A General Framework And Development Environment For Interactive Visualizations Of Evolutionary Algorithms In Java And Using It To Investigate Recent Optimization Algorithms That Use A Different Approach To Linkage Learning

Peter A.N. Bosman

Utrecht University

Department of Computer Science

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Preface

Evolutionary computation is a relatively new field in the world of optimization/approximation algorithms. Of late it has received an increasing amount of attention, broadening both the type of algorithms as well as its applications. Evolutionary computation is being used more and more often in industrial and commercial environments, making the diversity of applications of evolutionary algorithms even greater. For many problems stunning results have been achieved, making evolutionary algorithms a secret commercial weapon and increasing their popularity.

An important aspect that contributes to the popularity of evolutionary algorithms is the simplicity of implementation. A simple genetic algorithm is easily constructed using classical operators such as one–point and two–point crossover. Furthermore this simple genetic algorithm then leads to unexpectedly good results for most people that are just starting out in this field. This has lead to a great variety of implementations in many languages without any uniform framework except that of at some metalevel defined idealized description of evolution.

Next to many experimental implementations, an increasing amount of scientific research is done in the field of evolutionary algorithms. This has over the years led to theories and theorems. Given the complexity in providing any proof on the working of an evolutionary algorithm, more of the former exist than of the latter, but nontheless progress is made in research.

In both implementations as well as theories, a more explicit and mechanical setting has been rising of late. In the field of implementations some repositories and libraries have been created, providing frameworks in which evolutionary algorithms can be developed with both more ease and uniformity. In the field of research lessons are learned from prior experiments and enhancements are made so as to design evolutionary algorithms that are competent.

As proof is a hard thing to come by when working with evolutionary algorithms, visualizing results is essential to being confident about theories. When the evolutionary process is made interactive and the viewing continuous, the best of control is achieved over the execution. By applying changes interactively, theories can be stressed even better. Furthermore a general framework for developing evolutionary algorithms and the viewing of their results in just this interactive and continuous way results in both ease and uniformity.

Summing all of the former, a great tool for working with evolutionary algorithms and establishing an ease for their development is a system in which

1. information resulting from an evolutionary algorithm, both during its run and at its termination, can be visualized continously as well as interactively and
2. development of new algorithms is done by coding new instances of components that are placed in a general framework.

The latter argument relieves us of the necessity to write code for the entire evolutionary algorithm (all operators, genotypes, fitness functions, populations, etc.) and allows us to merely define instances of parts from an at the outset defined algorithm together with views that visualize the information we are interested in. The instances can then be put together to create an actual algorithm and the views can be placed so as to visualize the information. By doing all of this, we can both visualize theories in a powerful way and disregard a large amount of overhead in implementing a new evolutionary algorithm.

When going more into software implementation details, such a system could be made even more generally applicable if its code could directly be utilized on every platform, even when parts are added by a user regardless of his or her operating system or hardware. This is where the relatively recent development of Java comes in, as it is a platform independent language.

All of the former has been carefully considered and has led to the development of a Java program named *EA Visualizer*. This paper contains information on both the development of this system as well as using it to stress certain theories through interactive visualization. By doing so, we show that such a program is a highly valuable asset when working with evolutionary algorithms.

This paper is not intended to be a complete implementors guide, even though a full model description is given. A detailed description of the code is not found here as this paper deals at a higher level with the modelling of the *EA Visualizer*. A few implementation details are given, but this is only to show how certain aspects in the creation of such a system have been achieved within the *EA Visualizer*.

Furthermore neither is this paper a users manual, because the software is self–contained. The *EA Visualizer* is provided with a help system that is expanded as the system itself is expanded. It contains both information on how to use the program as well as a description of every component in the system, be it user defined or system supplied. Still in order to make this paper self–contained as well as the program, an overview is given on how to operate the system so as to make a description of the *EA Visualizer* complete.

Next to a description and the introduction of the *EA Visualizer* system, this paper also contains research information and results. The resulting system has namely been used to investigate a certain aspect of *linkage learning*. As recently a new approach has been given to this aspect which deviates from the approaches that evolved along the lines of the genetic algorithm, a brief investigation is conveyed and reported in this paper. The *EA Visualizer* is used to quickly gain insight into to what extend this new approach is competent in performing optimization. The easy way in which the system is used to this end demonstrates how easily and quickly a good insight to the algorithms in the system can be achieved through the interactive visualizations and the powerfull tool that is the *EA Visualizer*.

The contents of this paper are written for a reader that has at least some understanding of evolutionary algorithms. The first part in which the specification of the *EA Visualizer* system is given requires only minimal knowledge of this computation method that needs to be more broad and global than specific. The second part of this paper in which a study is presented regarding *linkage learning* requires a more thorough understanding of *genetic algorithms* as to how they work and process information.

Acknowledgements

In order for the contents of this paper to be written, the general idea for the *EA Visualizer* had to be proposed first. I would like to thank Dr. Ir. Dirk Thierens for thinking up the concept of the system as well as providing me with the possibility to write this paper as my graduation work. Furthermore, I am gratefull to him for making time for the conversations that mostly regarded the research part of this work and the listening to and incorporating of my own ideas and perspectives. The students that did valuable suggestions during the first serious test of the *EA Visualizer* are amongst those who I wish to thank for making me see beyond fixations that tend to appear when working on a system of this conceptual size, as well as for the reporting of bugs. Furthermore I'd like to thank Jilles van Gurp for the discussions regarding the latest JAVA tools as well as compilers and patches that have aided me in creating a more stable system. Also, great gratitude is expressed towards Astrid Tholen for the greatest support through the entirity of my computer science studies in which this final project is no exception. Finally, but certainly not in the least significant place I am *very* thankfull for the efforts of my father for creating an (unfortunately) temporary PC lab at our home in which the *EA Visualizer* ran for many weeks on a 24 hours basis on many computers, without which I could not have made this graduation paper contain the information in the thorough manner I wanted, as well as my mother for making working in that PC lab for many hours during both days and nights convenient and thereby feasible.

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Contents

1 A general overview

In this introductory section we provide an overview of the contents of the remainder of the paper. The preface at the beginning of the paper provided an introduction and pointed out what the subject is that is adressed in this work. The actual elaboration is done in the sections that follow the current one. As this elaboration is thorough and as a result rather large, it might be too much to ask of an interested reader to continue and read the full contents of those sections. Giving a good overview of what is presented or researched in those sections leaves it to the reader to determine whether the full contents of the following sections is to be read and yet leaves him or her with a good idea of what has been done in the light of this paper and what is discussed and worked out further on. As such, this section extends the preface by starting from the subject of interest introduced there and refrains from any type of detail that is used in the actual elaboration that is done in subsequent sections, giving the reader a complete impression of the work in this paper, without giving away the actual results.

The first and foremost point that this paper sets out to describe is the development of the *EA Visualizer*. This includes the decisions on behalf of the contents of the system as well as implementation issues that concern establishing those contents. Setting up a large software system which is what the *EA Visualizer* can become when set up right, requires a thorough investigation of the requirements, followed by the design of a model and subsequently the actual implementation which is in itself a cycle of validations and quality assesments that point back to more implementation decisions and model descriptions. For each system, especially the lager ones, first a requirements analysis needs to be conducted that tells us what is required from the resulting system, laying out what we need to incorporate in the system model as well as the resulting implementation. It becomes clear that the requirements of the *EA Visualizer* are that the information can be visualized both interactively and continuously, that the evolutionary algorithms in the system must be highly expandable and component–wise reusable, that in order to be of any scientific value it requires to have a multiple runs version that runs evolutionary algorithms a multiple of times independently such that results can be combined to draw conclusions in the field of expected results, that the system needs to be self–contained in that it has a help system that guides the user when needed, that it must be easily expandable in more terms than just the algorithms themselves and that JAVA applicability with respect to applets and thus usage directly over the web might be helpfull. These requirements that follow from the analysis result in a number of constraints that the system needs to constructed subject to, which is most important in the next phase of the engineering of the software, being the construction of the model.

Before getting to that however, one point that resulted from the requirements analysis is of great importance for what lies at the heart of the system, namely the EAs themselves. It becomes clear that it is best to decompose EAs such that we get a component–wise description together with an information flow through these components such that an EA is nothing more than a collection of actual instances for each of the components in the decomposition. As such, the actual instances for the different components need to be programmed only once and can then be used again in every other EA. By doing this, we establish that the EAs in the system are very much so expandable. As such, the first part in the modelling process is the decomposition of evolutionary algorithms. Starting from a framework for EAs by Bäck [1], noting the shortcomings in both detail and decomposition of EAs in this framework and subsequently expanding it to overcome these problems, a decomposition is reached that holds great expressional power with respect to evolutionary algorithms. The decomposition that thus results holds twelve components ranging from obvious such as the *Recombinator* and the *Genotype* to perhaps more unexpected such as the *Similarity* and the *Mater*. Based on this decomposition, the engine that lies at the heart of the *EA Visualizer* is easily created in its most basic form by implementing the information flow through the components and letting the components themselves do virtually all of the work. When the actual instances that are to be used for the components in the decomposition are provided, such an engine can be created by the system and started to actually run the EA. A mechanism using information objects is then used to gather information about the algorithm and thereby we have modelled (and almost implemented) the heart of the *EA Visualizer*.

Looking toward the requirements of viewing the results from the EAs, an MVC type of model is created for the system in which the model within the MVC is the engine just described, the viewer is a new class that is a container for views which are fed with the information coming from the model and the controller is the `EAVisualizer` class itself that is the main class and takes care of data flow in the system, which is mainly from the engine to the views, but also directly from the user to the system through mouse clicks and so on. Elaborating upon this MVC type of model description of the system, a general name system is introduced that allows for unique naming in the *EA Visualizer* and creator classes that are capable of creating instances for the components in the decomposition and views to actually perform the visualization. By setting up these classes as general and strictly according to rules as possible, the next step can be taken in creating a fully–fledged system that automizes updating the system with respect to the data administration required to notify the system of the presence of new instances or views. The actual result will be an even more powerfull editor version of the system that is capable of expanding the system in more ways than just mentioned, but such is found in the actual elaboration that is started in section 2. The editor is a complex task and brings along a large model that also incorporates the help system. Furthermore as many parts of the system are parameterized, a special structure for parameter definitions is required that also allows for automatic expansion towards multiple runs versions as such is to be facilitated by the system without extra requirements from the user.

Modelling the viewer brings along the definition of internal and external views that are mostly used for direct graphical visualizations and numeric visualizations respectively although such is not a constraint and thus it is possible to visualize information graphically in external views and numerically in internal views. All views are updated as the EA runs. It must be possible to define multiple runs and single runs views as different entities because running multiple runs or single runs mostly results in visualizing information in a different way (averaging results over multiple runs in graphs for instance or viewing the population contents for a single run). These different type of views are then updated through a slightly different mechanism that distinguishes a normal update from a *termination* update.

The implementation that follows brings along many details. Creating fully automated operations such as offered through the editor version of the system and the facilitation of multiple runs is a complex task and details to this end are placed in appendices A and B respectively. In this section we wish to refrain from any implementation details and leave this for as much as is interesting for the actual elaboration as found in section 2. That section closes with a demonstration of the resulting system by guiding the reader through a number of examples of EAs, both in a single run and over multiple runs.

The system that so results is ready to be used for testing evolutionary algorithms. Creating the system to be ready for this is a very time–consuming task as we are referring to the actual implementation which is greatly vast for the general framework constructed together with its complex automated tasks. Also in order to demonstrate the system, a number of instances and views need to be actually implemented in order to work with the system and visualize any results at all. This requires even more time, not to mention writing the code comment in a proper fashion during development as well as the help files in the system. To get an idea of the size and contents of the resulting system, we refer the reader to appendix C. In any way, when all the implementations are finally finished, we can indeed use the system to investigate the interesting new algorithms for optimization that use a different approach to linkage learning. In order to do this, an overview of what linkage learning is, where it came from and why it is required is given first. We refrain from going over the descriptions of the algorithms described in the process of doing so and state only that an historic overview is given which shows when the notion of *tight linkage* was introduced and resulted in linkage learning approaches. In this historic overview, the classical GA is visited as well as the mGA, the fmGA, the GEMGA and the LLGA. After thus having made clear what linkage learning is about, the recent algorithms with a different approach to linkage learning are introduced. Using the historic overview of the GAs that were evolved along the lines of the classic GA, the new approaches can be put in perspective by the reader.

After the introduction and the description of what linkage itself means, tests are run to investigate the competence of the recent new approaches. At first a couple of tests are run and compared to the classic GA. Based on results so achieved, it becomes clear that a number of items are interesting for further directed research. It is chosen to investigate the difference between the two recent algorithms that are introduced and to hopefully along those lines also find information about the boundaries of the approaches. As the main point however, we set out to find the implications of the difference between the two approaches that are MIMIC [6] and an approach by Baluja and Davies [3] that is supposedly an improvement over MIMIC. The results thus obtained are the final research results within this paper and the reader can read them directly if desired in section 3.3 as we shall refrain from duplicating those results here. Also as the time span in which the research was to be conveyed was unfortunately not too great as a good and usefull implementation of the *EA Visualizer* took a great deal of time. A number of topics are pointed out as a result from the testing that are interesting to visit as future research.

The testing in both the undirected and directed way results in a good insights as to how the recent new algorithms work. When relations are clearly required to be respected, the new approaches show an improvement over the classical GA, however it is unclear yet to what extent the complexity of the relations can be so that the new approaches are still capable of finding the right linkage to solve the problem *at all*.

This paper closes by drawing conclusions on the full contents of the work that was done and is described in the text that follows up on this overview section. As noted above, details of the system are incorporated in appendices to give the reader an idea of the complexity of the implementation and the convenience offered to the user by the automation that is thereby thus introduced. We close this overview section by noting that the testing of the recent new approaches in the *EA Visualizer* system is itself a test of the expressional power introduced by the decomposition as the new approaches aren't exactly standard GA material. However, they are evolutionary approaches and the decomposition proves to indeed be a powerfull description of EAs in general as the new approaches fit into the *EA Visualizer* without a problem, which is also the case for the different GAs that were described along the historic line that is provided on behalf of the explanation of linkage learning as even though they are not implemented, they are shown and explained how to fit in the system through implementation of new instances for components in the decomposition solely.

The remainder of this paper is organized as follows. A specification of the *EA Visualizer* system is given in section 2. This specification includes both the model design as well as some implementation issues. In section 3 the notion of linkage learning is introduced as well as the two recent optimization algorithms that use a different approach to linkage learning. Furthermore, the results of the tests as mentioned above are presented and investigated so as to finally be able to draw conclusions with respect to the competence of the new algorithms. In section 4 the final conclusions are drawn with respect to the material described in sections 3 and 2. In three appendices, detailed information is incorporated with respect to the *EA Visualizer* system. In appendix A it is explained how the system was made capable of being a fully automated system that includes an editor. Appendix B contains a description of the complex implementation of multiple runs EAs. Finally, in appendix C background information is given on the resulting system that is the *EA Visualizer*.

2 The EA Visualizer

The creation of large software systems of whatever kind is a process that is always divided over at least a few steps or layers. At the least it is very important to have a good model of the system in order to build something solid. This section describes the complete engineering of the *EA Visualizer* system. This ranges from analysing what the system should be capable of to the specification of the integration of evolutionary algorithms to implementation details.

In section 2.1 a survey is done of what functionality it is exactly that we want the system to have. It is decided what it is we want to use the system for and how broad our perspective should be with respect to evolutionary algorithms. This latter aspect is made precise in section 2.2, where according to the determined measure of granularity, the general framework of any evolutionary algorithm within the system is specified. In order to establish this, the highly idealized description of the evolution process that are evolutionary algorithms is divided over a certain amount of evolutionary components. The modelling of the system in an object oriented fashion is done in section 2.3. Some of the implementation details are discussed in section 2.4 and examples regarding the usage of the system are given in section 2.5. Finally, in section 2.6 the resulting system is evaluated in retrospective, glancing at options for future further enhancement.

2.1 Requirements analysis

In this section we describe what is required in order to establish a system as generally described in the preface. We have seen that the system should have two important properties, namely that of the interactive and continuous visualization of data and the expandability of the system through modularity of the evolution process. It is these issues that we will examine closer.

2.1.1 Visualizing information

Starting with the visualization side, in order to establish a flexible and expandable system with respect to the visualization/viewing part as well, this part of the system should be separated from the evolution process as much as possible. Furthermore it should have a highly modular structure so as to make it possible for the user to only define what it is that should be shown and how. The user should not be bothered with applying changes to the system in order to utilize the new view. This perspective leads to a MVC (Model–View–Controller) type of system in which the model (the evolution process) is separated from the view (the visualization part) and the system itself is controlled by the controller (the *EA Visualizer*).

Establishing the continuity of the visualization means that the controller will have to transfer information from the model to the controller after each generational step. Once the process has reached the next generation, all views should be updated by the system with the new data. It is then left to the views to decide if they need to provide the user with new information.

The other required aspect of the viewing system is for it to be interactive. We should be carefull when stating what level of interaction we allow the user to have with the system. If we want to have a direct influence on the evolution process through the views, the MVC separation as stated before becomes harder to establish as working with the views can then hold that the model should change directly. Furthermore if we are to create a modular setting for the evolutionary algorithms, allowing a change in settings directly through interaction with the views at a metalevel has no obvious or user–friendly definition. Next to that more problems arise when some combinations of components are not allowed (fitness functions are defined for certain genotypes for instance). This issue is not too difficult to resolve though because the viewing system should get all the information from the model as we cannot know in advance what it is a new view is going to visualize. This means that all instances of the components of the current evolution process will be passed on to the viewing system along with all information on what the instances have done the passed generation. As such any interactivity that is desired to alter parameters directly can be implemented as desired in a new view, as long as the views are allowed to receive input. It is therefore only required to make the system pass input information from the user to the views. This should at least be established for a mouse pointing device. By doing this, we will create a *possibility* of a far reaching form of interaction that extends from altering view characteristics to having an influence on the current evolution process.

2.1.2 Expandability for EA's

It is stated in the introduction in the preface that the system should allow for expandibility so as to easily compose evolutionary algorithms. A modular decomposition of the evolution process results in a description that consists of some components. The evolutionary algorithm uses these components and passes the required data between them. By doing this, a high level of expandability is created as each component of this definition can have a multiple of instances. The user never has to redefine the entire process. When for instance a new recombination operator is thought of for genetic algorithms, this recombination operator can be implemented without having to implement the binary string genomes, the desired fitness function and so on. Merely the recombination operator has to be defined. When using the system, the desired instances are selected to be part of the evolutionary algorithm without any changes whatsoever to the structure of the system.

This approach also has a drawback. By specifying any general framework except that of total freedom, the evolutionary algorithms that can be created are of a certain form. This implies that in order to have a general applicable system, the expressional power must be great. This is something of a problem though because evolutionary algorithms are subject to ideas and visions of many people and are therefore increasingly not conform to a specified structure. Nevertheless, in order to create a system that is easily utilized, it should be noted that the majority of evolutionary algorithms *can* be described within a general framework and this framework need not even be all too complex. Very specific evolutionary algorithms that go beyond the usage of single populations are harder to place within such a framework, but by not making certain requirements too explicit, even these types of evolutionary algorithms can be fit into one general framework.

By using such a structure, the evolutionary algorithm can be "clicked" together with ease. Furthermore, writing code for instances of components creates evolutionary utilities that can be used within other evolutionary algorithms without having to incorporate them over and over again. As the exact decomposition of the evolution process conform to which the evolutionary algorithms within the *EA Visualizer* will be composed is a fundamental issue determining the final applicability of the system in this field, a seperate section is devoted to this issue (section 2.2).

2.1.3 Single run and multiple runs

Evolutionary algorithms belong to the class of probabilistic algorithms because of their random aspect in applying operators with a specified chance, the creation of random genomes, etc. As such we can never rely on these algorithms in one single run to provide us with information from which we can then draw conclusions on how good or bad it is in any sense. It is for this reason that all experiments with evolutionary algorithms are always (or at least *should* always be) performed a multiple of times. The results over these runs are then combined (for instance by averaging).

The whole idea of setting up the *EA Visualizer* has been to create a new way to look at evolutionary algorithms, namely through interactive visualizations. As multiple runs are mostly conveyed when the user is occupying him or herself with other activities because they take a lot of time, these interactive visualizations imply the main utilization of the *EA Visualizer* be through the usage of single runs.

Nevertheless, the position of these single runs and the interactive visualizations within the research should be reviewed here. Not only are indeed continuous and interactive visualizations a great tool to learn about and research evolutionary algorithms, they are also a way to quickly establish satisfaction regarding intuitions. In order to then generate a thorough investigation, a multiple of runs is still needed. Next to that, using the single run version on beforehand guards the user from wasting a lot of time in computing results over a multiple of runs on wrong settings. Still in the end, the user will want to be able to perform a multiple of runs with different settings in order to compare results. It is important to realize that a general system for evolutionary algorithms is not complete or even nearly worthless if in the end one is not capable of running an algorithm a multiple of times and combining the results.

Furthermore, not only is it common practise (not only for *evolutionary* algorithms) to test an algorithm a multiple of times, but also to test it on problems with a different size or with different settings for the algorithm. As such, the availability of a multiple runs version that provides the option for running algorithms with different settings of all kinds is always a valuable and almost indispensable property.

2.1.4 Self contained systems

As is the case with an increasing amount of common systems these days, software distributions are intendend to be *self contained*. This implies that the software is all that is needed to get the system working and more importantly, to work with the system. Such is ofcourse a desirable property because it releaves the author from the writing of large documents like user manuals.

As the whole structure of the *EA Visualizer* will be a modular one, conform to the issues discussed above, a help system that contains information for every component in the system will allow for the system to become *self contained* on the condition that extensions to the system in new instances of the components *can be* and *are* documented properly within this help system. From the implementation view this implies that the help system is user friendly, allowing the user to click links to navigate between documents and so forth. Furthermore, the help system must be easily extendable so as to not make it an unattractive job to write help documentation for newly added instances. Finally, the help system must ofcourse be easily accessible from every part of the system.

Setting up a help system as described allows the system to be expanded world wide in a uniform way, allowing users to swap implementations without problems together with documentation within one system. This implies that all can be done electronically and without any overhead which makes the system yet even more attractive.

2.1.5 Easily expandable systems

An important property of quality systems is expandability. It is desirable to have a good modelling and a good implementation of some problem or algorithm within a larger system such that it offers user friendly operations and levels of abstraction, but in the long run, expandability plays the most important role.

So far we have seen that the *EA Visualizer* will be set up in a modular way with respect to many parts of the system. This is a very strong fundamentation on which to base the achievement of expandability. If we are capable of decomposing the system in such a way that parts are designed by descriptions such that implementations can be made in whatever way desired as long as they meet the demands of the description, we have a potentially expandable system. This is exactly the case with the *EA Visualizer* as argued in sections 2.1.1 and 2.1.2.

By achieving this, the system is not yet easily expandable, because certain parts may be significant within the system, as is the case with the *EA Visualizer*. This can imply that the system needs information on beforehand in order to work with the instances. This information could for example be a name that is administered in a name system to maintain consistency. The point is that adding new instances to the system will be accompanied by some means of an announcement to the system. This announcement becomes more difficult as separate systems or factories are created that maintain system information with respect to these instances and their availability to the system.

In order to once again make sure that extending the system does not become too unattractive so that the expandability property is lost after all, the system administration should be made as mechanical as possible so that extensions can easily and unambiguously be achieved. When we push this into a mechanical form, we can even form this extension process into a protocol form of action so that we can automate this as a *system update* operation. Such is a very desirable property.

Creating the editor makes using and expanding the *EA Visualizer* system even more attractive because just like taking away the overhead of the design and implementation of the complete evolutionary algorithm, the data flow within it and the data flow to the view part of the system, an editor takes away the overhead of updating and perhaps recompiling the system by hand, which in turn increases the self containedness of the system.

2.1.6 Java applicability

As we are to develop the system in the object oriented language Java we should ask ourselves the question what level of applicability we desire to have for the resulting program. Like most programming languages, Java can be used for the creation of programs that work on a computer under a certain operating system. In this respect it is no different from C or Pascal. One well known important difference is ofcourse the fact that Java is platform independent so we do not need to worry about which platform to choose to create the application for. Next to this great property, Java also comes in two approaches. Next to the normal programming language, Java also offers the option to create `Applet` classes that can be used in a WWW browser. As such, the resulting program is easily brought amongst a wide public around the world. There is an important sacrifice we must make though when choosing to develop the program so that it also works as an `Applet`. The point is that `Applet`s are not allowed to write to files as opposed to a normal application. This means that any results from algorithms that are normally written to disk or any settings that would be saved in some way can only be permanently stored if this is done by some other program that is running on the computer after using some copy and paste routine of the operating system. This latter type of operation is increasingly easy these days so this doesn't withold us from creating the option to not only distribute it over the web but also to put it *on–line* so that users can directly use the program when surfing the Internet.

Before closing this section, we note that any editor version of the program cannot be supplied as an `Applet` because we *must* be able to save in that program as that is the larger part of the functionality of it. So in conclusion we can say that the final application will created without any option to save data in whatever way with the exception of the editor version of the program.

2.1.7 Summary

In the above we have analysed what is required in order to build the system that was in a coarse grained way stated in section 1. In order to actually design a system model and implement the system based upon that model, we summarize the requirements.

1. The system should have a modular structure, decomposing the intended to be most flexible parts to an extent that they are easily expanded. This means that

   (a) visualizing the system is done by views that are implemented as seperate classes just as

   (b) the instances for the components of the evolutionary algorithm are implemented separately so that in working with the system a specific evolutionary algorithm is created by selecting what implementations to use for the components.

2. The views should be capable of processing user input at the least by using a mouse pointing device, making the visualization interactive.

3. The *EA Visualizer* as a controller should transfer information from the model to the views, transferring everything that could be of interest and as such allowing every view to be completely general or entirely specific as well as to offer an interaction that can indeed have a direct influence on the evolutionary algorithm.

4. The evolutionary algorithms that can be constructed within the system should be described by a general framework that is a decomposition of the evolutionary process. This decomposition should be made such that it holds a great amount of expressional power, but needs not to be defined for all specific cases, making it inherently too complex.

5. The *EA Visualizer* should offer the possibility of running evolutionary algorithms a single run as well as a multiple amount of runs in which in the latter a multiple of combinations of parameters can be set as well as a multiple of runs for each combination of parameters (and component instances).

6. The system should be self–contained through the containment of an easy to use extensive help system. This help system must be expandable for every other part of the *EA Visualizer* that is expandable.

7. The implementation of the *EA Visualizer* should be such that administration of all parts that can be extended is done in a mechanical way so that it can be automated, leading to the editor version of the system allowing for easy editing and expanding of the system.

8. The implementation should refrain from saving information to disk with the exception of the editor version of the program. This should result in the possibility to create an `Applet` version of the program that can be put on–line on the WWW.

2.2 Decomposition of evolutionary algorithms

In section 2.1 we have argued that the evolutionary algorithm should be decomposed. This means that we are to create a general framework in which we identify the components that have a clear and distinct functionality. As we shall implement the system in an object oriented language, a class will be created for each such object. We have argued furthermore that these classes should be a definition of what the components should be capable of. Instances of these classes will then be components that can actually be used for the task defined. To be more exact and more with respect to a JAVA implementation, these components will become *abstract classes* that cannot be instantiated. The instances that can actually be used will be the instances of subclasses of these components that specify how the functionality is exactly established.

2.2.1 Coarse grained decomposition

In order to create the decomposition, we distuingish two levels of precision. At the top level we are not concerned with how the evolution exactly takes place. We can see this as a coarse grained decomposition. At this level we define the most general framework which has become common in all approaches within *evolutionary computation* and as such is found in every type of evolutionary

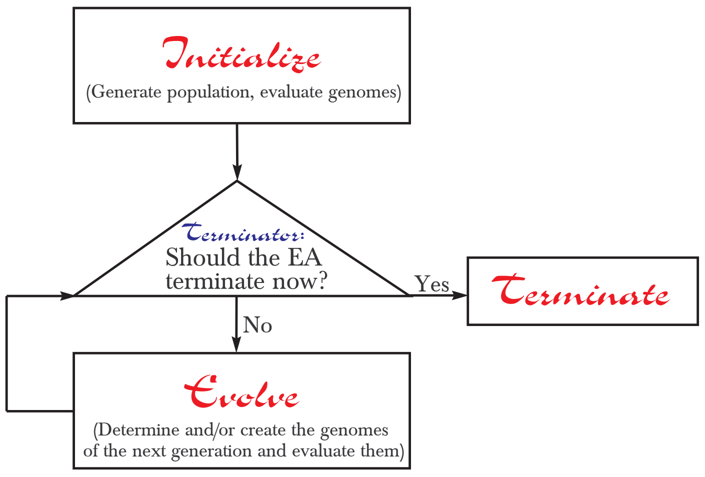

Initialize
(Generate population, evaluate genomes)
Terminator:
Should the EA terminate now?
Yes
Terminate
No
Evolve
(Determine and/or create the genomes of the next generation and evaluate them)

Figure 1: Coarse grained decomposition of evolutionary algorithms.

algorithm. This intersection of evolutionary algorithms is displayed in figure 1. Firstly, as is the case in almost every algorithm in every discipline, we have an initialisation phase. We generate the first generation genomes (most often at random) and evaluate their fitness values. Once this is done, we can perfom the body of the algorithm. As can be seen in the figure, this amounts to checking first whether the algorithm should be terminated on any behalf whatsoever (frequently used conditions are the amount of the genomes and the diversity of the population members). If this is the case, the algorithm halts and enters the terminated state. Otherwise, an evolution step is performed, bringing the population to the next generation. At this precision level we make no attempt as to specify further how this is established. All we require is that any new genomes in the population be evaluated so as to establish the invariant that every member of the population has been evaluated (so its fitness value is known) when the termination condition is to be checked. After this evolution step, the algorithm has reached the next generation and the termination condition is checked again.

From this top level model for evolutionary algorithms we can already derive a few components that are part of the decomposition. In the figure, this has been insinuated by suggestively posing the question “Should the EA terminate now?” to something named a *Terminator*. It is clear that we can vary the termination condition that is to be used. A termination condition can be based upon any information from the evolutionary algorithm. Modelling such a condition leads to a separate component which is named *Terminator*. This component signals based upon all information from the last generation step and the current state of the algorithm whether or not the algorithm should terminate.

Continuing in this manner, we could argue that the initialization process can be modelled within a component named *Initializor*. This component would then be requested to generate new offspring at the beginning of the algorithm. However, if we take a step back and view upon the framework from a global perspective instead of a component–wise one, we have already missed two of the most important components that are implicitly present in every evolutionary algorithm. These are the *Genotype* and the *Population* components. A subclass of the *Genotype* component is a description of what genetic material is used. It is a description of the material that is available to code solutions with. The *Genotype* component will therefore define access to fitness values and so forth for actual genomes that will occur in the population during the run of an algorithm. It cannot define relations with respect to the genetic material as this differs for each actual *Genotype* (like binary strings or evolution strategies tuples). The *Genotype* component is closely related to the *Population* component because the population consists of genomes. The *Population* component is therefore some collection that will for instance allow for adding and removing genomes. This component is also the component that holds information with respect to the global perspective in that it possibly defines relations between the individual genomes (such as clusters or subpopulations).

It is important to see that these components are of the greatest of fundamental importance as they allow for data storage. These components are never so obviously present in schematics or algorithm descriptions because these mainly consist of the usage of *operators*, which are obviously transformed to components according to our decomposition approach. We have identified the *Genotype* and the *Population* as fundamental components however and are therefore indispensable. We should also note that the fundamentality of these components could play an important role in the implementation of the general framework conform this decomposition. If we now look again at the part from figure 1 that lead to the definition of the two fundamental components *Genotype* and *Population*, the "Initialize" step, we can argue that a separate *Initializor* is superfluous. We can easily assign this functionality to the just discovered fundamental components. This implies that we define the *Population* component to be such that it can renew the entire population. This argument however is normally not strong enough to keep us from implementing that new component as it provides us with a higher degree of freedom. However, it also increases the complexity of the system as all these components are linked. Such is the case ofcourse for each of the components. The most important point is that initialization is in almost every case done at random, causing the addition of a new component to make the process more complex than need be. In the few cases that random initialization is not favored, we should note that we have *not* done away with the possibility of altering this phase of the evolutionary algorithm. We have only reduced the number of degress of freedom in putting an evolutionary algorithm together by selecting instances for its components. This reduction in amount of degrees of freedom has been justified by the argument that the dispensed degree of freedom is hardly ever utilized.

Finally, the least obvious part of figure 1 is the explanatory text between brackets. In these texts, it is twice mentioned that the genomes in the population need to be *evaluated.* Evaluation is always done by using a fitness function. Just as much as the *Genotype* and *Population* components, the *Fitness Function* is a fundamental component of every evolutionary algorithm. It is this part that can provide us with the information whether one genome is in some sense better than another. Moreover, the fitness function holds information regarding the domain. For instance, it contains information regarding distances between cities for a TSP instance. As such, this component has an important task beyond providing fitness values. It is also a holder of environment or domain information.

2.2.2 Fine grained decomposition

The part from figure 1 that has not been discussed yet, is the *Evolve* step. We cannot derive a new component from this, because it is a composite step. It is this step that we have argued in section 2.1 to decompose resulting in a high expressional power for composing evolutionary algorithms. In the light of the setting in this section, this is the second level of precision. We are now to make exact how to transform the state of the evolutionary algorithm from one generation to the next. This requires a fine grained decomposition.

In oder to obtain such a fine grained decomposition, we could regard general algorithm descriptions that have already been made, such as the following that was posed by Bäck [1]:

```
$t = 0$
$initialize(P(t))$
$evaluate(P(t))$
while not $terminate(P(t))$ do
    $t = t + 1$
```

```
        $P(t) = select(P(t-1))$
        $recombine(P(t))$
        $mutate(P(t))$
        $evaluate(P(t))$
    **od**
```

In this scheme, $P(t)$ denotes the population in generation t. This framework certainly contains essential operators such as *selection* and *recombination.* Furthermore, we recognise components that we have already identified in the coarse grained decomposition. We shall look at each of the operators from the above general framework by Bäck more closely (not in the same order) and determine what components to define on behalf of them.

Recombine
Recombination is the most prominent operator in evolutionary algorithms. The combination of genetic material that establishes the genetic exploration of the search space is classical and accepted to be the most important together with selection. This operator needs no further introduction and it is no less than required that it be a separate component in the decomposition. Just as we had the *Terminator* for the termination condition, we now have a *Recombinator* for the recombination operator.

It is important to determine what the input and output of the *Recombinator* component are. The algorithm by Bäck refrains from any specific details as it merely states that recombination be applied to the members of the population. More specific however, if we for instance look at the classical one–point crossover operator from genetic algorithms, it takes two parent genomes and generates either one or two offspring genomes. This is a better description of the recombination operator and it is only a logical definition to state that the *Recombinator* component takes as input a collection of parent genomes and returns a collection of offspring genomes. It is then up the general framework to supply the *Recombinator* with the parent collections that it wants to have recombined. It is this definition that we shall use.

While we are looking more precisely at the definition of the *Recombinator* component and having achieved the definition by looking at the one–point crossover operator from genetic algorithms, we could look a bit closer at this specific recombination operator. A fundamental issue in the definition of this operator, is the selection of a crossoverpoint. This selection is done at *random.* This is a good point to remember that evolutionary algorithms belong to the class of probabilistic algorithms and as such make use of pseudo random number generators. In the case of evolutionary algorithms, pseudo random number generators are even used *many* times during one run. It is therefore important to note that a good pseudo random number generator is of the utmost importance. Because of this, we should have a seperate *Pseudo Random Number Generator* component which is just as the *Genotype*, *Population* and *Fitness Function* components a fundamental component.

Mutate
An other operator that is frequently used in evolutionary algorithms and was regarded an essential operator in the early stages of evolutionary computation, is mutation. It is an operator that is included within evolutionary algorithms to follow the Darwinistic approach of random mutations. Just as the *Recombinator* component, this operator needs no further introduction as it is a classical one. It follows that we will require a *Mutator* component in the decomposition. We have already seen that random numbers are needed when we discussed the recombination operator. It is now even more obvious that these are needed, as mutation is almost always implemented as an operator that alters a genome in a random fashion.

Just as with recombination, the framework stated by Bäck refrains from filling in the details with respect to the application of mutation to the genomes in the population. When we regard the mutation operator by itself however, we should note that it is an operator that alters exactly one genome. We therefore define the *Mutator* component to have as input one genome and to output another genome which is a mutated version of the input. The general framework will then have to specify how to mutate *all* genomes.

Select
Together with recombination, the selection operator is known to be the most essential to the evolution process. Selecting in some way the better of the genomes in the population, this operator provides the search with a drift. There are many ways to select genomes from a population, but like can be seen from Bäck's algorithm, selection takes place *before* recombination and mutation. A more precise definition of the selection operator is that this operator selects the genomes that will serve as parents to generate offspring. There is one problem with this definition, namely that when we use the selection operator to, as it is stated in this definition, select genomes to serve as parents and then use them to generate offspring through recombination and subsequent mutation, there is no way of telling what genomes will be present in the next generation. Strictly speaking, in the former sentence we have *no* new genomes in the population whatsoever, since we have only made a selection from the old population and placed the results in a void. How then is this done in the general framework by Bäck?

If we look closely, we see that the selection operator is used in such a way that the selected parents replace the entire current population. From the looks of the remainder of the algorithm, recombination and mutation then directly alter these genomes within the population, whereas we have so far defined these two operators to create *new* genomes. Furthermore, the replacing of the entire population with the selected genomes might very well not be a satisfactory way to incorporate the genomes of the next generation. We could desire to in some way merge the genomes in the current population with the offspring genomes. This leads to the definition of a new component. It is a too strong requirement to state that based upon the selection on beforehand we are to continue the rest of the evolution process, forgetting the contents of the population at the current time. This would neither do justice to the definition of the traditional selection operator as just stated above. So in order to offer the possibility of merging the genomes of the current population with the offspring into the population of the next generation, we define to have a *Replacer* component that implements a replacement strategy. The input to a *Replacer* is the final collection of offspring genomes (after recombination, mutation, etc.) together with the current population. The output is a void as the component is to *replace* the genomes of the current population in some way, implying that the population is altered. So the *Replacer* component has a side effect in that it alters the current population.

We should now ask ourselves if we are content with the degree to which we are capable to select genomes either before or after creating offspring. The complete selection process now consists of the selection of parent genomes before generating offspring and placing the offspring within the current population after creating offspring. This is to a large extend satisfactory and contains a great expressional power with respect to the selection mechanism. For instance, the standard selection mechanism that allows us to clear the entire contents of the current population and replace it with only the offspring genomes is now achieved by using a selection mechanism to select the parents in any way that might be preferred (such as tournament or roulettewheel selection) and using a replacement strategy that only keeps the offspring genomes. Special selection strategies like for instance the (μ, λ) and $(\mu + \lambda)$ (μ parents, λ offspring) selection strategies from evolution strategies can now be incorporated as well. For instance when we desire to have a (μ, λ) selection mechanism (select surviving genomes from the λ offspring), we can implement the replacement strategy to be such that like with the standard selection mechanism it only keeps the offspring genomes, but it also applies some form of selection to those offspring. For $(\mu+\lambda)$, the replacement strategy would do almost the same, but the selection would then be from the total of offspring and parents.

Next to now being able to merge the genomes from the current population with the offspring, the *Replacer* component also allows us to establish an invariant with respect to the population size, which is a desirable property. We now need not to generate offspring and wait for the next round to be able to apply selection again (perhaps even in two phases so as to first select the surviving genomes and then the genomes that are to serve as parents). We can now use the

Replacer component to maintain the correct amount of genomes in the population. This means we have a nice invariant and that we can terminate the algorithm after each generational step (the *Evolve* step from figure 1.

Still there is one thing that is not satisfactory. This follows from the discussion above about implementing (μ, λ) and $(\mu{+}\lambda)$ selection strategies. We have argued there that implementing these strategies requires a selection functionality incorporated in the *Replacer* component. This implies that the framework will have the undesirable property of a need for code duplication. It follows from the discussion that we need to *select* genomes within the *Replacer* component. If we would want this selection to be a tournament selection, we would have to redefine it within the *Replacer* component as we ofcourse already have defined it for the selection operator. Such is very much undesirable. If we look closer, we see that we have implictly defined a composite functionality for the *Replacer* component. We had done this earlier with the *Genotype* and *Population* components with respect to the initialisation phase in section 2.2.1. In that case, the composition was argued to have no undesirable results at all. In this case however we need to factorize the current definition of the *Replacer*. Better put, we need to specify the definition of the *Replacer* more exact and introduce a new component.

If we are to remove the necessity for a selection part in some cases within the *Replacer*, we need to put a another selection operator directly after it. Then there is no need for a replacement strategy to have to select any genomes to survive, because this is done by the second selection operator. The *Replacer* than remains the same as before with exactly the same input and output, but without a possible selection property.

We have now come to the point where we can sum up the components that we shall use in the general framework. According to Bäck's framework we have a *Selector* component that selects from the population a certain amount of genomes. Furthermore we have a *Replacer* component that replaces the contents of the current population with a collection of offspring genomes according to some strategy. The application of the *Selector* component is twofold, whereas the application of the *Replacer* component is required once. The *Selector* component is used once at the beginning of a generation step to select the genomes that will serve as parents. The *Selector* component is then used again at the end of a generation step, directly after the *Replacer* component to select the genomes that are to finally survive the current generation step. As these two selection strategies need not be the same, we should facilitate in the definition of *Selector* components only once, but utilize them in two different locations. As such, we have two new components, namely the *Selector* and the *Replacer*, in which the *Selector* is defined *once* and used as a component *twice*, leading actually to three new components.

Putting the components together
We have now completely gone over the algorithm by Bäck that was stated at the beginning of this subsection. We shall therefore now review what we have discussed so far. To do this in the most brief way, we extend the general framework:

```
$t = 0$
$initialize(P(t))$
$evaluate(P(t))$
while not $terminate(P(t))$ do
    $sel = select(P(t))$
    $rec = recombine(sel)$
    $mut = mutate(rec)$
    $rep = replace(\ mut,\ P(t)\ )$
    $P(t+1) = select(\mathrm{rep})$
    $evaluate(P(t\ +\ 1))$
    $t = t + 1$
od
```

We have been more precise in the framework by stating what happens with the genomes that were selected, recombined and so on. We should note however that not everything is clear yet. For instance, after the before selection, recombination is applied to the result of the *Before Selector*. We have argued that the functionality of the *Recombinator* is defined with respect to a collection of parent genomes. The result from the selection however is a merely a set of genomes that are to serve as parents. It is most certainly not (always) the case that these genomes are all to be parents, generating offspring together. In genetic algorithms with one–point crossover, two parent genomes are required to apply the recombination operator. From a population of 100 members for instance, we might select 100 genomes (selecting some genomes most likely twice or more often) and make subsets of size two from this large set of genomes. These subsets can then be recombined one by one. Indeed, to go from the selection of genomes for offspring generation to the sets of parents that are actually recombined, we need some sort of mechanism.

Putting genomes togther is called a *mating* mechanism. It is therefore that we shall incorporate a new component in the general framework, called the *Mater*. This component has as input a collection of genomes and returns a set of sets of mated genomes, or in other words parents that have been put together to undergo recombination.

Continuing the inspection of the extended algorithm, we find that the specification of the application of mutation is not exact enough. We have already defined however that mutation is an operator that is to be applied to individual genomes. What we need to specify therefore within the algorithm is that we mutate every genome independently. Other than that, the algorithm has no unclear parts that lack detail.

An important property that has shown to improve the speed of evolutionary algorithms as well as their results is the consideration of problem specific knowledge in terms of non–evolutionary operators. These external approximation techniques that are mostly heuristics are applied to evolutionary algorithms so as to speed up the search for meaningfull genomes. This is especially desirable when the search space is rather large (for instance with $\mathcal{NP}$ complete problems). An example is the incorporation of a two–opt heuristic for TSP instances or a first–fit heuristic for bin–packing. Incorporating heuristics like these, makes an evolutionary algorithm be called *hybrid*. Just as the mutation operator, this "operator" is applied to every genome individually. Therefore it poses nothing new with respect to the framework, only an extension of what we have already seen. Concluding, we will allow for hybrid evolutionary algorithms by incorporating a new component called *Hybrid Searcher*.

We could now say that we have a full decomposition with a general framework that does not remain vague with respect to details and that holds a great expressiveness to define evolutionary algorithms. There is only one thing that is important and not yet present in the decomposition. One tends to easily forget about this component as it is rather invisible, even more than the *Genotype* and the *Fitness Function* components. It is common practise to compare genomes in some way, be it in a genotypic or phenotypic fashion. Moreover, when working on multimodal optimization, a measure of similarity is a very important item. Note that the framework is already complete in the sense that this type of information can be incorporated inside the components that are already present. However, if we were to not separate this similarity functionality and make it into a seperate component, we will once again have the situation we had before when we came to the conclusion that a second selection operator is needed. Therefore, we define that a *Similarity* component is part of the decomposition. It is nowhere visible in a framework description or figure, but it is passed on to the components so they can use this component, just like the pseudo random number generator. This component can be seen as fundamental as well, because it is used by other components. Its fundamentality is less obvious, but under a different naming this will become clear in the next section.

This concludes the decomposition of evolutionary algorithms. After inspecting evolutionary algorithms at two levels of granularity, we are now ready to state the resulting general framework and its components, both visible and invisible within the general algorithm that is part of the framework.

2.2.3 The final general framework conform the decomposition

In sections 2.2.1 and 2.2.2 we have deduced in a constructive way the components that need to be part of a general framework for evolutionary algorithms. This decomposition has led to the definition of the following components:

Name	**Description**
Population	A *Population* is a container for the genomes. When looked upon as a storage facility, the *Population* is nothing more than a collection of objects, but in the evolutionary algorithm it can come to hold more information than just such. For instance information on clusters or linkage between genomes can also be incorporated here, making the *Population* vastly more important than merely the holder of a collection of genomes. Like the *Fitness Function*, the *Population* serves as an environment. The difference is that the environment induced by the *Population* regards information about the structure and the linkage between genomes as opposed to information regarding the search space of the optimization problem.
Fitness Function	The *Fitness Function* rates the genomes and therefore the solutions according to their *fitness*. Very important alongside this definition is the fact that the *Fitness Function* ofcourse also defines what a “better” fitness value is (maximization or minimization for instance). Observing this definition in terms of the algorithm, it is clear that the *Fitness Function* defines a mapping from the solution space to the real numbers. This points out that the *Fitness Function* plays the role of the environment in the optimization problem. It holds the information that is specific for the problem instance. Finally, the *Fitness Function* implicitly defines a *genotype-phenotype* mapping. To be more precise, it denotes the exact location in the problem space for each genome. It is clear that based on this location, the *Fitness Function* computes its fitness values. Hence the *Fitness Function* can map a genome onto it’s phenotypic equivalent.
Genotype	A *genome* represents a potential solution to a problem. It codes the problem specific information that describes a point in the search space. How the solution information is coded within a genome, is determined by the *Genotype*. Like in imparative programming languages, it designates the type of a value container where in this case the value container is a genome instead of a variable.
Hybrid Searcher	The *Hybrid Searcher* is an extension to the conventional evolutionary algorithm as it need not make use of evolutionary operators. It facilitates the optimization of individual genomes outside the evolution process. After both the *Recombinator* and the *Mutator* have been applied, a *Hybrid Searcher* is used to optimize every single offspring genome. The *Hybrid Searcher* has no further knowledge on the execution of the evolutionary algorithm in the larger setting. The system will provide it with the genome it needs to locally optimize when needed.
Mater	The *Mater* is an operator that puts together the parent genomes that were selected by the *before Selector* in groups. These groups need not be disjoint, but such is usually the case. The genomes that are placed together in a group will produce offspring together, for it is the groups that result from this operator that are transferred one by one to the *Recombinator*.

Name	**Description**
Mutator	The *Mutator* implements the operation where the coincedental exploration of the search space takes place. The exploration is such because the mutation of a genome is mostly totally random. The *Mutator* has no further knowledge on the execution of the evolutionary algorithm in the larger setting. The system will provide it with the genome it needs to mutate when needed. These genomes are the offspring as resulting after the application of the *Recombinator* to the mated parents.
PRNG	In order to explore vast amounts of the search space (or at least to be able to do so), the usage of a certain random number generator can have a great effect. When using a random number generator that only generates so many different combinations, the exploration of any evolutionary algorithm is thereby inherently limited as well. In order to provide the user with a degree of freedom as to be certain of a well implemented *Pseudo Random Number Generator*, this functionality has been placed into a seperate component.
Recombinator	The *Recombinator* implements the operation where the inheritance of genetic material as found in nature takes place. This operator takes an amount of parent genomes and by combining the information that is stored within their genetic structure in some sense, creates new offspring. In this way an exchange in solution information information takes place, causing a traversal through the search space of a certain kind to take place . The *Recombinator* has no further knowledge on the execution of the evolutionary algorithm in the larger setting. The system will provide it with the parents it needs to recombine when needed. These groups of parents were compiled prior to the application of the *Recombinator* through usage of the *Mater*.
Replacer	The *Replacer* determines (before any optional *after selection* operator) which genomes will be in the population in the next generation. The replacement strategy implements a way to place the offspring back into the population and thereby possibly replacing already present genomes. The *Replacer* is provided with the current population as well as the offspring and relation between these offspring genomes and the parents that created them. Based on that information, a selection is made as to see what genomes survive. As such, this operator is part of the selection process.
Selector	The *Selector* is an operator that is capable of selecting genomes from a population. This selection process needs not to select any genome at most once. Individual genomes can be selected multiple times. It is not said that a *Selector has* to select the better genomes, but usually this will be the case. In the evolutionary algorithm framework used, selection is applied twice during the evolution of one generation. First, it is applied as the *before Selector*, selecting the genomes that will act as parents during the current generation. Who is to survive is not yet pointed out, as the *Replacer* specifies which genomes will eventually be placed in the population. Second, the selection operation is applied directly after replacement has taken place. Here, as the *after Selector*, it *does* define exactly who is to survive, for only the genomes that are selected this time are placed within the resulting population.

Name	Description
Similarity	In order to be able to compare genomes and using this information when defining evolutionary operators, the *Similarity* component is part of an evolutionary algorithm in the general framework. A *Similarity* component takes two genomes and determines to what rate they are equivalent. This information can for instance be used when mating genomes to create offspring or when replacing genomes in the current population to find the best or worst match.
Terminator	Eventually we want the evolutionary algorithm to terminate. For this task, a separate component has been created, being the *Terminator*. The component is provided with all the relevant information from the evolution process during the last generation. The terminator then determines based on this information whether or not the algorithm should terminate.

Starting from a general algorithm by Bäck [1], we have enhanced it by constructive development of the sections and we can now pose the final algorithm in the same fashion as we have done this before, yet now with all the details required. The graphic version of this algorithm consists of two parts. The first part is the top–layered framework that we had already encountered in section 2.2.1 and can be seen in figure 1. The second part is the elaboration of the *Evolute* step that we had not yet defined in figure 1 at the top layer. This part can be seen in figure 2. Combining these two figures leads to the final algorithm:

```
$t = 0$
$initialize(P(t))$
$evaluate(P(t))$
while not $terminate(P(t))$ do
    $sel = select(P(t))$
    $mat = mate(sel)$
    $rec =$ for each mated collection $m \in mat$ do $recombine(m)$
    $mut =$ for each genome $g$ in each recombined collection $r \in rec$ do $mutate(g)$
    $hyb =$ for each mutated genome $h$ in each collection $m \in mut$ do $hybrid(h)$
    $rep = replace(hyb, P(t))$
    $P(t+1) = select(rep)$
    $evaluate(P(t+1))$
    $t = t + 1$
od
```

2.2.4 A preliminary view on some implementation requirements

Even though we have now established a satisfactory general framework and have even set up a general algorithm along with it, we are not yet able to come up with an exact implementation. Firstly in order to set up a good piece of software, we need to create a model for the implementation based upon the components in the decomposition. Secondly, there are some details that have not been mentioned in the previous sections, but can already be noticed at this point. When establishing the implementation itself, more details will come forward, but a few issues we can already predict.

One detail is the fact that another form of approximation techniques named simulated annealing defines a property that is desirable within evolutionary algorithms as well. In simulated annealing, one solution is altered constantly. If an alteration results in a better solution, it is excepted. If it isn't better, it is accepted anyway with a certain chance. This chance becomes smaller as the algorithm proceeds. The acceptence criterium is thus time dependent or in simulated annealing terms temperature dependent. In evolutionary algorithms such time dependent operators could be

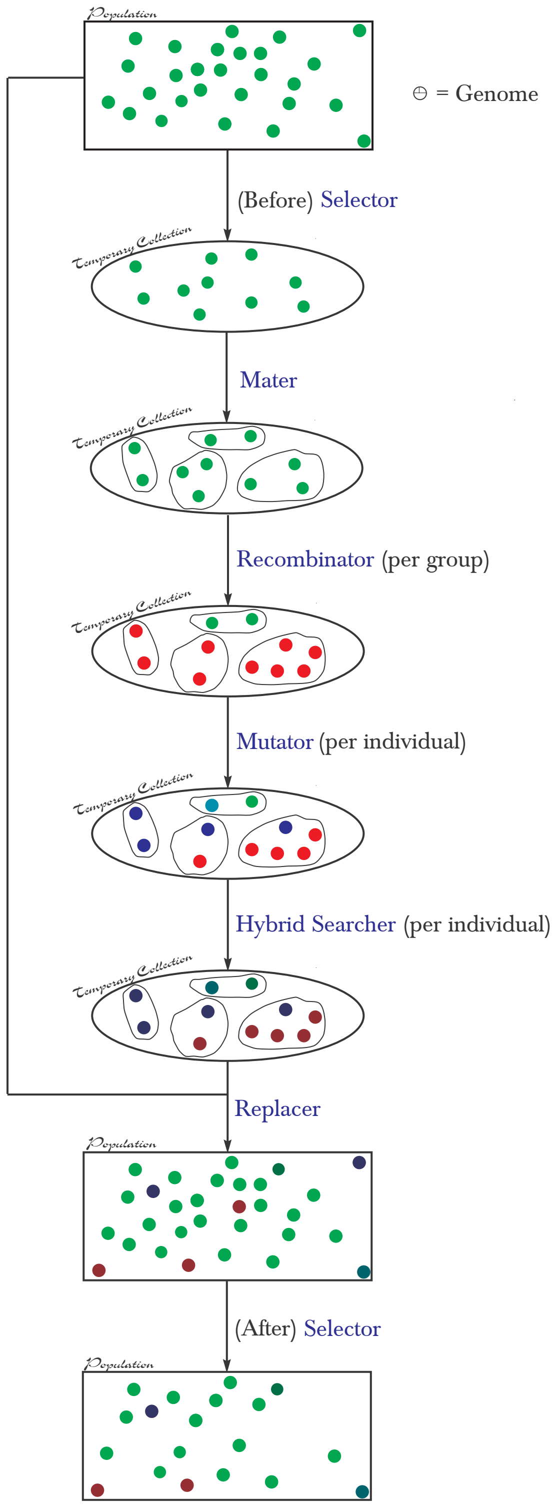


Figure 2: Fine grained decomposition of the generation step in evolutionary algorithms.

desirable in for instance acceptence criteria of selection operators. Therefore we note in advance that we should make the entire process generation counter dependent. Looking at the algorithm as stated in section 2.2.3, this remark seems superfluous as the generation counter is stored in variable t, but such will not be the case in our object oriented model in which the components all become separate classes that will be utilized by the system. As such, the system will have to pass generation counter information, making this remark important.

We have noted in the constructive deduction of the required components at several occasions that some components are rather important and we called them fundamental. These components are the *Genotype*, the *Population*, the *Fitness Function*, the *Similarity* and the *Pseudo Random Number Generator*. Their fundamentality is implied through their usage by other components. All these fundamental components hold information required by the other components. For instance, a mutation operator cannot be implemented without receiving the currently installed *Pseudo Random Number Generator*. This fundamentality aspect is interesting to know and leads to some additional implementation details because other components need to be provided with the currently installed instances of the fundamental components. More important though is that the availability of operators can depend on what kind of fundamental component is installed because it uses a fundamental component. This is ofcourse without meaning when we regard the *Pseudo Random Number Generator* component, because no component should be dependent on what kind of prng is used. This means that four out of the five fundamental components are *dependency imposing* components. For instance, we can only select to use two–point crossover as the *Recombinator* when we have selected binary strings as the *Genotype* for an evolutionary algorithm. This is an important implementation detail with respect to the functionality offered to the user in constructing evolutionary algorithms through selection of instances for each component as specified in section 2.2.3. When this is done correctly, this aspect can be disregarded when implementing the general algorithm. We can then simply assume that only correct combinations can be selected and supplied to the general algorithm.

Finally, it should be noted that even though the most important details have been clarified in the algorithm specified in section 2.2.3, the implementation details are most certainly not all layed out yet. This is mostly the case because of the object oriented design in which each operator will become a separate class. The system shall have to pass the information between the objects in order to provide the required information for certain components. In the general algorithm stated, all information appears to be globally available, but this will differ from the resulting implementation. Without making any further speculations as to the extend of these details, we merely predict that more details will have to be clarified and that for a good object oriented implementation the general algorithm is not yet explicit enough.

2.3 Model design

In this section we create the model of the *EA Visualizer*. We have argued in previous sections what elements should be part of the *EA Visualizer*, especially concerning the evolutionary algorithms themselves. We have created a complete decomposition of them in section 2.2, thereby determining the components that an evolutionary algorithm will consist of in the system. In order to build the *EA Visualizer*, we need to describe how we intend to divide the functionality over some object oriented structure. To achieve this, we shall briefly go over the aspects that were visited in previous sections as to what the resulting system should contain or be able to do and elaborate on this. The results will be summed up in UML (Unified Modelling Language) or OMT (Object Modelling Technique) like diagrams to provide an easy reference and a clear overview. Our goal in this section is to create a general overview and define the relations between the most promiment objects in the system. More specific details are layed out in the implementation sections. Furthermore, the most detailed description (which inherently fails to catch the larger picture of an overview) is found in the documentation of the program in *html* as generated by JAVADOC. That documentation describes the classes and all their methods in full detail. It is not contained within this paper, but within the software package of the *EA Visualizer*. Finally, the specifications of classes in the diagrams may not be complete with respect to the methods specified. We do not intend at all to be complete in this, as this would convey too many details. The models presented in this section are merely to give an impression of what the structure of the system is.

2.3.1 The main system

In section 2.1.7 we have summed up the requirements for the resulting system. In this section we are concerned with the system at the top level. This implies that the interesting points from the summary of the requirements section for this intend are 3 and 7. As we regard the editor version of the system to be a system in itself, we surpass point 7 for the moment as well and concentrate on point 3 for now.

As noted before, a good structure to base an application of this type on, is the MVC model in which the model, the view and the controller are separated. MVC implementations have actually a more fine grained structure that is worked out here, but the general idea of a MVC structure is a desirable aspect. We can work on the different parts of the system in a modular way, implying that we need not worry about making connections to the model from the view because this is already completely taken care of by the controller. In the *EA Visualizer* data must be transported from the evolutionary algorithm that is running to the viewing system that visualizes the information. A way to establish this is by using three classes for the three parts of the MVC structure. The main class is the controller, which is ofcourse the *EA Visualizer* system itself. This class is denoted `EAVisualizer`. The evolutionary algorithms that are used in the system are composed of different components as we have seen in section 2.2. The class that actually puts instances of the components together to form an evolutionary algorithm and is capable of running it, is called `EARunner`. Finally, the class that manages all the views and provides the system with a way to transport information to *all* views and store them in some way, is denoted as `EAViewer`.

Starting with the `EARunner`, we should realize that once we start running an evolutionary algorithm, we want to be able to continue using the system. For instance we want to interact with the algorithm as it proceeds, but we might also want it to stop at some point or otherwise influence the system. In order to do that, the `EARunner` must be a subclass of `Thread` so we can both start and stop it as well as do other things while it's running. Because the settings for an evolutionary algorithm can be changed when it is not running, we do not want the thread to stop at any given point when we feel like stopping the algorithm. Instead we want the algorithm to stop running after one generational step. In order to achieve this, the `EARunner` should have methods `brake()` and `gas()` because just like in driving a car, we can't stop the algorithm just like that. Instead, we signal that we want to stop. The algorithm will then stop as soon as the generational step is finished. To (re)start the algorithm and run until the termination condition is satisfied, the method `gas()` should be called (which is named such so that it is appropriate alongside the `brake()` method). Furthermore to provide the user with a greater functionality so the algorithm can be observed in "slow–motion", a method `runOnce()` should be supplied so the evolutionary algorithm is run for exactly *one* generational step. Finally, we have specified that the `EAVisualizer` should transfer information regarding the running evolutionary algorithm from the `EARunner` to the `EAViewer`. In order to do this, the system must be able to request the `EARunner` for information. A method `getInfo()` must be specified that returns an `EAInfo` object that contains all required information on the running evolutionary algorithm. The `EARunner` must be able to update the information in this information object, so the `EARunner` is therefore assumed to be an implementation of an `EAInfoUpdater`. This would not be required if we were to create a new `EAInfo` object every time the information is needed. However, once we employ a multiple runs option, we must remember that the installed components for the evolutionary algorithm and counters regarding how many steps have been done yet all need to be set, which will result in the necessity to have only *one* `EAInfo` object in the system which is referred to by both the `EARunner` and the `EAVisualizer`. The latter class will be the class that alters the information regarding installed components and so on and thus will be an implementation of the EAInfoSetter class that updates all the other information stored in an EAInfo object that cannot be altered by the EAInfoUpdater and vice versa. Once the EAInfo object is created, the EAInfoUpdater and the EAInfoSetter that have been announced at the time of the creation will be called upon to register the locations to place the updated information through methods setUpdateEnvironment and setSettingEnvironment respectively. The details with respect to the contents of the EAInfo class are omitted here.

From the model design of the EARunner it becomes clear that the EAVisualizer class requires methods that the EARunner can call upon when needed. For instance, a method will be needed so as to notify the system that the evolutionary algorithm has reached the next generation and that the views in the system should be supplied with the new available information. We name this method signalGeneration(). Furthermore, when the EARunner has been asked to stop by calling the method brake(), the EAVisualizer should be notified when the evolutionary algorithm has actually been halted by the EARunner. This is done by calling the method signalSuspended(). Furthermore, the system needs to be notified when the evolutionary algorithm has stopped out of itself because its termination condition has been satisfied. This notification is done by calling the method signalTerminated() in the class EAVisualizer. Finally, it almost goes without saying that the main(String []) method needs then to be placed within the EAVisualizer class as it is the main class of the system.

The last class in the general MVC type overview, is the viewing part of the system. What we require from the EAViewer is that views can be added and removed. This implies that we have methods like add(EAView), remove(EAView) and removeAll(), where an EAView is something that needs to be specified further. We refrain from that here and leave this for a later section (see 2.3.4). As we want to have views that are directly incorporated within the system and located together in one big window, we must be able to layout the views after we have for instance added or removed a view. This requires for a method relayout() to be present in the EAViewer class. Views may need to resize themselves when information changes or as a result of interaction with the user. As such, the EAViewer needs to be relayouted as well. However, when we allow for views to have a link to the EAViewer object, they are provided with too many possibilities like adding a view. Therefore, we must provide make the EAViewer an implementation of the EAViewsHolder class, that only contains the method relayout(). Nontheless, at some point in the system outside the EAVisualizer we might require that we can quickly add views. Then again we would not want to allow for removal so we need the EAViewer to be an implementation of another class as well, namely the EAViewsAddingHolder that allows for adding views only.

We have incrementally specified the most prominent classes that are required to set up the system (without the editor version) conform point 3 in the summary of the requirements (section 2.1.7). The most important classes are the EAVisualizer as the controller of the system, the EARunner as the model of the system and the EAViewer as the viewing part of the system. The requirements and more specific details regarding these classes can be found in the subsequent sections. The UML diagram that sums up the links and the functionality of the classes is given in figure 3.

2.3.2 The controller of the system

In section 2.3.1 we have argued that point 7 from the requirements summary in section 2.1.7 is part of the main system with respect to the editor version. In order to allow for the creation of an editor, the *EA Visualizer* should be designed so that any required administration with respect to expandable parts of the system is set up in a mechanical way so that updating the administration can be automated. This is stated in point 7 from the requirements summary as well as the desirable property of having an editor. Once again we leave the actual definition of the editor open for a later section, and now first concentrate on the design of the administration of the controller in such a way that it has a mechanical structure. The resulting UML diagram is depicted in figure 4.

The classes that are designed to this end are therefore automatically generated by the *EA Vi-*

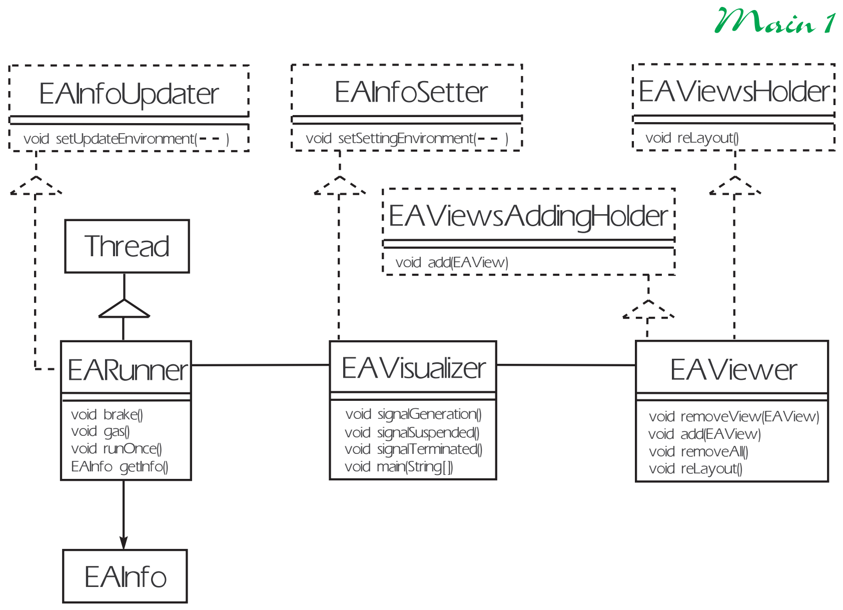


Figure 3: Model of main system, most important structure.

sualizer when needed. The data that is required will be stored in some format in a definitions directory. This data is parsed and stored in some data structure that can then be updated. When required, the classes can be generated and compiled and the data stored in the definitions files. One of the most commonly used issues in all software is the naming of elements of a system. In our case, we will have a name for every instance of a component from the decomposition (like "Binary String Random Mutator") as well as for every view and even more elements. These names are used in user interfaces and in the help system. As they are required in multiple places, we want a single location where the names are defined so that we cannot make mistakes when typing the name of an instance of a component anew. Because any name will have to be retrieved through this single repository, errors as those are rendered obsolete. To set up such a naming system, we require to store the name information with some key that is unique within the system and that is not subject to typing mistakes. For this, the JAVA runtime class system can be utilized. In this system, a `Class` is a class of which instances can be retrieved by using the method `getClass()` on an existing object. The naming of the runtime `Class`es is unique so we can use this as a key, defining a projection of `Class` names on used names. The resulting administration class that provides this functionality is called the `NameSystem`. By providing methods such as `findActualName( Object )` and `findActualName( String )` that return the name of the specified object (either through direct reference or through full runtime `Class` naming) as used in the *EA Visualizer System*. Storing this information in two ways, we can allow for bidirectional traffic in the `NameSystem` class through a method `findClass( String )` that finds the runtime class object for a name that is used in the *EA Visualizer*. This is required when the user is presented with some names from which a selection can be made and we are then required to know what classes have been selected by the user so we can make new instances of them. Finally, in order to create an index page in the help system that holds a link to every element in the system, a method `getAllClassNames()` that returns a `Vector` of names is required to list all names.

As argued before, the *EA Visualizer* will contain a general framework for evolutionary algorithms according to a decomposition in components. For each of these components instances can be created by the user. All these components can be selected to be part of an evolutionary algorithm in the system. This implies that these instances require to be administered in some way so that they can be created when required. To this end the `EAComponentCreator` class is defined. This class holds all information regarding the instances for the components of evolutionary algorithms in the *EA Visualizer*. The most important method that is incorporated here is the `create( String, Vector )` method that receives the name of the component to create along with a list of values for the parameters of the component specified. This method returns an `EAComponent` object that is the instance requested in which the parameters have been set. Once a new instance is added to the system, this creator class will be regenerated and it will reconstruct the database on which the functionality of the `create` method is based. In section 2.2 it became clear that four of the components in the decomposition are dependency imposing because they are used by other components in the system. This will be made explicit in section 2.3.3. For now, it is important to note that these dependency imposing components exist and that this information should be administered in the `EAComponentCreator` as it holds all information regarding the components. To this end, for each dependency imposing component a method must be defined that returns given the name of an instance a `Vector` of names of instances for a dependency imposing component that the specified instance is allowed to be selected along with. For instance a method `genotypes( String )` is defined that returns a `Vector` of genotypes that a specified component is allowed to be selected with. For instance for the BINARY STRING TWO–POINT CROSSOVER recombination operator, the result will be a `Vector` of size 1 containing the `String` BINARY STRING. Analogously we have methods named `fitnessfunctions( String )`, `populations( String )` and `similarities( String )`. Furthermore in order to provide the user with the names of the instances that are available within the system so that a selection can be made, this information must be provided by the `EAComponentCreator` as well. This implies that methods like `genotypesEAComponentsStrings()` are required that return a `Vector` of all instances of components that are available (in this case `Genotype` components). Finally, when the system is to indeed provide the user with these names, once a selection is made, the parameters for the components must be filled in as well. In order to retrieve what parameters can be set for the selected instance, the method `parameterComponents( String )` can be called that returns a `Vector` of `ParameterComponents` that denote the parameters that can be set for this component. The definition of parameter components will be given later on in this section.

Next to the `EAComponentCreator` class that provides all information required to create instances and provide the user with the correct combinations of all available instances for components of the evolutionary algorithms, we should have the same type of class for the views of the system. This implies that we must have a class named `EAViewCreator` with the same type of functionality of `EAComponentCreator`. Indeed, we need a method `create( String, Vector )` that given the name of a view and values for its parameters returns the actual `EAView` as a new object. Furthermore we need a method `EAViewStrings()` that returns a `Vector` with the names of all views that are available in the system. Because the views can be parameterized, just like in the `EAComponentCreator` a method `parameterComponents( String )` is required with the same functionality. The two classes differ in the fact that we have twelve different types of components, but only two different types of views. The views we can create can be defined for either a single run or a multiple runs evolutionary algorithm. In a multiple runs view, information over a multiple of runs can be depicted. This could be a simple averaging of results, but could also convey a visualization of a performance rate for two different strategies over an increasing population size for instance. In any way, we can add single run views to multiple runs algorithms, but we must prohibit the adding of multiple runs views to single run algorithms. In order to achieve this, a method `isMultipleRunsView( String )` is required that returns `true` if the specified view is a multiple runs view and `false` otherwise. Finally, in the `EAComponentCreator` a certain amount of methods is defined that allow for the handling of dependency imposing components. In the `EAViewCreator` these special components have no extra meaning over the other components as it is the views that we are selecting and not the components themselves. However, as we have never specified (and never will) any restrictions as to what information may be visualized and

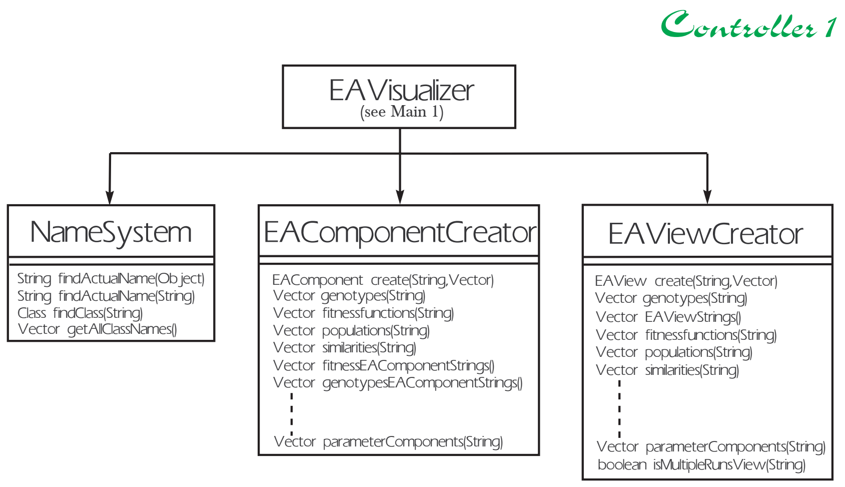

Controller 1
EAVisualizer
(see Main 1)
NameSystem
String findActualName(Object)
String findActualName(String)
Class findClass(String)
Vector getAllClassNames()
EAComponentCreator
EAComponent create(String,Vector)
Vector genotypes(String)
Vector fitnessfunctions(String)
Vector populations(String)
Vector similarities(String)
Vector fitnessEAComponentStrings()
Vector genotypesEAComponentStrings()
Vector parameterComponents(String)
EAViewCreator
EAView create(String,Vector)
Vector genotypes(String)
Vector EAViewStrings()
Vector fitnessfunctions(String)
Vector populations(String)
Vector similarities(String)
Vector parameterComponents(String)
boolean isMultipleRunsView(String)

Figure 4: Model of the controller, data administration.

what not, a view can be made dependent on any component in the decomposition. So in the `EAComponentCreator` not only do we need methods returning a `Vector` of names of components that a specified view is allowed to be selected with for the four dependency imposing components, but also for the other eight components.

Another part of the controller is the part of the user interfaces through which the user can specify parameters. All these interfaces are a window of some sort in Java terms. If we recall point 6 from the requirements summary, we need to set up a help system that is callable from any point in the system. This help system should furthermore contain all elements of the system. The latter requirement has been established as noted earlier in this section through the usage of the `NameSystem`. The former requirement implies that we create a structure that allows for the opening of a help window by pressing `F1` from anywhere in the system. To this end, we define the abstract class `EAFrame`. This class is a subclass of the `Frame` class from —Java— that implements a window. In the `EAFrame` class we redefine the `keyDown( Event, int )` method so that when `F1` is pressed, the help system is opened. Furthermore, we allow for other keys to be pressed and subsequently handled by the system by creating the new method `otherKeyDown( Event, int )` that can be overridden by subclasses of `EAFrame`. In order to actually open the help system, we must first of all have such a system in the form of a class. We name this class `HelpSystem` and provide it with the method `displayTopic( String )`. The system will contain a help directory with the help files that have a name that is in some way connected to the topic that can be showed in the system. When the method `displayTopic` is called, the file is read and the contents are displayed. In order to access the `HelpSystem` object, we need to provide the `EAFrame` with a link to the single `HelpSystem` object that is maintained in the system. It is too much control to allow for full access from a `EAFrame` object, so in the `EAFrame` we will keep a link to a `HelpSystemProvider` instead. This static link can be set only once and this is ofcourse done on the starting up of the system. The `HelpSystemProvider` contains a method `signalForHelp( Window )` that receives the window in which the `F1` button was pressed and opens the help system on the right page. The actual `HelpSystemProvider` that is used in the system will be the `EAVisualizer` as it will be this object that holds the link to the unique `HelpSystem` object in the system.

All the interfaces in the system could be made a subclass of the `EAFrame` class, but this class does not contain all information that is common for user interfaces in the *EA Visualizer*. In order to provide the user with feedback in the sense of system messages, we define a `MessageFrame` to be part of the system. The `MessageFrame` is a subclass of `EAFrame` and is nothing more than a window containing a text area to display messages on. One such object is created at the initialization of the system and is passed around all throughout the system so it can be used to display messages on. In order to alway have a link handy to such an object, this is contained in the `EAInterface`. Furthermore, to establish uniformity in appearance for the interfaces in the system, a `VisualPackage` class is created of which an instance is distributed throughout the system in the same manner as the `MessageFrame` object. The `VisualPackage` has methods like `getFont()` and `getBackground()` which provide the system with a one time specification of the colors and other visual attributes. A link to this instance is provided in the `EAInterface` as well. Lastly, the `show()` method is overridden so that any `EAInterface` is always displayed in the center of the screen on first appearance.

We are now ready to define the user interfaces and make all of them a subclass of the abstract `EAInterface` class. Already we had defined the `HelpSystem`, but we add the notion that it is a subclass of the `EAInterface` class. A certain amount of obvious and almost trivial interfaces is required to add and remove views from the system. Also, as the layouting of the views will be done from top to bottom and from left to right, the user might want to alter the order in which the views are registered within the system. To these ends, the following interfaces in the form of subclasses of `EAInterface` are created:

Class	**Description**
`EAViewAddInterface`	Facilitates the adding of views to the system.
`EAViewRemoveInterface`	Facilitates the removing of views from the system.
`EAViewOrderSwitchInterface`	Facilitates the alternation of the order in which the views are registered within the system.

Next to these almost trivial interfaces, we have yet to define interfaces for the two different types of runs that the *EA Visualizer* is to offer according to the fifth point in the requirements summary from section 2.1.7. This means that we have to create interfaces that provide the user with the available instances of the components and allows him/her to make a selection either a single time or a multiple of times for each component. In whatever way, note that a selection has to be valid with respect to the dependency imposing components. This requires that whenever a selection is made for a dependency imposing component, the other instances need to be filtered in order to only allow for valid selections. As this is the case for both the single run and the multiple runs selections, we create the abstract class `DependencyImposingComponentsHandler` that will be the superclass of the selection classes that regard dependency imposing components. As those will be user interfaces, the `DependencyImposingComponentsHandler` is made a subclass of `EAInterface`. The methods required in this class are of the form `filterImposersGens( Vector, Vector, Vector, Vector, String )` which takes the available instances for the `Genotype`, `FitnessFunction`, `Similarity` and `Population` components together with the selected `Genotype` and filters the supplied lists so that only the allowed instances remain. It follows that we require three more of these methods. Finally we require a method `fiterAll` that takes a `Vector` of instances for some component along with the currently selected instance as well as the currently selected instances of the dependency imposing components and filters that list.

Now that we have created the possibility to work with dependency imposing components so as to force valid selections by the user, we can continue to define the user interfaces for the single run and multiple runs evolutionary algorithms. Starting with the single run version, we define the `EASettingsInterface` class that provides the user with a multiple of lists containing instances for the components that are filtered when a selection is made amongst any dependency imposing components. Futhermore the user will be able to specify a mutation chance as well as a recombination chance. Methods that are required for such a class are `getMutChance()` and `getRecChance()` that allow us to retrieve the settings for the chances once all selections have been applied. For the same reason we need methods such as `getParameters( int )` and `getSelection( int )` that return the set values for the parameters as well as the instance name for the specified component.

We should realize that during the run of an evolutionary algorithm, the user might stop the run and go to the settings window in order to apply some changes to the algorithm and then return to continue the run with altered settings. We then need to know which components or parameter settings have changed so these changes can actually be carried out in the model. This completes our basic requirement for methods as we determine we need the methods `hasChanged( int )`, `parametersHaveChanged( int )` and `hasModified()` that specify whether a new instance has been selected for a component, whether the parameter settings have changed for an instance of a component and whether any changes have been made at all respectively.

Whereas we could suffice with one class in the single run version, we shall most definately not be able to do so with the multiple runs version. We require an user interface that allows for a selection of a multiple of instances for each component in the decomposition of evolutionary algorithms. For each of these instances, a multiple of parameter values can be selected. The result will be that for each combination of instances together with each combination of parameter values an evolutionary algorithm is created that is run a specified amount of times. This comes close to what we require, but is not totally satisfactory. First of all it is obvious that we don't always want to have a crossproduct of settings at all. For instance if we specify the population to have sizes 100 up to and including 1000 with a step size of 100 and we specify the same for the selection size of a selector, we most definately are not looking for the 100 different combinations of these settings, but only for the 10 different settings that result from an alternation in settings at the same time for both instances. We then say that these parameter values for these instances are *linked*. It follows that we require an interface that allows for a specification of such links so as to have control over what settings are actually used. Such a functionality is not without complex details as for instance we cannot have links within one component or links between subsets of a different size. Even more difficult is the final utilization of these links in order to enumerate the settings that result from the selection process by the user. The details of this complex task have been moved to a class named `EAMultipleSettingsEnumerator` which makes use of a counter system in which each set of instances as well as each set of parameters for each instance of each component is assigned to a counter variable. This assignment respects the links that were defined by the user and thereby creates the desired combinations of settings. The complete details of this process are beyond this paper but can be found in the software package. Finally, before we start defining the resulting user interfaces we should realize that the process of working with dependency imposing components has become more difficult. Each addition of a depency imposing component requires the filtering of lists that contain already added instances of components as well as the lists that the user may select these instances from to add in the first place. Removal of an instance for a dependency imposing component requires once again filtering of all lists that the user is allowed to select from. And in all of this the most complex is the fact that we have to ask ourselves what it means to have two different types of population instances selected for instance that impose different dependencies on the other components. What instances may we now select and what not? If we allow for neither instances that are specified by the dependencies from the population component, we are cutting off too much, but if we do not we are allowing too many settings which could result in an invalid combination of settings. In order to overcome such difficulties, we should separate the selection of depency imposing components from the selection of the instances for the other components, resulting in one combination of instances for dependency imposing components for each multiple runs settings. In other words, when defining the settings for a multiple runs evolutionary algorithm, we first choose which dependency imposing components we desire to use just like when using the `EASettingsInterface` for a single run version. When the user has selected these instances (one for each dependency imposing component), the other instances and their parameters may be filled in according to the multiple runs settings as just defined. It is important to note that it is only the selection of instances for the dependency imposing components that brings along the too complex task of incorporating everything in one selection phase. The parameters for the instances of these components have nothing to do with it and therefore we should allow these parameters to be filled in together with the rest of the settings after the selection of the dependency imposing components. In order to still provide the user with the full functionality that allows for a multiple of settings with respect to the dependency imposing components as well, we should allow for a multiple times of the complete settings process to be carried out. This results in a multiple of multiple runs evolutionary algorithms. We are now ready to define the user interfaces required for the multiple runs version of running evolutionary algorithms in the *EA Visualizer*.

Contrary to opening a `EASettingsInterface` for a single run evolutionary algorithm, selecting the settings multiple runs version starts with the `EAMultipleMultipleRunsInterface`. As argued above we need a multiple of the restricted multiple runs evolutionary algorithms as defined above as well. This interface allows for the user to manipulate such a multiple of multiple runs evolutionary algorithms, defining both the settings and the links for it as well as the amount of times every combination should be run. The complete result of settings must be returnable after all settings have been applied, so we require to have a method `getAllSelectedAndLinked()` in this class. As argued when defining the settings for multiple runs evolutionary algorithms, we require first to select the instances for the dependency imposing components. This functionality is brought about by the `EAMultipleRunsDependencyImposingComponentsInterface`. In order to retrieve what selection has been made, we require the method `getSelection( int )`. Because in this interface we have to select instances with respect to the dependency imposing components, this class needs to be a subclass of the `DependencyImposingComponentsHandler` class that we specified earlier. As noted, once this selection is done, the actual multiple of settings that is valid with respect to the selection of dependency imposing components and conform the arguments above can be selected. This is done by the multiple runs version of the `EASettingsInterface` class, namely the `EAMultipleSettingsInterface` class. We have already mentioned what the functionality of this class should be and this specification implies that we have methods `getAllSelections()`, `getSelectedInstances()` and `getSelectedParameters()` in order to retrieve all information with respect to the settings that have resulted from this interface. The functionality of the methods needs no further explanation. Finally we require to define the links between the settings so as to prohibit the system from taking the crossproduct. This information can be specified in an interface that can be opened from the `EAMultipleMultipleRunsInterface` when desired. The functionality of the interface has been layed out above and it has been argued that the process is quite complex. We shall therefore refrain from going into the details in this paper and merely note that the class is named `EAMultipleRunsLinksInterface` and has a method `getAllLinks()` which provides us with the settings made in this interface with respect to the links between the actual settings for the multiple runs evolutionary algorithm once the definition of the links has been applied.

Before closing the constructive discussion regarding the user interfaces, we should note that we have completely left out a very tricky detail that yet brings along a lot of work. This is the creation of backups before opening any interface so that when the `Cancel` button is pressed, the old values can be restored. As each user interface really holds a completely different structure, this needs to be defined anew for every one of them. The resulting interface overview without these details is depicted in figure 5.

As has become clear from the above, many parts of the *EA Visualizer* are parameterized. For both the single run as well as the multiple runs version of the algorithms that can be used in the system, parameters have to be set for instances of components. In many cases, these parameters will all be of the same type but with a different name. For instance an integer number needs to be entered to determine the string length or the population size. Furthermore, a multiple of parameters is required for one instance. In order to prohibit from doing the same work over and over again in defining parameters, it is best to define a specialized parameter structure that can be utilized in an uniform way. Remembering the outset to make the structure of the *EA Visualizer* as modular as possible and allowing for extensions, we define the `ParameterComponent` class that models a parameter for which a value can be set. The type of value is determined by the parameter component. If we have such a class, for each new instance that we create, we define what parameter components are required to set all parameters for the instance. When

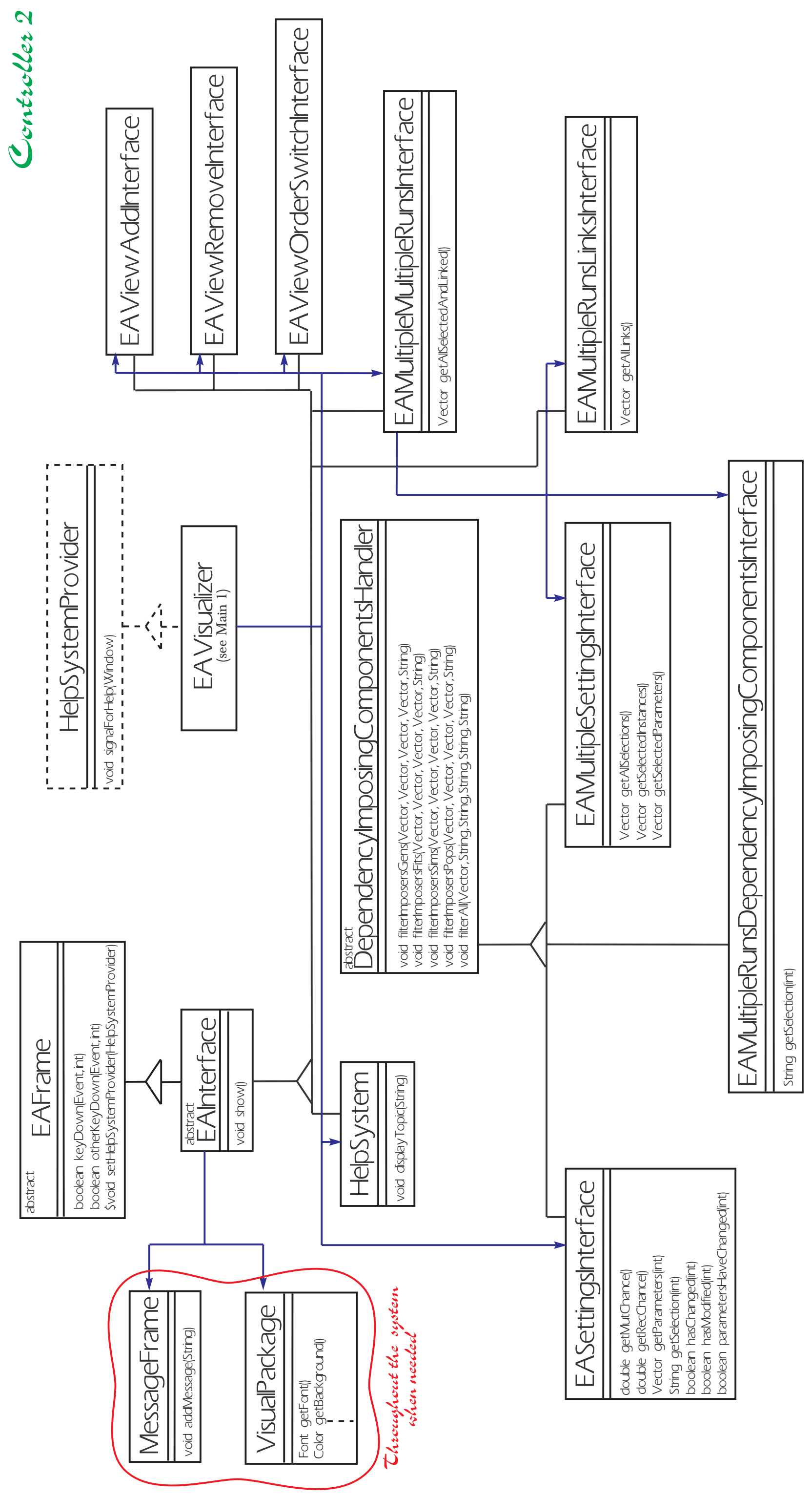

Controller 2
EAViewAddInterface
EAViewRemoveInterface
EAViewOrderSwitchInterface
EAMultipleMultipleRunsInterface
Vector getAllSelectedAndLinked()
EAMultipleRunsLinksInterface
Vector getAllLinks()
HelpSystemProvider
void signalForHelp(Window)
EAVisualizer
(see Main 1)
abstract
DependencyImposingComponentsHandler
void filterImposersGens(Vector, Vector, Vector, Vector, String)
void filterImposersFits(Vector, Vector, Vector, Vector, String)
void filterImposersSims(Vector, Vector, Vector, Vector, String)
void filterImposersPops(Vector, Vector, Vector, Vector, String)
void filterAll(Vector, String, String, String, String, String)
EAMultipleSettingsInterface
Vector getAllSelections()
Vector getSelectedInstances()
Vector getSelectedParameters()
EAMultipleRunsDependencyImposingComponentsInterface
String getSelection(int)
abstract
EAFrame
boolean keyDown(Event,int)
boolean otherKeyDown(Event,int)
$void setHelpSystemProvider(HelpSystemProvider)
abstract
EAInterface
void show()
HelpSystem
void displayTopic(String)
EASettingsInterface
double getMutChance()
double getRecChance()
Vector getParameters(int)
String getSelection(int)
boolean hasChanged(int)
boolean hasModified(int)
boolean parametersHaveChanged(int)
MessageFrame
void addMessage(String)
VisualPackage
Font getFont()
Color getBackground()
Throughout the system when needed

Figure 5: Model of the controller, user interfaces.

the parameters are prompted to be actually set, the system opens an interface showing these parameter components. This is the case for instance in the `EASettingsInterface`. The interface showing the components does not worry about the physical structure of the parameter components and defines a general way to display them so that the user can specify the required values. That interface is named the `ParameterInterface` and it thus administers a set of `ParameterComponent` objects. Methods that we require on such an interface are `amountOfParameters()` to find out how many parameter components are contained in the interface, `getName()` to find out the name of the interface as in *Parameters for ...* and `parameterName( int )` to return the name of the parameter specified (for instance "String Length"). Any caller of the `ParameterInterface` should hold links to the `ParameterComponent` objects provided so that the values can be retrieved afterwards. As the `ParameterInterface` is an user interface for setting parameters, we shall require an `Apply` button together with a `Cancel` button as is the case in almost every user interface in the *EA Visualizer*. Furthermore, this interface will be a subclass of the `EAInterface` class that was introduced earlier. Methods required in the `ParameterComponent` class are `acceptInput()` which returns whether the component is satisfied with the current input, `getActualComponent()` which returns the JAVA component that will be added to an interface, `getSelectedValue()` and `getCloneSelectedValue()` so as to determine the resulting value as well as to retrieve a backup value respectively, `getName()` to retrieve the parameter name and `setValue()` to complete the required methods for creating a backup so that old values can be restored to the parameter component.

It is at this point that we should realize that the structure we have now laid out is very much suitable for the single run version of evolutionary algorithms in the system. For instance to specify real numbers as parameters, we define a `DoubleRangedParameterComponent` that only accepts `double` values in a specified range. We should remember though that we also have a multiple runs version that requires a multiple of settings for the parameters. This requirement is quite easily accomodated by creating a `MultipleValuesParameterInterface` that creates for every parameter of an instance a list of `ParameterComponent` objects instead of just one. This approach lacks ease of use however because we would like for instance to specify that we want to run an evolutionary algorithm with population sizes between 100 and 200 with a step of 2. It would render the system as uneasily incomplete when such an expression were to be absent. In order to allow for this, we subdivide the `ParameterComponent` idea further over two abstract classes: `SingleValueParameterComponent` and `MultipleValuesParameterComponent`. The first class is actually the class for parameters we first set out to define. The second class is the new class that allows for an ease in defining multiple values. Methods required in this new class are `amountOfSingleValues( Object )` and `toSingleValues( Object )`. These methods determine for an `Object` that was returned by the parameter component out of how many single values it consists without actually computing them and what these values exactly are (eg. actually computing them) respectively. This is required as we should note that the values that are in the end needed are single values as the evolutionary algorithm is provided with parameter settings just as is the case in the single run version, with the only difference that now this is done a multiple of times. To neatly finish up on the possibility of defining parameter components for multiple values, we should note that this type of parameter component might still not be self sufficient. For instance, the user might want to specify that all values between 100 and 200 be used and all values between 200 and 1000 with a step size of 5. This cannot be specified with one multiple values ranged number parameter component of some sort. However, for some parameter components we might be able to define some multiple values parameter component that *is* self sufficient. In any way, such needs to be facilitated in the model design. This results in the method `isSelfSufficient()` that returns whether or not the parameter component holds enough expressional power to specify a multiple of values in all possible ways or all possible desired ways. This information is used in the multiple values parameter interface. When a parameter component is marked to be self sufficient, it is not placed in an additional list to specify a multiple of values. The method is placed in the `ParameterComponent` class and is overriden in the single value version and defined to always return `false`.

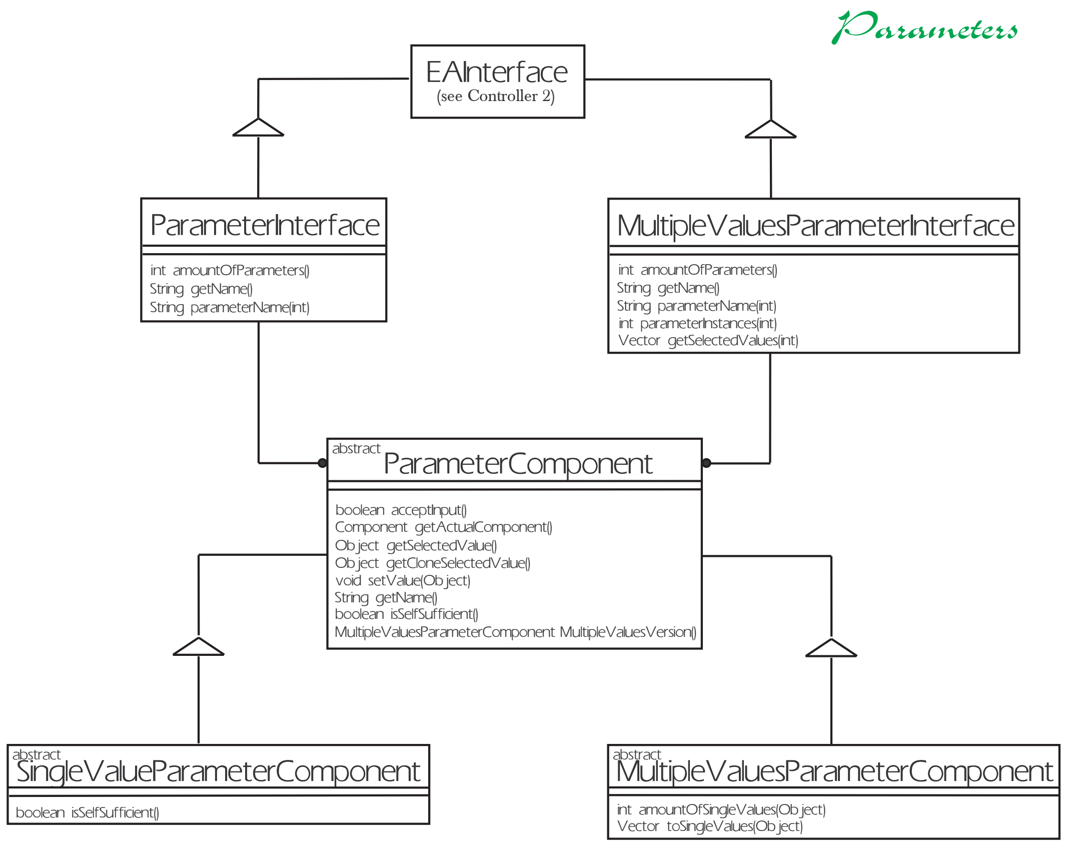

Parameters
EAInterface
(see Controller 2)
ParameterInterface
int amountOfParameters()
String getName()
String parameterName(int)
MultipleValuesParameterInterface
int amountOfParameters()
String getName()
String parameterName(int)
int parameterInstances(int)
Vector getSelectedValues(int)
abstract
ParameterComponent
boolean acceptInput()
Component getActualComponent()
Object getSelectedValue()
Object getCloneSelectedValue()
void setValue(Object)
String getName()
boolean isSelfSufficient()
MultipleValuesParameterComponent MultipleValuesVersion()
abstract
SingleValueParameterComponent
boolean isSelfSufficient()
abstract
MultipleValuesParameterComponent
int amountOfSingleValues(Object)
Vector toSingleValues(Object)

Figure 6: Model of the parameter structure in the *EA Visualizer*.

We have specified everything but for the contents of the `MultipleValuesParameterInterface` class. It requires the same methods as in the single value version, but additionally it needs be supplied with methods `getSelectedValues( int )` and `parameterInstances( int )` because the task of retrieving the parameters that were actually set is no long trivial as in the single value case. Here the `ParameterComponent` objects are used so that they can either be placed in a list or not. In any way the task is not very complex but impossible to fullfill based solely upon the `ParameterComponent` objects. The specified methods return all of the selected values and the amount of selected values respectively for a specified parameter. This completes the modelling of the controller from administration to the user interfaces to the parameter structure. The latter topic is not directly related to the controller of the system but closely to the user interfaces and is therefore placed in this section. The UML diagram that results for the parameter structure is depicted in figure 6.

2.3.3 The model of the system

In the context of modelling the system in a MVC manner as we are doing in this modelling section, the model of the system as denoted by the title of this subsection is the evolutionary algorithms themselves. We have already determined through a thorough investigation in section 2.2 what the components are that the definition of evolutionary algorithms in the *EA Visualizer* consists of. Next to that we have also determined in general what the functionality of these components should be. In this section we investigate these components closer, defining more precise their functionality and establishing the object oriented model for the general framework. This will be done conform point 1 from the requirements summary in section 2.1.7. This is actually not much more than a logical extension of the decomposition that we have defined earlier, because there we already introduced *separate* components. Now we establish the actual presence of these components in the system by explicitly incorporating them in the model. The resulting UML diagram is shown in figure 7.

The first thing that must obviously be incorporated into the model is the fact that the `EARunner` class must have a link to each separate class that constitutes the decomposition of evolutionary algorithms. As the `EARunner` uses the components to actually run an evolutionary algorithm, this is a fundamental requirement. Secondly all components can be parameterized. This has been emphasized in subsection 2.3.2 by defining a structural framework for parameters. In general, all components will have something in general and as such we should define a superclass for all of the components and name it `EAComponent`. In this abstract class the method `setParameters( Vector )` is required to allow the system to set the parameters that were selected by a user. Furthermore, the names for the parameters might be required at a later stage, so `setParameterComponentNames( Vector )` is also a required method. In reverse, we should ofcourse also be able to retrieve the data that we have set so it can be used. It follows that we require methods `getParameters()` and `getParameterComponentNames()` that retrieve the parameters and the lastly set values for these parameters respectively. Finally, we will want to allow the user to reset an algorithm so as to perform a run over again with exactly the same settings without redefining the entire algorithm. Therefore we must have a method `reset()` that will be called exactly when the algorithm is requested by the user to be reset.

Having specified the outset of the model, we are now ready to define in a more detailed manner the functionality of the components that will appear as seperate abstract classes.

Genotype
This class codes the information of a solution in some way and as such it can be seen as a datastructure in itself. Some general methods that we should have are `cloneGenotype()` and `equalsGenotype( Genotype )`. These two methods facilitate the creation of an identical genome and the inspection whether two genomes are identical. The latter method seems to be superfluous as we have defined to have a `Similarity` component that expressed measures of simililarity. The larger difference however is that a similarity component is defined to be more general as we can express a measure of similarity in some range. This method only specifies when two genomes are completely equal and it facilitates ease in programming for instance the oftenly used termination condition that specifies that termination should occur when all genomes in the population are identical. The `cloneGenotype()` method could also be regarded as superfluous because we could always create a new genome since such must be facilitated in a `Recombinator` for instance and then transfer all information. Once again, cloning genomes is a frequently used operation and for ease of programming and speed of running an evolutionary algorithm, this method is defined. A third more general method that we require is `newGenome` that receives a prng as a parameter and randomly resets the genome. This method is needed in order to facilitate the initialization process.

A more complicated question is that of where to store fitness values. In order to allow for efficient execution, we require to store the fitness values so that they do not need to be recomputed unless a genome has altered. The question is where to place this information. As all genomes are stored in the `Population` class, this could be a good location to place this information. The drawback of such a choice however is that the `Population` then needs to define another datastructure in which the fitness values are kept. Furthermore a fitness value is something that is an attribute of a genome like a price tag to a sound card in a computer store. Also, letting the `Genotype` class hold the fitness information results in the possibility to keep the information consistent with changes to a genome. Whenever changes are applied, this is marked in some internal structure so that the `Genotype` can report that its current fitness value might not be valid anymore. From this discussion it follows that we require methods `getFitness()` that returns the fitness value that is currently stored with a genome, `haveFitness()` that reports whether the currently stored value is valid for the contents of the genome and `setFitness( double )` that sets a new fitness value.

It follows from the discussion above that the `Genotype` and the `Population` components are tightly linked. This is ofcourse actually quite obvious since a `Population` is a container for multiple `Genotype` objects. It is therefore most usefull to know what the physical position of a genome in the population is. For instance, when using a replacer that determines that some parent genome should be replaced by some offspring genome, this replacement cannot be carried out efficiently unless we know where the genome is located in the population so that it can be replaced directly. As such, we require to have the additional methods `getPopulation()` that returns the `Population` object that a genome is stored in, `getPosition()` that returns the position of a genome in that population, `setPopulation()` that sets a new `Population` object that a genome is stored in and `setPosition` that sets a new position for a genome in the population.

Population
We have already seen in the discussion regarding the `Genotype` class that the `Population` class is tightly linked to the `Genotype` because the `Population` class holds a multiple of genomes. This container functionality can be established by introducing methods such as `addGenome( Genotype )` to add a genome, `removeAllGenomes()` to wipe the entire contents of the population and methods such as `getGenome( int )` and `setGenome( Genotype, int )` to retrieve a genome from a specified position and to replace a genome at a specified position in the population by a new genome respectively. Furthermore it is no less than obvious that a method `popSize()` is needed that returns the current size of the population.

We have seen in the discussion regarding the `Genotype` class that the fitness values are stored directly with the genomes. The computing of these fitness values is called evaluation and is normally performed after the evolution of one generation and directly after initialization. We have argued that this evaluation is to be implemented with the use of both the `Population` and the `Genotype` class in combination with the `FitnessFunction` class. We have therefore provided the `Genotype` class with fitness manipulation methods. In order though to facilitate actual evaluation, we need to provide the `Population` class with an `evaluate( FitnessFunction, Similarity, long )` method that receives the fitness function to actually compute the fitness values, a similarity component to compute information regarding linkage between genomes (such as clustering information) and the generation counter that as discussed earlier in section 2.2.4 may have an influence on the evolution process. It might be required that at some point all the new genomes are to be re–evaluated no matter what their internal state might be. To signal such a request, the method `invalidate()` should be provided that states that the fitness values for all genomes need to be recomputed (for instance when the fitness function has changed but not the genomes themselves).

In order to facilitate the resetting of only the population instead of all components of the evolutionary algorithm, we have to define a `renewPopulation()` method that randomly regenerates all genomes in the population. In order to do this however, the `EAComponentCreator` class is needed to actually generate genomes. This class might not be available when required, so a method should be defined that is used to set a link to the used instance of that class. The same is true for the `PseudoRandomNumberGenerator`. As such, a method `setEnvironment` is required that receives both the name of the `Genotype` that is used as well as its parameters, the component creator and the prng of the system. Finally, a method `shuffle` should be defined in order to facilitate a mixing of the order of the genomes in the population. This can be needed quite often because we need to make sure that we do not keep on having the same ordering. This might imply that we keep on testing the same genomes together for some measurement for instance. As such, instances of components may need to mix the ordering of the genomes. To facilitate this at the outset, we define to have a method in the `Population` class that shuffles the genomes.

FitnessFunction
The fitness function defines a measure of performance for genomes and as discussed in section 2.2

also holds information regarding the environment of the problem as it contains problem instance specific information. This second aspect needs no modelling in the sense that we need to define extra methods that establish the containment of such information. This information is held within the component and is used implicitly when computing fitness values. As such, the method that must obviously be defined is `fitness( Genotype, long )` that computes a fitness value for a given genome. The second parameter is the generation counter. This method however is not the only method required because in order use the fitness values we still need to know when one fitness value is better than another (we could minimize or maximize for instance). So, in order to complete the functionality of a fitness function component, we need to define a method `betterFitness( double, double, long )` that specifies exactly when one fitness value is better than another (at a given "time").

Similarity
The last of the dependency imposing components is the `Similarity` component through which a measure of equality is expressed for genomes. We need to define only one method:

```
compare( Genotype, Genotype, FitnessFunction, long )
```

that compares two genomes and returns a value between 0 and 1 where 0 means that the two genomes are totally different and 1 means they are completely identical (according to the measurement) because such is the only thing required from a similarity component. The fact that a `FitnessFunction` is required is implied by the definition of the fitnessfunction to also hold problem instance specific information. For instance, we require information from a TSP fitnessfunction for a measure of similarity when we base this information on the location of the cities. Finally the generation counter is also specified as a parameter conform the discussion in section 2.2.4.

Selector
The four non–dependency imposing components are somewhat more complicated than the remaining components as will become clear from the remainder of this subsection. Especially the `Genotype` and the `Population` classes require a great deal of administration so as to facilitate a good information storage. The remaining components all have a specific meaning as has become clear in section 2.2 and this specific meaning can be implemented in one method, making these components at first glance contain less complexity. The first of these components is the `Selector`. From the results from section 2.2 we deduce that the selector is to select an amount of genomes directly from the `Population`. As such we can define the `Selector` has having one method:

```
Vector select( Population, FitnessFunction, Similarity,
               PseudoRandomNumberGenerator, long )
```

The result of this method is a `Vector` of genomes that constitutes the result of the selection process. These genomes were selected directly from the supplied `Population`. The `FitnessFunction` might be required because of its problem specific information as well as the `Similarity`. Such will be the case for each of the remaining components, so we shall not repeat such justifications anymore. The same is true for the `long` variable that is the generation counter. In section 2.2.4 we have already argued the necessity of this variable and we shall refrain from repeating the arguments here or later in this section. Finally, the `PseudoRandomNumberGenerator` was already in section 2.2 denoted as a *fundamental* component, but we have disallowed it to be a dependency imposing component because we do not want to have such dependencies as a prng should provide random numbers as good as possible regardless of the problem. So in any of the following we shall disregard the specification of the `FitnessFunction`, `Similarity`, `PseudoRandomNumberGenerator` and the `long` (generation counter) parameters.

Mater
Before applying recombination, the `Mater` places the selected genomes together in groups. This is the only functionality of this component and it can be facilitated by the following method:

```
Vector mate( Vector, FitnessFunction, Similarity,
             PseudoRandomNumberGenerator, long )
```

The returned `Vector` contains a multiple of `Vector` objects that contain the actual `Genotype` objects. The `Vector` objects that are contained in the resulting `Vector` are the mated groups. The parameter `Vector` is the `Vector` that was returned by the before `Selector`.

Recombinator
The `Recombinator` class is slightly more complex in its definition because of the possibility that this component might be surpassed in the running of evolutionary algorithms when the recombination chance is less than 1. When this is the case, the system might decide at some point that a mated group should not undergo crossover. In such a case the system must clone the original genomes in some way. The problem is that the system cannot simply clone *all* genomes that are contained in the mated group. This is because of the fact that a recombination operator might have more or less parents than offspring. Because of this we require an additional method `offspringArity()` that returns how many offspring a `Recombinator` generates. If this amount is to be variable, -1 should be returned, resulting in the cloning of all genomes in the mated parental group by the system.

The actual functionality of the `Recombinator` can be facilitated by a method

```
Vector recombine( Vector, FitnessFunction, Similarity,
                  PseudoRandomNumberGenerator, long )
```

This method returns a `Vector` with the offspring genomes. The recombinator is supplied with one mated group at a time. The system will make sure itself that the `Recombinator` is applied to *all* mated groups and that the results are combined. The `Vector` that is provided as a parameter contains the parent genomes. In order to actually generate offspring genomes, we should note that to do this *neatly*, the `EAComponentCreator` should be passed on to the method[1]. However, even though the `EAComponentCreator` is one of the most neat and well structured classes, it also grows in size and creation of components therefore becomes slower. As the creation of genomes is one of the most prominent actions in an evolutionary algorithm because of the need for creation of offspring, this action should be done as quick as possible. Therefore, the user should simply create a new offspring by for instance stating `new BinStringGenotype()` and then using some means of administration offered by the system that is normally done by the `EAComponentCreator` so as to have the fastest way of creating genomes. It is for this reason that the `EAComponentCreator` was removed from the method. The same is the case for the methods in the `Mutator` and the `HybridSearcher` that are also classes that generate *new* genomes and therefore have the same problem. The speedup gained after employing the new strategy was a factor 2.1. This factor will only increase when the system expands. We therefore emphasize once more that for an automated administration that allows for easy expansion of the system, the `EAComponentCreator` is a completely great and high tech class. Its usage is very much so justified when the system creates the components for an evolutionary algorithm once at the outset. However during the run of the evolutionary algorithm, using the creator class to generate genomes ever so many times results in a drawback and slows down the algorithm. Therefore we should not allow the user to utilize the creator class when generating new genomes.

Mutator
The mutation operator has a functionality that allows it to mutate a single genome. As such we must define the method that establishes mutation by receiving a single `Genotype` object that it should mutate. The system will provide the component with all genomes that should be mutated one after the other. This leads to the definition of the following method in this class:

```
Genotype mutate( Genotype, FitnessFunction, PseudoRandomNumberGenerator,
```

[1]That was the original implementation of the method.

```
                    double, long )
```

The resulting offspring should not be the mutated genome that was received, because of the information that might be extracted for visualization later on. Mutation takes place with a specified chance. Even though in the *EA Visualizer* it is possible for a `Mutator` to have its own definition for such a chance, because the usage of it is classical, it is also defined at the outset (but can ofcourse be eliminated by simply disregarding it). As opposed to the usage of chance in combination with the `Recombinator`, the chance at mutation is not taken to be the chance that mutation be applied to a genome in general, but as a chance that be used when mutating a genome. As such the chance at mutation is supplied as a `double` parameter.

HybridSearcher
To a certain length the `HybridSearcher` is similar to the `Mutator` class because it receives a single genome and returns the genome that results from searching in some way starting at the solution specified by the genome to search. As such it alters a genome and returns the altered version which is viewed in this way no different from the `Mutator` class. Therefore the definition of the method required in the `HybridSearcher` is not much different:

```
Genotype search( Genotype, FitnessFunction, PseudoRandomNumberGenerator, long )
```

As with the `mutate` method from the `Mutator`, the resulting `Genotype` object should not be the given `Genotype` objec that was altered, because of information that might be extracted (for instance the performance of the hybrid searcher) at the visualization stage.

Replacer
The `Replacer` is really the point where all the results come together because at this point the offspring need to be placed back in the population and therefore the results from the former components need to be used, resulting in the definition of the following method in the `Replacer` class:

```
void replace( Population, Vector, Vector, FitnessFunction, Similarity,
              PseudoRandomNumberGenerator, long )
```

The `Population` parameter is the original population at the beginning of the evolution step. The first `Vector` is the `Vector` of `Vector` objects with the mated parents that resulted from the `Mater`. The second `Vector` is also a `Vector` of `Vector` objects, but the `Vector` objects in the main `Vector` in this case contain the offspring genomes that resulted *after* the application of the `HybridSearcher` component. In this we should note that the system should provide the `Vector` parameters in such a way that `Vector` number x in the parent `Vector` gave `Vector` number x in the offspring `Vector`.

Terminator
As specified before in section 2.2, the `Terminator` component specifies whether an evolutionary algorithm should terminate given the state of the algorithm. This state has been defined in subsection 2.3.1 to be contained in the `EAInfo` class. As such, the definition of the one method in the `Terminator` becomes quite simple:

```
boolean terminate( EAInfo )
```

Through such a liberal definition we have no problems whatsoever regarding restrictions in expressional power. This is completely conform the definition of the `Terminator` component because we cannot say in advance what it is that we want the algorithm to stop on behalf of.

PseudoRandomNumberGenerator
Finally, the least evolutionary but very much so fundamental of the components in the decomposition is the `PseudoRandomNumberGenerator` component. We mention again that evolutionary

algorithms belong to the class of probabilistic algorithms and as such rely on random numbers for their performance. We must therefore note again that this component is very important even though it is almost assumed to be a trivial thing and not obviously present in descriptions of evolutionary algorithms. We require to have some standard ways of doing things "randomly", be they the determination of numbers or the execution of an event with a certain chance. Examples of these methods are `chanceEvent( double )` that returns `true` with the specified chance and `false` with the complement of the specified chance, `nextRandomNumber()` that returns the next random number from the cycle, `randomNumber( long )` that returns a random integer number in the range $[0..x-1]$ where x is the integer parameter received and `setSeed( long )` that sets the seed for the pseudo random number generator.

2.3.4 The viewing part of the system

We have specified in the requirements summary in section 2.1.7 in point 1b that the viewing system needs to be set up in a modular way, creating separate classes for each new view. Furthermore we have specified that the views should be capable of processing user input by at least using a mouse pointing device. It is these requirements that we need to take into account in refining the `EAViewer` class we introduced in subsection 2.3.1. Before defining what views look like, we must ask ourselves how a visualization comes into being. Mostly this is done in some graphical way as in drawing graphs. But the visualization could also be merely a list of numbers. Typically the latter type of data is desired to be saved to a file. In point 8 of the requirements summary however we have stated that we are not to save information in any way. Concluding we are now facing the problem that we want to offer the option to create views that graphically visualize information without much overhead in defining a new system in which a drawing of any type can be made, as well as the option to easily create text–based output that can be copied and pasted to save the information to a file after all. The solution exists in creating two types of views.

Using Java we can create a `Canvas` object which allows for unrestricted drawing. Therefore we can supply the *EA Visualizer* with a large canvas to be the body of the system. On this canvas we can then place views that can directly draw information on this `Canvas` using a `Graphics` object. The `EAViewer` can assist in this process by managing a multiple of such views to be placed on the `Canvas`. The `EAViewer` will layout the views as being rectangles and place them in rows underneath each other. Each view is thereby assigned a location of the canvas and the `EAViewer` signals the views to draw themselves when needed. This is done so that the `Graphics` point of origin is translated to the left upper corner of the view so that the coordinates that the view can be drawn in are totally free from the actual coordinates on the canvas, which allows for a good separate development of the views. Every view should ofcourse in this setting provide its dimensions so the layouting can be done properly. Any visualization should not go beyond these bounds even though this cannot be forced. This type of view fullfills the first need for views and allows for graphical visualizations without the creation of a new system or mechanism.

Establishing the other type of view that allows for easy output of text, we can provide a second type of view. We could specify this to be some kind of text component, but a more liberate definition seems to be more in place. If we regard the `Canvas` views we have just defined, all these views have been stated to be placed on one large `Canvas` that is part of the system (the main window). As such, we will call this type of view `EAInternalView`. It only seems to be appropriate to therefore define the other type of view to be an `EAExternalView` and allow for total freedom in the creation of these components. This total freedom is done by having a link to an `EAExternalViewFrame` which is the window that is actually displayed as the external frame. In order to make it so that the help system can be opened from this window as well, we make it a subclass of the `EAFrame` class. In the `EAExternalViewFrame` class we actually only require to redefine the `paint( Graphics )` method so that is calls upon the `draw()` method from the `EAExternalView` that it is linked with. This whole liberal specification does not stroke well with the definition that we want to provide the user with an easy way to output text. In order to

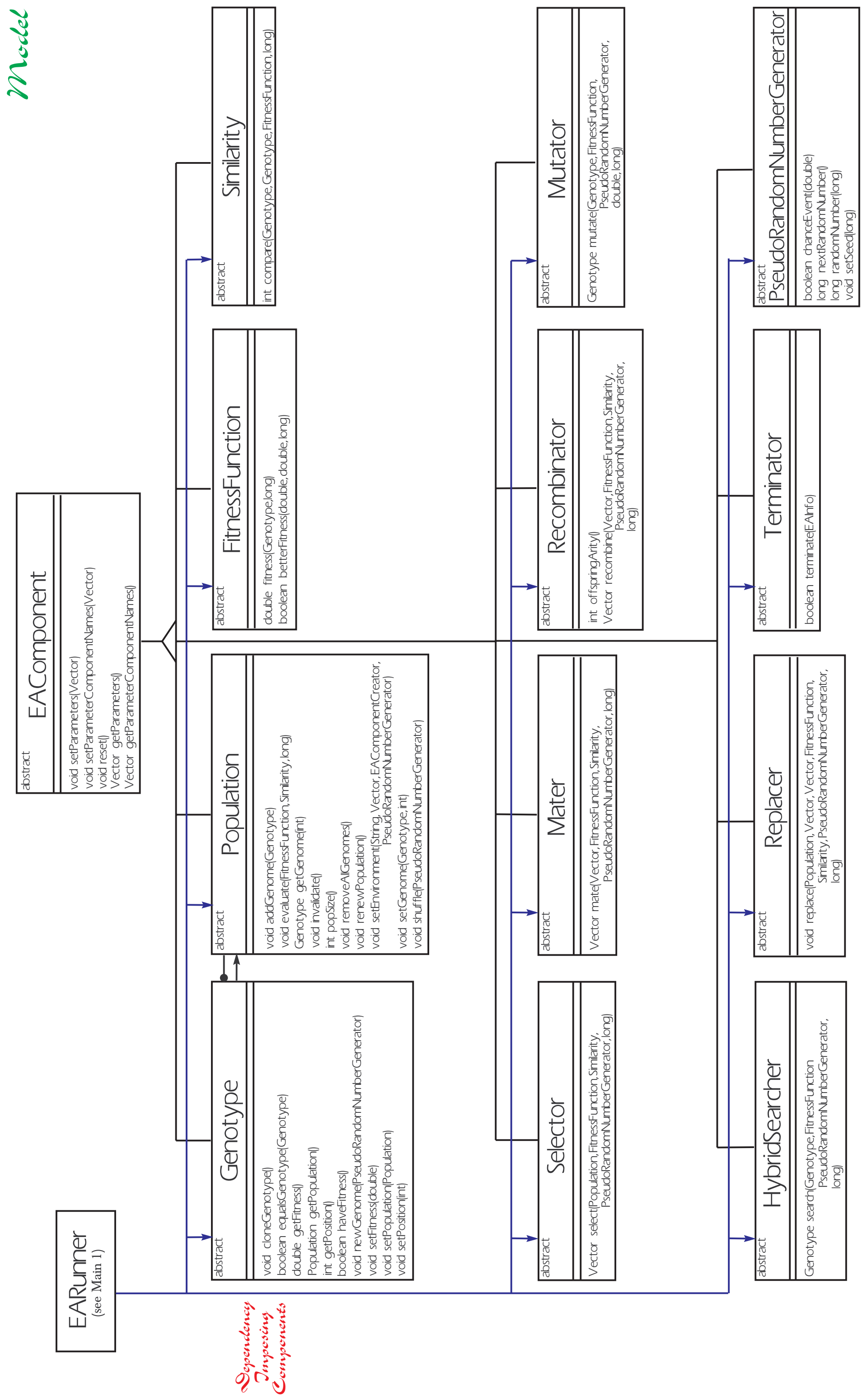

Model
abstract
EAComponent
void setParameters(Vector)
void setParameterComponentNames(Vector)
void reset()
Vector getParameters()
Vector getParameterComponentNames()
EARunner
(see Main 1)
Dependency Imposing Components
abstract
Genotype
void cloneGenotype()
boolean equalsGenotype(Genotype)
double getFitness()
Population getPopulation()
int getPosition()
boolean haveFitness()
void newGenome(PseudoRandomNumberGenerator)
void setFitness(double)
void setPopulation(Population)
void setPosition(int)
abstract
Population
void addGenome(Genotype)
void evaluate(FitnessFunction,Similarity,long)
Genotype getGenome(int)
void invalidate()
int popSize()
void removeAllGenomes()
void renewPopulation()
void setEnvironment(String,Vector,EAComponentCreator, PseudoRandomNumberGenerator)
void setGenome(Genotype,int)
void shuffle(PseudoRandomNumberGenerator)
abstract
FitnessFunction
double fitness(Genotype,long)
boolean betterFitness(double,double,long)
abstract
Similarity
int compare(Genotype,Genotype,FitnessFunction,long)
abstract
Selector
Vector select(Population,FitnessFunction,Similarity, PseudoRandomNumberGenerator,long)
abstract
Mater
Vector mate(Vector,FitnessFunction,Similarity, PseudoRandomNumberGenerator,long)
abstract
Recombinator
int offspringArity()
Vector recombine(Vector,FitnessFunction,Similarity, PseudoRandomNumberGenerator, long)
abstract
Mutator
Genotype mutate(Genotype,FitnessFunction, PseudoRandomNumberGenerator, double,long)
abstract
HybridSearcher
Genotype search(Genotype,FitnessFunction PseudoRandomNumberGenerator, long)
abstract
Replacer
void replace(Population,Vector,Vector,FitnessFunction, Similarity,PseudoRandomNumberGenerator, long)
abstract
Terminator
boolean terminate(EAInfo)
abstract
PseudoRandomNumberGenerator
boolean chanceEvent(double)
long nextRandomNumber()
long randomNumber(long)
void setSeed(long)

Figure 7: Model of the model part of the system, defining the structure of EA's.

establish that as well, we define a class named `EAExternalMessageFrame` that is a subclass of the abstract class `EAExternalViewFrame` and is a class that can actually be used as an external frame (for clarity: the external *frame* is what the user sees, the external *view* defines the functionality of the view). This class is nothing more than an external view frame analogon of the `MessageFrame` class we saw earlier. It merely holds a text area on which messages can be placed and as such allows exactly for the easy output of text that is required.

We are now ready to specify the structure of views in the system. At the top level, we define the abstract class `EAView`. This class is the general definition of the functionality of a view in the system. It contains methods such as `setName( String )` that sets the name of the view and `setParameters( Vector )` that sets the parameters for the view that were set by the user through the parameter structure of the *EA Visualizer*. Most importantly, it contains the method `updateInfo( EAInfo )` that is called upon by the system every generation to supply a view with new information comming from the `EARunner`. This information is however not enough for a multiple runs view as such a view requires to be notified when a run terminates as well. Mostly it is the information at that point that is gathered and used in a multiple runs view anyway. In order to account for this, the method `runTerminated( EAInfo )` is placed in the class that is called by the system exactly when a run terminates. As we have seen, we require to define two different types of views, the internal and the external ones. Doing just this, we define a class `EAInternalView` that denotes the kind of view that is placed on a large canvas in the *EA Visualizer* itself. A required method is `draw( Graphics )` that actually does the visualization and draws the information in some way. This is automatically called by the system when needed. Furthermore the class contains the method `setEAViewsHolder( EAViewsHolder )` to specify the object that is containing this view and the method `size()` that returns the dimensions of a view. In order to establish the interactivity through the mouse pointing device, the methods `mouseDown( int, int )`, `mouseDrag( int, int )` and so forth are defined that are called by the system if such an event occurs within this view. For the external views, we have the class `EAExternalView` that contains the methods `draw()` and `getView()` that actually draw the view (note the liberal definition) and return the window in which the visualization is done respectively.

The only thing left to define is the role the `EAViewer` plays in all this. It is obviously a class that holds a multiple of `EAView` objects. Furthermore it will redefine the mouse event methods so as to check in which internal view an event took place in order to notify that view of the event. Furthermore it contains methods like `updateInfoAll( EAInfo )` and `runTerminatedViews( EAInfo )` that pass on the information on events already specified above to all of the views in the system. Other contents of this class were already given when the main system was discussed in section 2.3.1.

Even though we have now fully specified the general outset of the view system, we have skipped the part of the layouting of the internal views. This part is rather tricky because we have to describe in some way how to layout a collection of views neatly. Are we going to compute what is the best fit to some measure or are we going to apply a simple first fit heuristic? The latter approach may very well result in an undesirable layout. However, the latter approach also maintains the order in which the views were added and it is the most simple to implement. Furthermore if we are to allow the user to switch the order of the views in the management of the `EAViewer`, causing the layout to change as well, we need not worry about any not so good looking layouts. If some ordering is not satisfactory, the user can change it if desired. In order to employ a first fit heuristic however, we are to place views in rows from top to bottom, layouting them with equal space on all sides in one row. If a view does not fit on a row any longer, it is shipped to the next row. The row length is taken to be the maximum of the width of the widest view and the width of the canvas that the views are to be displayed upon. The layouting and the placing of the views is the easiest when all views in one row are thought of to have the same height and a total width that equals the maximum width. To this end the `EAInternalViewWrapper` class is defined. It implements a rectangle that is larger than an actual view but is invisible to the user. This wrapper makes it easier to do the layouting because we can at first determine what views will end up on what row, then determine the sizes of their wrappers so that the views have an equal amount of spacing between them on all

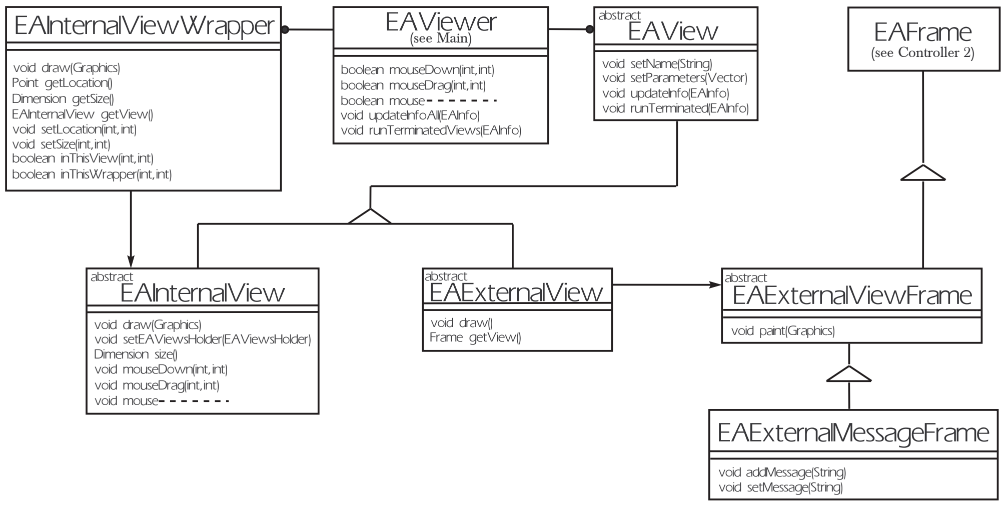


Figure 8: Model of the view part of the system.

sides so that they are centered as well. Finally all views are simply located in the center of their wrappers. The methods required in the `EAInternalViewWrapper` are `draw( Graphics )` that draws the view after translating the origin to the left upper corner of the view, `getLocation()` that returns the location of the left upper corner of the wrapper, `getSize()` that returns the dimensions of the wrapper, `getView()` that returns the view that is being wrapper and some more obviously needed methods that need no further explanation such as `setLocation( int, int )`, `setSize( int, int )`, `inThisView( int, int )` and `inThisWrapper( int, int )`. The final result is depicted in an UML diagram in figure 8.

2.3.5 The editor version of the system

We have described the structure of the *EA Visualizer* with respect to the operational side in the previous subsections. We have however remarked in the requirements summary in section 2.1.7 that the existance of an editor version of the program is highly desirable. This editor would have to provide the user with a way to expand the system. We have seen that the expandable parts of the *EA Visualizer* are the *EA Components* and the *EA Views* by definition because this is what the system is all about. Next to that we have created in the process a structure that allows for an expansion of *Parameter Component*s in the same way. In whatever way, the need to manipulate classes within the system presents itself. In this subsection we model the editor version of the program that will allow for the expansion of the system.

Starting with the main class of the editor, we realise that the `EAVisualizer` class is still by far the most important one. Very likely we will have some sort of structure that is initialized regardless of whether the editor or the operational version is to be started. This argument leads us to define a new class, the `EAVisualizerEditor` of which one instance is created on initialization of the system by the `EAVisualizer`. This new class should be a subclass of `EAFrame`. The editor will ofcourse allow for editing and browsing classes that are currently in the system as well as images after some selection procedure. It is very important to realize that any changes to classes in the system must be saved to disk by means of a system update. If we for instance add a new class to the system but do not regenerate the `EAComponentCreator` class, we have perhaps defined a great new recombination operator, but the system will not know that it exists. To remedy this, we require a method `synchronizeSystem()` that will save any required information to disk and will regenerate the classes `NameSystem`, `EAComponentCreator` and `EAViewCreator`. Furthermore, it is always convenient to directly view the results by running the program, so we should have a method `runEAVisualizer()` that starts up the operational version of the system.

The editor is mainly a system that provides the user with an extensive collection of user interfaces through which the system can be extended. In the end it is the user that defines the interesting parts as he/she writes new pieces of JAVA code. Therefore we shall require a lot of interfaces, for which the earlier defined class `EAInterface` comes in handy again. If we start off easy, we note that the system will have a directory containing images that can be used within the system. Images are required to clarify the working of the *EA Visualizer* from the help system, so such a directory will most certainly be present. In such a case we should have interfaces that allow for addition and removal of images from the system. When removing from the system, we should not allow the user to select any images that are required by the system. The contents of these interfaces are of no further importance and their functionality is apparent. The classes are called `AddImageInterface` and `RemoveImageInterface`. A third interface that does not come as a surprise and the contents of which are not very important here is the `ClassSelectorInterface`. Through this user interface the user will be able to specify a class to edit, browse, remove or add.

The more interesting part comes into view now that we have defined most all important aspects except for the most prominent operations supported by the editor. These operations are the browsing and the editing of classes directly within the system. Before going further into this aspect, we note that the help system can be incorporated in the exact same way as defined earlier in subsection 2.3.2. This becomes even more apparent when we once again point out that we have re–used the `EAVisualizer` class that acts as the provider of the help system.

Before defining an editor and a browser for class files that are part of the *EA Visualizer*, we note that an editor and a browser have a lot in common. Both display the source code and have access to all properties. The difference is that the editor is allowed to save, edit and compile the class files and their properties. This suggests a general setup in which the editor and the browser are a subclass of some higer form of a text manipulator. Realising that the main part that is edited or browsed in a class file is the source code itself which is no more than text, we should create an even cleaner structure that contains a general text browser and a text editor at a higer level than the class browser and class editor. At the top level we shall require a text manipulator, to which end we create the abstract class `TextManipulator`. In the construction of this class we can think of a general text editor and incorporate a standard collection of methods allowing for functionality issues that make text editing easier and more user friendly. These methods include `canEdit()` which returns whether or not the manipulator can edit the text, `displayMessage( String )` that displays message on a message bar that is located below the menu bar, `find( String, boolean )` that finds the next occurrence of a string and selects that string and either does this search case sensitive or insensitive, `replaceNext` and `replaceAll` methods that are the replace analogon of the `find` method, `getText()` that returns all the text that is being edited, `gotoLine( int )` to jump to a line and `handleClose()` in which it can be specified what must be done before the manipulator can be closed (close other windows first or such). In order to facilitate the well known find and replace operations from text editors, we shall also need pop up windows that allow for the user to specify what is to be found and replaced with and so forth, so links to a `FindFrame` and a `ReplaceFrame` user interface will be required. Continuing in this fashion now poses us with the requirement to define the `TextBrowser` and the `TextEditor` classes that are the two types of text manipulators desired. Both classes are abstract and define some general methods that can be overridden by subclasses. These methods will be called by the superclasses when needed. The `TextBrowser` holds nothing more interesting that is mentionable here. The `TextEditor` for instance requires extra methods such as `canClose()` that specifies if the editor window can close (usually when all data has been saved), an overridden method `handleClose()`

and the method `handleSave()`. The classes that are actually used in the `EAVisualizerEditor` are ofcourse the `ClassBrowser` and `ClassEditor` classes that are subclasses of `TextBrowser` and `TextEditor` respectively. The definitions of these classes is not very complex, but as opposed to that very extensive and not very interesting as such. We shall therefore refrain from further specifications with respect to the contents of these classes but only mention what functionality they should hold and what user interfaces are required to establish this functionality.

There are five things that can be of interest for a class in the *EA Visualizer*. These are the help information, the name, the parameter components, the dependencies and most of all the code. Not all of these items are always available for a class that can be edited or browsed. For instance a parameter component will have nothing to do with parameters that can be set for it or dependencies with respect to the dependency imposing components. Having mentioned this issue, we do not elaborate on it any further. We have specified exactly the items that are of interest and that are still to be defined in an user interface. As mentioned we require browsing and inspection of dependencies. For editing we define to have a class named `DependenciesEditor` in which these dependencies with respect to the dependency imposing components can be specified. Likewise, we define to have a class named `ParameterComponentsEditor` through which the user can specify by selection what parameters are required for an instance of a component of the evolutionary algorithm decomposition or for a view. On the browsing side, we could define to have similar classes but altered to have the suffix `Browser` instead of `Editor`, but the browsers for these subjects are hardly interesting as all that needs to be displayed is a list of items. As such, we define to have a `ItemsBrowser` that can display a list of items. The `ClassBrowser` will thus have a multiple of these classes, namely two. An even simpler interface is the editor of the name of the class (remember that names have a special administration in the *EA Visualizer*, see subsection 2.3.2). The functionality of both the editor and the browser is trivial and we specify no more than that we should have classes `NameEditor` and `NameBrowser`. The final interfaces that are required are more interesting. They regard the help files for the classes. As stated in the requirements summary in section 2.1.7, the help system must be expandable for every category of classes that is expandable. This is ofcourse achieved by allowing the user to edit the help file for the class that is being edited. This implies the editing of text and therefore we require a class named `HelpEditor` that is a subclass of `TextEditor` and a link to which is held in the `ClassEditor` class. Analogously, we require a `HelpBrowser` class that is a subclass of `TextBrowser` for the `ClassBrowser` class.

The only thing we have not clearly specified in the definition of the editor version of the *EA Visualizer* is the option to compile class files. The text editor will contain a mechanism to compile files into the system and report any errors. As we will define a language similar to LaTeX and comparable to HTML in which to write the help files, such a mechanism will also be available to the help editor as required. The required compiler or parser needs to be specified by a subclass of the `TextEditor`. We refrain from further specifying the compile mechanism and leave its specification at the mentioning of its availability. The implementation is not so much tricky as it is quite analogous to the "Save file" mechanism that has already been specified quite clearly and is very well known, implying that we need not spend more time on specifying any details. The resulting UML diagram for the editor version of the `EA Visualizer` is shown in figure 9.

2.4 Implementation

In this section we briefly go over some low level implementation details. The model that was presented in section 2.3 covers the fundaments of the *EA Visualizer*, but the actual implementation brings along some extra details. This section is not intended to contain and be explanatory for all details of the system, for such is not what this paper is meant for. Nevertheless, some fundamental details that stand out are described. This shows that the system implementation is not trivial once a model has been created.

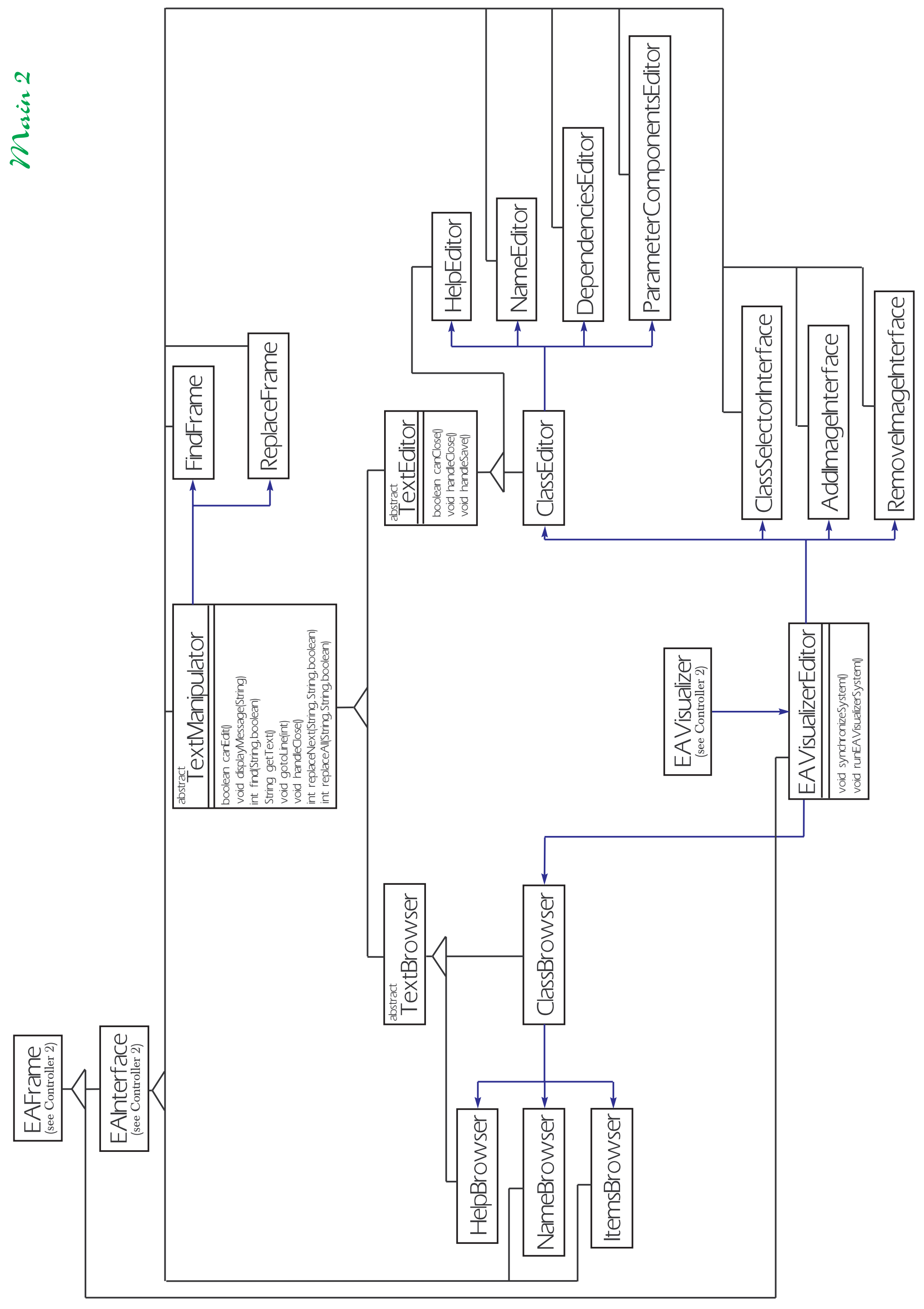


Figure 9: Model of the main system in EDITOR mode.

In section 2.4.1 we discuss the implementation of the general framework. Sections 2.4.2 and 2.4.3 describe the viewing part of the system and the main system respectively. The resulting implementation contains many files. In order to easily find something back amongst all the files, they are ordered according to what part of the system they belong to. This subdivision is made precise in section 2.4.4 where the *packages* that contain the files according to some subdivision are introduced. Finally, the resulting system is briefly presented in section 2.5. In that final subsection both the resulting system and its appearance are demonstrated and a description of how to use it is given to give the reader a feel for what the system looks like and how all considerations have come into being.

2.4.1 The evolutionary algorithms engine: `EARunner.java`

We have seen that the `EARunner` class is the class that implements the general framework for the evolutionary algorithms. As such, it is of great importance since it is evolutionary algorithms that we are essentially working with in the *EA Visualizer*. Because of this importance we have also already seen its contents in quite some detail. We have already specified fully the components the general framework should consist of in section 2.2 and have defined a model for it as well as for its components in section 2.3.3. The flow of information through the evolutionary operators is therefore already fully specified. What remains is to specify the creation of the `EARunner` and the outflow of information through the `EAInfo` object that we have been vague on so far.

First of all, the `EARunner` is a class of which we create an instance with the correct parameters. These parameters will mainly be the actual instances that should be used for the components in the decomposition. Other than that some means of connection to the `EAVisualizer` is required so as to notify the main system of termination for instance. Details like such shall not be observed any closer. The more important thing is the multiple runs evolutionary algorithms. Over a multiple of runs, the components and parameters change. This could imply the creation of a new `EARunner` for each change in parameters. However we could do better (more efficient) if we were to only change the components or parameters directly. This direct reference method is justified by the fact that we wish to offer the user a way of resetting the algorithm anyway. This implies that we can change the components and the parameters directly and then reset the algorithm just like the user would do. This will then have resulted in a new evolutionary algorithm that is initialized. It refrains us from holding a reference to all components that are currently installed together with their parameters and installing all of them in a new algorithm. We can now use some enumeration techinique to enumerate all the settings and make this enumeration work directly on the links that are kept in the `EARunner` so that changes in settings are directly put through to the model. Then as mentioned before, we can reset the algorithm and start it over.

The only thing that is therefore not specified as of yet, is how to neatly allow for direct access to the links within the model. In section 2.3.1 the way for this information flow has already been paved however. We have defined two interfaces `EAInfoUpdater` and `EAInfoSetter`. The exact specification of the methods within these interfaces has been left out and we shall not provide such information here either. Nevertheless, the solution to the implementation problem lies within the definition of these interfaces. A crucial role in all of this ofcourse is the contents of the `EAInfo` class. We have mentioned on several occasions that this class contains all information required to visualize any information from the evolutionary algorithms in any way. As such amongst all of this data the instances for the components from the general framework must be stored in this class as well. The solution to the problem now lies in the making this class the global container for the instances that are used in the evolutionary algorithms defined by the `EARunner` class. Global data is however an undesirable aspect so we should prohibit ourselves from making access completely global. But this is exactly what is established through the two interfaces `EAInfoUpdater` and `EAInfoSetter`. The `EAVisualizer` sets the information for the `EARunner` and the `EARunner` updates information coming from the algorithm. As such the information flow within the program that we have argued for has been established.

2.4.2 View management: `EAViewer.java`

Managing the views in the system that visualize the information from the evolutionarry algorithms is done as we have seen by the `EAViewer` class. This class contains methods to add and remove views. Furthermore we have argued that we should have two types of views in the system, namely internal and external views. The external views are quite simple as they leave the user with the greatest of freedom in filling in the contents of such an external frame. The internal views however need to be layouted on some large canvas. This has been noted earlier and we have already described how to layout such views. Implementing such functionality in JAVA however leads to some tricky details which in turn lead to the introduction of a new type of AWT component, the *free* component.

The `EAViewer` is defined to be subclass of a `Panel` as it must come to hold a multiple of views. As we have mentioned earlier however, these will all be graphical views and as such we could suffice with a `Canvas` on which we can draw. With an eye towards future extensions, we do not wish to impose such a constraint. This in turn implies that the `Canvas` that we want to use for now must be added to the `Panel` that is the `EAViewer`. Furthermore we need to have control over that `Canvas` because we need to establish the interactivity and therefore need to reroute the mouse events to the right view. This rerouting depends on the physical placing of the views on the canvas. The normal way to solve such a problem is to create a new class that is a subclass of `Canvas` and implement the functionality there. This does not rid ourselves of all problems however, because it will be the other class that contains this new class that needs to handle the actions. This in turn can be solved as well by transferring all information to the new class, but this leaves us with a new sort of information rerouting. In the case of the `EAViewer` this problem could be solved by rudely leaving the `Panel` thought aside, but the problem is not solved as we have defined the user to be able to define `ParameterComponent` classes that hold JAVA AWT components that are added to an interface to actually display them to an user. These components can be composite (for instance a geometric TSP problem that can be clicked together by a canvas and is presented with a button that can clear the current contents) and hence we once again have the same problem because we cannot make the actual parameter component a subclass of any AWT component since it *must* be defined as a subclass of `ParameterComponent`.

To solve such problems, we create *free* components when needed. For instance we now require the `FreeCanvas` class. These *free* components catch the AWT event flow and call methods of users of these free components that will in turn handle these events. For instance, we have a `FreeCanvas` class that contains a `mouseDown( int, int )` method that is called automatically by JAVA as the `FreeCanvas` is a subclass of `Canvas`. The `FreeCanvas` then calls the `FreeCanvasMouseDown( int, int )` of the `FreeCanvasUser` that was defined for it. The most important thing is ofcourse that the `FreeCanvasUser` entity is a JAVA interface. As such the `EAViewer` has a class definition that looks like this:

```
public final class EAViewer extends Panel
  implements EAViewsHolder, EAViewsAddingHolder, FreeCanvasUser,
             FreeScrollbarUser
```

Hence when the mouse goes down in the `Canvas` that is contained in the main interface of the *EA Visualizer*, the `EAViewer` is called upon because it is the `FreeCanvasUser` of that `Canvas`. This allows us to in turn implement the desired interactivity because we can now put the events through to the correct internal views. So in general we now have the option to define *free* components together with their users that allow for the inclusion of AWT components in a class and have control over them without defining a new subclass of such an AWT component.

Another quite crucial point is that of the displaying of information while the evolutionary algorithm is still running. The visualization that is done by the views is such that at a certain point (mostly after each generation) the information is gathered from the evolutionary algorithm and placed in an `EAInfo` object. This object is then shipped to the `EAViewer` by the `EAVisualizer`. The `EAViewer` in turn will ship this information to the views in the system, both internal and external. At that point the views will update their internal state and are then asked to redraw themselves. In the mean time, the `EARunner` continues to run the evolutionary algorithm and might place update information again when the views are still updating their internal structure or are just repainting some visualization based upon some link to the information within the `EAInfo` object. Furthermore as the views might be drawn over again because of some JAVA update event (a window that was blocking the view has been lowered for example), the view might have to be redrawn as well which is even more likely to occur during an update from the `EARunner`. As such, we require to have some means of mutual exclusive access to the information placed in the `EAInfo` object. In order to achieve this, we must first determine the type of mutual exclusion required. The views are allowed to read the information and the `EARunner` is allowed to write the information. Reading and writing may not happen at the same time. Furthermore, as the running of the algorithm has the highest priority, writing should have a preference over reading. Finally, we have a multiple of views which are allowed to all read at the same time, but we have a single `EARunner` that is capable of writing information. This is the description of the classical readers/writer problem with writers preference. To facilitate the usage of such mutualy exclusive access, we create a `ReadersWriter` class that contains methods `requestRead()`, `releaseRead()`, `requestWrite()` and `releaseWrite()`, the functionality of which is obvious.

Continuing in this perspective, it might very well be the case that a view needs to redraw itself because its interior state has changed not as a result of the updating of information from the `EARunner`. For instance, the view might define some means of interaction that causes its shape to change on clicking or dragging (3–D model rotating, checkbox clicking or multiple ways to view information that can be toggled by clicking for instance). In such a case, the view needs to redraw itself without the system asking it to redraw itself. The difference is that in the latter case the system will ensure its mutually exclusive access with respect to the writing of information by the `EARunner`. In the former case it follows that the view needs to request access so as to ensure mutual exclusive access. To this end, we have ensured to provide each and every view with a link to an `EAViewsHolder`, which is actually the `EAViewer`, but any holder of a link to a `EAViewsHolder` cannot use the full functionality of the `EAViewer`. The functionality that can be used ofcourse is the specially implemented methods `requestGraphics( EAView )` and `releaseGraphics()` that request reading access from the system and releases that resource respectively. These methods must be called by any view when any update must be peformed that is not system initialized to avoid problems, but it cannot be forced by the system that these methods are called.

Another important detail is the difference between single– and multiple runs views. We have defined an explicit separation of these types of runs with the multiple runs version being the most elaborate. The multiple runs algorithms therefore can also have different types of views as visualization of data over a multiple of settings can be much more complex. The kind of visualizations for multiple runs is mostly some aggregation over values. A lot of details come forward from defining visualizations such as the mapping of evolutionary algorithms and their settings to table entries, but the main thing is that we require to know when a view is defined for multiple runs. This information is provided by the `EAViewCreator`, but the subject is not closed with that statement. The point is that when using a single run version, the information we want to see is the direct behaviour of the algorithm. When we use a multiple runs version, we are mostly only interested in the final result that is computed over a large variety of settings during a long night or so. The information flow we have discussed so far has been specified to move from the `EARunner` to the `EAViewer` after every generational step. This is clearly too fine grained in most cases as the information that we want to aggregate is mostly some value based upon the results at the termination of a single run. As such we should provide the default setting for multiple runs views that they are updated only on the termination of a run. Furthermore, the density issue of shipping information from the evolutionary algorithms to the viewer can also be experienced as being too often perhaps in some cases when running a single run version. The visualization brings extra overhead because results need to be computed and visualized. As such, the actual algorithm runs slower. When information coming from the algorithm *every* generational step is too often, this must be changeable to shipping information every so many steps.

A final small detail is that for setting up the help system, we have already specified that the *EA Visualizer* should be constructed so that in every user interface the user can press the F1 key for help. This has been taken into account in the definition of the model in section 2.3.2. A not so very user friendly item though is that because the instances of the components of the decomposition of evolutionary algorithms as well as the instances of the internal views are not windows in the system, we can in no way therefore ask for help on them directly. Such must always be done through the index on the help page. This is acceptable for the instances of the components but much less for the internal views, because they are very much so visible to the user on the large canvas in the main window. But pressing F1 there leads according to the earlier definition to the opening of the help system on the page for the *EA Visualizer* itself and not for the view that the mouse pointing device is pointing at. This is a very desirable extra aspect and should not be neglected. So we allow the user to point at a view with a mouse pointing device and request for help on that view by pressing the F1 key together with the `Ctrl` key. This completes the discussion of the most prominent details on the views in the *EA Visualizer*.

2.4.3 Putting things together: `EAVisualizer.java`

The main class of the system is the `EAVisualizer` class as it is this class that not only contains the `main( String ps[] )` method but also implements the main window of the system and is the main point of data flow through the system. This is most prominent when regarding the information flow from the `EARunner` to the `EAViewer`. The runner notifies the main class of the fact that it has reached the next generation or that it has terminated. The main system then requests the runner for information on the evolutionary algorithm if updating is required and puts this information through to the viewer which in turn distributes this information to the views. Furthermore the information regarding the settings for the single run or multiple runs evolutionary algorithms is reported to the `EAVisualizer` class, which in turn processes this information to set up the evolutionary algorithm or an entire environment for enumeration of different settings. We note here that the views have an implicit link back to the model through the information that is passed on to them. As discussed in subsection 2.4.1 the information is gathered in an `EAInfo` object that also holds all instances of the components of the decomposition. As such, the views have access to the parts of the model. We should also note that the views cannot *alter* what instances are installed in some evolutionary algorithm because they are not defined to be an `EAInfoSetter` and even if they were, the system would not use this property. This thus results in a desirable connection between the views and the model and a complete freedom in the choice of visualization of data.

Next to being the nerve system for data flow through the system, the `EAVisualizer` class also implements the setting up of the system as we have defined it to also be the main user interface. Thus the `EAVisualizer` sets up all required data structures in order to allow for data flow. The main point we are trying to emphasize is that the `EAVisualizer` is an important class and by placing most of the software aspects in this class we can disregard these scientificly uninteresting details in other parts of the system. So here we will for once and for all denote some of the choices that were made and some implementation issues that are stored in the `EAVisualizer` and are no longer required at any other point.

First of all, we require some sort of protection for the system itself. We do not want any other parties to alter parts of the internal system or to expand the system by not using the editor. Furthermore the information required to generate the `EAComponentCreator` class and other automatically generated classes needs to be stored in some way. Lastly we want the files that belong to the system and components that are contained in the default package of the *EA Visualizer* not to be editable or removable through the editor. What we therefore require is some means of cryptography on the data. We have chosen to implement some cryptography scheme and to thereby encrypt the data. This data concerns the components that are available in the system as well as the views and the naming of all components. This information is updated or extended when using the editor. The information is completely read into memory where it is encrypted and decrypted when needed. Ultimately we need to store the data on disk to be able to use it next time the system is started. We have now protected the data that concerns the components of the system and their naming. This implies that the user cannot expand the system because the encrypted files cannot be altered in the right way except by using the system. This does not however solve all our problems because we still wish to protect the system from being edited. To prohibit the user from doing so, once we generate the program version of the system that can be used for distribution, not *all* JAVA files are distributed. For instance all the more prominent files are not included such as `EAVisualizer.java` and `EARunner.java`. Furthermore the contents of the `eavctrl.interf` package is restricted to the `.class` files only. This does not save us yet from any harm because the files can be reverse engineered even though this is illegal and is stated in the `readme.txt` file to be just that. The user could reverse engineer the `.class` files and alter the resulting `.java` file and recompile the system. To prohibit the user from doing this, upon generation of the system checksums are computed over all system files. These files include *all* `.class` files, the images and the help files. This information is stored in an encrypted file and is read every time the system is started. All files are then checked to see if they still have the same checksum value. Recompiling any part of the system after altering it results in alternation of `.class` files and hence will give them a different checksum value[2]. Any problems that occur during startup that are not solvable (this even includes the creation of two `NameSystem` objects for instance) causes a large red window to appear that notifies the user of a *fatal error*. In the center of the window the problem is stated. Upon such an event the system will not continue the startup sequence.

It is now clear that the `EAVisualizer` also serves as the startup class that builds the `NameSystem`, the `HelpSystem` and the creator classes. This is done by decrypting the data stored on disk and storing this data in some data structures. A problem therefore arises when implementing the editor version of the program. Making a new program would then mean copying parts of the startup information. This makes the system harder to update for ourselves however and also makes it potentially weaker because we then have stored some crucial security information in two different places. To overcome such problems, we create a new class `EAVisualizerEditor` conform the model we saw earlier in section 2.3.5 but do not place the information regarding startup and such in this class. This implies that the `EAVisualizerEditor` is not placed in the same physical place as the `EARunner` and the `EAVisualizer` but rather in the `eavctrl.interf` package. We expand the `EAVisualizer` in such a way that on starting it up an extra command line flag `-editor` can be specified to start up the editor instead of the "normal" main system. The startup sequence is then done just as in the case of the "normal" system with some exceptions. After that the `EAVisualizer` creates the `EAVisualizerEditor` object, leaves the controls to that class and does not show itself.

The most important details of implementing the main part of a software system like the *EA Visualizer* have now been discussed. Next to the tasks specified for the *EA Visualizer* so far, this class is rather large also because it is the holder of the main user interfaces for settings and therefore has a lot of administration to process. Other than that the *EA Visualizer* is a well known user interface type of program. With that remark we can close the discussion of the details and the tasks of the main class of the system, the `EAVisualizer` class.

There remains one thing that one tends to forget easily but is essential to the system. We have argued in several cases that the resulting system is self–contained through the extensive help sytem that can be opened at any time by pressing the `F1` button. The user however is expected to write such help files for new instances of components that he or she defines. Furthermore the help files are displayed within the help system through some mechanism. This mechanism typically involves

[2]This need not always be the case but the chances at this not being the case are extremely slim.

the reading of some structured text and the displaying of that text in some form. When at some point for a new version we decide to have a new look for the help files or have a better way to format the text, we do not wish to re–edit all the help files to adapt them to some structure, but rather only to rewrite the displaying mechanism so that the same files can still be read. Such is the case for instance with HTML documents for the WWW and with LaTeX documents. To achieve a desirable structure that allows for exactly the rewriting of only the displaying and formatting mechanism, we have defined a LaTeX kind of language in which text can be written with special environments to format the text. As such we have defined a language in which the help files should be written. The files are then parsed and subsequently formatted. To give some idea of what this looks like, we specify the commands that can be used:

- Normal text.
- `\emph{...}` for emphasizing.
- `\bold{...}` for bold font.
- `\color[r,g,b]{...}` for colored text.
- `\seealso[subject]` for a crossreference (`subject` is fully specified classname).
- `\image[filename]` for an image.
- `\\` for a forced newline.
- `\backslash` for a backslash symbol.
- `\{` for a curly brace open symbol.
- `\}` for a curly brace close symbol.

2.4.4 Organizing the implementation neatly: packages

As the *EA Visualizer* is set up modularly by establishing functionality through generalization and abstraction in seperate classes, the amount of classes that result for the final implementation is rather large. Furthermore, the part of the system that is interesting and expandable for the user consists of a multiple of separate classes. The complete implementation therefore contains some structure and we should utilize this structure to divide the classes that constitute the implementation over packages that each stand for some distinct part of the system so as to organize the implementation neatly and to build a good piece of software.

It has become clear from the discussions about the model of the system as well as the implementation so far that the *EA Visualizer* is built up according to a MVC structure in which model, view and controller are separated. Hence, dividing the classes in the most general way gives us the three packages `eavmodel` for the components of the evolutionary algorithms as determined in section 2.2, `eavview` for the views of the system and `eavctrl` for the parts that constitute the functionality of the system. A few classes however are not contained within these packages as they are the true system classes. These are first of all the `EAVisualizer` for this class contains the main class of the system and is therefore the leading controller class, second of all the `EARunner` and the `EAViewer` as these are the leading model and viewer class respectively as has become clear from the discussion about the model in section 2.3.1 and third of all the `EAVisualizerApplet` which is a class we have not discussed so far. We have argued however in section 2.1 that we wish to set up the *EA Visualizer* in such a way that it can be immediately used over the internet by creating an applet version. In such a case it is not the `EAVisualizer` that we need to start, but the `EAVisualizerApplet`. The latter class is not much more than a shell around the `EAVisualizer` class to allow access to it through an appletviewer. We shall now inspect each of the three packages closer in turn.

Evolutionary algorithm components: package `eavmodel`
In determining the model of the *EA Visualizer* that logically followed the results from the decomposition of evolutionary algorithms, we already saw the components that constitute this decomposition and their functionality through a specification of the methods in these components. This package is set up just for these components and therefore contains the part that defines what is being modelled in the *EA Visualizer*: evolutionary algorithms. The package itself consists out of two files and eleven more packages. The two classes it contains are `EAComponent` and `EAComponentCreator` that have been defined in sections 2.3.3 and 2.3.1 respectively. These classes contain a higher level of abstraction than the actual components of the decomposition which are placed in the subpackages.

It is subpackages such as `eavmodel.Genotype` and `eavmodel.Replacer` that we are referring to. It is clear that for each of the classes that can be seen in figure 7 (except for `EAComponent` and `EARunner`) one of such packages is available, which sums up to a total of twelve packages. One such package contains the abstract class that is the component that defines the functionality of it in the general framework for evolutionary algorithms. In that same package the actual instances are placed that can actually be used in the *EA Visualizer*. The editor will place any new classes in the right package so that the organisation of the model components stays intact. For example the package `eavmodel.Selector` contains the abstract class `Selector` which we have seen in section 2.3.3 as well as classes such as `TournamentSelector`, `RouletteWheelSelector` and `TruncationSelector` which are actual implementations of selection strategies.

Visualization of results through views: package `eavview`
We have seen that the views in the system through which the visualization of aspects of evolutionary algorithms is established are set up in a similar fashion with respect to the components of the decomposition of evolutionary algorithms. We have internal and external views which are defined through abstract classes. Actual views that can be used in the system are subclasses of these classes. This package contains all that is required for defining the views and consists of two classes and three subpackages. The two classes are analogous to the `eavmodel` package the `EAView` and the `EAViewCreator` that have been introduced in sections 2.3.4 and 2.3.1 respectively. The actual views are placed in the subpackages and just as is the case with the `eavmodel` package the classes contain a higer level of abstraction.

The subpackages in package `eavview` are `internal`, `external` and `viewutil`. The internal views are defined in package `eavview.internal`. The most important class found in this package with respect to structure of the system itself is `EAInternalView` that defines the methods that are available on any such view. Furthermore it contains the actual internal views that are thus placed directly on the canvas and are graphical of nature. For instance the package contains the `StatisticsView` class that is capable of drawing graphs concerning statistical information. The package `eavview.external` contains the external views. Analogous to the internal counterpart it contains the class `EAExternalView` that holds the methods for any such view. As an example, this package contains the class `ExternalStatisticsView` that displays numbers instead of a graph with statistical information. Finally, the package `eavview.viewutil` contains utilities that are specifically required for the views. Here we for instance find the class `MultipleRunsLegend` that provides a legend that can be used when visualizing an evolutionary algorithm over a multiple of runs, combining information from different types of evolutionary algorithms in one graph.

System specific components: package `eavctrl`
The last of the packages is the package that contains classes that are required to build the system or are just general utilities that could also be used outside the *EA Visualizer*. Mostly however it is meant to contain classes that hold some functionality with respect to the system itself. This means user interfaces, backup structures for data flow or algorithms for data processing and such. The package itself contains no classes but is subdivided into four other packages, `eavutil`, `genutil`, `interf` and `pc`.

The package `eavctrl.eavutil` contains those classes that have been developed as utilities especially for the *EA Visualizer*. All these classes have some information about the structure of the system and can therefore not be seen as general utilities. It contains classes such as `NameSystem` and `MultipleSettingsEnumerator` that define the system in which the naming of components of the *EA Visualizer* is organized and the enumeration of the settings for the evolutionary algorithms over a multiple of runs is defined respectively. All these classes constitute some larger part in the system and are therefore denoted as specialized utilities. The package `eavctrl.genutil` contains classes that are general utilities and could be used outside the *EA Visualizer* just as easily as they hold no specific information on any system components. Classes in this package are for instance `Triple` that defines a triple containing exactly three links to data items, `BinaryStringDictionary` that defines a dictionary that can be built in $O(n)$ time when the data is specified initially or in $O(n^2)$ time incrementally and can be searched binary in $O(\log n)$ time. Furthermore it contains for instance all `Free` components and their users which are classes that we have introduced in section 2.4.2. The package `eavctrl.pc` contains all parameter components that can be used in the system. We have introduced parameter components in section 2.3.2 as being part of a general framework for specifying parameters in the *EA Visualizer*. In this package, classes such as `LongRangedParameterComponent` that allows the user to enter an integer number within bounds are found. Finally, the package `eavctrl.interf` contains all the user interfaces in the system with the exception of the main window of the *EA Visualizer*. All parameters and other settings that can be entered are displayed to the user through a graphical user interface in a new window. These windows are defined in this class. All these classes contain information about settings, have backup procedures themselves and so on. This is the largest package in the system as the settings that can be entered can sometimes be rather complex, especially when this also brings along some type of backup procedure that is required to implement a `Cancel` button. Examples of classes that are found here are `EASettingsInterface` and `EAMultipleRunsLinksInterface` that have been introduced in section 2.3.2.

2.5 The resulting system and how to use it

Even though the system is self–contained, meaning that the software package in which the *EA Visualizer* is distributed can be used without further documentation because it already contains all the documentation it requires, we wish to provide some means of a user manual in order to give the reader some idea of what the system looks like after reading all the theoretical definitions and the modelling of the system to see how it all comes together in order to finally create the system that is the *EA Visualizer*. This also makes this paper in itself rather self–contained and it is our perspective that this paper would not be complete unless some means of system usage is incorporated in it.

To establish some form of a system description with respect to its actual usage, we could provide figures of the system and explain all components within it, describing all menu items and buttons in the system. Such is however already done in the help system. This means that when the user doesn't understand something, by simply pressing `F1` the required information is displayed. Placing that information in this paper as well would result in a redundant information presentation which is undesirable. However there is something that is not contained in the system as it is hard to provide a place for it unless we create a commercial product and incorporate a lot of external documentation in terms of short movies that explain how to use the system. What we are referring to is some means of how to use the system by example. The system is provided with information on every part of it, but it does not have some means of showing the user how to typically run an algorithm and visualize the results. This addition is provided in this paper. We describe four examples of visualizations done and algorithms run with the *EA Visualizer*. As we have two distinct ways to use the system, namely trough a single run and a multiple of runs, we provide an example for both cases. In section 2.5.1 we provide an example for a single run evolutionary algorithm as we inspect some recombination operator for the TSP and in section 2.5.2 we provide an example for a multiple runs evolutionary algorithm as we inspect some more interesting theoretical problem that sheds some light on the requirements for genetic algorithms. To illustrate the platform independence of the resulting system, the figures for the single run example were grabbed on a SUN computer running UNIX and the figures for the multiple runs example were grabbed on a PC running WINDOWS 95. The program running on the SUN computer was altered so that the background is white because the available JAVA implementation was not entirely errorfree in the sense that the menubar was given the same color as the background, making it black with black letters. Next to these two examples, we have included some less standard examples to give an impression of the diversity of the program. In the research section 3 an even greater diversity which incorporates deviating evolutionary algorithms is either described in detail or actually implemented. The examples in this section are compared to those more traditional. In section 2.5.3 we demonstrate the usage of crowding, preselection and deterministic crowding (in this case specifically for multimodal function optimization) in the *EA Visualizer* to show that such additions to classical GAs are easily incorporated in the system. The last example is given in section 2.5.4, in which a different evolutionary algorithm is installed, being the *Evolution Strategies*. Furthermore at the same time the use of an elitist mechanism is demonstrated so as to show that truely any combination required for an EA is possible in the system. The images for both these two additional examples were taken on a PC running WINDOWS 95.

Before describing the settings in the *EA Visualizer*, we wish to note at this point that the examples shown in the following subsections are not to prove anything or to achieve interesting results with respect to evolutionary algorithms. They are merely meant to demonstrate the usage and the capabilities of the resulting system. The program is used for interesting matters in section 3.

2.5.1 A first single run example: edge map recombination for the TSP

The standard package of the *EA Visualizer* contains a basic working set for the 2–dimensional geometric travelling salesman problem. This problem states that we are to find the shortest path between a given set of cities in the 2–dimensional plane in such a way that every city is visited exactly once and the city where we start is also the city where we end. The distances between the cities are the Eulerian distances. It follows that the resulting tour is a Hamilton cycle. The 2–dimensional geometric version of the TSP (Travelling Salesman Problem) was chosen because easy visualizations that are both interesting and fun to see can be created. In this section we see how to use the *EA Visualizer* to try to find an usefull approximation to the problem using evolutionary algorithms.

At the outset we choose to use one of the better recombination operators for the numbered list presentation of the solutions to the TSP[3]. This recombination operator is the *edge map* recombination strategy. This is one of the better "blind" operators that stem from the first generation of operators for the TSP. Blind operators do not utilize any domain specific information from the problem at all. Only the information from the parents is used to generated new tours. The edge map recombination operator has turned out to be one of the best of this kind. Mathias and Whitley [28] have shown that the edge crossover can even be improved further, which resulted in an edge–2 and an edge–3 crossover operator. The edge map recombinator uses a so called *edge map*. This edge map is a table in which each city is stored. Behind each city a list is placed which holds the cities that are neighbours to this city in the parent tours. These lists therefore all have a length no larger than four cities. The recombination process is then performed as follows:

1. Select first city from one of both parents to be the current city.
2. Remove the curent city from the edge map lists.
3. If the current city has any remaining edges, go to step 4, otherwise go to step 5.

[3]The only representation for TSP tours in the current standard package of the *EA Visualizer* is the numbered list.

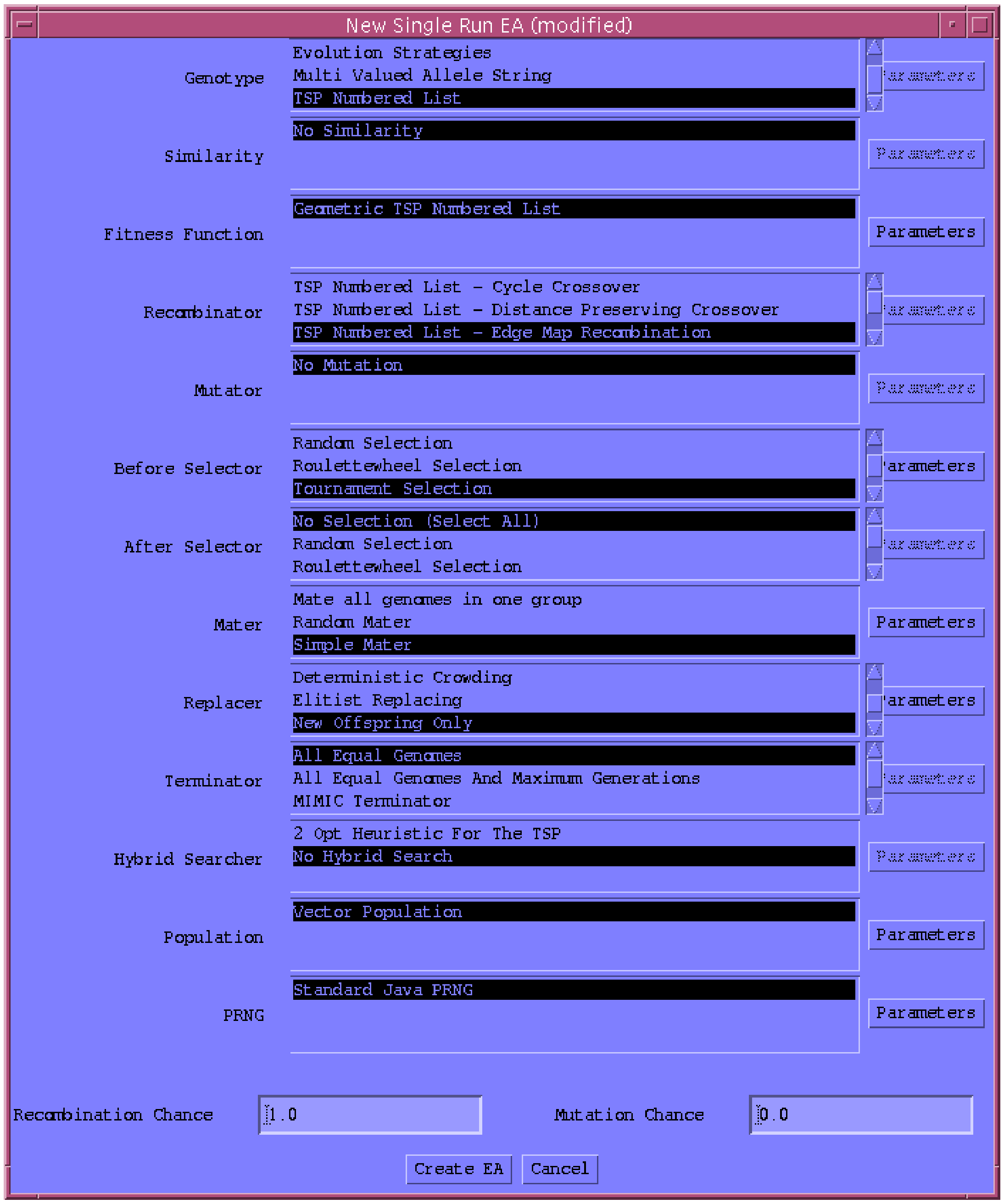
4. Choose the new current city from the edge map list of the current city as the one with with shortest edge map list
5. If there are any cities left, select the city with the shortest edge map list to be the current city and go to step 2.

It follows that the operator according to the above definition creates 1 offspring genome for every two parents. This means we have to select twice as many parents so as to get enough offspring back to replace the current population and retain the invariant with respect to the population size.

We are now ready to enter the settings of the evolutionary algorithm. By pressing `F4` in the main window or by selecting New Single Run EA from the EA menu, we open the settings window and enter the settings as is depicted in figure 10. At the top of the window we select to use the `TSP Numbered List` as the genotype. The similarity component is not interesting as we are not concerned with niching or any other means of similarity usage. We therefore select the only thing we are allowed to select: `No Similarity`. The fitness function is one of the most interesting parts of the settings. We select the `Geometric TSP Numbered List` and notice that the `Parameters` button on the right of it is enabled. By pressing that button we can specify the parameters for the component which in this case is ofcourse the locations of the cities. As this is an unusual type of parameter component, we show this situation in figure 11. At the top we can enter the coordinates of the cities. We can also directly enter the cities by clicking them in the white rectangular area. We specify some 50 cities in arbitrary configurations. By pressing `Apply` we select to go with the entered settings.

We continue to enter the settings for the evolutionary algorithm by selecting that we wish to use edge map recombination as the recombination operator and no mutation whatsoever as the mutation operator. The outset of the evolutionary algorithm determines how we should select our remaining components. We choose to select some classical configuration by installing a selector on beforehand and using only the offspring genomes as the genomes of the next generation. This leads to selecting tournament selection as the before selector. We enter to select 400 genomes from the population with a tournament size of 2. Note that the tournament selection strategy is found by scrolling down the list of available selectors. The after selector is set to no selection and the mater to the simple mater that is to create mating groups of size 2 so as to achieve the classical configuration as requested. Continuing on this note we select to have the `New Offspring Only` as the replacement strategy which is once again located in the lower part of the list. Furthermore we employ no hybrid searcher and select to use the standard population implementation, namely the `Vector Population`. We specify to have 200 genomes in the population which is correct with respect to the selection of 400 genomes by the before selector because the recombinator creates one offspring genome for every two parents implying that the 400 selected genomes are recombinated into 200 offspring. Finally we select to use the standard prng that is provided within any Java distribution. We finish entering the settings for the evolutionary algorithm by pressing the `Create EA` button, accepting the chance of 1 for recombination and 0 for mutation (of which the latter is not of interest anyway because we have a non contributing mutation operator).

Once the evolutionary algorithm has been created, we press the `F8` button or select `Add View` from the `Views` menu to add views in order to visualize information about the evolutionary algorithm. The window that appears resulting from this action is shown in figure 12. We select to add four views. First of all we wish to see directly some of the solutions. The most interesting solutions are the best and the worst genome. As we are approximating a 2–dimensional geometric TSP, we add two `Geometric TSP Tour` views that show the best and the worst tour in the population. Below these views we specify to have two statistics views to have some statistical feedback on the evolution process over a multiple of runs. These views are both `Fitness Statistics` views that display the fitness average of the population and the fitness variance. These numbers are displayed as a function of the generation counter. After adding all these views, we press the `Close` button in the `Add View` window and we are ready to run the evolutionary algorithm.



New Single Run EA (modified)

Genotype	Evolution Strategies Multi Valued Allele String **TSP Numbered List**	Parameters
Similarity	**No Similarity**	Parameters
Fitness Function	**Geometric TSP Numbered List**	Parameters
Recombinator	TSP Numbered List - Cycle Crossover TSP Numbered List - Distance Preserving Crossover **TSP Numbered List - Edge Map Recombination**	Parameters
Mutator	**No Mutation**	Parameters
Before Selector	Random Selection Roulettewheel Selection **Tournament Selection**	Parameters
After Selector	**No Selection (Select All)** Random Selection Roulettewheel Selection	Parameters
Mater	Mate all genomes in one group Random Mater **Simple Mater**	Parameters
Replacer	Deterministic Crowding Elitist Replacing **New Offspring Only**	Parameters
Terminator	**All Equal Genomes** All Equal Genomes And Maximum Generations MIMIC Terminator	Parameters
Hybrid Searcher	2 Opt Heuristic For The TSP **No Hybrid Search**	Parameters
Population	**Vector Population**	Parameters
PRNG	**Standard Java PRNG**	Parameters

Recombination Chance: 1.0
Mutation Chance: 0.0

Figure 10: Entering the settings for a single run.

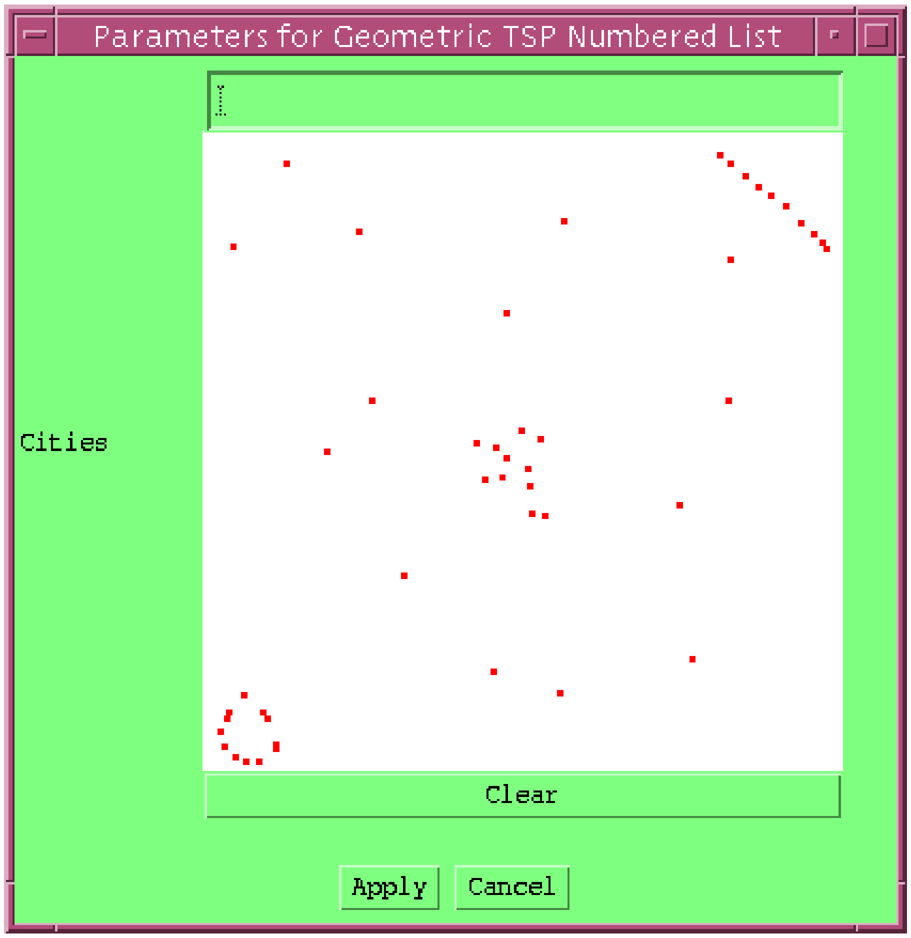


Figure 11: A special kind of `ParameterComponent`, entering parameters for the 2–dimensional geometric TSP.

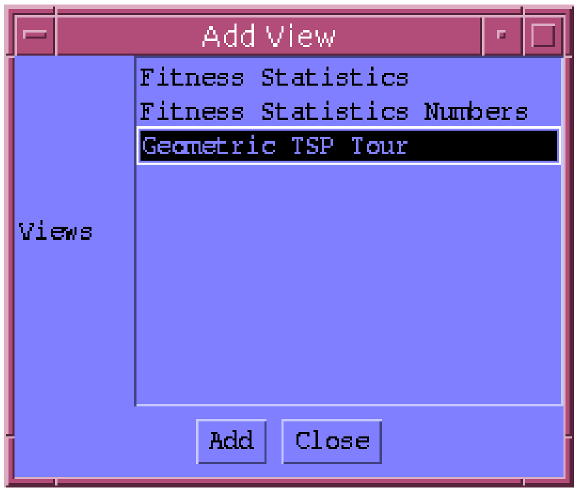


Figure 12: Adding views to visualize information.

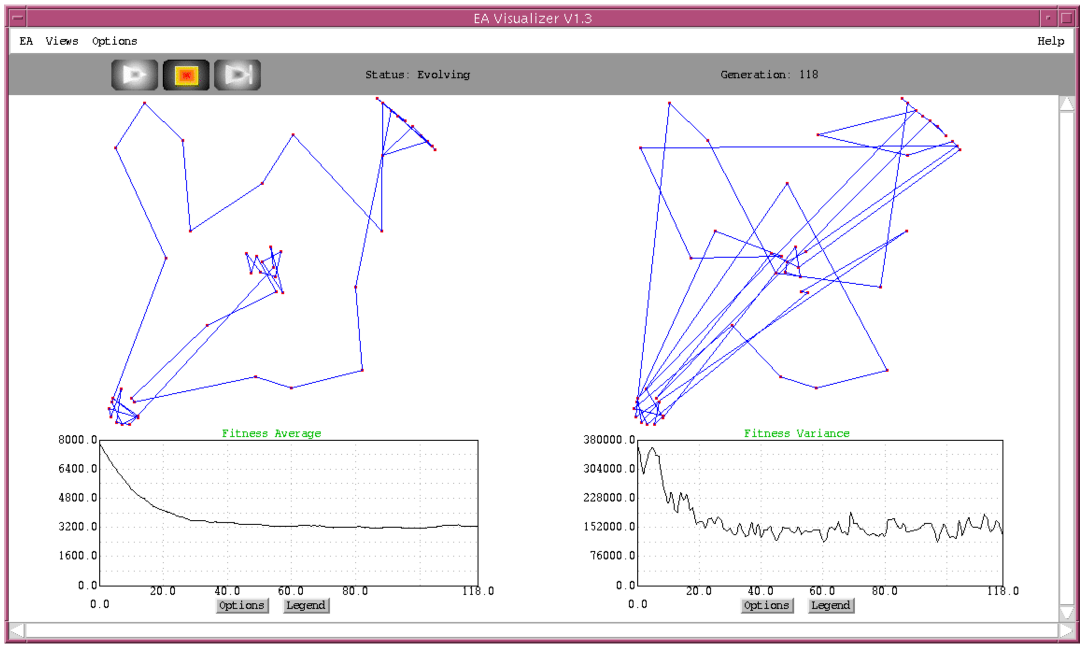


Figure 13: The evolutionary algorithm in progress.

Running or stopping the evolutionary algorithm is done by using the three buttons underneath the menubar in the main window of the system. The buttons have been chosen similar to those of a CD or cassette player and are therefore intuitively easy to use. The leftmost of the buttons is the “play” button and can be used to start or continue the algorithm. The button in the middle is the “stop” button and can be used to stop the algorithm at some point. Finally the rightmost button can be used to do *one* generational step and is called the “step” button. All buttons are grey when they are disabled. They turn to a yellow–red combination color when they are enabled. By pressing the “play” button, the evolutionary algorithm starts and we can observe the best and the worst tours that it contains each generation as well as the fitness statistics we chose to view. In figure 13 the situation is displayed after 118 generations while the system is running the algorithm.

After these 118 generations we observe that the fitness average of the population is not decreasing fast enough anymore to our satisfaction and the tours are far from something interesting yet. The variance is still rather large, but seen the fitness average this tells us only we have some rather bad and even worse tours. So after 119 generations we stop the algorithm by pressing the stop button and edit the settings of the current evolutionary algorithm by pressing `F5` or by selecting `Settings Current Single Run EA` from the `EA` menu. We select to use the 2–Opt hybrid searcher for the TSP and use the step button to do one step in the algorithm. The results are shown in figure 14. This demonstrates the influence the user can have directly on the evolutionary algorithm and the conclusions that can be drawn when applying some new strategy somewhere right in the middle of a run.

Because we have no interest in this section to investigate any properties of the evolutionary algorithm or the selected recombination operator specifically, we do not draw any conclusions about any results here. As we are demonstrating the system itself and we want to provide an example of typical usage, we would for instance at this point like to just let the original algorithm run until the termination condition is satisfied (all tours are identical). We establish this ofcourse by editing the settings of the current evolutionary algorithm and removing the hybrid searcher. Then by pressing the play button, we await termination. After 316 generations the algorithm terminates

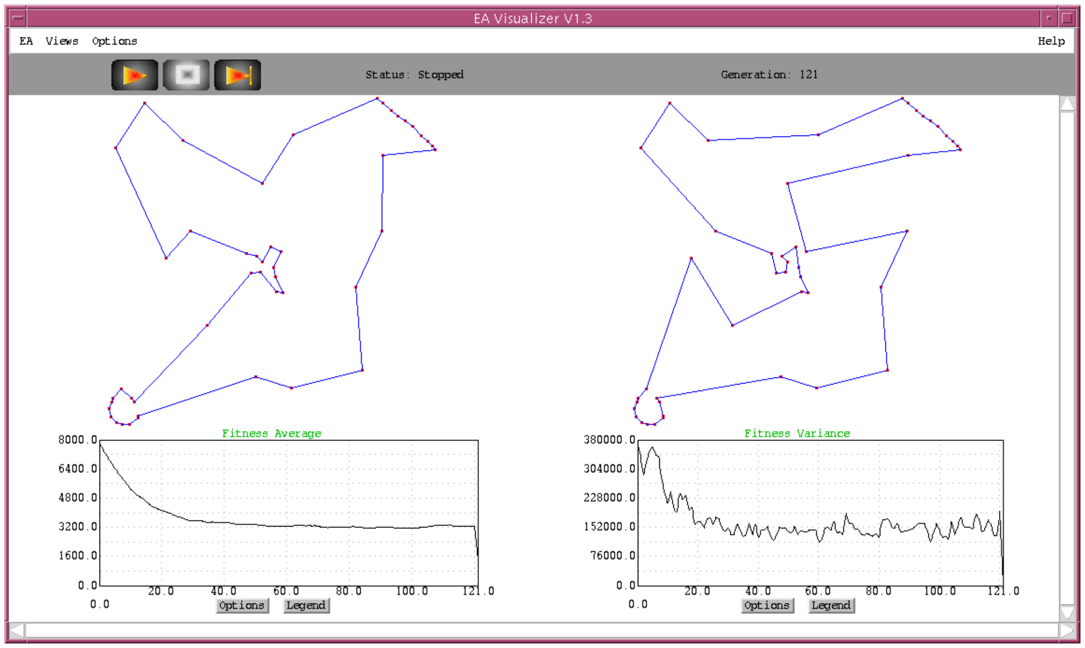


Figure 14: A single step of the evolutionary algorithm with a 2–Opt heuristic.

with a tour that is slightly better than the one first found when using the 2–Opt searcher that made the evolutionary algorithm hybrid. This situation is depicted in figure 15. Note how all the buttons are now disabled and the status is marked as `Terminated`.

Finally, we use the *EA Visualizer* to magnify the result by enlarging the view. This is done by selecting the view in the `Views` menu and altering its dimensions. Once again we note that we are not interested in drawing any conclusions about the results for any reason, but we do wish to finish this example by providing a nice view of the results. The tour that was finally found is depicted in figure 16 and is a rather acceptable result at first glance. This concludes our stereotypic example of using the system with a single run version. The number of options is far greater than demonstrated here and can be made as great as required by implementing some interesting usage of the interactivity offered by the *EA Visualizer*. We merely set out to provide some feeling for how to use the system and what all the modelling and implementation issue discussions have led to, which is exactly what we have established.

2.5.2 A first multiple runs example: population sizing

A more interesting example than the simple test run for some recombination strategy as given in section 2.5.1 is that of the testing of the population sizing theory. Evolutionary algorithms have quite a lot of parameters and the question ofcourse is what parameters are the best. One of the most prominent parameters is that of the population size. Clearly a population that is too small does not potentially hold enough information to solve a problem. G. Harik, E. Cantu-Paz, D.E. Goldberg and B.L. Miller [17] wrote a paper that concernes the problem of determining the required population size for a given optimization problem. They defined a function that predicts what size the population must be to converge with some probability to the optimum. We shall disregard that theory here but only use it in the *EA Visualizer* to test the soundness of that function. For starters we therefore need to do tests over a multiple of population sizes because we want to see the response for many population sizes (the empirical probability that the evolutionary algorithm converges to the optimum) within a specific range. Furthermore as we do not wish to

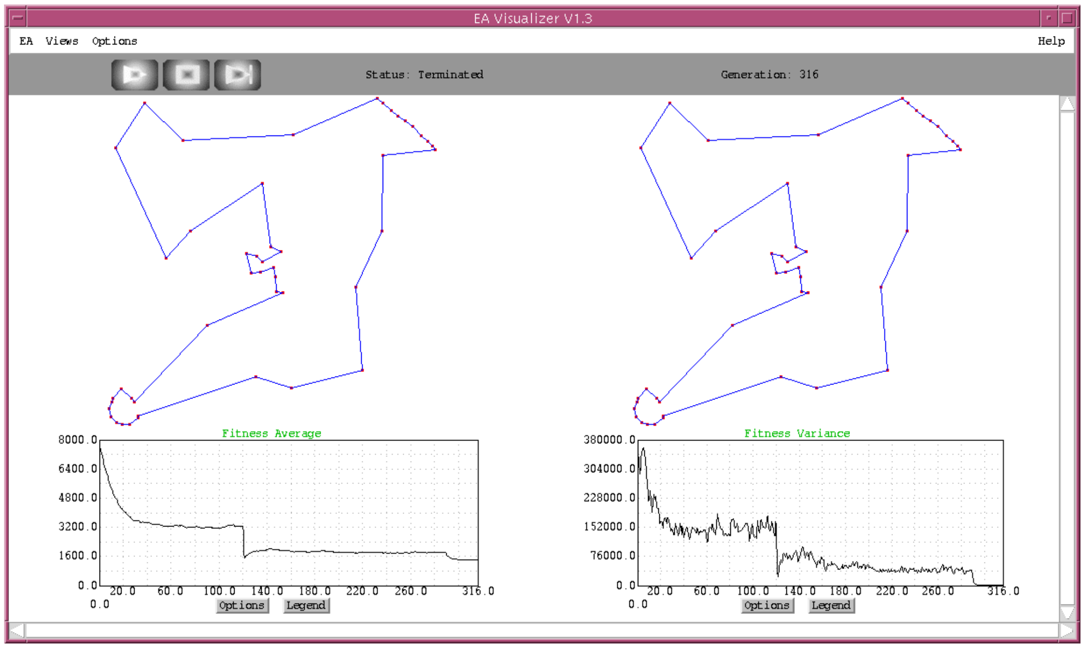


Figure 15: The resulting visualizations upon termination.

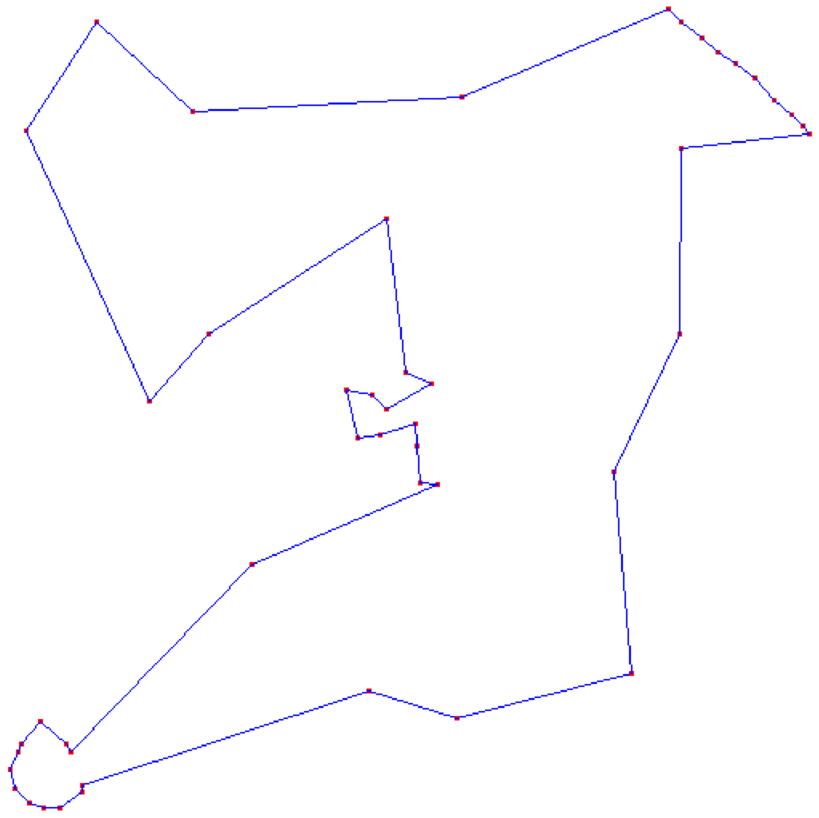
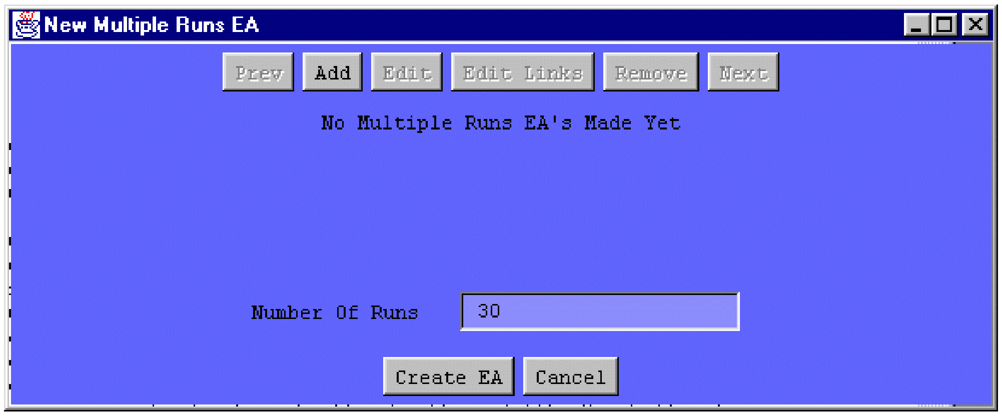


Figure 16: The resulting tour, displayed magnified by the system.



No Multiple Runs EA's Made Yet

Number Of Runs 30

Figure 17: Creating a new multiple runs evolutionary algorithm.

rely on a single run, we want to average the results over a multiple of runs. This implies we require a multiple runs evolutionary algorithm in terms of the *EA Visualizer*. Because this is the case, we can enhance the tests we are about to run and test different recombination strategies at the same time.

The optimization problem that is inspected is known as *trap functions*. This fitness function has parameters that allow it to be made an easy problem or a fully deceptive problem which tricks the evolutionary algorithm into a suboptimum. The problem is defined especially for genetic algorithms, which is the type of evolutionary algorithm we shall therefore inspect here. The fitness function is parameterized with parameters k, n and d. The parameter d is called the signal and is the difference between the optimum value 1 and the suboptimum value $1 - d$. The parameter n denotes the length of the problem and k denotes how many of these problems we have. Therefore it implies that the trap functions fitness function is applied a multiple of times on one binary string and all these applications are subproblems. Therefore the maximum fitness for a total string equals k. The fitness function for *one* subproblem is as follows ($o(x)$ denotes the amount of ones in string x):

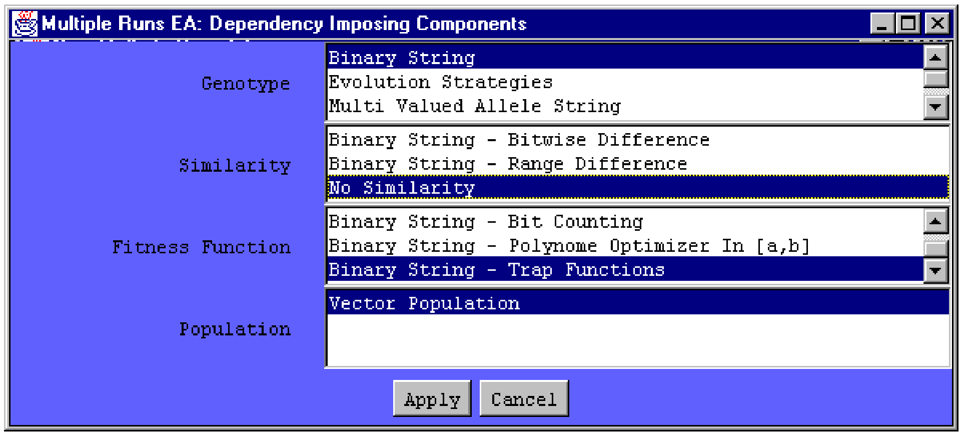
$$f(x) = \begin{cases} -\frac{1-d}{n-1}o(x) + 1 - d & \text{if } o(x) < n \\ 1 & \text{if } o(x) = n \end{cases}$$

Without inspecting this fitness function further because once again it is not our goal here to inspect interesting aspects or to achieve scientific results, we continue the example by showing how to use the *EA Visualizer* to do an interesting test run for the problem. By pressing `F2` or by selecting `New Multiple Runs EA` from the `EA` menu in the main window of the system, we select to work with a multiple runs evolutionary algorithm. The window that appears requests from us that we enter the amount of runs we wish to average over. We set this amount to 30. The buttons at the top of the window indicate that we can create a multiple of multiple runs evolutionary algorithms. This is conform the discussion of setting parameters for multiple runs evolutionary algorithms and handling dependency imposing components (section 2.3.2). We shall only require one of such multiple runs evolutionary algorithms because we will have only one combination of dependency imposing components. The image of the current user interface is shown in figure 17.

By pressing the `Add` button in the current user interface, a new interface appears that allows us to specify the dependency imposing components as can be seen in figure 18. We select to use `Binary String` as the genotype, `No Similarity` as the similarity (which doesn't matter for the same reasons as the single run example), the trap functions as the fitness function and the `Vector Population` as the population component. By pressing the `Apply` button we confirm these settings after which the user interface from figure 19 appears. At the top of the interface four buttons are located that allow us to enter the settings for the dependency imposing components. We enter for the genotype to have 40 bits. The fitness function parameters are set to a signal of 0.1, 8 subproblems and a length of 5 for each subproblem. The additional parameters that can be set for the trapfunctions that are scaling constants deal with the scaling of the fitness contribution of the blocks themselves. We are disregarding these options in this case and thus leave the scaling type to uniform at a scale factor of 1.0 which does not alter the fitness response of a single building block and thus gives us the fitness function as described. As presented in section 2.3.2, the parameter structure of the *EA Visualizer* creates the multiple values parameter structure itself. As an example in figure 20 the parameters for the trap functions are shown set. As the original parameter components for the problem are numerical parameter components, they specify that there exist multiple values versions of these components that are not self sufficient. These versions are used here as can be seen for they all have an `Increment` field in which we can specify with what stepsize we wish to step through some specified range. The non self sufficientness returns in the addition of the buttons on the right side of each parameter component that allows us to enter again a multiple of these perhaps multiple values (which is not needed in this case). We specify the population sizes to come from a range of 2 to 500 members with a stepsize of 4. Having specified the parameters for the dependency imposing components, we continue with the remaining components and enter the recombinators we wish to use. By pressing `Add` on the right side of a list, we can add a new instance to use. We select to use both one–point, two–point and uniform crossover, the latter of which is deemed truly uniform crossover by employing a crossover probability of 0.5. The mutator we set to be `No Mutation` as we do not wish to use mutation anyhow (it causes the algorithm not to terminate based on the equality condition). The before selector is chosen to be tournament selection. We must remark that the settings for the selection size must be specified to be the same as the population size, namely from 2 to 500 with a stepsize of 4. Furthermore we employ no after selection strategy, a simple mater that mates the parents in groups of two, the new offspring only replacer to use the offspring only for the next generation, no hybrid search and the standard JAVA prng. The termination condition is specified to be the point when all genomes in the population are identical. We finish the specification of the parameters by entering that the recombination chance is always 1 and the chance at mutation is always 0. The resulting contents of the user interface can be seen in figure 19. By pressing `Apply` we once again agree to go with the specified settings and we return to the first user interface that was displayed. This interface now displays the selected four dependency imposing components for the multiple runs evolutionary algorithm we are editing. We can select to add a new multiple runs evolutionary algorithm, to edit the current one or to remove it. Finally we can select to edit the links. As we are still to connect the population sizes to the selection sizes so as to let the evolutionary algorithms select x genomes from a population of x members and not y genomes from a population of x members for all combinations of y and x from the numbers between 2 and 500 with stepsize 4, we select to edit the links by pressing the `Edit Links` button.

The complex user interface that appears allows us to specify the links between the components and/or parameters that are not to be enumerated separately. From the instances list we therefore select `Vector Population (Population)` and then select from the parameters list `Population size`. We then press the `Add Link` button below that list and see that the rightmost list now contains that parameter. The arity of the link is specified to be 125, which is the amount of numbers in the range between 2 and 500 with a stepsize of 4 ($\lceil \frac{500-2}{4} \rceil$). All parameters and components that do not have the same arity disappear when adding to a link for the first time. The only parameter that remains is the `Selection Size` of the tournament selector. We add this one to the link as well and end up with the configuration of the user interface as displayed in figure 21. Pressing `Apply` once again confirms the settings and returns us to the first interface. We can now press the `Create EA` button to finally create the evolutionary algorithm that was requested.

As with the single run example, we have now reached the point where we are to decide what views to add to visualize the information about the evolutionary algorithm. Continuing to work analogously to the single run example, we wish to view some problem specific information along



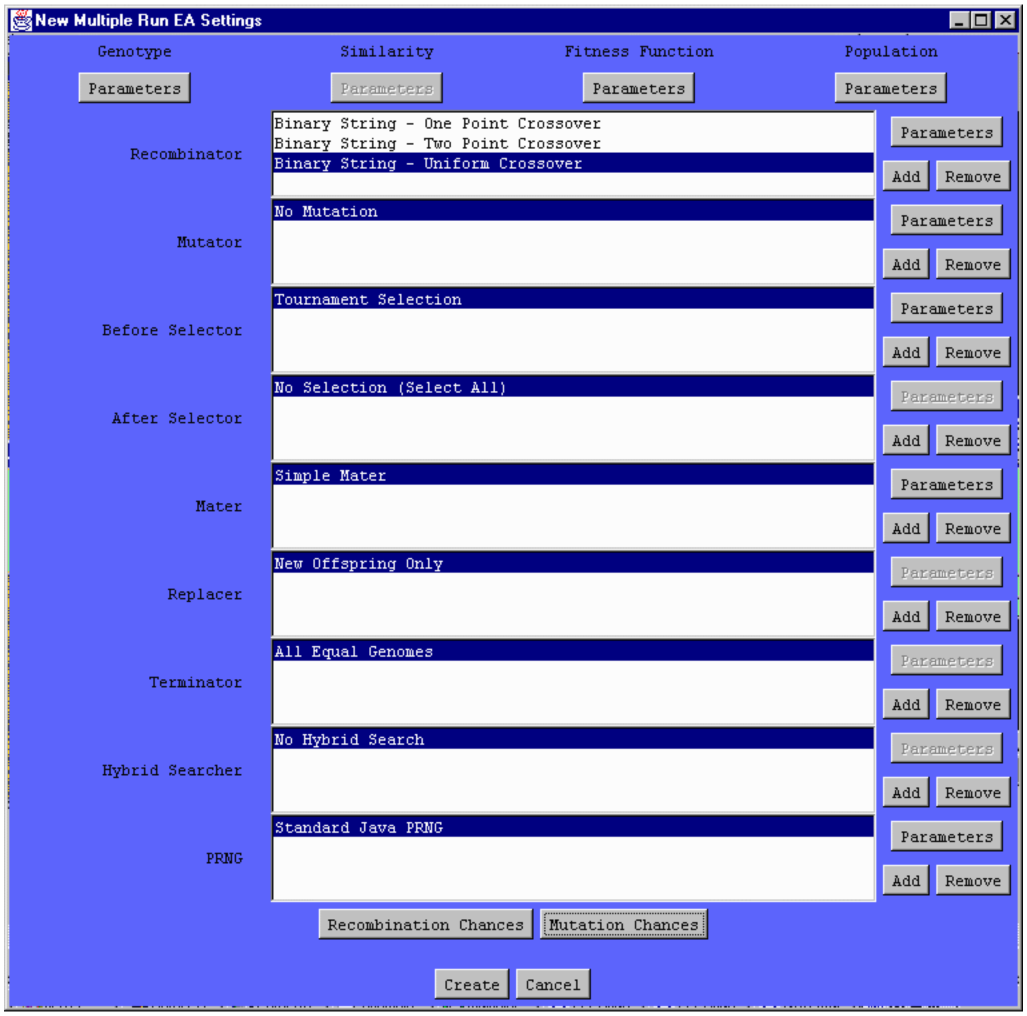
Genotype: Binary String | Evolution Strategies | Multi Valued Allele String (selected: Binary String)

Similarity: Binary String - Bitwise Difference | Binary String - Range Difference | No Similarity (selected: No Similarity)

Fitness Function: Binary String - Bit Counting | Binary String - Polynome Optimizer In [a,b] | Binary String - Trap Functions (selected: Binary String - Trap Functions)

Population: Vector Population

Figure 18: Selecting the dependency imposing components for multiple runs.



Recombinator: Binary String - One Point Crossover | Binary String - Two Point Crossover | Binary String - Uniform Crossover

Mutator: No Mutation

Before Selector: Tournament Selection

After Selector: No Selection (Select All)

Mater: Simple Mater

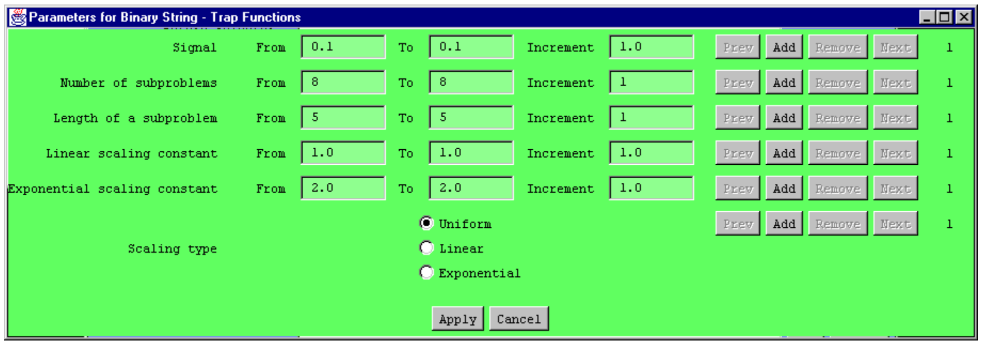
Replacer: New Offspring Only

Terminator: All Equal Genomes

Hybrid Searcher: No Hybrid Search

PRNG: Standard Java PRNG

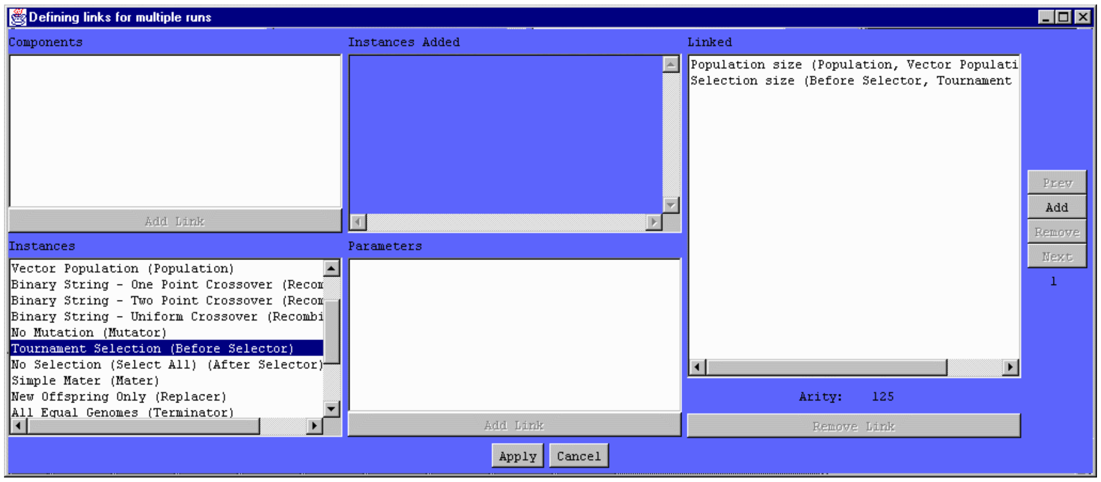
Figure 19: Entering the settings for one multiple runs evolutionary algorithm.



Signal	From	0.1	To	0.1	Increment	1.0	1
Number of subproblems	From	8	To	8	Increment	1	1
Length of a subproblem	From	5	To	5	Increment	1	1
Linear scaling constant	From	1.0	To	1.0	Increment	1.0	1
Exponential scaling constant	From	2.0	To	2.0	Increment	1.0	1

Scaling type: [✓ Uniform] Linear Exponential 1

Figure 20: Multiple values parameter components for the trap functions.



Instances

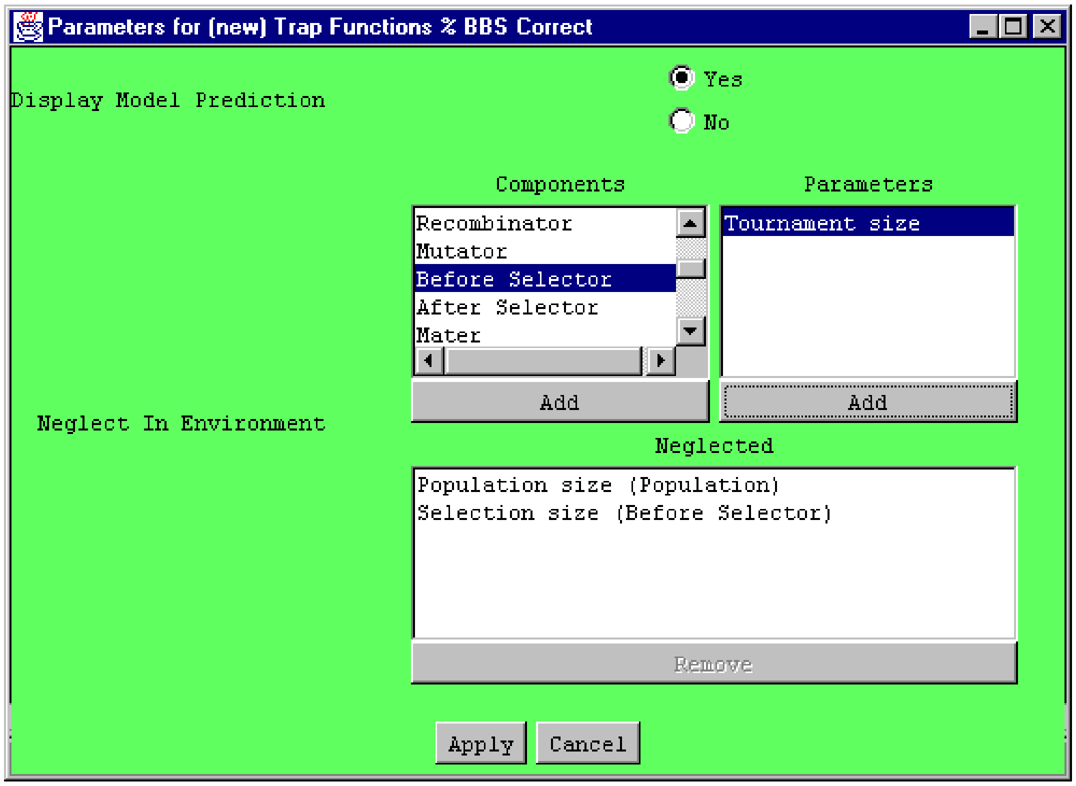
```
Vector Population (Population)
Binary String - One Point Crossover (Recom
Binary String - Two Point Crossover (Recom
Binary String - Uniform Crossover (Recombi
No Mutation (Mutator)
Tournament Selection (Before Selector)
No Selection (Select All) (After Selector)
Simple Mater (Mater)
New Offspring Only (Replacer)
All Equal Genomes (Terminator)
```

Linked

```
Population size (Population, Vector Populati
Selection size (Before Selector, Tournament
```

Arity: 125

Figure 21: Linking the instances and the parameters to avoid crossproduct enumerations.


Parameters for (new) Trap Functions % BBS Correct

Display Model Prediction [✓ Yes] No

Neglect In Environment

Components: Recombinator, Mutator, Before Selector, After Selector, Mater

Parameters: Tournament size

Neglected:

Population size (Population)
Selection size (Before Selector)

Figure 22: Entering the settings for a special multiple runs view for the trap functions.

with some statistical information. Starting with the problem specific information, a special view has been developed that can be used to visualize the results and compare them with the population sizing function from the paper that was specified earlier. This view is named `Trap Functions % BBS Correct`. When we add this view, we are prompted with the parameters for the view as always, but this time the parameters are quite complex. First of all we are to specify the size of the view, which is nothing new. At the bottom of the parameter interface however, we are to specify what to neglect in the environment. This is needed because we have a multiple runs evolutionary algorithm and the results are gathered over runs with different settings. By selecting what to neglect in some environment, we specify what runs belong to the same evolutionary algorithm. As such we specify to neglect both the population size of the population and the selection size of the tournament selector because we do not want an evolutionary algorithm with all the same settings except for the population size to be seen as a different evolutionary algorithm, especially because we are displaying the results as a function of the population size. The resulting settings can be seen in figure 22.

Second of all we thus wish to add some information about statistics as we did for the single run in which we inspected some evolutionary algorithm for the TSP. Such information can be added through a view called `Multiple Run Fitness Statistics`. We want to display the resulting numbers under the same cicumstances as with the specialized trap functions view, meaning we want to display them in a graph as a function of the population size and mapped by selecting what to neglect in the environment in the same way. The only thing that it is a little harder to select is the right combination of statistics as we are prompted to make a selection for the kind of `Statistic` we want to see and how we want to see it `Over All Runs`. We want to display the average over a multiple of runs as well as the variance for we are doing the visualization analogous to the single run example. Plotting the variance however is in this case rather superfluous as we do not let the algorithm terminate untill all genomes are the same. They will therefore all have the same fitness value, which will result in a variance value of 0 over the board. So the only variance value we would want to display that is meaningfull is the variance value over the fitness averages over the 30 runs per setting. We decide however to keep the amount of views for this example (it is still merely an example) low to avoid clutter in the example. As such we will select to display as the statistic type the `Fitness Average`. Over all runs we want to see this value `Averaged`.

Finally, because we are visualizing a multiple runs evolutionary algorithm that runs over a multiple of settings a multiple times, we want to know how far the system has come yet in doing all combinations when coming back to the computer at a certain time. This can be viewed by adding a `Progress Indicator` that is specifically defined for a multiple runs evolutionary algorithm. This indicator shows a bar that grows when more settings and combinations have been run. As such this progress indicator cannot be used to extrapolate linearly how much more time the system will require to finish the entire run because the settings may very well be such that the size of the problem instance will increase or decrease making the process slower or faster respectively. Once again we can press the "play" button when we have finished adding all the views. The system starts to enumerate all settings and combine the results in the views. As we have specified a very large number of combinations, the system will take some time before it completes the total computation. The reader can try out this example and see the results upon termination. In this example we present in figure 23 the system while it is still running after having computed a portion of all combinations. The names of the views allow the reader to deduce what is displayed where. We are once again not concerned with the implications of the (intermediate) results, but can see that uniform crossover (the dotted–dashed line) can only reach the deceptive attractors, certainly when the population size increases. When the population is small, the evolutionary algorithm might get lucky and find some good building blocks in most relatively fit strings. Furthermore, the solid line in the upper graph is the predictive function we discussed earlier. If it is to denote a good prediction for the population size, experimental results should show that the actual results must be above the solid line. The dotted line is one–point crossover and the dashed line is two–point crossover in the upper graph. In the lower graph, the solid line is one–point crossover, the dotted line is two–point crossover and the dashed line is uniform crossover. We can deduce that the theory seems to be rather sound for one–point crossover, but the two–point crossover operator is rather destructive after all as it seems to make the genetic algorithm perform worse and even below the predicted value.

2.5.3 Something less standard: crowding, preselection, deterministic crowding and sharing schemes

Crowding and preselection are two notions in the world of genetic algorithms that have been around for some time. Both are meant to preserve the diversity in the population. It has been shown however that in practice stochastic errors in the replacement of population members work to create a significant amount of genetic drift, causing unsuccesfulness at preserving population diversity as noted by Mahfoud [27]. At this point we are not going to take a closer look at reasons or experimental explanations to confirm these results in a scientifically justified way. What we will do however is briefly go over the crowding and the preselection scheme as well as the scheme that was introduced by Mahfoud [27] to overcome problems introduced by crowding and preselection. Subsequently we shall look at the most popular way in GA history to achieve multimodal function optimization, which is *sharing*.

Crowding
The crowding strategy makes use of a crowding factor CF which is the number of genomes from the current population that are grouped together. This group is randomly chosen from the entire population. The genome from the next population to add then finds from this group the most similar genome and replaces that one in the population. The implementation in the *EA Visualizer* disregards the newly added genomes in the subsequent replacement of all the new genomes of

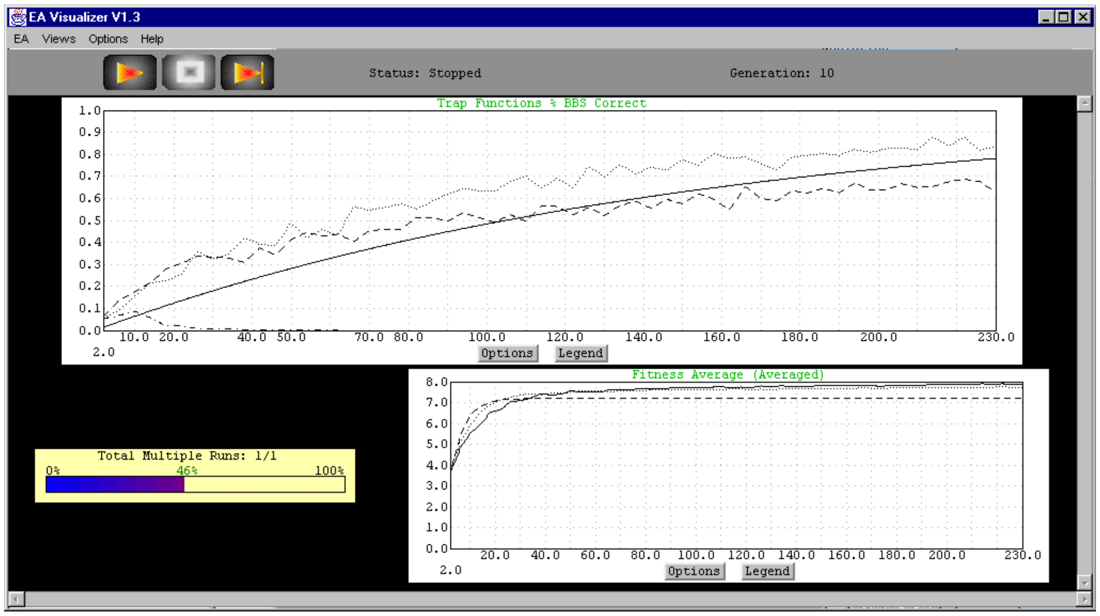


Figure 23: The multiple runs being run by the *EA Visualizer*.

the new generation. In order to find the most similar genome, the *Similarity* component is used. The true crowding strategy also employs a *generation* gap G which is a percentage that specifies the portion of the population that is to be selected and subsequently replaced in the population through the crowding factor replacement.

Preselection
The preselection replacement strategy works directly on the offspring and the parents that created the offspring through recombination. To place an offspring into the population, the worst parent is found. If the offspring is better than that parent, it replaces that parent.

Deterministic Crowding
The deterministic crowding replacement strategy was presented as an improvement over *crowding* and *preselection*. For each offspring, the nearest parent according to some distance measure is found and if it's better, it replaces that parent in the population. In order to find the most similar genome, the *Similarity* component is used.

According to Mahfoud [27], his deterministic crowding mechanism would be an improvement over normal crowding and preselection and he experimentally verified this through showing results using the three strategies on multimodal function optimization. This form of optimization concerns the finding of more peaks than just the optimal one. Peaks that stand out in general are required to be found. The most extreme type of example in this field is maximizing the $sin(x)$ function with $x \in [0, 8\pi]$ for instance. The maximum value is found for $x = \pi(2k + \frac{1}{2})$ with $k \in \{0, 1, 2, 3\}$ and so there isn't a single solution for x. An example of multimodal function optimization for functions that do not have maxima all at the same value is the maximization of the polynome $\frac{4}{1000}x^9 + \frac{5}{1000}x^7 - \frac{4}{5}x^5 + 5x^3 - 8x$ with $x \in [-2.9, 2.9]$. This function is depicted in figure 24. The maximum value for the polynome is obtained for $x \approx -0.80145$ and equals approximately 4.1. In the light of multimodal function optimization however it is not the goal to find only this optimum, but also the other peaks which are local optima in terms of optimization. As crowding, preselection and deterministic crowding are said to allow for preservation of population diversity, this should result in the finding of all peaks. We shall now turn to installing the three different algorithms in the *EA Visualizer* and running them to observe the results.

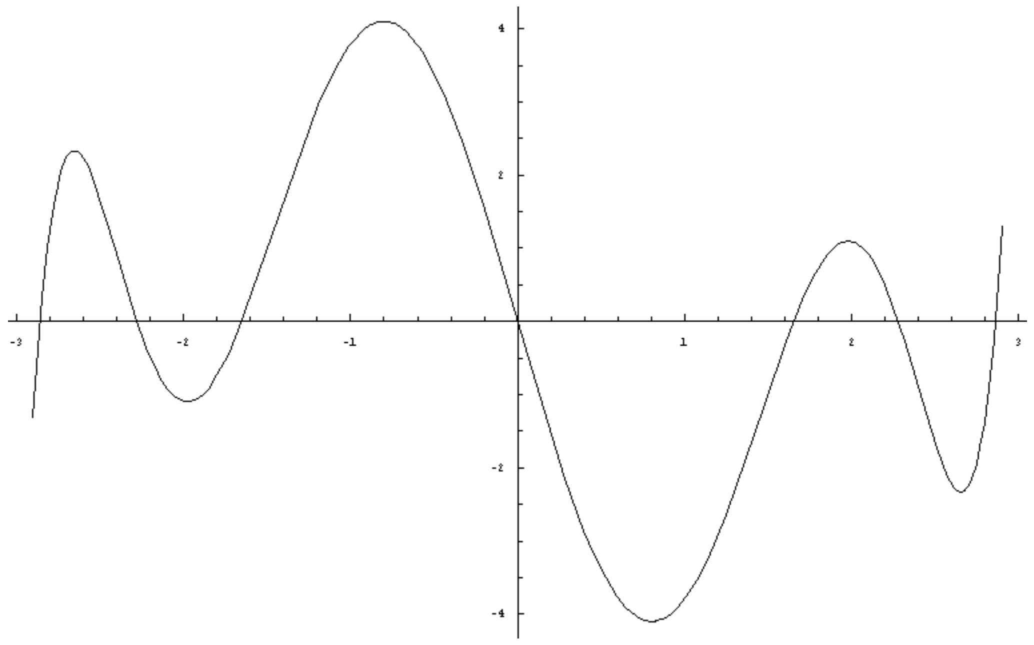


Figure 24: The polynome $\frac{4}{1000}x^9 + \frac{5}{1000}x^7 - \frac{4}{5}x^5 + 5x^3 - 8x$ with $x \in [-2.9, 2.9]$.

We start out with the crowding scheme. From the menubar in the *EA Visualizer* we select to create a new single run EA. As we are to tackle the problem using genetic algorithms, we select to use the `Binary String` as the *Genotype* and set the string length to 25 bits. The *Similarity* component is of great importance now as it defines during the run to what extent two binary strings are similar. We start out with the simplest of similarity measures, being the `Bitwise Difference`. This difference measure is equal to the amount of bits that are matched, scaled to $[0, 1]$. In other words, the *Hamming* distance is expressed through this *Similarity* component. The fitness function is ofcourse set to be the polynome optimizer with its parameters set according to the specifications above. The *Recombinator* is set to be the classical one–point crossover with two offspring. As we do not wish to have mutation in the algorithm, we specify to use `No Mutation` as the *Mutator*. The effect of this is the same as selecting any other mutator and keeping the mutation chance at 0. The *Before Selector* is taken to be tournament selection with a selection size of 100 and a tournament size of 2. The *After Selector* is not to be used so we set this to be verb—No Selection (Select All)—. The *Mater* is to mate the selected genomes in groups of two so that they can be sent in exactly these groups of two to the *Recombinator*. Therefore we install the `Simple Mater` as the *Mater* and set the grouping size to 2. The simple mater does nothing more than go over the population from top to bottom and mate the genomes in groups of the specified size. As such this approach is the fastest. Only slightly slower (negligable speed reduction) is the random mater that goes of the population in a random order until all genomes have been mated. We can however suffice with the simple mater because the tournament selection mechanism shuffles the population to go into a new tournament round. This indeed means that when no selection is used as the *Before Selector*, the random mater must be used so as to make sure that there no restrictions are introduced in what genomes can be mated. This is all explained in the help system as well which can be reached by pressing `F1` on the keyboard at any time. Continuing on the settings, the *Replacer* is set to be the `Crowding` replacer with a crowding factor of three[4]. If the crowding mechanism indeed succeeds in maintaining the population diversity, it is no use to select to have a *Terminator* that terminates when all genomes are equal because that will then never happen, so we select to have the `Maximum Generations` instance for the *Terminator* component with 100

[4]Note that in the classical sense of crowding, we have a generation gap of 100%.

as the maximum of generations. We employ no hybrid searcher and set the population to be the simple and standard `Vector Population` with a population size of 100 genomes. The prng is set to be the standard JAVA prng with a seed of 902480582260, which is the time in milliseconds at which the parameter component in which the seed can be specified was made. It doesn't matter what number it says here. The recombination chance is set to be 1.0 and the mutation chance to be 0.0. When we presented the single run example in section 2.5.1, we already showed the interface in which to enter the settings (the interface coded in the `EASettingsInterface` class) in figure 10. The following table with the instances to select for the components and the parameters to set for these instances should therefore suffice for the reader to try out the example him or herself.

Component	**Instance**	**Parameters**
Genotype	Binary String	String length 25
Similarity	Binary String – Bitwise Difference	—
Fitness Function	Binary String – Polynome Optimizer in $[a, b]$	Function `0.004x^9 + 0.005x^7 - 0.8x^5 + 5x^3 - 8x` Lower limit (a) -2.9 Upper limit (b) 2.9 Optimization Maximize
Recombinator	Binary String – One Point Crossover	Offspring Arity 2
Mutator	No Mutation	—
Before Selector	Tournament Selection	Selection size 100 Tournament size 2
After Selector	No Selection (Select All)	—
Mater	Simple Mater	Grouping size 2
Replacer	Crowding	Crowding Factor 3
Terminator	Maximum Generations	Maximum generations 100
Hybrid Searcher	No Hybrid Search	—
Population	Vector Population	Population size 100
PRNG	Standard Java PRNG	Seed 902480582260

After the `Apply` button has been pressed, we are ready to add views to the system to observe the events as they evolve. By pressing `F8` we are presented with the views we can add. In the light of what we set out to achieve, namely multimodal function optimization, it is no use to trace the best and worst genome or the fitness average. It is more interesting to inspect things like cluster analysis and replacement errors. These have not (yet) been implemented in the *EA Visualizer* however, but if the reader finds it interesting, it is a good excercise to implement exactly this in a view. For now, we select to add the `Locations On Polynome` view to actually see in a phenotypic sense where the genomes are going over the generations. The maximum value for the graph is set to 5 and the minimum to -5. The result is a graph in which a blue line is the polynome and the red crosses are the locations of the genomes [5]. Furthermore to view what happens with the genetic material in the population, we add a `Binary String Population Dots` view that will show every bit in every genome in the population from top to bottom. As we have a string length of 25 and 100 genomes in the population, the width/height ratio should be $\frac{1}{4}$ to have every bit to be a square instead of a non–square rectangle. We therefore set the width of the view to be 100 pixels and the height to be 400 pixels. The result is a view in which every red dot is a `1` symbol in the population and every blue dot a `0` symbol. The genomes themselves are the rows in the block. At this point we are ready to start the algorithm to see what happens and so we "press play" in the menubar. After only a few generations, we indeed see that the population does not directly converge to the maximum value and that the suboptima are also kept populated

[5]Note that the polynome is completely point symmetric in $(0, 0)$.

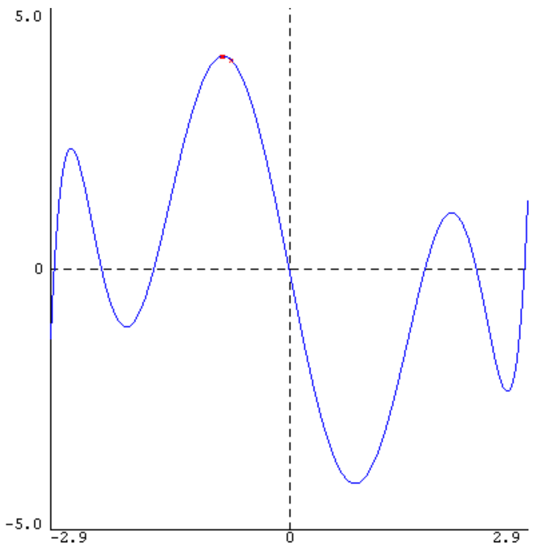


Figure 25: Polynome locations after 100 generations using crowding and genotypic similarity.

by genomes. However this is only shortlived and after some time only the largest peak is still populated, however not all genomes are at the same position as crowding still keeps them apart. The population dots view shows us indeed that in some sense the diversity is keept as the least significant bits (the rightmost) are still quite random. This poses exactly the problem with the approach because the observed diversity in in genotypic space, while we wish to keep the diversity in phenotypic space ofcourse. The resulting polynome and the locations of the genomes on it is depicted in figure 25 and the resulting population contents are shown in figure 26.

Even though we have at this point deduced that it will be much better to have a similarity measure in phenotypic space, as this is only an example we will hold that thought for the moment and first now try preselection with the same similarity measure. To do this, we press `F5` or select `Settings Current Single Run EA` from the `EA` menu. We alter the *Replacer* to be `Preseletion` instead of `Crowding` and note how the `Parameters` button is immediately disabled because there are no parameters to be set for preselection. It is at this point that we must realise that the preselection operator in the *EA Visualizer* only accepts a single offspring genome to set back amongst its parents. As such we need to alter the parameters of the one–point crossover operator installed and set the amount of offspring it generates to one. After installing the new *Replacer* and altering the parameters for the *Recombinator*, we press the `Apply` button and note in the `System Messages` window how the system reports that a new *Replacer* has been installed and that the views have been checked to still be valid for the altered contents of the evolutionary algorithm. The EA remains however in the `Terminated` state and we must first reset the algorithm before we can continue. At this point we point out that there are two ways of resetting the algorithm, namely through `F6` and `F7` which represent the resetting of the entire algorithm and only the population respectively. Resetting the entire algorithm means that the system notifies each instance that is currently installed that it has to reset itself. This must be used when instances are installed that have some sort of memory which must be reset when a new independent run is to be started. In our case it sufficies to only reset the population which is done by pressing `F7`. Note how the generation counter is also reset when we do so. This is done because in the `Options` menu the `Resetting Population` option is set to also reset the generation counter upon resetting of the population through the pressing of `F7`. We now have a completely reset EA but now with preselection instead of crowding and we once again start the algorithm by clicking the play button. The results are shown in figures 27 and 28. The results are even worse than for crowding because the population has converged almost to a single point. Indeed if the other peaks could be populated

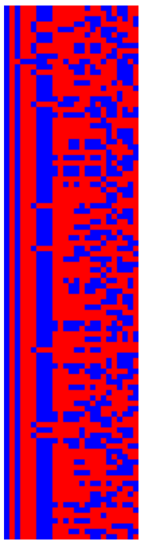


Figure 26: Population contents after 100 generations using crowding and genotypic similarity.

as well in a similar fashion, the preselection operator would work better here because the genomes converge more to a single point in that optimum whereas crowding kept more diversity. Note that the remark that preselection works better is ofcourse restricted to this problem. Also, during the run with preselection, the diversity witnessed again was in the genotypic sense, providing us with yet more assurance that a phenotypic distance measure is essential in this type of problem. On a practical note, we mention at this point that the views here presented are directly captured from the *EA Visualizer*. This has been done by using the copy and paste methods of WINDOWS 95. On the SUN machine used in section 2.5.1 this was done using the program `xv`.

Concluding the triple of crowding, preselection and deterministic crowding approaches, we wish to test deterministic crowding. In order to do this, we select to edit the settings for the current single run EA and set the *Replacer* to be the `Deterministic Crowding` replacer. As this operator can handle again two offspring, we set the offpring arity for the one–point crossover operator back to two. After pressing the `Apply` button and resetting the population, we are ready to press again the play button to start the algorithm. Behaviour similar to that of preselection is observed and rather quick convergence to the highest peak takes place. The deterministic crowding replacer shows again results that point out that the genotypic matching is all wrong for problems such as these. We shall not go into details further at this point since this is only an example. The results upon termination after 100 generations are depicted in figures 29 and 30.

Even though at this point we have clearly demonstrated how easy it is to incorporate mechanisms such as crowding, preselection and deterministic crowding, the feeling is rather unsatisfactory as the results with respect to the problem of multimodal function optimization are very poor. We noted before however that a phenotypic similarity measure is required for this problem and so in figure 31 we present all the results for the three mechanisms anew, but now using the `Binary String - Range Difference` similarity measure that uses the locations of the genomes with respect to the x range to use as similarity measure, meaning that two genomes are said to be more equal when their x coordinates are closer together. Indeed the results are much better now as can be seen in figure 31.

To illustrate further how less standard items are easily incorporated in the *EA Visualizer*, we will shortly describe and operationally introduce the most popular approach to multimodal function optimization in genetic algorithms, which is called *sharing*, and should be able to achieve better results than seen so far. The sharing scheme that we will test is an extended sharing scheme

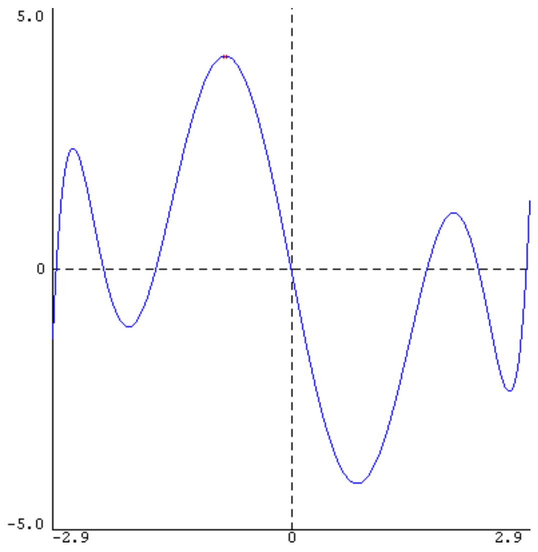


Figure 27: Polynome locations after 100 generations using preselection and genotypic similarity.

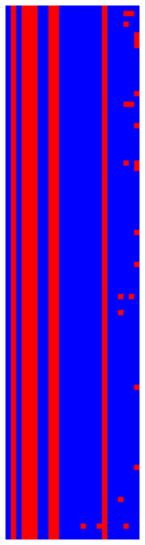


Figure 28: Population contents after 100 generations using preselection and genotypic similarity.

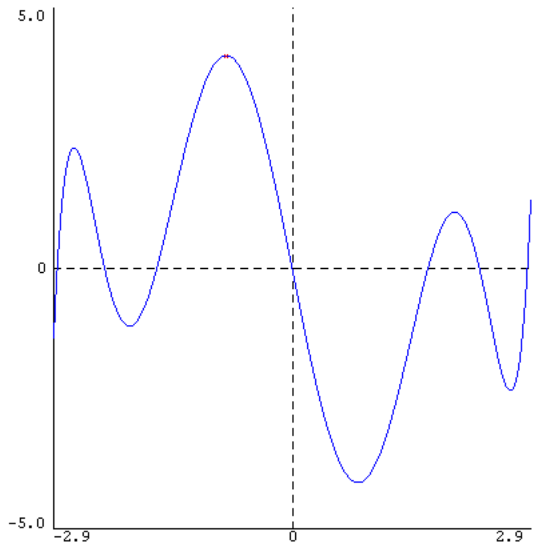


Figure 29: Polynome locations after 100 generations using deterministic crowding and genotypic similarity.

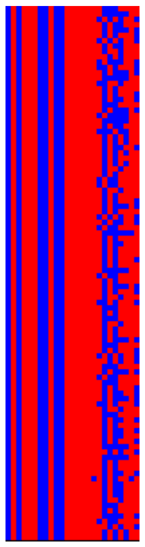


Figure 30: Population contents after 100 generations using deterministic crowding and genotypic similarity.

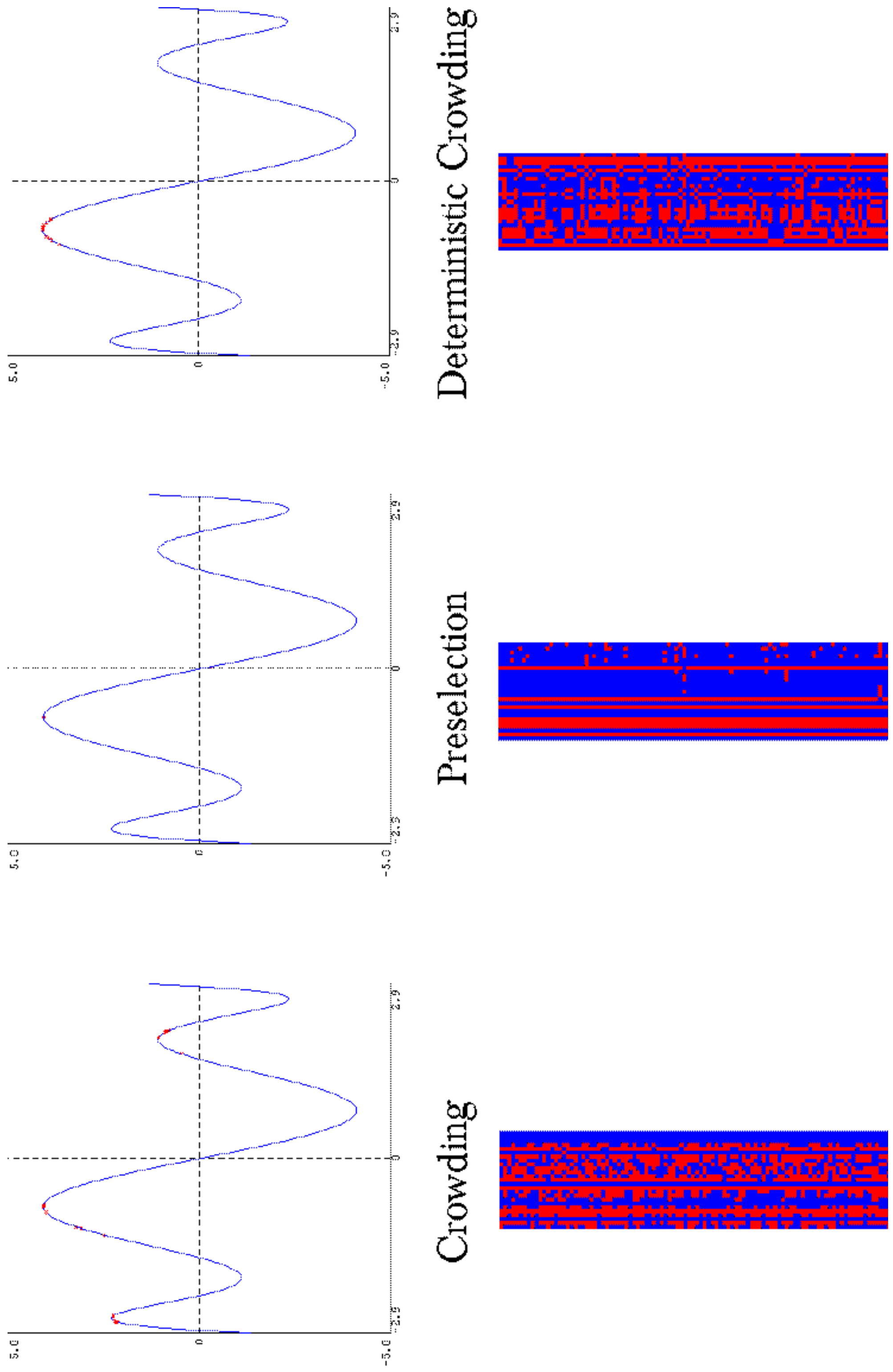


Figure 31: Results after 100 generations for all replacers using phenotypic similarity.

that uses cluster analysis methods especially for multimodal function optimization. The general idea is to divide the population in clusters that are adaptively formed and to degrade the fitness of the members in a cluster by an amount that is dependent on the amount of genomes in the cluster. This way the overpopulated clusters will have lower fitness values for their members and subsequently we will more likely get a good spread over the suboptima as well as their fitness is relatively better as the amount of individuals in a cluster at that point are less in number. To implement this, we need a new kind of expansion for the *EA Visualizer*. We need to create a new *Population* that acts as an environment with information on the whereabouts of the genomes. The result is the `Sharing Clustered Population` which we shall introduce next.

The `Sharing Clustered Population` is an implementation based on a sharing scheme as proposed by X. Yin and N. Germay [30]. The additional information that this population holds over the standard population (the `Vector Population` in the *EA Visualizer*), is the clusters over which the population is divided. Each genome is assigned to a cluster. To find these clusters, a distance measure is needed, which is established through the usage of the *Similarity* component. The clusters are determined with the *Adaptive MacQueen's KMEAN Algorithm*. The implementation of the clustering algorithm together with the sharing scheme is as follows (taken from the article by Yin and Germay [30]):

> After the reproduction and the crossover processes in each generation, the clustering algorithm is applied to cluster all the individuals in the population into different niches. The number of individuals in each niche are determined. Then, for individual i, its potential fitness f_i is divided by the approximated number of individuals in the niche to which it belongs m'_i:
>
> $$f'_i = \frac{f_i}{m'_i}$$
>
> with $m'_i = n_c - n_c * (d_{ic}/2 * d_{\max})^{\alpha}$ for each x_i in cluster c.

In the above n_c is the amount of genomes in the cluster, d_{ic} the distance between individual i and its niche's centroid, $d_{\max}$ is the maximum distance between clusters (parameter for the Adaptive MacQueen's KMEAN Algorithm), and α is a constant. The KMEAN algorithm is an algorithm that finds clusters amongst data entries based upon a distance measure between those data entries. In our case the data entries are the genomes in the population and the distance measure is the *Similarity* component. We set out to test the clustering sharing method on the same problem using as many similar settings as possible. We initiate the example using the same views as before and the following settings for the single run EA (the settings for the population were taken from the paper by Yin and Germay [30], except for the maximal centroid distance, which was increased specifically for this problem):

Component	**Instance**	**Parameters**
Genotype	Binary String	String length 25
Similarity	Binary String – Bitwise Difference	—
Fitness Function	Binary String – Polynome Optimizer in $[a, b]$	Function `0.004x^9 + 0.005x^7 - 0.8x^5 + 5x^3 - 8x` Lower limit (a) -2.9 Upper limit (b) 2.9 Optimization Maximize
Recombinator	Binary String – One Point Crossover	Offspring Arity 2
Mutator	No Mutation	—
Before Selector	Tournament Selection	Selection size 100 Tournament size 2
After Selector	No Selection (Select All)	—
Mater	Simple Mater	Grouping size 2
Replacer	New Offspring Only	Report popsize warnings Yes
Terminator	Maximum Generations	Maximum generations 100
Hybrid Searcher	No Hybrid Search	—
Population	Sharing Using Adaptive Clustering	Population size 100 Initial Number Of Clusters 10 Minimal Centroid Distance 0.05 Maximal Centroid Distance 0.5 Alpha 1
PRNG	Standard Java PRNG	Seed 902480582260

Note that we have again started out using a genotypic similiarity measure. We have seen above in the examples for crowding, preselection and deterministic crowding that such a similarity measure leads to unsatisfactory results as the similarity measure does not allow for clusters to form in a space that we want the clusters to form, namely the phenotypic space which for this problem is the range of the x axis. Now using this explicit clustering mechanism it is even more obvious that a phenotypic similarity measure is required, because that is the only logical space to base the cluster creation on. The results of both the genotypic and the phenotypic similarity measure are depicted in figure 32 and from the results for the genotypic similarity only it is already obvious that the search for clusters is more powerful in the sharing scheme as can be observed from both the resulting population contents as well as the locations on the polynome.

Finally, the article by Yin and Germay closes with the introduction of a mating restriction. This mating restriction implies that only genomes that come from the same cluster are allowed to be mated together and thus to produce offspring. This encourages the forming of tight clusters even further. Unfortunately however, as can be seen from the results in figure 33, the restriction is just a little too tight for the settings that we entered and the amount of clusters is reduced to exactly one, being far from the desired result. To remedy the too fast selection, we can introduce a mild random mutation. Doing this in itself shows the diversity and ease in use of the *EA Visualizer* because after the 100 generations that resulted in the undesired effect, we simply select the `Binary String Random Mutation` as the mutator and set the mutation chance to 0.01. Furthermore we alter the termination condition to have a maximum of 1000 generations just to be able to continue evolving with the current result. After these changes, we start the algorithm again and witness that after another 100 generations, the diversity is already a lot greater, even with the slight mutation rate. These results are shown in figure 33.

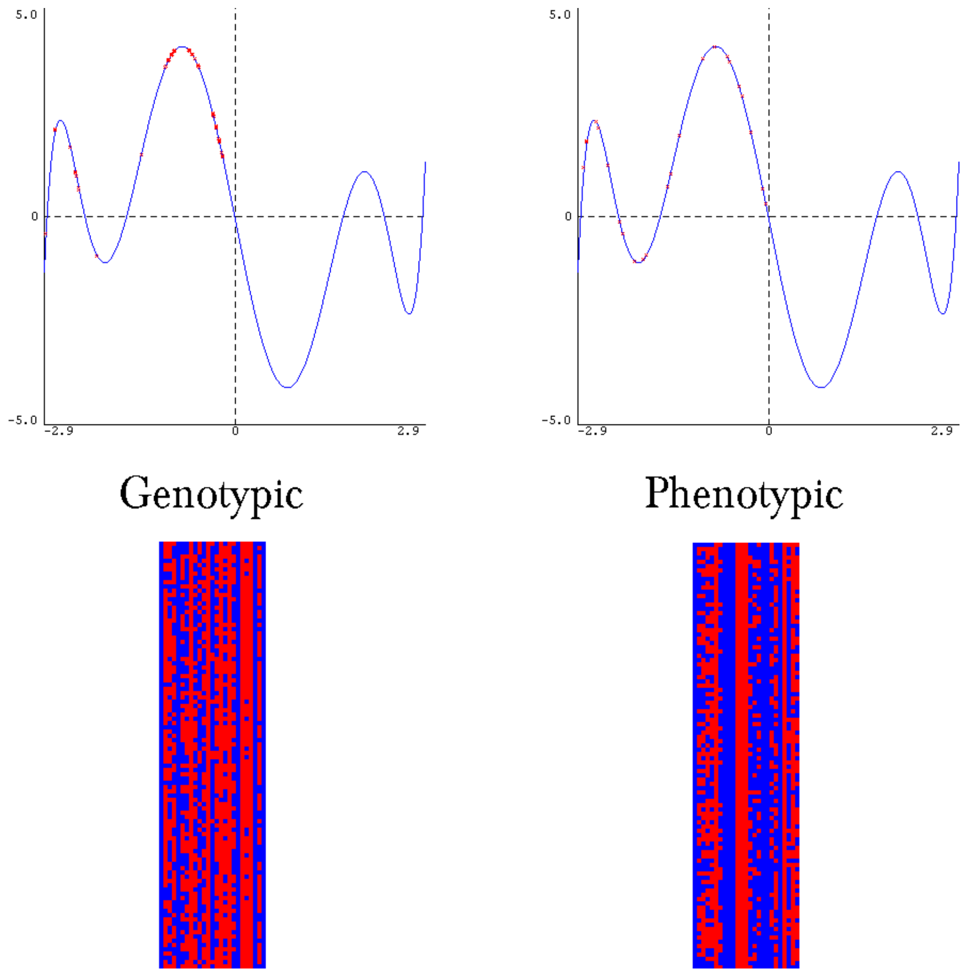


Figure 32: Results after 100 generations for the clustering sharing scheme using genotypic and phenotypic similarity.

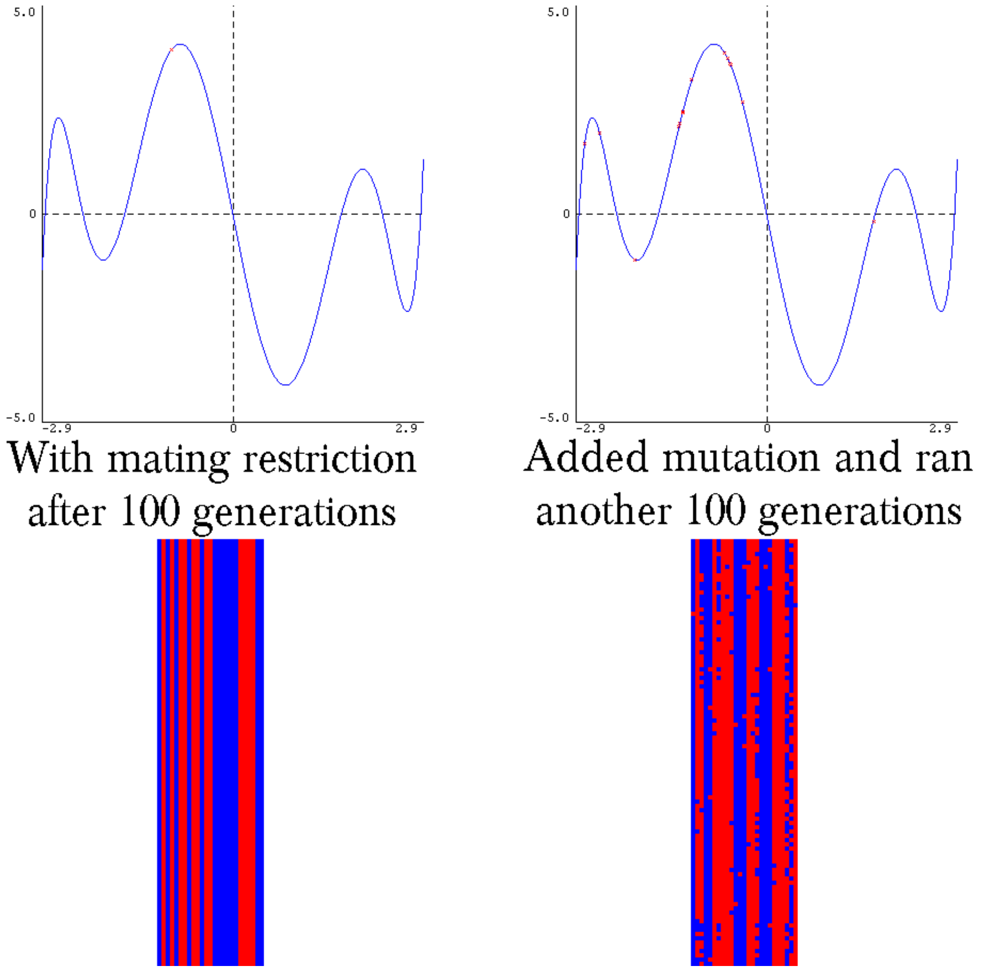


Figure 33: Results after adding a mating restriction and subsequently mutation.

2.5.4 A final and composite example: evolution strategies and elitist recombination/replacing

To once again show the diversity of the resulting system that is the *EA Visualizer*, we briefly go over an example that goes over the evolutionary algorithm known to be well suitable for real function optimization, being *Evolution Strategies*. The evolution strategies are reviewed in an article by Bäck [2]. The main difference with the genetic algorithm is the representation which in the case of evolution strategies (ES) a vector $(x_1, \ldots, x_n, \sigma_1, \ldots, \sigma_n)$, consisting of n object variables and their corresponding n standard deviations for individual mutations. The mentioned standard deviations for individual mutations are commonly referred to as the *meta*–parameters. The coding of the problem is done through the x_i parameters. Mutation is done as follows:

$$x_i' = x_i + z_i$$

The x_i parameters are thus adapted through the addition of a variable z_i. The z_i variables are normally distributed with $z_i \sim N(0, {\sigma'}^2)$. The meta–parameters themselves are mutated as well:

$$\sigma_i' = \sigma_i \cdot e^{s'} \cdot e^{s_i}$$

In this expression, s' is chosen once for every individual and is normally distributed with $s' \sim N(0, {\tau'}^2)$. Furthermore, the s_i variables are chosen for every x_i in every individual anew and are normally distributed with $s_i \sim N(0, {\tau_i'}^2)$. The values for τ' and τ_i have been suggested based on experimental and theoretical research and have found to best be set at $\tau' = \frac{1}{\sqrt{2n}}$ and $\tau_i = \frac{1}{\sqrt{2\sqrt{n}}}$. The mutation operator is the main operator for evolution strategies as opposed to genetic algorithms. General recombinators have been specified in the past of which the classical are *intermediate* and *discrete* crossover. Discrete crossover acts as uniform crossover and determines per entry in the string from which of the two parents the entry must be inherited. Intermediate crossover takes the average value for the entries in the chromosomes. Both crossover operators can directly be used to support more than two parents. Research has shown that the best results are achieved when discrete recombination is used for the object variables and intermediate recombination for the meta parameters.

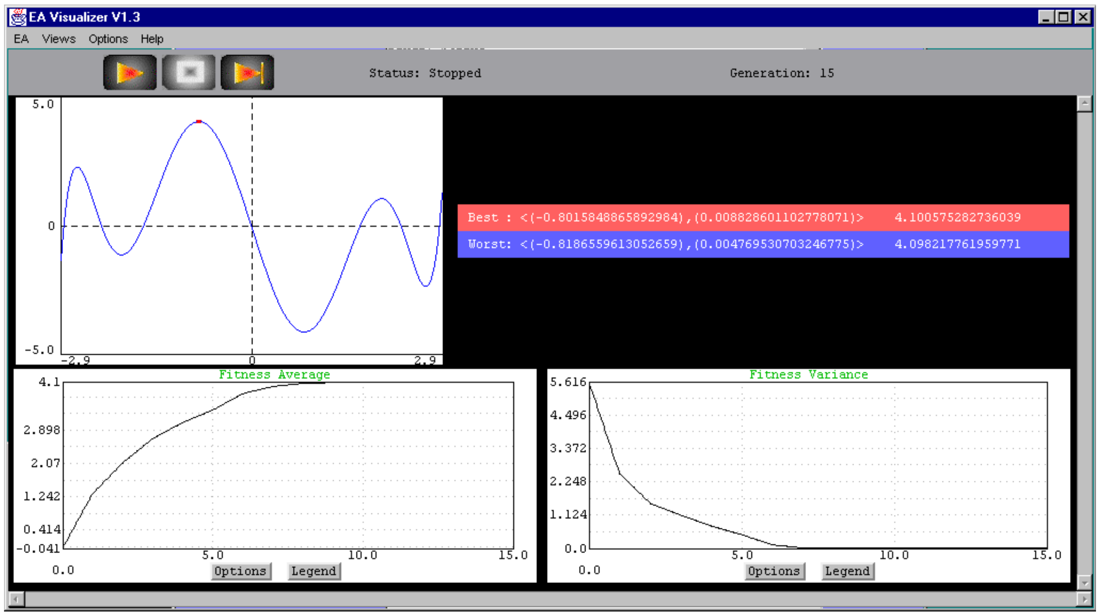
Next to the specialized mutation and recombination mechanisms, the selection operator is also of a special form in evolution strategies. For the sake of showing the diversity of the *EA Visualizer*, we shall restrict ourselves to the $(\mu + \lambda)$ selection mechanism. This mechanism states that there are μ parents and λ offspring. The μ genomes selected to survive are in the $(\mu + \lambda)$ selection mechanism chosen from the both the parents and the offspring (hence the + in the name). How this selection is done is in the strictest of senses unspecified, but normally this is achieved by simple truncation selection that selects the μ best genomes.

Incorporating evolution strategies in the *EA Visualizer* means that a new *Genotype* needs to be created, along with a new *Mutator* and a *Recombinator*. This is exactly what has been done alongside the expansion of the polynome optimization component to also allow for evolution strategies genomes. The requirements to thus install a classic ES in the *EA Visualizer* that optimizes the same polynome as we used for multimodal function optimization in section 2.5.3 are now clear and the following table shows how to actually configure the *EA Visualizer*:

Component	**Instance**	**Parameters**	
Genotype	Evolution Strategies	Length	1
		Min. init range values	-2.9
		Max. init range values	2.9
		Min. init range meta–parameters	0
		Max. init range meta–parameters	1
Similarity	No Similarity	—	
Fitness Function	Evolution Strategies – Polynome Optimizer in $[a, b]$	Function	`0.004x^9 + 0.005x^7 - 0.8x^5 + 5x^3 - 8x`
		Lower limit (a)	-2.9
		Upper limit (b)	2.9
		Optimization	Maximize
Recombinator	ES Crossover	Crossover type for values	Discrete
		Crossover type for meta–parameters	Intermediate
Mutator	ES Mutation	General Tau	0.7071067811865
		Individual tau	0.7071067811865
Before Selector	No Selection (Select All)	—	
After Selector	Truncation Selection	Selection size	100
		Percentage	50
		Which To Use	Selection size
Mater	Random Mater	Grouping size	2
Replacer	Add Offspring To Population	—	
Terminator	All Equal Genomes	—	
Hybrid Searcher	No Hybrid Search	—	
Population	Vector Population	Population size	100
PRNG	Standard Java PRNG	Seed	902497035020

The recombination chance and mutation chance are both set to 1.0. After creating the EA by pressing the `Create EA` button, views can once again be added to the system. As we are looking for the optimum value, we are interested in the best and worst value so far in the system. Therefore, we add a `Best & Worst Evolution Strategies Genome` to the views. Next, we add two `Fitness Statistics` views that show us the average and the variance in fitness values over the population. Lastly, a locations on polynome view is added to actually see where the individuals in the population are located on the polynome. Using all standard sizes however, we have now created a clumsy ordering of the views. With the `1024x768` pixels as the screen resolution that is used to write this example alongside, the two statistics views are situated next to each other and just fit in the width of the window, separating the best and worst view from the locations on the polynome view. Putting these latter two views next to each other would save height and perhaps save us from having to use the scrollbar as is now required because the total height of the view is larger than the available viewing space height. To remedy this, we select from the `Views` menu the option `Change Order Of Views` and move the polynome locations view all the way to the top. When we apply the view order switching, the system relayouts the views and indeed we save a lot of height, but we can yet not see everything without scrolling vertically. To this end we change the dimensions of the polynome locations view by selecting it from the `Views` menu. We set the `Width` to be 400 pixels because we seem to have some width left in the first row of the views and for the sake of the example would like to use that width. Furthermore we reduce the height to 250 pixels. After applying the results, finally everything fits on screen and we are ready to start the algorithm by pressing the play button.

After fifteen generations the optimum has already been found to a very high precision as can be seen in figure 34 and can be compared with the maximum value for the polynome that was stated in the previous example section (section 2.5.3). However, the algorithm can proceed beyond



```
Status: Stopped                    Generation: 15
```

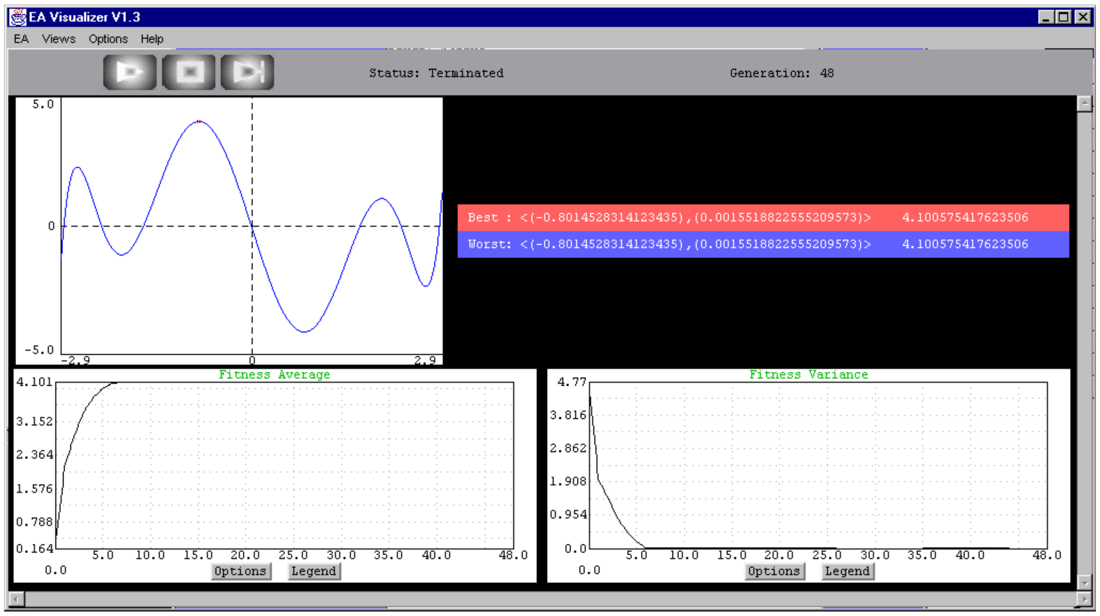
```
Best : <(-0.8015848865892984),(0.008828601102778071)>     4.100575282736039
Worst: <(-0.8186559613052659),(0.004769530703246775)>     4.098217761959771
```

Figure 34: The results of running the ES after 15 generations.

the fifteen generations because not all genomes are totally equal yet. This is ofcourse a problem in evolution strategies because the mechanism takes very long to terminate as the offspring are always mutated and it takes a long time to get a population with 100 members without finding any better ones at all under the circumstances of the precision offered by the ES genotype. After 300 generations we decide to stop the algorithm ourselves.

In order to speed up the termination of the algorithm that uses the ES genotype, we could introduce the *elitist* recombination strategy. Elitist recombination is an augmented recombination operator that creates offspring and then uses elitist behaviour to see which of the parents and offspring will survive into the next generation. This truncation selection kind of behaviour is thus done in a local fashion for each pair parents and offspring. What the elitist recombination operator is thus actually doing is performing replacement. In the *EA Visualizer* to this end a special *Replacer* component has been created. Indeed, the elitist recombination specification is a composite one and is therefore not a neatly one. The elitist behaviour described is a replacement strategy as it selects which of the parents and offspring that were involved in a single *Recombinator* application are to be placed in the population to go into the next generation. Therefore the name *elitist recombination* is wrong and it should be *elitist replacing* and indeed in the *EA Visualizer* a *Replacer* component instance is created called `Elitist Replacing` that is the implementation of the elitist behaviour as stated.

Incorporating the `Elitist Replacing` replacement operator at the expense of the currently installed operator (`Add Offspring To Population`) will generally make an evolutionary algorithm terminate much faster as offspring are directly not selected if a recombination and subsequent mutation has resulted in a lesser offspring than the parent. So instead of global behaviour, the elitist replacement strategy is much strickter and has local behaviour that speeds up convergence, but also very easily causes premature convergence because of quick loss of diversity in the population. We do not address the theory of that further at this point as we only serve to provide the reader with the example. The resulting algorithm is thus a composite algorithm that uses both the evolution strategies approach but without the truncation selection globally on both the parents and the offspring afterwards but with the elitist replacing that is actually truncation selection locally on both the parents and the offspring. The only parameter for the `Elitist Replacing` instance



```
Status: Terminated                    Generation: 48

Best : <(-0.8014528314123435),(0.0015518822555209573)>     4.100575417623506
Worst: <(-0.8014528314123435),(0.0015518822555209573)>     4.100575417623506
```

Figure 35: The results of running the adapted ES with tournament selection and elitist replacing.

of the *Replacer* component is the `Selection Size` which specifies how many genomes should be selected from both the parents and the offspring that are concerned with a single application of the *Recombinator* operator. To set the correct value for this parameter, at this point it should be noted that the `ES Crossover` *Recombinator* takes n parents and creates only a single offspring because of the possible intermediate crossover which obviously allows only for a single different offspring to be generated. Concluding, in order to keep the population at a size of 100 every generation, the local elitist replacing strategy should select 2 out of the 3 genomes involved in the recombination process because the *Mater* creates 50 groups of 2 genomes from the 100 population members, so from each of these groups 2 genomes should again be selected. Setting these parameters however seems to make the altered ES converge even slower and easily go over 300 generations again. To really speed up the convergence process and to see how easy it is to alter settings and incorporate new strategies and make new combinations, we select to have tournament selection as the *Before Selector* that selects 100 genomes instead of the selection mechanism that simply selects all genomes. Now we have a two fold selection scheme actually and the pressure is very high, leading to much quicker convergence. Indeed, after 48 generations the so constructed new EA terminates with a near optimal solution as can be seen in figure 35. The best and worst view for the ES shows the best and worst string upon termination which are ofcourse the same because of the termination condition that signals termination upon equality of all genomes. The strings are indeed of length 2 as we require for this one–dimensional problem only a single object parameter x_1 and thus we have also a single meta parameter σ_1, which are exactly the entries in the string that can be seen in the best and worst view (meaning that the first number in the string found there is the value for x in optimizing the polynome $p(x)$). Behind the strings the fitness value (which equals the polynome response value $p(x)$) is stated.

2.6 Possible future extensions

In this section we look at the *EA Visualizer* in retrospective and glance ahead toward things that could be done to extend the system. In the case of a program such as the *EA Visualizer*, extensions can be made in many ways and the program in itself is never finished. The software package that has come into being now however is to some degree complete. It is a system specifically designed for evolutionary algorithms that contains a development environment for extending it as well. Hence in some sense it is a self–contained and self–sufficient software system. Furthermore we can say that what we have set out to accomplish as written in section 2.1, has actually been achieved and the current system is at least as extensive as described in that section. This implies that we can only glance forward and describe in what ways the *EA Visualizer* can yet be extended. In the following we shall propose extensions to the system, ranging from obvious to very pretentious.

The first and most trivial way in which the system can be expanded is through the creation of new instances for the components in the decomposition of evolutionary algorithms as defined in section 2.2 as well as new views that (interactively) visualize information. This is what the *EA Visualizer* is built for next to the actual working with evolutionary algorithms and so this option for expansion does not come as an unexpected surprise. However, the way in which the expansion takes place could make a difference in that expectation. We refer to the actual performing of such expansions by the user. To be more precise, to what extend will the expansions be done and who will do them? The possibilities of this system are very great and as such this system could come to serve as an important software repository for evolutionary algorithms. We shall come back to this later in this section.

The only expansions or better said adaptions to the system that do not involve a direct extension of the system is the restoration of the applet version of the *EA Visualizer*. In section 2.1 we noted that we wanted the system to work as an applet as well. Stricktly speaking this is the case, for an appletviewer that is provided with any Java implementation can be used to start the applet version of the system. However, the general structure of the system has become such that the creator classes have a very neatly organised structure to store methods for the classes in the system so that the classes can be regenerated when required by the system. This requires however using the Java runtime system to inspect classes and such has been found to not be allowed within browsers for the WWW such as Netscape. This renders the applet version for its original intention useless. There can therefore not be a place where the applet is provided for anyone on the Internet, making it much less accessible and making popularity chances as well as chances at growth in interest in evolutionary computation both at an amateur as well as at a professional level a great deal more slim. Therefore the restoration of the applet version of the *EA Visualizer* could very well be an important extension of the system.

One of the reasons why reading and writing of settings and/or results to disk has been banned at the outset was the availability of an applet version that could be used over the Internet. Applets are not allowed to write data and therefore such functionality has been factored out of the system. Nevertheless, it is a desirable aspect to be able to save work to continue it at a later stage. Furthermore, entering settings can be an extensive exercise when this has to be done over and over. As such it would be a definite addition to the system if such would be possible. Furthermore the writing of results from views directly to disk would also be a great addition as images need then no longer be grabbed from the screen or numerical results be copied through the operating system. Such writing however does not stroke with the applet version of the system, which implies that the writing of data must be disabled when the system is run as an applet.

We have in section 2.2 made an extensive decomposition of evolutionary algorithms as we have determined in section 2.1 that such a decomposition would lead to the most usefull framework. However, we are aware of the fact that some evolutionary algorithms that are more recent of date contain exotic variations to evolutionary algorithms and tend to not fit well into our decomposition. The most prominent of such variations to the "standard" evolutionary algorithm are the evolutionary algorithms in which multiple populations are used. These populations themselves mostly are evolved according to some evolutionary algorithm with some stategy. The populations interact through migration schemes and competitions for limited resources. Even though this still fits in the decomposition, defining a new `Population` instance that holds information with respect to what population every genome is actually assigned to, this is not the natural definition that strokes well with the idea of a multiple of populations. What fits that idea better is an `EARunner` for each separate population and a new mechansim to define interactivity between the populations. This is a whole new scheme and it could be added to the system. The visualization mechanism through the `EAVisualizer` class need not change in such a case, only the model.

It is known that evolutionary algorithms are surprisingly easy to parallelize. The power of computing grows when algorithms can be parallelized because more computing power can then be applied, allowing for greater instances of problems to be solved. In the case of evolutionary algorithms such is not less true. Because of this, a very intensive but interesting extension of the system would be to prepare it for networking. Selecting one computer to be the main machine where the results are visualized and deeming the rest (either computers or processors in a system) to be slaves, the evolution process can be performed much more extensive and much faster. Moreover, once the applet version of the program is restored, any number of machines over the entire Internet can be used. This requires some caution because the parallelization should then be such that the communication time is drastically minimized, otherwise the speed of computation is quickly lost. At least the usage percentage of processors involved will be very low, leading to a higer phone bill than incoming funding for the results achieved. In any way, networking or parallelization by some means is a very at least interesting extension for the *EA Visualizer* system.

Even though it is exterior to any reviews on the *EA Visualizer*, it is totally in place to make some remarks about JAVA since this is the language in which the *EA Visualizer* has been written. The platform independent language JAVA is developed by SUN and distributed freely as a *development toolkit* also known as the JDK. Commercial versions are also available from companies such as SYMANTEC and MICROSOFT. The EA VISUALIZER was developed with the JDK verions 1.1.4 and at a later stage 1.1.6 by SUN. This development toolkit software is available free of charge and can be downloaded from the WWW site of SUN[6]. Eventhough the newer versions of JAVA - versions 1.1.x - offer better utilities and a better implementation to many parts, very efficient and good JAVA implementations are not yet satisfactory created to our perspective. The development of the *EA Visualizer* was initiated using a 1.0.x version that showed to have enough bugs to render a good software system nearly impossible to create. The newer JAVA version turned out to work quite well, but the trajectory leads us to place the remark here that even though not all parts of the *EA Visualizer* might seem satisfactory, this need not be a problem caused by the software that is the *EA Visualizer*. Furthermore, the speed is an important thing to note. It is well known that C implementations are the most common because compilers exists for most any platform that are highly advanced and generate code that runs quickly. The *EA Visualizer* runs in a JAVA runtime enviroment which means that the software runs within another framework and is therefore interpreted by the virtual machine that is JAVA. The main point to note is that running evolutionary algorithms (or any algorithm for that matter) in JAVA, especially in a system as large as the *EA Visualizer*, makes the runs take a lot more time as computation is done slower. A quick and all too easy decision is to conclude that the *EA Visualizer* is a bad piece of software because it runs relatively slow at first sight. We must emphasize though that as JAVA implementations become better and more efficient, the system will run faster. We must also note that the speedup will never allow the implementation to result in the same execution times as for instance when written in C, but the situation will definately still improve. Furthermore, the *EA Visualizer* is now portable without *any* alterations *whatsoever* which makes it accessable to people from all levels of profession ranging from an amateur on a PC to a professional with a superior SILICON GRAPHICS machine. We conclude this discussion by repeating the argument that JAVA implementations will yet improve and make the *EA Visualizer* system more efficient and faster so one should not judge the system on its speed of performance compared to some specific C or assembler implementation.

We wish to conclude this section on future prospects for the *EA Visualizer* by continuing on the arguments started above with respect to seeing the *EA Visualizer* as an important software repository for evolutionary algorithms. The *EA Visualizer* is a system that is self contained and allows for easy extensions in both visualizations and instances for components. Furthermore the system allows for documenting these additions through the help system. Therefore the system

[6]`http://www.sun.com/java`

is one that can be extended anywhere around the world and implementations can be transferred between users of the system on different computers easily. The modular structure of the *EA Visualizer* results in the property that anything that is once coded can be used over and over again in many combinations. Once defined, any code for an instance of a component in the decomposition of evolutionary algorithms needs never be duplicated anymore as is the case with many specifically developed implementations. Furthermore the standard package that is the *EA Visualizer* (which tends to grow over the years) contains basic items so that any new people in the field of evolutionary computation can directly get a feel for the contents, the power, the pros, the cons and the ease of evolutionary algorithms. As such, the *EA Visualizer* is very much suitable for educational purposes. Furthermore for all the arguments as noted before, the *EA Visualizer* is very suitable for scientific research. Easy visualizations which can be made interactive allow for quick and efficient research and once many people over the world use the system, implementations are easily transferred. Concluding, the *EA Visualizer* is potentially a very strong, efficient and extensive central scientific research library and software repository for evolutionary algorithms which in the future could be exactly its role and place in the world of evolutionary computation or more generally in computer science.

3 Recent optimization algorithms using a new approach to linkage learning

In the history of evolutionary computation and more specifically genetic algorithms, research has led to the acknowledgement of the importance of linkage. In general, the notion of linkage concerns the relations that genes (bits in a genetic algorithm) in a problem coding string have amongst each other. Acknowledging these relations and not violating them will aid the EA in the quest for optimization especially for problems in which blocks of bits are necessarily related. In the last ten years, GAs have evolved along the lines of linkage learning to incorporate the notion of linkage to achieve competent algorithms in optimization. Of late a new flow of algorithms that uses a more statistical approach to learning relations and constructing new individuals in accordance with these relations has been introduced. In this section a survey with respect to the capabilities of these new approaches is described.

In section 3.1 an extensive overview on what linkage learning is about is given as well as what progress along the lines of the GA has been made in the field of linkage learning in the past decade. In section 3.2 the recent algorithms with a different approach to linkage learning are introduced and investigated. Finally, section 3.3 closes the linkage part of this paper by summarizing and drawing conclusions on behalf of the research on the new algorithms.

3.1 Linkage learning

Evolutionary computation is a relatively new field in the world of optimization techniques. The contents of the field with respect to the algorithms has grown rapidly over the more recent time. Evolutionary algorithms are becoming vastly more competent in solving difficult and large optimization problems reliably (meaning that the results of a single run are always "good"). This has caused a lot of applications to have emerged in both the scientific and the commercial world. Without asking questions about as to why things actually work, many programmers have implemented evolutionary algorithms for their purpose. With a large portion of the implementations thus created being implemented and used by people that had no understanding of the dynamics of what was created and used, the results were not always as good as hoped for. Especially in the case of the the earliest algorithm in the world of evolutionary computation (the genetic algorithm invented by John Holland [19, 20]) that is so easy to implement, the results from the many implementations were of a precarious form. A good understanding of the dynamics of the sytem at hand was (and an integrated theory still is) required to know in what cases optimization would be succesfull.

To this end, scientific research has been active since the very beginning of evolutionary computation. John Holland's pioneering work [20] provided good ideas about the information processing by genetic algorithms in optimization. Of late, more thorough investigations have provided results that have brought both insights in the the shortcomings of (standard) genetic algorithms as well as new algorithms that cut off some of these shortcomings. All the research is part of designing competent evolutionary algorithms that rapidly and accurately solve difficult and large optimization problems. Most of the research has been directed toward some form of *linkage learning*, which is what is investigated in this paper to a certain extent. In the following we shall provide a chronological overview of the progress in research with respect to this subject. Analysing the quest for competent evolutionary algorithms, we shall see how the term linkage learning has come into being, what it stands for, why it is deemed important, what new work it has led to and where we stand today in theoretical evolutionary computation with respect to linkage learning. The progress in research is accompanied by the introduction of new algorithms. For each of these algorithms we shall also give an operational summary and show how they could be incorporated in the *EA Visualizer*, showing again that it is an extremely competent general framework.

In the section that follows up on the introduction given in this section we contribute to the research in the field of linkage learning as we investigate a new evolutionary type of algorithm that attempts a form of linkage learning in a more direct statistical manner. This new perspective on linkage learning is also part of the historic overview that follows. As the results have heavily tended toward coding solutions with binary strings, we shall only concern ourselves with just those codings. This tendency is the direct result of the search for an integrated theory on the working of the classical genetic algorithm. To first find answers in this field is to create the fundaments for good results in all evolutionary computation, which is why researchers have mostly narrowed down their problem coding of interest to only chromosomes consisting of `0` and `1` symbols. As such, the reader can for the remainder of this paper restrict his or her view on evolutionary computation to the field in which binary strings are used. In the remainder of this section we now behold the past, the present and the future of linkage learning or whatever it is that lies beyond that interesting concept.

3.1.1 Laying the foundations and learning lessons: *Genetic Algorithm*

Genetic algorithms are found to be the cradle of evolutionary computation. The work by John Holland [19, 20] brought about a new optimization algorithm which is based upon the natural mechanics of selection and recombination. For many years, with results for the better as well as for the worse, the genetic algorithm (GA) was the most prominent algorithm in evolutionary computation. With results sometimes being remarkably good, implementations relatively easy, but explanations and theories for the reasons that GAs work seemingly unfindable, this breed of algorithm received a good deal of attention by both end users as well as researchers.

The genetic algorithm in its classical form is best explained by presenting the algorithm itself. For this algorithm as well as the subsequent ones in this section however, we shall be very brief in providing this operational description as we assume that the reader is at least to some extend familiar with the fact that evolutionary algorithms work with populations that contain individuals that code solutions in some search space and are assigned fitness values that denote their value–"goodness" in this search space and that the individuals are combined over subsequent generations to find new solutions from which in some way members are selected to survive. Have made the reader realise this, we can now provide the operational description of the classical GA:

```
$t = 0$
$initialize(P(t))$
$evaluate(P(t))$
while not $terminate(P(t))$ do
    $sel = select\ proportionally(P(t))$
    $mat = mate\ in\ groups\ of\ two(sel)$
    $rec =$ for each mated collection $m \in mat$ do $recombine(m)$
    $mut =$ for each genome in each recombined collection $r \in rec$ do $mutate(g)$
    $P(t+1) =$ each mutated genome $h$ in each collection $m \in mut$
    $evaluate(P(t+1))$
    $t = t + 1$
od
```

In this algorithm, recombination is one of *one–point*, *two–point* or *uniform* crossover, where *one–point* is the true classical recombinator that recombines material from two parents in order to generate two offspring:

$$\begin{array}{c} 11111111 \mid 11111 \\ 00000000 \mid 00000 \end{array} \rightarrow \begin{array}{c} 11111111 \mid 00000 \\ 00000000 \mid 11111 \end{array}$$

For every subsequent pair of genomes in the population, recombination (by crossover) is performed with a specified chance p_c. This implies that some parents may yet survive unharmed the recombination phase. All offspring (and perhaps unharmed parents) are then put through the mutation phase in which every bit in every string is negated with a specified chance p_m. Termination occurs when some termination condition is satisfied. This is no different from later algorithms, but in the most classical sense the termination condition has either been the point at which the population has converged (all equal genomes) or when a specified maximum amount of generations has been reached. To be complete, we note that initialization is the creation of a certain amount of random binary strings and that evaluation denotes the assigning of fitness values to the different strings in the population.

With respect to the working of GAs, John Holland [20] took some first steps to investigating the dynamics of the genetic algorithm. Before stating his results, we shortly introduce the notion of *schemata* for binary strings. A schema is a string consisting of symbols from a slightly larger alphabet that the binary strings themselves. Next to '0' and '1' symbols, a schema may also contain asterisks: '*'. Such a symbol is called a *don't care* symbol and it informally means that it doesn't matter what kind of a symbol is placed at that position. We say that schemas *match* binary strings. The strings that a schema matches are the strings that have exactly the same symbols as in the schema, except for the '*' symbols, for which we *don't care* whether the actual string has a '1' or a '0' symbol. For instance, the schema 0**1 matches the string 0111, but also the string 0101, but not the string 1001 since the first symbol in the string does not match with the first symbol in the schema. Furthermore we introduce the notion of *schema fitness*, which is defined as the average fitness of all the binary strings that match a given schema. Finally the *order* of a schema is equal to the amount of fixed symbols it contains. By fixed symbols we mean all symbols except the don't care symbols.

We define $\delta(S)$ to be the *defining length* of a schema, being the amount of possible crossover positions between the outer two fixed bitpositions. So $\delta(01***10*1**) = 8$ and $\delta(1*1) = 2$. Next to that, we denote the order of a schema S by $o(S)$. The population size is denoted with POP-SIZE and we denote the fitness of the entire population by $f(t)$. This implies that we have $f(t) = \sum_{i=1}^{\text{POP-SIZE}} f_i(t)$, with $f_i(t)$ being the fitness of the i–th individual in the population at time t. Furthermore the average fitness is written $\overline{f_t}$, implying that we have that $\overline{f_t} = \frac{f(t)}{\text{POP-SIZE}}$. Continuing, we define the amount of individuals that match schema S at time t in the population as $\xi(S,t)$. The chance at applying crossover is denoted p_c and the chance at applying mutation is denoted p_m. Finally we use $eval(S,t)$ to denote the average fitness of the individuals that are matched within the population by schema S.

Given all these definitions, John Holland showed that the behaviour of a genetic algorithm can to some extend be written out mathematically. The total fitness of the matched individuals at time t equals $\xi(S,t) \cdot eval(S,t)$. Because proportionate selection is used, the part that the schema contributes to reproduction equals $\xi(S,t) \cdot eval(S,t)/f(t)$. The amount of matched individuals in the next generation now becomes equal to $\xi(S,t+1) = \xi(S,t) \cdot \text{POP-SIZE} \cdot eval(S,t)/f(t)$, which is the same as $\xi(S,t) \cdot eval(S,t)/\overline{f_t}$. We now still have to regard crossover and mutation. These two operators can cause an individual that was matched by a schema to no longer match that schema after the application of the operator. An individual remains matched when its fixed positions remain unharmed. Regarding mutation only, we get $(1-p_m)^{o(S)}$. Given the fact that normally $p_m \ll 1$, we can estimate this chance to be $1 - o(S) \cdot p_m$. The crossover operator is taken to be one–point crossover. The chance at destruction by crossover disregarding possible reconstruction by the inherited part from the other parent becomes $p_c \cdot \frac{\delta(S)}{l-1}$ with l the string length. Combining all of these results, the *schema growth equation* can finally be stated:

$$\xi(S,t+1) \geq \xi(S,t)\frac{eval(S,t)}{\overline{f_t}}[1 - p_c\frac{\delta(S)}{l-1} - o(S)p_m]$$

This equation shows that *if* the part behind the term $\xi(S,t)$ is greater or equal to one, there will be an exponential growth that looks like of $\xi(S,t+1) = \xi(S,t) \cdot (1+\varepsilon)^t$. The term $eval(S,t)/\overline{f_t}$ denotes the ratio between the average fitness of the matched individuals with respect to the average fitness of the entire population. The part that is derived from the chances shows that the exponential growth will be achieved sooner when both $\delta(S)$ and $o(S)$ are small and the schema is thus short and is of a low order. This is exactly what is stated in the so called *schema theorem*:

> **Schema Theorem**: Short, low–order, above–average schemata receive exponentially increasing trials in subsequent generations of a genetic algorithm.

An hypothesis that is directly derived from this theorem is the following:

> **Building Block Hypothesis**: A genetic algorithm seeks near–optimal performance through the juxtaposition of short, low–order, high–performance schemata, called the building blocks.

From the above schema theorem and the building block hypotesis, it follows that we must realise what the GA processes: building blocks. It has also become apparent however that the building blocks that are processed are those that have bitpositions that belong to building blocks close together. This is where the requirement of tight linkage comes in. The representation (binary strings) allows for codings that contain building blocks not coded as blocks of adjacent alleles. As Kargupta [23] mentioned:

> One–point crossover also fails to generate samples for the intersection set of two equivalence classes in which fixed bits are widely separated. For example, in a 20–bit problem, single point crossover is very unlikely to generate a sample from the intersection set of $1\#\ldots\#$ (first bit is fixed) and $\#\ldots\#1$ (last bit is fixed). In biological jargon, this is called the *linkage problem*.

It is thus clear that the coding of problems in binary strings is an important issue when we wish to work with these classic genetic algorithms solely. Any coding that does not have the crisp building block structure that is required, will most surely not give satisfying results. What is required is thus *linkage*, or in other terms: knowledge about the cohesion of the bits in the coding string with respect to the fitness landscape (search space). Interesting to note is that even though the research towards linkage learning has really only come into reality some nine years before this writing, Holland [20] already called for *tight linkage* in 1975 after his investigations that led to the results in the processing of building blocks by GAs.

The reason why classical genetic algorithms fail is thus the fact that the ordering of the bits in the string is important. The coding is such within the genetic algorithm that items are coded at fixed positions in the string. There are two things that can be done to resolve this problem. On the one hand, we could code the problem in such a way that we know for sure that the genetic algorithm will have clear building blocks that can be processed which are set up so that bits within a building block are adjacent or at least in close vicinity of each other. Knowing so much however is usually a sign that we know already much more about the problem we are investigating. In other words, on beforehand it is usually unkown what bits make up a building block. Another solution has been proposed by Holland as he introduced the *inversion* operator. It has been shown however [10] that eventually the use of this operator does not come soon enough and the population will have already converged before any goals can be accomplished by the inversion operator.

Even though we have in the above made it clear that linkage learning is an aspect that is missing in GAs and that optimization will be for the better when acknowledging the importance of linkage and taking appropriate steps in algorithms to utilize this knowledge, the extent of the devastiation with respect to the performance of the classical GA because of this negligence has not been made clear. How bad is it that there is no room for tight linkage? Research by Goldberg and Thierens ([14, 15]) with respect to the mixing of building blocks has provided answers in that direction. A mixing model determined two times t_x and t_s for mixing and selection respectively. The model imposes that $t_x < t_s$ in order to have a succesfull GA. Otherwise, the genetic algorithm will not have enough time to mix the building blocks and selection will (most likely) drive the algorithm to the wrong answer. The exact constraint that follows by deriving expressions for t_x and t_s is $p_c < (e^{l/n}\ln(s))/(n\ln(n))$ where p_c is chance at applying crossover, s is the selection rate[7] and n is the population size. Furthermore, Goldberg and Thierens made explicit [15] that the sample complexity grows *exponentially* with the problem size for solving bounded deceptive problems using a simple GA with uniform crossover. They showed that the precise detection of schemata and mixing of schemata takes exponential time for a simple GA using uniform crossover.

So we conclude that the classical GA even though complex in its dynamics and sometimes powerfull in optimization capabilities, has shortcomings that have to be acknowledged. Ensuring tight linkage and juxtaposition of bits that make up building blocks pave the way for a GA to solve a problem efficiently. So in order to make that possible, the classical GA had to be expanded to somehow include the evolution the *position* of the bits in the strings that the GA processes.

3.1.2 Acknowledging the importance of linkage: *Messy Genetic Algorithm*

Before Goldberg and Thierens made their statement on the mixing of building blocks, providing a better understanding in that field, studies were already being undertaken toward the inclusion of linkage information as it had already been established that linkage was something that would add to the power of the GA. The result of this work was the *messy Genetic Algorithm* [13]. The addition *messy* to the GA comes from the fact that the messy genetic algorithm (mGA) allows for strings that are variable in length and may over– or underspecify the contents of the true coding string. In other words, the true binary string still exists in mGAs as the coding of the problem, but the strings that are being evolved are no longer directly those strings, but a new brand of strings that specify the contents of the coding strings. The specification can thus be complete, incomplete or overcomplete. We shall discuss the contents of the mGA and then provide an algorithm outline just as we did earlier for the classical GA.

To allow for linkage information to be processed, it followed from the research with respect to the working of the genetic algorithm, information about the location of the bits should be taken into the evolve process in order to form tightly linked building blocks. This is exactly what is done in the mGA. The strings that the mGA works on contain tuples instead of bits. The tuples contain two values that specify the *locus* of the bit and the *value* for the bit and are stored as pairs (*locus*, *value*). The string thus specified is still a binary string just as was explicitly used in the GA, but that structure is now only regarded when the solution that is coded is required, for instance when evaluation of the string is required. The following example should serve to make the notion of the new coding clear:

mGA string	**Binary string to match**
((1,1)(0,0)(2,1))	011
((1,1)(2,1)(0,0))	011
((2,0)(0,0)(1,1))	010
((0,1)(1,1)(2,1))	111

Note that the first two strings in the example are in the problem space identical since they denote the same problem coding string. For the mGA however, the two codings have different meanings as the locations are placed in a different order, implying different relations. The above examples are examples of complete and exact specified strings. In mGAs however, during the runnning of the algorithm, such is not required to be the case. We already noted that strings may be under– or overspecified. This implies that for a five bit problem, we are allowed to have strings such as ((1,1)(3,1)) and ((0,0)) which only partly tell us how to fill in the problem coding string, as well as strings such as ((1,1)(1,0)(1,1)(2,1)) and ((0,0)(1,1)(2,1)(0,2)(3,0)(4,1)) that contain more than

[7]To be exact, s is the tournament size where in binary probabilistic tournament selection where the better individual is selected with probability p_t.

one specification for values at the same position. Overspecification is dealt with by scanning from left to right and taking the first entry found for any position (locus). This implies that in the string ((1,1)(1,0)(1,1)(2,1)) only the first and the last tuple are actually used when finding the problem coding string and we thus find 11### where the # symbols denote undefined entries as a result of underspecification. The underspecification is resolved by introducing *templates*. One template is maintained as global data which fills in the gaps introduced by underspecified strings. A template is no more than a fully specified binary string such as 10011 for our five bit problem. Any undefined entries are taken directly from this template, so our incomplete string 11### is filled up with the entries from the template to get 11011 as the string that codes a solution to the problem. The templates themselves are altered in a wise way as we shall see shortly.

Important to note from the way the problem coding strings are coded is that because both the locus and the value are contained, building blocks may now achieve tight linkage because the alleles that are part of a building block can now be placed closed together in the coding that is used by the algorithm, contrary to what was the case for the classical GA as the positions of the bits could not be altered[8]. This variable locus coding was introduced especially to tackle the linkage problem. Kargupta [23] mentioned that every member of the mGA population represents an equivalence class of a certain order. He points out that where the GA uses individuals that are only order–l classes with l the problem coding string length, the mGA strings can be of any arbitrary non–zero order. Kargupta's work on BBO (Black Box Optimization) and his SEARCH framework [23] poses a new perspective toward BBO based on relations and classes in which he points out that BBO optimization algorithms should separate sample, class and relation space where sample space stands for the problem coding strings themselves, class space stands for the way in which the samples can be grouped in classes (according to relations) and relation space stands for the relations between the alleles in the problem coding strings. In this light, Kargupta thus points out that the mGA decomposes the search space into the sample space and the class and relation space, but not into all three spaces separately. Concluding, he points out that because of this decomposition, better decisions can be made by the algorithm than is the case for the classical GA.

We continue our description of the mGA by discussing the operators that are used to combine the mGA strings. The one–point crossover operator used in the classical genetic algorithm cannot be directly used by the mGA since the strings are not required to be of the same length. The mGA variant is therefore slightly different. The recombination operator in messy genetic algorithms is called *Cut and Splice* and takes two parent strings and produces two offspring strings. In each of the parents a cutpoint is randomly selected and the parts starting from those cutpoints are swapped between the parents to thus generate the offspring. Actually the only difference with the one–point crossover recombination in GAs is the fact that because of the variable length strings there are now two cutpoints instead of one. The *cut* operation is performed with chance $p_c = (\lambda - 1)p_\kappa$ where λ is the length of the messy string. The *splice* operation is directly after the cutting performed with chance p_s. In other words, after parts have been cut off, these parts need not always be put back. We present an example in which both *cut* and *splice* are performed:

$$\begin{array}{lcl} ((0,1)(1,1)(1,0)(3,1) \mid (5,1)(4,1)(7,1)) & \multirow{2}{*}{$\rightarrow$} & ((0,1)(1,1)(1,0)(3,1) \mid (5,0)(1,0)(4,0)) \\ ((6,0) \mid (5,0)(1,0)(4,0)) & & ((6,0) \mid (5,1)(4,1)(7,1)) \end{array}$$

Next to this recombination method, a special variant of tournament selection is employed especially for the messy strings. The tournament selection is always taken to be binary (selection size equals two) but the selection isn't always applied given a pair to select from. Selection is permitted to be performed when the two strings subjected to the selection mechanism share at least a threshold θ of genes. The amount of genes shared is equal to the amount of loci that are contained in both strings. For instance the strings ((0,1)(4,1)(3,1)) and ((3,1)(0,0)(0,1)(2,2)) share two genes since the loci 0 and 3 occur in both strings. Given length l_1 of the first string and length l_2 of the second

[8]Note that still the positions of the bits are actually not altered, only the new coding that trough indirection forms the old coding allows for position changes.

string, the threshold θ is set to be $\theta = \frac{l_1 l_2}{l}$ where l is the length of the problem coding string. This value is chosen because the expected number of genes in common between two randomly chosed strings of length l_1 and l_2 is hypergeometrically distributed and the value of θ is exactly that expected number, as is described by Deb and Goldberg [8].

A mutation operator is in the description [8, 9, 23, 13] of the messy genetic algorithm mostly not mentioned. However, a mutation operator is no more difficult that it is in the classical GA. With a specified chance at mutation p_m, a bit in a messy genetic string can be flipped. Alternatively, a mutation operator could adapt either randomly or like is done in evolution strategies based on proximity the locus of a bit with a specified chance at mutation. However, if we regard the way in which the cut and splice operator, the threshold selection and the three phases of the algorithm that are discussed below are used, it is understandable that mutation is something that is better not used as the whole setup is a more exact way that enforces the dynamics as specified. In other words, the setup is *meant* not to include a mutation operator.

The tools for the mGA have now been described and we can now state the bigger picture of the algorithm itself. Basically the mGA works in three phases, being the initialization, primordial and juxtapositional phase. In the initialization phase a population is created with a single copy of all substrings of length k. This causes the population to contain all building blocks of the desired length. If the genetic processing then respects the good building blocks and recombines them, good solutions can be expected to be formed. The problem is however that there are 2^k strings of length k and we can select $\begin{pmatrix} l \\ k \end{pmatrix}$ combinations of k loci out of a total of l available loci, implying that$2^k \begin{pmatrix} l \\ k \end{pmatrix}$ strings are created and evaluated in the initialization phase. Furthermore it is often unkown in advance what value of k is required to solve the problem and taking $k = l$ is no option as we are then better off enumerating all possible solutions. Finding the right value for k is therefore done differently as we will see shortly.

The second phase is the primordial phase and it constitutes the selection of the better strings that were made in the initialization phase. The above thresholding selection mechanism is applied here. No evaluation takes place because such is not required as no new strings are introduced. It is furthermore common practice to adjust the population size to be appropriate for the next phase. The population size is namely quite large at the beginning of the primordial phase, since initialization left us with a total of $2^k \begin{pmatrix} l \\ k \end{pmatrix}$ strings. The reduction of the population size is usually done by halving the population size at a priori set intervals.

The third and final phase is the juxtapositional phase which is meant to recombine the material. During this phase just as in the classical GA selection and recombination are performed, be they for the mGA thresholding tournament selectiond cut and splice recombination respectively. In this phase evaluation evidently needs to take place again as opposed to the primordial phase, since new strings are introduced as a result of applying the recombination operator.

As mentioned before the value for k in the initialization phase is unkown at the outset and some means of finding the appropriate value is required. As Goldberg, Deb, Kargupta and Harik describe [9], the initial tests with the mGA were indeed performed with a preset value for k, but the need for a competitive template that is optimal with respect to the previous level recommended the idea of level–wise processing. In other words, we should remember the fact that we need *templates* to resolve the problem of underspecification in the messy strings. It has not been made clear yet how these templates are created. The idea of competitive templates provides the solution. Competitive templates are strings that are locally optimal to the previous level denoted by the building block length k in the initialization phase. Strings that are fitter than the template must by definition contain building blocks at the next level or higher. The idea for level–wise processing to find the required template thus implies starting the mGA at level $k = 1$ and an order–zero template which is any random string. Upon termination of the three phases, the resulting structure should be optimzal to order–one and thus we can update the template with the optimal string found. This process is iterated until the time to terminate has come. Termination is hard to specify under these conditions, but a maximum in level processing can ofcourse be specified or termation could be signalled when no improvement over the values are found after some specified amount of subsequent levels. The whole of the mGA is thus the three phases looped, starting with $k = 1$ and continuing until some termination condition is met. We are now ready to provide the operational description of the mGA:

```
$level = 0$
$template = random\ binary\ string$
while not $terminate(P(t), level)$ do
    $t = 0$
    $initialize(P(t), level)$
    $evaluate(P(t), template)$
    while not $terminate\ primoridal\ phase(P(t))$ do
        $P(t+1) = select\ by\ thresholding\ tournament(P(t))$
        $t = t + 1$
    od
    $P(0) = P(t)$

    $t = 0$
    while not $terminate\ juxtapositional\ phase(P(t))$ do
        $sel = select\ by\ thresholding\ tournament(P(t))$
        $mat = mate\ in\ groups\ of\ two(sel)$
        $rec$ = for each mated collection $m \in mat$ do $cut\ and\ splice(m)$
        $mut$ = for each genome in each recombined collection $r \in rec$ do $mutate(g)$
        $P(t+1)$ = each mutated genome $h$ in each collection $m \in mut$
        $t = t + 1$
    od

    $template = best\ string(P(t), template)$
    $level = level + 1$
od
```

An interesting sidestep at this point is to advert our attention from the history of linkage learning and specifically the role of the mGA in that history and think about implementing the above scheme in the *EA Visualizer*. We posed that the decomposition of evolutionary algorithms is general enough to incorporate virtually any evolutionary algorithm, so surely it should be able to incorporate this algorithm. It seems however that the structure of the algorithm as outlined above differs fundamentally from the algorithm that uses the decomposition that was stated in subsection 2.2.3. However we should guard ourselves from being too fast in drawing conclusions to this end. We should not forget that the idea behind the creation of the general framework in the *EA Visualizer* is defined at a *meta* level that should be seen as very general to the fact that it poses some way of generating new samples or selecting from old samples to have more or less samples in the next step of the algorithm. Acknowledging this, we see that the primordial phase in itself fits in the framework perfectly, with the *Before Selector* a new selector that should be implemented (something named like `Messy Threshold Binary Tournament Selector`) and a noncontributing *Recombinator*, *Mutator*, *Hybrid Searcher* and *After Selector*. The replacing mechanism can be based on whatever strategy is required. To this end we should remember that it is common to reduce the size of the population, which is easily done with the help of the `Truncation Selection` component as the *After Selector*. But most likely a new component named `Messy After Selector` will be used as after selector. In a similar fashion we note that the juxtapositional phase can be easily implemented in the *EA Visualizer* with new component implementations for the *Mutator* and the *Recombinator*. Furthermore, the evaluation now depends on templates and a messy string can have no mapping to the actual problem coding string without it. In any way it should be clear that a new *Genotype* is required, named the `Messy Binary String` or something of such kind that is the string of tuples. As a template *must* be globally available, the new genotype will have to incorporate a `static` reference to such a template as well as a `public` method that will generate a problem coding binary string[9]. The only thing that might seem impossible is the fact that there are three evolutionary algorithms combined into one, where one of the algorithms even contains the other two that are sequential. The problem is not as large as it seems however as we must recognise that all the really new operators we are introducing are especially for the mGA anyway. As such we can specify for instance that the `Cut And Splice` recombinator and the `Messy Mutator` that will be created for the mGA, respect the two phase operational semantics. This means that when we specify to store this global information in a global (in JAVA: `static`) fashion in the specially designed *Genotype* for the mGA, this information can help to distuinguish between the different phases and trigger the *Recombinator* to actually work or not. So really we require only a single new recombination operator[10] that performs cut and splice but also respects the global information within the *Genotype* with respect to the two phases in the algorithm. The same goes for the *Mutator*, *After Selector* and the *Terminator*. The latter class will require a new instance as well for the mGA that will *internally* signal the ending of the two distinct phases in the mGA through the global information in the *Genotype* and through the common way signal termination for the mGA as a whole to the system in order to terminate the entire algorithm. The level information could also be placed in the *Genotype* class because it seems to refrain ourselves from implementing a new *Population* instance, but it would be more justified if the level information were placed in just such a new instance as this information really only has to do with initializing the population which in itself is of a specialized structure, implying that we need a new *Population* class anyway. Concluding, we can say that the mGA even though at first glance perhaps looking impossible, indeed fits very nicely so into the structure of the *EA Visualizer* and when done neatly will have a very nice structure.

Returning to the mGA, we are at the point where we close up the discussion about the mGA. We have seen how the first approach to tackling the linkage problem has come into being. We have also seen that the algorithm probably takes far too long seen to the extensive initialization phase. Goldberg, Deb and Korb [12] even wrote out the complexity estimates for the original messy genetic algorithm when executed in a serial fashion:

Phase	**Serial**
Initialization	$O(l^k)$
Primordial	0
Juxtapositional	$O(l \log l)$
Overall mGA	$O(l^k)$

It follows that the computation is dominated by the initialization phase. The difference between the initialization and juxtapositional phase is even so significant, that the next step in the direction taken by the mGA would obviously be to get these two phases more aligned in running time.

Despite the running time problems, the mGA does solve a lot of problems encountered by the classical GA. Most important ofcourse is that it directly succesfully tackles the linkage problem. Kargupta [23] points out that one of the most important aspects of the mGA is that it realizes the importance for finding appropriate relations. Unlike the classical GA, the search for proper relations in the mGA is more accurate and less susceptible to error because of the explicit enumeration and the use of a locally optimal template for class evaluations. However, Kargupta also points out that there are still deficits to the mGA approach, mainly in the decomposition of the search space. The main point he too points out is the computation bottleneck imposed by the initialization

[9]Both the template and the result of the required `public` method can be a JAVA `BitSet`, which is indeed also used by the `BinStringGenotype` class that implements the binary strings for GAs.

[10]If we implement this neatly we create an abstract superclass for messy recombinators that respects the two phase structure.

phase. Whereas the classical GA had the advantage of implicit parallelism as Holland [20] pointed out, the mGA no longer posesses this quality. The implicit paralellism stems from the fact that parallel evaluation of different equivalence relations can be done at the cost of evaluating a single relation. The work of Kargupta resulting in the SEARCH framework [23] makes this explicit. The mGA enumerates all the order–k equivalence classes however as they are *all* generated and evaluated in the initialization phase. This implies that for problems that require even moderate values of k (order of decomposability in building blocks), the population size in the initialization phase and moreover the running time renders the mGA no longer practically applicable.

3.1.3 Taking shortcuts: *Fast Messy Genetic Algorithm*

Even though the mGA overcame most of the problems imposed by the classical GA and succesfully tackled the linkage problem, the main downside to the algorithm is its running time. The initialization phase takes far too long for it to be of any practical use when larger building blocks require detection. In order to dispose of this problem, a new version of the mGA has been created by Goldberg, Deb, Kargupta and Hark [9] as a direct extension to the mGA, called the *fast messy genetic algorithm*.

During the research on the mGA, the inventors already realized the computational bottleneck imposed by the initialization phase because of its enumerative method and tests were run with smaller populations and longer strings. This was done so to try and capture more building blocks within a single string to get some means of implicit parallel processing to vastly speed up the running time. Eventhough the first tests deemed the approach unsuccesfull, later rigorous investigation and further expansion came up with results similar to that of the mGA, but at a much lower time complexity.

The most direct difference is the way in which the initialization phase takes place. Instead of full enumeration of order k building blocks over all possible loci assignments from l loci, the population is initialized so as to be *probabilistically complete*. Furthermore the idea of the longer strings is incorporated so as to try and achieve implicit parallellism. However, the first tests that failed using the longer strings did so because of the fact that those longers strings were directly used in the mGA. Recall however that the mGA initialization method left the mGA with only strings of length k and no longer. To merge these two approaches, building blocks are filtered during the primordial phase. Instead of only applying selection to find the better building blocks and ensuring more copies of the strings carrying those blocks, the strings that are now thus initialized at a greater length are during the primordial phase reduced in length in such a way that the better blocks are at the end still found in strings of length k or close to length k. The juxtapositional phase is altered as well in the sense that the thresholding selection operator is altered (implying another chance in the primordial phase as well since this operator is used there too). We shall now discuss the altered contents of the different phases and operators.

First and foremost, the initialization of the population is now thus done so as to create a population that is *probabilistically complete*. In order to do this, we must understand what this means. In the original mGA, the population created was simply complete because all possible combinations existed and for each good building block we most certainly had at least one entry in the population. The probabilistic approach dictates that we have in the initialized population one single entry of each building block *on average*. To achieve this, it should first be recognised that the string length l' for each individual in the initial population (the population created in the initialization phase) has at least length k and at most length l, where k is the same as in the mGA and l is the length of the problem coding string. The amount of strings of length l' creatable when only regarding the locus information when we have l options is ofcourse equal to $\binom{l}{l'}$ as we are selecting l' loci out of a total of l possible. So we have hereby specified how many different strings we can create of length l'. Recall that in order to specify the total amount of possible messy strings of this length, we should multiple this number by $2^{l'}$ as this is the amount of value combinations for the

l' positions, which would bring us back to the amount we had before. We shall turn to the value combinations shortly. On the other hand we wish to take a string of length l' and determine in how many ways a combination of loci of length k can occur in such a string because ultimately we are interested in supplying enough building blocks of length k no different than in the mGA. To compute this value, we state that the k loci too have to come from the l available loci, just the same as the total of l' values for one string. In other words, if we fix the k loci in the string of length l', we have $l' - k$ loci to choose from a total of $l - k$ loci, which gives a number of $\binom{l-k}{l'-k}$ combinations. Combining these results gives the probability of randomly selecting a combination of size k of loci in a string of length l' that is constructed as a subset of a total of l available loci $\{1 \dots l\}$ [9] as we have specified the amount of combinations required and the total amount of combinations possible:

$$p(l', k, l) = \frac{\binom{l-k}{l'-k}}{\binom{l}{l'}}$$

As the above probability expresses the chance at the existance of a required building block of length k with respect to the loci, it is basic mathematics that states that a population of size $n_g = 1/p(l', k, l)$ with random created strings contains on average one instance of the required locus combination. It can be shown that for large values of l and l' $n_g \approx (l/l')^k$. Furthermore it is obvious that for $l = l'$, $n_g = 1$ and that for $l \approx l'$, n_g is a constant that does not depend on l. We should also not forget that for larger values of k, the expression $\binom{l-k}{l'-k}$ becomes much greater, implying that the required population size n_g increases drastically. So even though we are halfway through to ensuring a faster running time than the *mGA*, we are still looking at possible drawbacks due to very large populations.

The part not yet included in the probabilistic complete population initialization is the assignment of values to the initialization strings. Recall that every entry in the messy string is a (*locus*, *value*) pair and so far we have only discussed the probabilistic completeness for the *locus* part of the pair. The inclusion of the *value* part requires a population sizing equation that accounts for building block evaluation under the influence of noise. In other words, a model is needed that predicts how large the population requires to be in order to make the right decisions among building blocks given a random initialization. For classical genetic algorithms, Goldberg, Deb and Clark [11] provided such a model and Goldberg, Deb, Kargupta and Harik improved upon that model in creating a more accurate prediction [17]. The original model is however used in the original fmGA and gives us $n_a = 2c(\alpha)\beta^2(m-1)2^k$. In this expression, k stands for the building block length just as it has before. Furthermore, m stands for the amount of building blocks in a string, implying that $mk = l$. Continuing, β stands for the squared root–mean–squared subfunction inverse signal–to–ratio or $\frac{\sigma^2_{rms}}{d^2}$, where $\sigma^2_{rms} = \frac{\sigma^2_M}{m-1}$ and σ_M is the variance of the average order–k schema which is in turn computed as the variance of two competing schemata H_1 and H_2: $\sigma^2_M = (\sigma^2_{H_1} + \sigma^2_{H_2})/2$. Finally, $c(\alpha)$ stands for the value such that $z(\alpha) = \sqrt{c(\alpha)} = \frac{d^2}{2\sigma_M}$ with d being the signal difference between the two schemata: $d = f_{H_1} - f_{H_2}$ and $z(\alpha)$ is the ordinate of a unit, one–sided normal deviate. Perhaps not all of these terms are directly clear, but the main thing to notice is that there exists an expression that tells us how large to take the population size based on the values for the messy string tuples in order to be able to make the right decisions when choosing between building blocks. The only problem with this approach is that we require some prior information with respect to the fitness function to actually compute the values of the variables in the formula to find n_a. This is however not possible in most practical applications and in such a case we are back to guessing the population size, but this is no different than was the case for the classic GA. If we just observe the expression $n_a = 2c(\alpha)\beta^2(m-1)2^k$, we see that it's a factor $\gamma 2^k$ where 2^k is thus the same value as we had in the mGA before to account for the different value combinations. We multiplied the value of 2^k there with $\binom{l}{k}$ to compute the total amount of strings required to generate to get all possible combinations of building blocks of length k. We now have a different value for $\binom{l}{k}$, but also introduce noise when deciding amonst the strings we introduce instead of the enumerative $\binom{l}{k}$. The population sizing formula predicts how many individuals are required to overcome this problem. So where we actually had $n_g = \binom{l}{k}$ and $n_a = 2^k$ and wrote $n = n_g n_a$ to get the total amount of strings to generate *enumeratively* and thus *deterministically* in the initialization phase of the mGA, we now have two new expressions for n_g and n_a and find a new formula that specifies the total amount of strings to generate *randomly* in the initialization phase:

$$n = \frac{\binom{l}{l'}}{\binom{l-k}{l'-k}} 2c(\alpha)\beta^2(m-1)2^k$$

The only open parameter left at this point is what value to choose for l', the length of strings in the initialization phase. Increasing l' makes n_g decrease quickly, but also increases the error probability since additional noise is introduced by additional bits. However, decreasing l' quickly increases dramatically the population size and setting $l' = k$ will bring us back to the same running time as in the initialization phase of the mGA. So values close to l seem to be appropriate and the original fmGA used a value of $l' = l - k$. With this choice, it has been shown that assuming problems of bounded difficulty, n_a is $O(l)$ [11]. This implies that the population sizing becomes $O(l)$ overall as it was stated before that for $l \approx l'$ n_g is a constant that does not depend on l. The result is thus a very large difference with respect to the mGA in favor of the fmGA.

Now that the initialization phase is complete, the primordial phase initiates as we recall from the mGA. The algorithm is now left however with strings of length l' instead of k with l' being close to l. In order to start the juxtapositional phase, the strings have to be decreased in size to become close to k because that will make the mGA function properly. The only way to get strings of this length is by deleting entries from the strings, which is exactly what is done in the primordial phase of the fmGA in addition to the primordial phase of the mGA. If we state that the initial length l' is equal to $l^{(0)}$ and we have successive lengths $l^{(1)}, l^{(2)}, \ldots, l^{(n)} \approx k$ such that $l^{(i-1)} > l^{(i)}$, we can define the reduction ratio as $\rho_i = l^{(i)}/l^{(i-1)}$. It is clear that during stage i, $l^{(i-1)} - l^{(i)}$ genes (entries) are deleted from every string. To be more precise, the fmGA deletes these genes at random. After the deletion, the selection is invoked some number of generations. In other words, every so many generations next to selection also deletion takes place. The selection rounds are meant to give more copies to the strings containing the better building blocks so as to get more copies of the best building blocks. This is required since as the deletion is performed every so many generations, building blocks disappear.

It is clear that the deleting of the building blocks must not overrule the selection because otherwise the required building blocks are gone before we can make more of them. To see how much deletion can be performed, the same approach can be taken as in the initialization phase. As before it is required to have building blocks of length k, but now we have strings of length $l^{(i)}$ to place them in and strings of length $l^{(i-1)}$ to chose the loci from. In other words, the total amount of possible combinations equals $\binom{l^{(i-1)}}{l^{(i)}}$ as we have $l^{(i)}$ loci to choose from and furthermore the number of ways a string of size $l^{(i)}$ can contain a loci combination of size k where the loci are selected from $l^{(i-1)}$ options after analogy of the initialization equals $\binom{l^{(i-1)}-k}{l^{(i)}-k}$. Combining these results, it follows once again that the amount of strings required to have one expected copy of the desired building block (which we call the building block repetition factor γ here) equals:

$$\gamma = \frac{\binom{l^{(i-1)}}{l^{(i)}}}{\binom{l^{(i-1)} - k}{l^{(i)} - k}}$$

Once again, we have that for large values of $l^{(i-1)}$ and $l^{(i)}$ compared to k, γ varies as $(l^{(i-1)}/l^{(i)})^k$. This implies that we are able to set $l^{(i)}$ to any value such that γ is smaller than the amount of duplicates generated by the selection operator. If the amount of duplicates generated by the selection operator is less than γ, this implies that we expect less than one copy of the desired building block to survive the disruption as the formula expresses exactly how large the population size must be in order to after the random deletion have one expected building block left. It remains ofcourse to set an exact value for the reduction factors ρ_i so that it is clear how many genes must be deleted each generation. The inventors of the fmGA (Goldberg, Deb, Kargupta and Harik, [9]) posed to assume to have a fixed repetition factor γ. They pose that if t_s is taken to be the amount of selection repetitions per length reduction, γ should be fixed to a value less than 2^{t_s} as it is expected that the binary tournament selection will roughly double the proportion of best individuals during each selection repetition. Noting that $\gamma \approx (l^{(i-1)}/l^{(i)})^k = \rho_i^{-k}$, it follows that the assumed fixed γ roughly imlies a fixed reduction ratio per deletion round $\rho = \rho_i$, $\forall_i$. Now it is possible to compute the number of deletion rounds required to reduce the string length to $O(k)$. The authors do this by taking a value $\zeta \geq 1$ such that the final string length equals ζk. It then follows that the amount of deletion rounds t_r with reduction ratio ρ follows from $\frac{l'}{t_r} = \zeta k$ and is thus equal to $t_r = \frac{\log(l/\zeta k)}{\log \rho}$. Thus, accepting a constant factor ρ and recalling that the population size is of $O(l)$, the initialization phase and primordial phase together take no more than $O(l \log l)$.

The final adaptation of the mGA to create the fmGA lies in the chance of the thresholding selection operator. Kargupta [23] mentions that ideally we would want to set θ to the string length so as to only let classes that belong to a particular relation compete with each other. He also mentions that the search for appropriate relations which needs to filter the bad relations that are introduced because of the probabilistic complete initialization however, requires to have a smaller value of θ so that competition among classes that share some instead of all common genes will occur. The amount that θ should be decreased is based on the work of Deb [7], who set the original value of θ for the mGA to be $\frac{l_1 l_2}{l}$. From experiments it showed that for the fmGA this value was too much of a decrease from the stringlength. A more conservative value was posed by Goldberg, Deb, Kargupta and Harik [9] as they suggested using $\theta = \lceil \frac{l_1}{l_2} + c'(\alpha')\sigma \rceil$ where σ is the standard deviation of the number of genes that two randomly chosen strings of possibly differing lengths have in common and $c'(\alpha')$ is once again the ordinate of a one–sided normal distribution with tail probability α. Deb [7] also stated the variance of the hypergeometric distribution that is required: $\sigma^2 = \frac{l_1(l-l_1)l_2(l-l_2)}{l^2(l-1)}$. The selection is implemented to select a string for the tournament and then to check other strings to see if they meet the threshold requirement with a limit to the amount of strings checked. This completes the adaptation of the mGA to become what is called the fmGA and we are now ready to provide its operational description:

```
template = a template

t = 0
initialize(P(t))
evaluate(P(t), template)
while not terminate primoridal phase(P(t)) do
        if $t_s$ mod $t = 0 \wedge t > 0$
        then del = delete genes(P(t))
                P(t + 1) = select by (new $\theta$) thresholding tournament(del)
        else  $P(t+1)$ = select by (new $\theta$) thresholding tournament($P(t)$)
        $t = t + 1$
od
$P(0) = P(t)$

$t = 0$
while not terminate juxtapositional phase($P(t)$) do
        sel = select by (new $\theta$) thresholding tournament($P(t)$)
        mat = mate in groups of two(sel)
        rec = for each mated collection $m \in mat$ do cut and splice($m$)
        mut = for each genome in each recombined collection $r \in rec$ do mutate($g$)
        $P(t+1)$ = each mutated genome $h$ in each collection $m \in mut$
        $t = t + 1$
od
```

Note how the level wise processing has been left out of the process. The initiators of the fmGA suggested that for practical purposes level wise processing should be employed, which was in turn one of the two modifications suggested by Kargupta [23] to improve on the fmGA. The extension of the above algorithm however to include such level–wise processing should be clear from the mGA operational description given earlier. Next to that, how to incorporate the fmGA into the *EA Visualizer* should also be clear at this point as the operational requirements with respect to the system are not much different than those of the mGA.

Results for the first fmGA showed amongst other things that for a deceptive trapfunction problem, the function evaluations required to solve the problem by the mGA are of $O(l^5)$ with l the problem length, whereas the fmGA appeared to be subquadratic. So we can conclude that the fmGA took the next step in the direction taken by the mGA and both made the messy search algorithm of more practical applicability as well as improved on the relation search and thus stood stronger yet in tackling the linkage problem. In all modifications, the search for good relations was of central importance and the importance of linkage was thus acknowledged once again. Furthermore, given even more attention to this end improved the results further as the deletion phases and the adapted thresholding that weren't in the mGA made the fmGA score even better.

However, the fmGA was not the endpoint of the search for competent GAs. For starters, Kargupta [23] pointed out both two modifications as well as shortcomings the fmGA still has. The one modification as the level–wise processing that the initiators of the fmGA themselves also already pointed out. Kargupta also posed an alternative approach to the building block filtering or deletion phase. He showed that the filtering schedule as contained in the fmGA that is based on the assumption that binary thresholding selection continues to evenly grow all the building blocks is not correct. Test runs showed that during the late stages of the primordial phase, one of five building blocks started to grow at a much higher rate, leading three other building blocks to the verge of extinction. Kargupta mentioned that the thresholding selection works to create niches in which two strings are members of the same niche if they can compete with each other in the thresholding selection. Thresholding selection allows for comparisons between strings of the same class but also allows for some cross competition to get rid of the bad relations. Now if a niche for string is too small, the growth of the string is restricted, but if the niche is too large, the cross competition will be very high and the string will be able to compete much more, possibly giving it many more copies. Therefore, one possible design objective for choosing a filtering schedule is to minimize drastic changes in the size of the niche, which is what Kargupta stated and implemented. This change improves further on the fmGA since the relations are now better balanced so that the algorithm can process them better. Once again, a closer look to relations led to better results.

Still not everything is perfect in the fmGA, even after the extensions provided. The first and foremost point as stated by Kargupta [23] is that the fmGA only adequately adresses one problem of the mGA, which is the lack of implicit parallelism. The other problems of the mGA are therefore still present in the fmGA. The main problem is that maintaining all the good building blocks during the filtering stages may become difficult because of cross competition amongst classes of good relations because of the way thresholding selection works. Also, the use of a single template might impose problems as gaps are always filled in from the same and single template which seems to be very narrow minded.

3.1.4 Neatly decomposing the search: *Gene Expression Messy Genetic Algorithm*

After the first two generations of messy genetic algorithms and gaining insight in the points where they are not fully competent, a new generation of messy GAs emerged, initiated by Hillol Kargupta [23, 21, 4]. Kargupta founded the framework named SEARCH wich offers a new perspective to BBO (Black Box Optimization) which concerns the optimization problems in which nothing is known about the structure of the problem on beforehand. In other words, all that is conceptually available is a black box which can be fed points from the domain to receive a function response. The goal then is ofcourse to find the point that when fed to the black box will either result in the maximum or the minimum value that the black box can return. This type of optimization problem implies that the search for the optimal solution has to be an inductive process that draws conclusions about the results gathered along the way. Kargupta [23] also noted that without any relation among the members of the search space, induction is no better than enumeration, which is exactly what we wish to prevent ofcourse, since the search space can be astronomically large. This calls for the search to find relations and this in a way confirms the need for linkage learning as already found in the early days of the classical GA.

In the history of the messy GAs, the relations sought really have been the type that help solve order k delineable problems. These type of problems are the ones that can be solved by observing no higher than order k relations. Even though the original mGA and the fmGA had a new representation that allowed a search for tight linkage, the linkage itself was not explicit enough and as witnessed, a lot of cross competition was introduced between strings from different classes. As such, the decisions made in class and relation space often interfered. Linkage was expressed by the juxtaposition of genes and the comparing of strings was allowed or not allowed following some threshold mechanism that observed the amount of common genes, which is exactly where the problems arise. To overcome this, a new representation is required in which the linkage is made even more explicit and handled more explicit. In the first good relation search performance version of the new messy GA [21], the GEMGA, that was created to this end, a more explicit search was done to find the order k relations. A first transcription phase sought for the appropriate order k relations and a second transcription phase determined the clusters of genes precisely defining the relations among those instances of genes. After in such a way creating the linkage sets, selection and recombination were used to make more instances of the better classes and to swap material respecting the linkage constraints respectively. The resulting algorithm is an $O(2^k(l^2+k))$ sample complexity algorithm that has been shown to indeed work properly for order k delineable problems. The reason that we do not further describe this algorithm however is the fact that the GEMGA is liable to quite frequent changes as its initiator Kargupta looks more closely for the equivalence with natural evolution. We therefore wish to only discuss the latest version of the GEMGA that is described by Bandyapadhyay, Kargupta and Wang [4].

Before describing this algorithm, we should give a brief review of the things Kargupta found when investigating more thoroughly the results found in biology about genetics and evolution. As we shall see later this section, the way natural evolution actually works might show that the creation of algorithms in evolutionary computation have yet been too narrow minded. The main point emphasized in the work of Kargupta is the importance of search space *symmetries*. A definition symmetry is the way in which a certain pattern does *not* change when some transformation is applied to it. The pattern under observation in the case of BBO is the objective function value since how good a certain class of solutions within the search space is, is determined by the objective function values of the members of the class. For instance, a class with only good members (all high fitness values for maximization) has a symmetry in a qualitative sense since the fitness value remains high under the transformation that turns one member of that class into another member of that class. It thus follows that a set of symmetries defines a set of different classes, which in turn define a relation. There are a lot of details that follow this important notion and can be read in the work of Kargupta [22]. We shall only report the result which notes that the search for relations really exists in two steps, being on the one side the search for the appropriate functions using some basis that captures the local symmetries or in other words not more than the idea of linkage learning so far. On the other side, there is the notion of finding a basis over which to find the symmetries or in other words, chancing the representation in such a way that the symmetries can be captured. The ideas this is based on are found later in this section. As a summary, we note that the foundation to this idea is what has been called *gene expression* in biology.

The notion of *gene expression* is the transformation of the information coded in DNA to the proteins which are responsible for almost every activity of a living being. Thus, gene expression constructs representation in natural evolution, whereas *all* current attempts in evolutionary computation work on no more than a priori defined representations. The new messy GA, called the GEMGA or the Gene Expression Messy Genetic Algorithm, is no exception to that unwritten (and in the future to be broken) rule. Really, the GEMGA pays better attention to linkage than did the mGA and the fmGA and as such is a novel algorithm. It searches for the set of symmetries in the search space to make the right decisions in defining relations and classes for order k delineable problems. Once again we point out however, that the GEMGA uses a fixed representation just as do the other GAs so far, even though the gene expression term in the name suggests otherwise. Given this background on the GEMGA, we shall now introduce the parts that make up this new messy genetic algorithm based upon the latest known version of the GEMGA [4] at the writing of this paper.

The representation that the GEMGA works on is just as much a redirection to a binary string as was the case for the original mGA and the fmGA. In other words, the GEMGA uses a coding that defines values and loci which together tell us how to make up the problem coding string that is represented. Whereas the mGA had a pair for every entry in the string, the GEMGA has a triple which contains the locus, value and capacity for the entry, which is really called a *gene*. The locus and value are no different than they were in the mGA, but the capacity is a new notion which is no more than a positive real value. The string is however not restricted to genes only as has been the case for the GA, mGA and fmGA. Strings in the GEMGA also contain a linkage set which is a set of weighted linkage lists. Each of such lists contains a list of loci that determine which genes are related. Furthermore for each such list a weight, goodness and trails field is reserved. The weight of a list measures the number of times that the genes in that list are found to be related in the population. The goodness is a value that indicates how good the linkage of the genes is in terms of its contribution to the fitness and the trial field indicates how many times the linkage list has been tried so far. The complete linkage set defines the relation space of the GEMGA and is thus *completely* separated from the sample space as opposed to earlier (m)GAs. Finally, the string has to be completely and precisely specified, implying that we need to templates to fill in the gaps and that we do not have multiple genes with the same locus (overspecification). Note how the explicit linkage sets are different from the mGA and removes the need for some thresholding selection scheme which was deemed a problem.

The size of the population in GEMGA is dependent on the value for k, just as was the case for the mGA and the fmGA. As the GEMGA searches for symmetries using schemata, it requires to have at least one instance of the optimal order k schemata in the population. This implies that the population must be of size 2^k at the least to expect to have one instance of an optimal order k schema. Not knowing the value of k on beforehand and setting the population size to some constant times 2^k, it must be noted that the order of relations processed equals $k = \frac{\log(n/c)}{\log(2)}$.

The first phase in the GEMGA is the transcription phase, the name of which stems from the transcription operator that is found in nature which forms mRNA from DNA and thus translates strings in one code into strings in another code. As was stated before, the GEMGA uses only one representation and thus transcription is restricted to a transformation over the given basis to detect search space symmetries. What happens is that for every string, each bit is flipped and the change in fitness is observed. If the change results in an improvement of the fitness value, the original gene value does not belong to the instance of the best schema because the fitness value can be further improved. The capacity of the gene is then set to one, indicating that the gene has a capacity to change by one. Otherwise, the capacity is set to zero. The original bit value is restored to the gene. If the capacity was reduced to zero, the bit is placed in the initial linkage list, which is the first list in the linkage set. This list is assigned values 1, 0 and 0 for the weight, goodness and trial factors respectively. What thus has happened is that all bits that by flipping only their value alter the fitness value for the better, receive a capacity value of one and are said to be linked initially.

The transcription phase is followed by a phase in which solely a new operator is applied, being the recombinationexpression operator. The operator deviates from most of the recombination operators seen in many GAs for the fact that a lot of time is spent on the investigation of the linkage information. In other words, whereas the most recombination operators in the history of GAs directly swapped information, the recombinationexpression operator of the GEMGA is a more composite operator that does more explicit searching and exploration. To be more precise, the recombinationexpression operator consists of two phases, the prerecombinationexpression and the actual recombination phase. The prerecombinationexpression operator takes two strings and investigates the initial linkage list (recall this is the first list in the linkage set of the string as created in the transcription phase). For each locus in the initial linkage list, if both the value and the capacity of the gene indicated by the locus are the same for both strings, the locus is added to a new temporary linkage list. When all loci in the initial linkage list have been iterated, the algorithm checks to see if the thus created temporary linkage list is already present in the linkage set of the first string. If this is so, the weight of that list in the linkage set is increased, otherwise the temporary list is included as a new linkage list in the linkage set of the first chromosome. When a certain amount of times this prerecombination operation has been undertaken, a matrix is constructed with conditional chances $p(X_i|X_j)$ for entries (i, j) that indicates the chance that gene i occurs in a linkage list of a chromosome that already contains gene j. Based on this matrix, the final linkage is computed. This is done by iterating the rows of the matrix and for each row i finding the maximum value. Every gene j that has its probability value $p(X_i|X_j)$ within some value ε of the maximum value is included in a new linkage list that also includes gene i which receives the average probability of every gene in the set as its weight. If the list is not already present in the linkage set, it's added to the set. The construction of the matrix and the gathering of the final linkage is done for every string in the population anew. After all of this, the actual recombination takes place iteratively on pairs of chromosomes. This is exactly what is written down in the original presentation of the new GEMGA [4] and it is unclear (as are many factors in this unfortunately very blurred and unprecise description of the GEMGA) how many times the recombination is applied, but we expect this to be $\frac{n}{2}$ with n the population size as it is stated that the pairs are taken iteratively, leaving it to the imagination that from the entire population two strings are picked until there are no strings left to pick. In any way, the recombination operator that handles exactly two strings selects from the first string one of the linkage lists based on a linear combination of goodness and weight. All linkage lists that are disrupted in the other chromosome because of possible swapping of the genes in the selected list are iterated and the maximum weight, maximum goodness and maximum trials are found among them. A linkage list is disrupted if the selected list contains loci that are not contained in the linkage list. Any swapping then violates the linkage relations in that linkage list. If the maximum goodness found among those disrupted lists is smaller than the goodness of the selected list, the gene swapping is actually performed by swapping the values at the loci in the selected list. The linkage sets are adjusted accordingly as is stated by Bandyopadhyay, Kargupta and Wang but it is nowhere mentioned how and why this is done. The fitness values of the two adapted strings are determined and if the new string from which the linkage list was *not* selected is better than its old version, the selected list is good and its goodness is increased in the new string and the old string from which the linkage list was selected. Otherwise, the goodness value is decreased. Finally, two strings are selected to be retained at the end of the recombination phase. Concluding, once again the operator pays direct attention and respect to the linkage information contained in the strings in an explicit manner. It is expected that the relations sought should very well be found in this way. We are now ready to provide the operational description of the GEMGA:

```
$t = 0$
$initialize(P(t), k)$
for each genome $g$ in $P(t)$ do
    for each locus $i$ in $g$ do
        $transcription(g,i)$

$t = 0$
while $t \neq t_{\max}$ do
        repeat $NoOfLinkageExpt$ times
        $preRecombinationExpression($ $randomMember($ $P(t)$ $)$, $randomMember($ $P(t)$ $)$ $)$
        for each genome $g$ in $P(t)$ do
            $m = computeMatrix($ $g$ $)$
            $getFinalLinkage($ $g$, $m$ $)$
        for $\frac{n}{2}$ random unique genome pairs $(g1, g2)$ from $P(t)$do
            $recombination($ $g1$, $g2$ $)$
        $t = t + 1$
        od
```

Incorporating the above framework in the *EA Visualizer* is really quite simple when a new *Population* object is created especially for the GEMGA, which takes care of the initialization and transcription phase as the complete initialization phase. Furthermore it is obvious that a new *Genotype* will need to be created to store all the extra data required. Finally, the whole of precombination and recombination can be seen as one *Recombinator*, making the GEMGA really a very limited algorithm in terms of requirements from the *EA Visualizer* and as such *easy* to implement.

The GEMGA algorithm above has a sample complexity of $O(2^k l)$ with k the order of relations to still be detected and l the problem coding string length. It is clear that the initialization takes already that complexity as there are $O(2^k)$ population members of length l to be randomly initialized. The transcription phase loops over all the population members as well as their positions again with an $O(1)$ function call, making that phase not violate the running complexity bound. As the maximum of generations as well as the amount of times the prerecombinationexpression function is called, are regarded as constants, the entire complexity to run the algorithm is still $O(2^k l)$ as the complexity to compute the matrix as well together with getting the final linkage is $O(l)$ and is performed for every genome in the population and finally recombination is applied $O(2^k)$ times and takes $O(l)$ sample complexity. The running time for this however seems to be $O(l^2)$, minded that the total length of the linkage sets can become up to $\sum_{i=1}^{l} O(l) = O(l^2)$. This is however nowhere mentioned in the work of Bandyopadhyay, Kargupta and Wang [4] that introduced this version of the GEMGA. Experiments show that indeed the GEMGA scales up perfectly linear with the amount of function evaluations for test problems and that it always finds the optimal value.

The GEMGA as we have seen is thus a logical step in the direction of linkage learning and actually even calls for goals beyond that type of relation learning. These larger goals have not been adressed so far, but the set up and the background against which the GEMGA was created holds an interesting thought for the future. The linkage problem is now adressed with almost full explicitness as the linkage is kept completely separate from the rest of the genetic material. The way in which the linkage information is processed shows that the GEMGA acknowledges the class space and the search for symmetries to find relations which in turn account for solving the linkage learning problem. This all is accounted for by trying out bit flips and witnessing their influence in the fitness landscape to in such a way determine the symmeteries that make out the classes. Concluding, the GEMGA cleanly decomposes the search in class, relation and sample space just as proposed in the SEARCH framework and does away the linkage learning problem completely, albeit with a restriction to the order of relations that can be detected, namely those of order k or less.

3.1.5 Not to put too fine a point on it: *Linkage Learning Genetic Algorithm*

The latest algorithm in the quest for solving linkage learning or in the larger picture in the quest for finding competent GAs, is the linkage learning algorithm invented by Georges Harik [16]. Beholding the name of the new GA, we ofcourse expect that the linkage problem is solved by this algorithm as there is not put too fine a point on it that this algorithm is designed especially to tackle this problem. Having learned from problems imposed by the first and subsequent attempts to tackle the linkage problem and all the interesting theories that followed from it, the linkage learning GA (LLGA) overcame once again problems of previous attempts just as did the predecessors. After first employing investigation to a new approach to linkage learning [18], the LLGA was initiated [16] and subsequently improved upon to allow for a larger variety of problems to be solved efficiently [25]. The work described here is the most recent in the field of linkage learning published at the time of writing of this paper.

The strings that the LLGA works on are no different from the ones used in the mGA. In other words, a string contains entries which are (*locus*, *value*) pairs that specify what *value* (`0` or `1`) the problem coding string has at what *locus* (binary string index). There are however three differences in using the string. First of all there is a conceptual difference in interpretation. Whereas strings in the past have always been handled as the equivalent of a line with a starting and an end point, the string in the LLGA is extended with an interpretation point from which the string should be read to the right until the interpretation point is found again, starting at the head of the string when the end is reached. In other words, the string is the equivalent of a circle instead of a line. The genes are located in a circle, meaning that there normally is no beginning and no end, which is why the interpretation point is introduced, from which the string is read in a clockwise fashion. There should actually be no need to read the string in any direction if the string were to be precise and complete in its representation, but overspecification is once again allowed as was the case for the mGA, justifying the need for a reading direction along the circle. The form of specification is the second difference with the mGA strings. The strings are not allowed any underspecification, which does away with the need for templates. However, overspecifications are allowed. To be more precise, for every locus it is allowed to have one entry for the expressed allele and at most two (and at least one) entries for the unexpressed allele. In other words, when the string is read clockwise and starting from the interpretation point, the first time any locus i with $i \in \{1 \ldots l\}$ and l the problem coding string length is found, this is called the expressed allele as this value is place in the problem coding string that is represented by the LLGA string. Any other entries in the LLGA string found with the same locus i furtheron in the string is just as was the case for the mGA neglected in constructing the problem coding string but thus is also only allowed to have the opposite of the bitvalue the first entry with locus i had. Furthermore, only two of such extra entries with locus i are allowed. This is called the extended probabilistic expression (EPE–2) introduced by Harik [16]. The third difference with the mGA string (which is really not a difference with the string but with the way they are used by the algorithm) is that non–coding genes are allowed. This means that the string is allowed to have genes that contain loci that do not contribute to the problem coding string. For instance, if the problem coding string has length l, the amount of different loci to choose from could for instance be set to $3l$, meaning that all loci $l+1, l+2, \ldots, 3l$ point to problem coding string positions that are not present. The EPE–2 expression for the coding *does* apply as well to these non–coding genes however, implying that the problem coding string length in our example could yet be seen as having length $3l$ but when computing fitness, the extra bits are discarded after all.

The idea of incorporating non–coding material stems from research in biological systems in which it is found that about 97% of human DNA is non–coding for instance. These non–coding genes are sometimes called *introns* in the evolutionary computation community. It should be noted at this point that the inclusion of genetic material as is done in the LLGA allows for maintenance of diversity of building blocks because of the EPE–2 expression mechanism which always holds every complement value at each locus at least once in the string. The interpretation point changes the actual problem coding string that is represented. The problem that was introduced by the use of the thresholding selection that was required for the underspecified strings of the mGA is no longer needed here because underspecification is not allowed. Also, a single copy of the desired building block had to be present either for sure (mGA) or probabilisticly (fmGA). In the case of the LLGA, all building blocks are actually present in all strings because every problem coding string is a combination of the material in the LLGA string as for every locus, both the binary values `0` and `1` are present. So a recombination operator working on the juxtaposition of loci that make up building blocks, just as was the case for the mGA should always have enough material present to work with.

The recombination operator indeed is one that once again makes the algorithm look for tight linkage through the juxtaposition of loci that make up building blocks as was the case with the mGA and the fmGA. The improvement made by the GEMGA by removing this less explicit form of linkage was one way to solve the problem really introduced by thresholding selection. The new representation in the LLGA with the always overspecified and never underspecified string however is a solution as well because thresholding selection that introduced cross competition in the search in the class space is eliminated. The recombination operator shares much with the two–point crossover operator from the classical GA. For every two parents a single offspring is generated. One parent is marked the donor and one parent is marked the recipient. In the donor string two cross points are selected which make up the part of the circle that will be transferred to the recipient. The part chosen from the circle is the part found by traversing the circle–string direction used when constructing the problem coding string, namely clockwise. In the recipient string a single grafting point is selected where the material will be injected. This point will also be the new interpretation point (starting point for finding the problem coding string) for the offspring. After the injection of the donor material in the recipient string, the so constructed offspring is traversed starting from the interpretation point in clockwise direction so as to delete genes that make the new offspring no longer be a legal EPE–2 string.

Research has been done with respect to the implications of the usage of this exchange operator. An important issue is ofcourse whether the learning of linkage can be done fast enough with this operator to outrun the selection operator because in the case of the classical GA and the proposed solution to the linkage problem, the inversion operator, it showed that selection was too fast for the linkage to be learned. Harik [16] showed that when the selection rate is chosen properly, the crossover operator above brings the genes that constitue a building block closer together. Harik also showed that the LLGA is very efficient in the solving of problems with exponentially scaled building blocks, just as much as it doesn't perform that good on uniformly scaled problems. Results showed that a requirement for solving these problems efficiently is an exponentially growing amount (with the amount of building blocks) of non–coding genes. To remedy this, the latest addition to the LLGA is the coding of *compressed* introns.

The introns themselves are hardly interesting as they will never have an impact when finding the problem coding string that is represented. Therefore the information contained in them is really superfluous and the only thing that is interesting is the fact that they are there. Minor detail in this is that the introns *do* obey the EPE–2 coding, making it slightly more interesting than just to know that they are there. Neglecting this latter detail however, subsequent introns can be compressed into a single compressed intron that does no longer code (*locus*, *value*) pairs but only the amount of introns it replaces. This implies that the string will never be longer than $6l$ with l the problem coding string length because every expressed allele appears exactly once, meaning l genes, every opposite of the expressed allele appears at most twice, meaning at most $2l$ genes and in between every of these $3l$ genes placed in a circle a compressed intron can be placed, meaning another $3l$ (non–coding) genes. In other words, the LLGA string length is $O(l)$ and no longer exponential in size with the increasing amount of building blocks or for that matter dependent of the amount of building blocks at all. Working with the compressed introns is not much more difficult. The only adaptation is the recombination operator since the introns had nothing to do with the problem coding string anyhow. Choosing crossover points can however still be done as if there were so many genes, splicing compressed introns when necessary to make the transferred substring to the recipient. As before, no genes are deleted from the transferred (also called grafted) material and coding genes that destroy the EPE–2 coding are deleted from the rest of the material. This was before also done with the non–coding genes, which is now impossible as the exact information about the contents of the introns is lost within the compressed introns. To remedy this and thus to simulate the deletion of non–coding material according to the EPE–2 scheme, n introns are removed uniformly from the compressed introns where n is the amount of introns represented in the grafted material. All of this is no more than a logical and not difficult extension to the original LLGA with explicit introns. Results [25] show no problems and virtually the exact same performance of the LLGA with and without the compressed version of the introns on the exponential problems. We shall therefore regard the compressed introns version of the LLGA as the LLGA as it was introduced to remedy certain problems and it didn't degrade the performance in other fields and we can now provide the operational description of the LLGA:

```
$t = 0$
$initialize(P(t))$
$evaluate(P(t))$
while not $terminate(P(t))$ do
        $sel = select\ by\ tournament(P(t))$
        $mat = mate\ in\ groups\ of\ two(sel)$
        $rec$ = for each mated collection $m \in mat$ do $recombine(m)$
        $P(t+1)$ = each offspring genome $g$ in $rec$
        $evaluate(P(t+1))$
        $t = t + 1$
od
```

The initialization phase is done at random and as is clear from above, tournament selection is used as a standard. The similarity with the classical GA is very much so apparent and the only thing missing really is a mutation operator. This mutation operator has been left out on purpose however since it does not stroke with the learning of linkage that has been made rather explicit in the setup of the LLGA. The selection round might have to select twice as many individuals as was the case for the classical GA because the recombination operator for the LLGA has only a single offspring genome. This information is nowhere found however in the description of the compressed introns LLGA [25]. The above outline algorithm for the LLGA is so greatly similar to the classical GA and bears certainly no more complexity than the mGA and the fmGA which we already showed to fit within the *EA Visualizer*, that we really must conclude that fitting the LLGA into the *EA Visualizer* is almost trivial and that it should be clear to the reader how this is done.

The results of the LLGA are quite interesting. An interesting fact to note is that it is nowhere mentioned what building block sizes can be processed given what size of the population which was the case for the messy GAs as described earlier. The population sizing issue is actually mentioned nowhere in the work that this summary was based on, but some means of this factor must really be present. It is stated however [25] that for the type of problems tested (crips building blocks introduced in artificial problems) the initial supply of building blocks dominates the population sizing as correct decision making is secondary since there is almost no noise coming from the other partitions.

Concluding, this last breed of linkage learning algorithms has together with the GEMGA a great potential for finding that breakthrough GA that will efficiently and robustly solve problems both easy and hard (under certain conditions). Using the right instruments and codings, the potential of the new GA that directly supports the learning of linkage is indeed very large.

3.1.6 A different perspective: *using a probability density estimator*

Of late, new approaches to GA like problem optimization have come into being that can be placed in the history of linkage learning. Linkage learning is a term that has come forward out of the classical GA history and is therefore deemed to be tackled by a GA that allows for finding relations to aid its selection and recombination of material. However the notion of linkage learning can be taken in a much more general fashion just as was stated at the introduction of linkage learning, namely as the cohesion of the bits in the coding string with respect to the fitness landscape (search space). The important thing is thus finding structure amongst the bits and exploiting the thus found structure. In terms of GAs the idea was to find the building blocks and respect the building block borders in the exchange of material between strings. However, this is not the only way in which the linkage information can be processed. When the linkage information is made more explicit in terms of statistics, one might be able to say things such as bit i is set to 1 with chance 0.9 when bit j is set to 0 implying that a certain linkage has been found between bit j and bit i. This is exactly the new perspective that has been employed by De Bonet, Isbell and Viola in the creation of MIMIC [6] and in an extended version by Baluja and Davies [3].

The exact contents of this novel approach initiated in 1996 and extended in 1997 are in a detailed manner set out in section 3.2.1, so we shall refrain from that here. In a historic overview of processing linkage information however, we need to note this new approach and therefore we thus present this notion here. Even though the GA approach has a much richer history through the mGA, fmGA, GEMGA and LLGA over the past ten years, the new approach is interesting and prooves that we should not fall into a closed world assumption. Incorporating explicit statistics is actually something that the GEMGA was already making use of as it computes a conditional probability matrix based on information found in the individuals. The GEMGA prooved to be a good algorithm so it is natural to question ourselves how much better the new approach is in which the concept of explicit statistics is fundamental and the more random GA approach is disposed of. Furthermore, it is very interesting to note that *no* restrictions are posed a priori with respect to the order of building blocks in the problems that can be solved. If only for these reasons it is already interesting to investigate this approach more closely and perhaps to find if GA history can be dispensed of or that the new approach is really lacking insight and can never be compentent enough. As in this section we are only interested in the history of linkage learning, we refrain from further expedition along these lines and refer to section 3.2.1 for a detailed description of the new approaches and to section 3.2 in general for an investigation of their competence.

3.1.7 Beyond linkage learning: *scrutinizing the ways of natural evolution*

The field of evolutionary computation received its name because of the attempted equivalence in operational dynamics with behaviour observed in nature. It is hypothesized that nature has constructed through evolution highly advanced, complex and efficient structures such as mankind and plantlife. Under this hypothesis it is important to understand the ways of nature as close as possible. Many things in natural evolution as well as the biology of current life however are not understood yet. On the other hand, this real–life research equivalent of evolutionary computation has also undergone progress over the years just as well and gradually more of nature is understood.

As researching the ways of nature and subsequently drawing parallels to evolutionary algorithms incorporating equivalences of behavioural observations of nature is the way in which evolutionary algorithms will be lead into new generations and hold technologically innovative methods, a closer look at the natural evolution is of the essence.

Whereas we shall refrain at this point from introducing novel discussions or ideas to this end, the future will most certainly hold investigations thereof. To give an idea of the impact this approach may have, we shortly go over the work of Kargupta and Stafford [24] and earlier by Kargupta alone [22] so as to take a closer look at the coding in real life, which is DNA, and how life comes into being from that coding. The work was done in the line of the SEARCH framework by Kargupta [23] that already brought forward ideas about relations and classes in a more general setting than simple gene linkage as well as led to introducing the GEMGA which we discussed earlier.

As we are discussing the past, present and future of linkage learning and at this point actually only the future part, it is interesting to note that linkage learning in its basic concept has after some ten years perhaps come to its end. The basic concept of linkage learning is the identification of equivalence relations between gene loci. Kargupta and Stafford [24] mention that this is a restricted form of finding patterns in the search space as there are symmeteries in the search space that are not to be captured by only similarity subsets such as the pattern induced by two strings 1111 and 0000 in which thus the building blocks are not important but the patterns themselves. Looking toward the way nature works with codings and search spaces, the sought equivalent might very well be found in the concept of DNA. The coding that is DNA is the carrier of genetic information, which is the equivalent of the problem coding strings in genetic algorithms. Information flow in evolution is taken to be two–fold, namely extra–cellular and intra–cellular where extra–cellular is the storage, exploration and transmission of genetic information over generations or in other words the recombination and mutation as found in GAs over the years. The intra–cellular flow of information however is little observed so far. In nature, proteins are responsible for almost every activity of a living being. Proteins are created through a process called gene expression of which not all stages are understood, but it involves the transcription of DNA into mRNA and the transformation of mRNA into proteins. Without going into details, Kargupta and Stafford [24] noted that transformations from mRNA into proteins are fitness invariant symmetry transformations with interesting characteristics. The transformations seem to define relations that define fitness invariant patterns (that thus define classes) of the search space. These patterns are not restricted to the restrictive linkage learning that has so far been sought to incorporate in GAs.

Summarizing, the concept of linkage learning as the detection of related genes is quite restrictive as noted by Kargupta and Stafford [24]. Intra–cellular flow is something hardly adressed by GAs so far (with the exception of the GEMGA which contains mediocre equivalences to this issue) and might yet be capable of capturing important relations that lay out the structure of the search space to subsequently allow for fast optimization. The main conclusion should be here that where GAs were initiated with as the underlying metaphore natural evolution and was subsequently scrutinized to find shortcomings and to address these to amongst other things find more shortcomings, remembering that the parallel is natural evolution and acknowledging that through observing progess in biology and drawing parallels with that field of science is an important aspect in finding efficient methods and ways to perform optimization that have yet been missed in evolutionary computation but are of such fundamental importance, implying that the future of evolutionary computation and the broader aspect of linkage learning is still open and holds still to bestow upon us more interesting features for finding competent GAs.

3.2 Linkage through explicit probability density estimators

In section 3.1 we gave an history overview of the efforts towards linkage learning. It became clear in that section how the notion of linkage has come into being and why it was and is deemed important. We have also seen a subsequent amount of trials to tackle the linkage problem so as to construct a competent GA or at least one that distuinguishes itself from the classical GA in performance because of the acknowledgement and usage of linkage information. In section 3.1.6 we briefly introduced a special type of algorithm that has a different approach to processing linkage information. We refrained ourselves from specifying the details of the algorithms in the new field but provided a notion of how these algorithms work.

The new approach consists of the incorporation of explicit statistical information with respect to linked bits in the problem coding string. Unlike the classical GA or any of the subsequent linkage variants, there is no recombination operator in the classical sense that swaps genetic material between parent strings. Rather there is a mechanism for generating samples (problem coding strings) and a way to extract explicit statistics from them, which are subsequently used to generate more samples. This novel approach to finding relations amongst bits is interesting to further investigate as the GAs adapted for linkage learning have been well tested and understood in what they can and can't do. The new approaches however are merely introduced and hardly put to the test. The introductory tests by the authors showed interesting results and we question ourselves therefore what the competence of this novel approach is and whether the evolutionary approach that has been with us for some 25 years has been surpassed by explicit statistics that have much less to do with nature and evolution.

It is therefore interesting to see what makes the algorithms under the new scheme work and to what extend they are capable of solving problems that contain building blocks both uniformly and exponentially scaled which are the problems tested by all the for linkage learning adapted GAs. It follows that there are many interesting questions to be answered through investigation. Such investigation we shall employ in the remainder of this section in an experimental fashion, using the *EA Visualizer* to help us in establishing both insights in the competence of the new algorithms as well as a futher confirmation of rudimentariness of the system as these from more classical evolutionary algorithms deviating algorithms are fit into the *EA Visualizer*.

In section 3.2.1, a detailed description of the new frameworks that incorporate the explicit statistics is given. In the following section, section 3.2.2, we show how the new algorithms fit into the *EA Visualizer*. This is a more extensive description than we gave for the algorithms in the description of the history of linkage learning as we want to show here more precisely how the incorporation is done to provide the user with yet more a feel for the system. As the frameworks are actually implemented, the detailed description is yet more called for as well as very precise. Section 3.2.3 describes the running of tests for the first time on the new frameworks and observing their behaviour. Conclusions are drawn as to why things go right or wrong. In section 3.2.4 we attempt to find out what makes one algorithm better than the other under the new framework as we investigate the influence of differences between them. Finally, in section 3.2.5 topics for future research are summed up that have not been adressed here but are interesting in the light of what was found in section 3.2.

3.2.1 In theory: MIMIC and beyond

In this subsection we present two frameworks that attempt optimization through the direct usage of probability density estimators. The most fundamental of the two is named MIMIC, which we shall discuss first. The other framework is based upon MIMIC and extends it by using a less restricted way for the generation of probability distributions. We present the theory for both frameworks by giving background information as well as actual algorithms.

MIMIC
The framework known as MIMIC [6] is the first to attempt to find optima by estimating probability densities. MIMIC stands for *Mutual Information Maximizing Input Clustering* which expresses the general idea of the framework: trying to find clusters in the coding structure by maximizing the linkage information between pairs of bits. Before going into details that specify how this is

achieved within MIMIC, we should think about what this means. To this end we picture binary strings like in genetic algorithms. Finding linkage information between pairs of bits would then mean that we find for every bit some other bit that it is linked to according to some measure. This measure should be the implementation of something like the following expression:

> When bit a is linked to bit b, this means that there is a meaningfull relation specifying that when bit b is set to 1, bit a is set to 1 with a certain chance.

In more mathematical terms, this would mean that there is a conditional chance $p(a = 1|b = 1)$ that "makes sense" when we link bit a to bit b. Now since we work with *pairs* of bits, for every bit there is exactly one other bit that it will be related to when we wish to create a full probability distribution. To keep the distribution connected, we do not wish to generate subcycles and we will get some form of a tree in which each bit has at most one parent bit in the tree. In the light of what we just noted above, the child bit is then bit a and the parent bit is bit b. Note that indeed linking bits is in this way a *one–way* relation. If the relation was not *one–way* we could get direct subcycles and we would not get a connected distribution. Both MIMIC and the framework in the next paragraph work with such restricted models, which is why we introduce this notion. As we shall see, MIMIC further restricts the form of probability distribution to a specialized tree: the chain. The more recent framework in the next paragraph removes this restriction. We shall now move to more specific and mathematical terms to make precise the MIMIC framework. In the following, parts and fragments from the introductionary paper for MIMIC [6] are repeated.

The joint probability distribution over a set of random variables $X = X_i$ is

$$p(X) = p(X_1|X_2 \dots X_n)p(X_2|X_3 \dots X_n) \dots p(X_{n-1}|X_n)p(X_n)$$

From a practical and engineering point of view this reads from right to left something like:

> We can set bit n to 1 with a certain chance $p(X_n)$. Once we do such, we can set bit *n-1* to 1 with a certain chance because we have been given the value for bit n and we know the conditional chance $p(X_{n-1}|X_n)$ which tells us with what chance to set bit *n-1* given the fact that bit n is valued either 0 or 1. The remainder of the expression to the left is analogous.

Ofcourse what the expression says is that the chance at X having some value, or to be more precise the chance at every X_i having some value a_i, is equal to the chance that X_n has value a_n multiplied by the chance that X_{n-1} has value a_{n-1} given the fact that X_n has value a_n and so on. Why this is true is explained in the following simple general example with $n = 3$:

$$\begin{aligned} p(X) &= p(X_1 = a_1|X_2 = a_2 \wedge X_3 = a3)p(X_2 = a_2|X_3 = a_3)p(X_3 = a_3) \\ &= p(X_1 = a_1|X_2 = a_2 \wedge X_3 = a3)\tfrac{p(X_2=a_2 \wedge X_3=a_3)}{p(X_3=a_3)}p(X_3 = a_3) \\ &= p(X_1 = a_1|X_2 = a_2 \wedge X_3 = a3)p(X_2 = a_2 \wedge X_3 = a_3) \\ &= \tfrac{p(X_1=a_1 \wedge X_2=a_2 \wedge X_3=a_3)}{p(X_2=a_2 \wedge X_3=a_3)}p(X_2 = a_2 \wedge X_3 = a_3) \\ &= p(X_1 = a_1 \wedge X_2 = a_2 \wedge X_3 = a_3) \end{aligned}$$

The last expression in the above derivation is trivial and something we all agree on being the expression for stating the chance that each random variable has a certain value.

So what we have now is a different expression for the same thing. The only difference is that we now use *conditional* probabilities. These conditional probabilities however are exactly what we described above in the intuitive description of finding linkage between pairs of bits. The only thing is that we were merely to use *pairs* of bits. This means that we cannot have subexpressions such as $p(X_1|X_2 \dots X_n)$ as each bit was only allowed to be linked to one other bit[11]. This implies

[11] So actually we are only regarding second order statistical information.

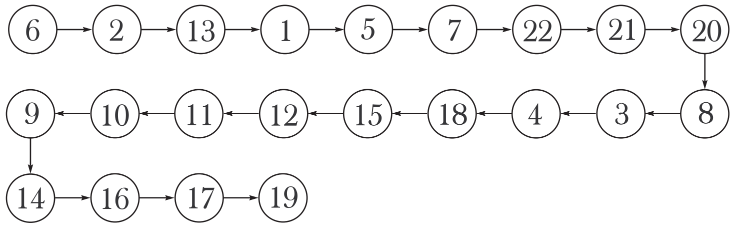


Figure 36: An example of the chain of dependencies generated by MIMIC.

that we can only create distributions of the following kind:

$$\hat{p}_\pi(X) = p(X_{i_1}|X_{i_2})p(X_{i_2}|X_{i_3})\ldots p(X_{i_{n-1}}|X_{i_n})p(X_{i_n})$$

In this expression π stands for a permutation of the numbers between 1 and n, $\pi = i_1 i_2 \ldots i_n$. The distribution $\hat{p}_\pi(X)$ uses π as an ordering for the pairwise conditional probabilities. The goal is then to find the permutation π that maximizes the agreement between $\hat{p}_\pi(X)$ and the true distribution $p(X)$. This agreement is measured in the paper on MIMIC [6] by using the Kullback–Liebler divergence, which is a nonnegative distance measure which is zero when two distributions are identical. When written out, it becomes clear that the optimal π is the one that minimizes the following expression:

$$J_\pi(X) = h(X_{i_1}|X_{i_2}) + h(X_{i_2}|X_{i_3}) + \ldots + h(X_{i_{n-1}}|X_{i_n}) + h(X_{i_n})$$

The fact that we have already chosen to use a permutation of $1 \ldots n$ to approximate the true joint distribution, leads to the fact that the resulting tree of dependencies will be a chain as can be seen in figure 36. To find the optimal permutation π, all $n!$ permutations could be searched. When n becomes even but medium large however, the amount of permutations to search is already intractably high. So in the interests of computational efficiency, the creators of MIMIC employ a straightforward greedy algorithm to pick a permutation:

1. $i_n = arg \min_j \hat{h}(X_j)$.
2. $i_k = arg \min_j \hat{h}(X_j|X_{i_{k+1}})$, where
   $j \neq i_{k+1} \ldots i_n$ and $k = n-1, n-2, \ldots, 2, 1$.

In this algorithm, $\hat{h}()$ is the empirical entropy. Given a discrete random variable X over an alphabet α, the entropy $h(X)$ is defined as follows:

$$h(X) = -\sum_{a \in \alpha} p(X = a) \log p(X = a)$$

The algorithm also uses the notion of conditional entropy $h(Y|X)$ where in the algorithm $\hat{h}(Y|X)$ is used to denote once again *empirical* entropy instead of true entropy. To work with the algorithm, we must provide the definition of conditional entropy first when we are additionally given a discrete random variable Y over an alphabet α':

$$h(Y|X) = h(X,Y) - h(X) = -\sum_{a \in \alpha} \sum_{b \in \alpha'} p(X = a \wedge Y = b) \log p(X = a \wedge Y = b) - h(X)$$

The only factor that is now unclear is the term *empirical.* This means no more however than the fact that the information on which the chances $p(x)$ are based, is computed from the information at hand. In the case of the MIMIC framework, this means that the required chances are computed from the individuals in the population. For instance, in the first line of the algorithm, the index of the variable with the lowest entropy is determined. We have seen that to compute the entropy $h(X)$ however, we need chances $p(X = a)$ for each $a \in \alpha$. We will be working with binary strings, so our alphabet α will be none other than $\{0, 1\}$. This means that we need to have $p(X_j = 0)$ and $p(X_j = 1)$, where the X_j are the random variables that represent the bit at the j–th position in the binary string. So we determine the empirical chance $\hat{p}(X_j = 1)$ by regarding every individual in the population, looking at the bit at position j in each such individual and counting the amount of 1 symbols we encounter. If we have counted m_1 ones at position j over the population which holds m individuals, we have $\hat{p}(X_j = 1) = \frac{m_1}{m}$ and ofcourse $\hat{p}(X_j = 0) = 1 - \hat{p}(X_j = 1)$, since our alphabet α has size 2. The computation is analogous for finding the values for $\hat{p}(X = a \wedge Y = b)$.

To compute all these empirical probabilities, we require for each string a running time of $O(n^2)$ where n is taken to be the length of the binary strings in the population. Over the entire population this implies a running time of $O(mn^2)$, which is the running time for the greedy algorithm presented above for finding the permutation.

What has been established so far is the creation of a probability distribution. A search component is still required, as we have only seen what to do given a number of samples to update the distribution but not the population. Given that distribution however, we can generate new samples in a straightforward manner as is described in the paper on MIMIC [6]:

1. Choose a value for X_{i_n} based on its empirical probability $\hat{p}(X_{i_n})$.
2. For $k = n - 1, n - 2, ..., 2, 1$ choose element X_{i_k} based on the empirical conditional probability $\hat{p}(X_{i_k} | X_{i_{k+1}})$.

There is nothing new here anymore since we have already shown how to compute the empirical probabilities that are required. The only thing that isn't directly clear from the algorithm is something that has been clarifed above already when we gave an engineering view on the joint probability distribution over a set of random variables $X = \{X_i\}$. The first step of the algorithm is clear, but the second step leaves it to the user to understand that once the value for X_{i_k} has been chosen to be a_{i_k}, the value for $X_{i_{k-1}}$ is equal to $a \in \alpha$ with chance $\hat{p}(X_{i_{k-1}} = a | X_{i_k} = a_{i_k})$ which is what we explained in words earlier. It means that to create a new sample, the string should be built up dynamically, from the right to the left with respect to the permutation π, incorporating the decisions made along the way.

The full MIMIC framework can now be specified:

1. Generate a random population of m candidates chosen uniformly from the input space. Extract the medium fitness and denote it θ_0.
2. Update the parameters of the density estimator of $p^{\theta_i}(x)$.
3. Generate more samples from the distribution $p^{\theta_i}(x)$.
4. Set θ_{i+1} equal to the Nth percentile of the data. Retain only the points less than θ_{i+1} (in case of minimization).
5. If the values of $C(x)$ have ceased to improve, stop. Otherwise go to step 2.

Steps 2 and 3 in the algorithmic framework above are the algorithms we saw earlier in this paragraph. Concluding, we can state that MIMIC attempts optimization by subtracting second order statistics from the better part of a population, using these statistics to pairwise relate bits and then to generate more samples from the established probabilistic relations, hoping that these samples will be better the the ones seen previously as the evidence for the linkage that was used to generate the new samples was subtracted directly from the better genomes in the population.

Baluja and Davies optimal dependency trees
In 1997 Baluja and Davies came forward with an extension [3] to the MIMIC framework. The idea at the outset is the same as with MIMIC. The approach is to try to learn the structure of the search space through the usage of a density estimator based on second order statistics. At first glance the only restriction dropped with respect to MIMIC is the form of the graph that is allowed for the linkage relations. Whereas MIMIC allowed only one chain of relations to exist to express the linkage between pairs of bits, the framework of Baluja and Davies (which has not been given a name) allows for probability distributions where each random variable is linked to exactly one other variable. The restriction is thus dropped that each bit also is allowed to *be linked to* by exactly one other variable. This means that the structure that can be used to estimate the true joint probability distribution of the set of random variables as introduced in the former paragraph, is now a tree in which each node is thus allowed exactly one parent but multiple children. Any bit that is now a node in the tree is linked to its parent. Just as with MIMIC there is one bit that is not linked, which is in this case ofcourse the root of the tree. How the structure of the tree is actually determined we shall see later on in this paragraph.

Even though the new structure for the probability distribution is the most obvious difference between MIMIC and the framework by Baluja and Davies, there are more nuances that just might make the approach fundamentally different after all. Just as with MIMIC, the framework by Baluja and Davies generates samples at each generation and just as with MIMIC the better few are chosen. However, this selection is now done from the generated samples only, whereas MIMIC retained the best samples selected from both the generated samples and the best samples seen so far. In other words, MIMIC has an elitist component that the framework by Baluja and Davies does not contain. This might just make the approach to be fundamentally different.

We shall now move again to more specific and mathematical terms to make precise the framework. In the following, parts and fragments from the introductionary paper for the framework [3] are repeated.

Even though MIMIC is the one that "remembers" the better individuals from the past, the framework by Baluja and Davies does not completely "forget" them. In the new framework an estimator array is maintained that holds for every (i, j, a, b) with $i \in \{1..n\}, j \in \{1..n\}, a \in \alpha, b \in \alpha$ a value that is an estimate of how many recently generated "good" bit strings have had bit i set to a and bit j set to b. To stress the influence of recently generated strings, the array is multiplied by a decay factor (a real value between 0 and 1) every generation. Just as with MIMIC, unconditional and conditional probabilities are determined empirically every generation. These values are however now computed directly from the estimator array. The array itself is updated every generation by looping over all strings in the population and incrementing the array at (i, j, a, b) when bit i has value a and bit j has value b. Based upon the mutual information measure $I(X_i, X_j)$ between all pairs of variablies X_i and X_j the tree is then generated. The mutual information measure is somewhat similar to the entropy measure used in MIMIC:

$$I(X_i, X_j) = \sum_{a,b \in \alpha} p(X_i = a \wedge X_j = b) \log \frac{p(X_i = a \wedge X_j = b)}{p(X_i = a)p(X_j = b)}$$

The mutual information measure is a measure for how closely two parameters are linked. The higher the mutual information, the greater the linkage. So in any algorithm that searches for the tree of dependencies we will want to find pairs that maximize the mutual information measure[12].

The final part missing in the description of this new framework is the creation of the tree. The authors have used a method for finding the optimal model within the restrictions posed for the probability distributions that was presented by Chow and Liu [5] in 1968. We shall not repeat that algorithm here, as it is part of the framework and is therefore part of the algorithm found at the end of this paragraph. The results are that the tree constructed minimizes the Kullback–Liebler

[12]This is contrary to the approach in MIMIC where the goal was to *minimize* the entropy. Note that the idea is the same, only the measures differ.

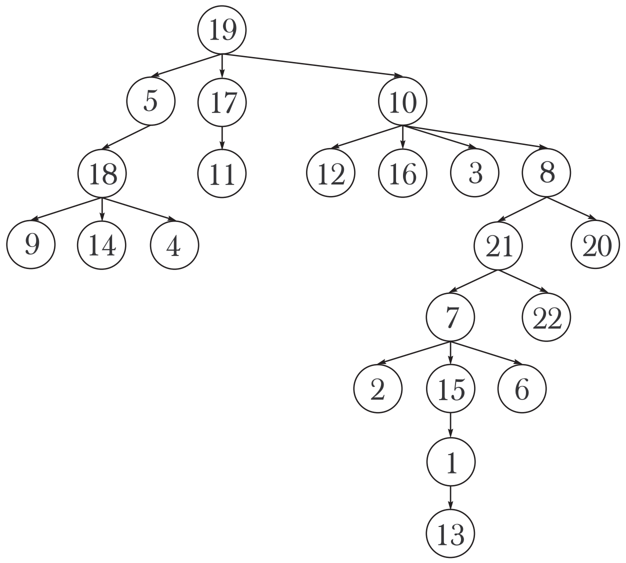


Figure 37: An example of the tree of dependencies generated by the framework by Baluja and Davies.

divergence posed in the paragraph on MIMIC that we sought out to minimize in the first place. An example of the tree structure that can now be found for the pairwise linkage between bits can be seen in figure 37.

The full framework by Baluja and Davies can now be specified (the following algorithm is a quote from the original paper [3] that introduced the framework):

INITIALIZATION:
For all bits i and j and all binary assignments to a and b, initialize $\mathbf{A}[X_i = a, X_j = b]$ to $\mathbf{C}_{\text{init}}$.

MAIN LOOP: Repeat until Termination Condition is met.
1. Generate a dependency tree

- Set the root to an arbitrary bit X_{root}.
- For all other bits X_i, set bestMatchingBitInTree$[X_i]$ to X_{root}.
- While not all bits have been added to the tree:
  - Out of all the bits not yet in the tree, pick the bit X_{add} with the maximum mutual information $I(X_{add}, \text{bestMatchingBitInTree}[X_{add}])$, using $\mathbf{A}$ to estimate the relevant probability distributions.
  - Add X_{add} to the tree, with bestMatchingBitInTree$[X_{add}]$ as its parent.
  - For each bit X_{out} still not in the tree, compare $I(X_{out}, \text{bestMatchingBitInTree}[X_{out}])$ with $I(X_{out}, X_{add})$. If $I(X_{out}, X_{add})$ is greater, set bestMatchingBitInTree$[X_{out}] = X_{add}$.

2.Generate $\mathbf{K}$ bit–strings based on the joint probability encoded by the dependency tree generated in the previous step. Evaluate these bit–strings.

3.Multiply all of the entries in $\mathbf{A}$ by a decay factor α between 0 and 1.

4. Choose the best **M** of the **K** bit–strings generated in step 2. For each bit–string **S** of these **M**, add 1.0 to every $\mathbf{A}[X_i = a, X_j = b]$ such that **S** has $X_i = a$ and $X_j = b$.

Concluding, we can state that the framework by Baluja and Davies attempts optimization in a way very similar to MIMIC. In fact, we could just as well call this second framework MIMIC as the difference is not all that much except for a greater expressional power in the same (limited) space of second order statistics. The fact that the two approaches are quite alike already becomes clear from the fact that the general introduction in the paragraph on MIMIC already really poses the natural result of the tree for the probability distribution. The tree could just as well have been taken as the chain, which would have caused MIMIC to be even closer to the framework by Baluja and Davies than it is now. Once again we state that the one difference that we wish to remain sceptic on at this point is the fact that MIMIC retains samples from previous generations and the framework by Baluja and Davies does not.

3.2.2 In practice: Implementing and using it in the EA Visualizer

In subsection 3.2.1 we have in detail described both theoretically and to some extend operationally to clarify the methodology, two evolutionary frameworks that attempt to perform optimization through pairwise linkage between bits. The theory brings a novel approach and it differs in some ways from evolutionary algorithms seen so far. For instance, classical genetic algorithms contain recombination and mutation operators that work on subsets of two individuals from the population and single individuals respectively. Furthermore with the whole structure that admits selectors, replacers and terminators, the classical genetic algorithm fits perfectly in the structure of the *EA Visualizer*. One could even say that the *EA Visualizer* was to a large extent fine tuned to work perfectly for such algorithms. How then do we incorporate a different framework such as MIMIC? Certainly it is an evolutionary framework as it uses old samples, learns from these samples and generates new samples that are again evaluated, but there is not an obvious operator such as recombination that directly swaps information between parents. However, we claimed the *EA Visualizer* to be a most general framework and part of the proof is ofcourse given in putting it to the test by implementing such alternative evolutionary frameworks as MIMIC. We shall first explain how MIMIC fits into the structure of the *EA Visualizer*. It is clear from the similarities between MIMIC and the approach by Baluja and Davies that the latter will most definately fit as well if we can make MIMIC fit into the *EA Visualizer*. We shall therefore concentrate on MIMIC and then briefly show how the other framework has been implemented as well.

MIMIC

To see how MIMIC can be incorporated in the *EA Visualizer* we should first reconsider the notion of *Recombinator* the way it was introduced when we set up the *EA Visualizer*. We should not be focused on wanting to have some direct mechanism that swaps alleles between two parents for instance. This is rather tempting ofcourse since such is the approach of many evolutionary algorithms, especially the classic ones. In general however, as we stated before, the *Recombinator* is an operator that simply receives parent genomes from the system and is required to generate offspring genomes. As such it is obvious what part of MIMIC this applies to. In MIMIC, all genomes are treated at the same time as information is extracted from the entire population. Therefore we require the *Recombinator* (which we will also call MIMIC in the *EA Visualizer*) to receive one group of parents per generation where this group is nothing less than the entire contents of the population. To ensure this, we require a new *Mater* that will mate all the parents into a single group.

We have now insured that every generation all the genomes from the population are passed on to the MIMIC *Recombinator*. It should be clear that this new operator implements most of the algorithmic contents of the MIMIC framework. The MIMIC *Recombinator* will generate the distribution (the linkage chain, see figure 36), generate the samples and return these samples as the offspring. The generation of the distribution and of the samples are exactly the two algorithms we saw in the paragraph on MIMIC in section 3.2.1. This however does not complete our incorporation of MIMIC in the *EA Visualizer*. The MIMIC framework also has its own way of retaining genomes. It generates more samples and then retains the Nth percentile as is written in the paper on MIMIC [6]. This is however something we can incorporate easily as we made the *EA Visualizer* capable of handling extensive selection mechanisms. We simply take as the *Before Selector* the selector that selects all genomes (which is really hardly any selection at all) so that all parents are preserved when shipping the contents to the *Mater*. The resulting parents from the *Recombinator* are then put through to the *Mutator* which we set to be the mutator that doesn't mutate any genomes at all. The thus resulting genomes are replaced into the population through the *Replacer* and it should be clear by now that we need to use the replacer that adds the offspring to the population so that the *After Selector* that is set to truncate the population at the Nth percentile will select the better genomes from both the old parents as well as the newly generated offspring.

The requirements for the settings of the other components is trivial, except for that of the *Terminator*. The termination condition is something that in the description of the MIMIC framework has not been made completely clear. Termination is supposed to occur "when values of $C(x)$ cease to improve". This could mean for instance that the average fitness does no longer improve, but it could also mean that the best fitness does not seem to improve. However, for as long as the genetic material within the population is not equal for every genome, the MIMIC framework might yet induce a new probability distribution that generates even after some time of no improving fitness values, better offspring. When we look more precise, what we are saying is that as long as the probability vector does not seem to have stabilized, we could yet find better values. Still yet, even when the probability vector *has* stabilized, we could still generate offspring we haven't seen before, unless it has stabilized with chances only set to 0 or 1. Under the assumption that the latter will happen, the *Terminator* that terminates when all genomes are equal can indeed be employed. To save ourselves from the situations in which the framework has problems with coming up with only equal genomes (for instance the probability for the last bit in the distribution is not 1 or 0 and all others are, resulting in two genomes that dominate the population), a maximum of generations is set.

The following table contains the settings that need to be employed to install the MIMIC framework in the *EA Visualizer*:

Component	**Instance**
Genotype	`Binary String`
Similarity	Any
Fitness Function	Any
Recombinator	`MIMIC`
Mutator	`No Mutation`
Before Selector	`No Selection (Select All)`
After Selector	`Truncation Selection`
Mater	`Mate All Genomes In One Group`
Replacer	`Add Offspring To Population`
Terminator	`All Equal Genomes And Maximum Generations`
Hybrid Searcher	Any
Population	`Vector Population`
PRNG	Any

Baluja and Davies optimal dependency trees
It should now be clear how the framework by Baluja and Davies can be implemented and installed in the *EA Visualizer*. In the following we shall briefly describe how this has actually been established.

Just as with MIMIC, a new recombinator is generated that does most of the mathematics that was introduced in the paper [3] that introduced the framework. This new recombinator prepares the estimate array by multiplying it by α, updates the estimate array from the samples by counting the different combinations for pairs of bits, generates the dependency tree from the estimate array and returns the newly generated samples as offspring. The selection mechanism for the framework is slightly different as the parents are not retained. This means no more than that we use as the *Replacer* the replacer that places only the offspring in the population. Just as was the case with MIMIC we decide to simply select to install the terminator that signals termination when all genomes in the population are identical or a maximum of generations is reached. The rest of the settings remain unaltered with respect to MIMIC (Note that all that had to be added to the system is the implementation of the *Recombinator* for the new framework, all other parts were allready present in the system and could simply be selected to be part of the evolutionary algorithm when running the *EA Visualizer*):

Component	**Instance**
Genotype	`Binary String`
Similarity	Any
Fitness Function	Any
Recombinator	`Baluja And Davies Optimal Dependency Trees`
Mutator	`No Mutation`
Before Selector	`No Selection (Select All)`
After Selector	`Truncation Selection`
Mater	`Mate All Genomes In One Group`
Replacer	`New Offspring Only`
Terminator	`All Equal Genomes And Maximum Generations`
Hybrid Searcher	Any
Population	`Vector Population`
PRNG	Any

3.2.3 Running tests and analysing the results

In this section we run tests on the frameworks introduced in section 3.2.1. We compare the tests to the results from classical genetic algorithms and draw conclusions. We shall introduce the different testfunctions one at a time and investigate the results thoroughly. For each test we will provide the settings that were used for the different algorithms. In the following we shall first present the test functions that were used, followed by a report on the results and explanations for the observed behaviour, moving from the simplest test function to the trickiest one.

The test functions
The simplest of the three test functions is the maximization of the polynome $p(x) = 0.007x^5 - x^3 + 25x$ with $x \in [-10, 10]$. The polynome in the given range is depicted in figure 38. This function obtains its maximum value at $x \approx -8.73842738$ with $p(x) = 92.13837146$. A suboptimum is found for $x \approx 3.05845883$ with $p(x) = 49.72544247$. Finally there are is a suboptimum at the boundary for $x = 10$ with the value of 50. The maximization of the polynome is fairly simple as the peaks in the search space are scarce, continuous and have nice gradient properties (eg. no needle in a haystack type of function). Any random population most likely already has some samples that are in the range of largest peak of the polynome and by recombining these, the greater peak will quickly be climbed. Only for very small population sizes the problem will probably not be solved. So on beforehand we note that this fitness function should be rather easy.

Coding solutions for the polynome means the coding of real values with binary strings. To this end we require a mapping from real values to values in binary coding. This mapping is obvious

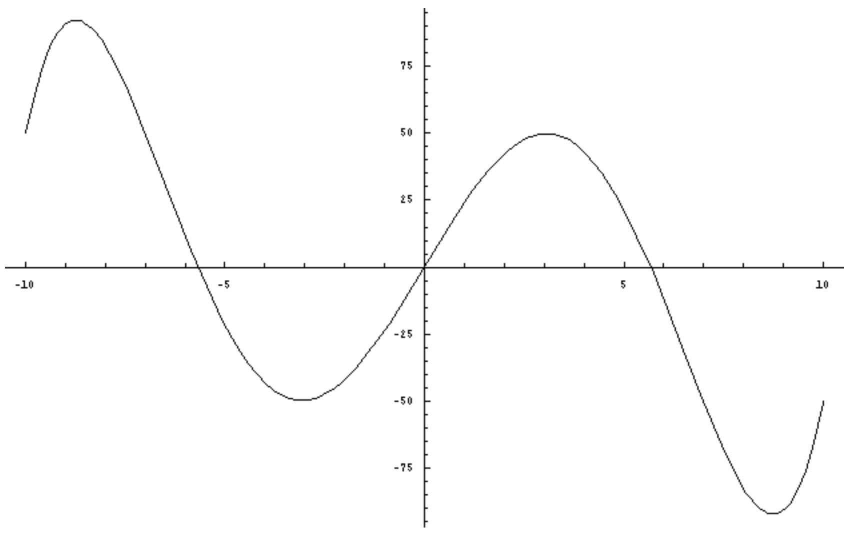


Figure 38: The polynome $0.007x^5 - x^3 + 25x$ with $x \in [-10, 10]$.

if we denote $d(x)$ to be the decimal value for a binary number x. Given the string length l, we can map any binary number onto a range in the real domain as we know that there are exactly 2^l values codeable with a binary string of length l. The mapping $m(x, a, b)$ for any binary string x onto a range $[a, b]$ becomes:

$$m(x) = d(x)\frac{b-a}{2^l - 1}$$

Note that we are very much so discretising the real space that we are truly searching. To remedy this, we can use more bits to increase the precision. We employ a length of 20 bits as this shall grant us enough precision to approximate the solution close enough (if any solution is found ofcourse).

The second function is also a continuous function, but one that consists first and foremost of multiple variables. The function maps n real numbers to a single real number, in other words, the function mapping is mathematically defined as: $\mathbf{R}^n \rightarrow \mathbf{R}$. The function is known as *Ackleys function* and its exact definition is the following:

$$f(\overrightarrow{x}) = -20e^{-0.2\sqrt{\frac{\sum_{i=1}^{n} x_i^2}{n}}} - e^{\frac{\sum_{i=1}^{n}\cos(2\pi x_i)}{n}} + 20 + e$$

In this expression we have that $x_i \in [-30, 30]$ $(\forall_{i\in 1\ldots n})$. The goal is to minimize the function. The mimimum value is obtained when all variables are 0. The function then evaluates to $-20 - e + 20 + e = 0$.

Coding solutions in binary strings implies the coding of all the variables. In the case of the polynome, this is not so difficult as we have a standard mapping for real values from a certain range onto a binary string which we gave above when we discussed the polynome fitness function. All we do is put the coding for every variable one after the other in a longer string. This implies that if we work for instance with a precision of 16 bits and 30 dimensions, the amount of bits required is 480. The amount of 30 dimensions is the amount that is generally used for Ackleys function. However, as the framework of MIMIC and that of Baluja and Davies has a complexity of $O(mn^2)$ where n is the amount of bits in the string, a large amount of bits becomes rather intractable in terms of computability. As such we shall drastically reduce the amount of dimensions as well as the precision for the different variables. To be precise we use merely 5 dimensions and code each variable with 10 bits. We must not only remember the fact that we are dealing with a less difficult function, but also that we are discretising the search space more than in the case of the

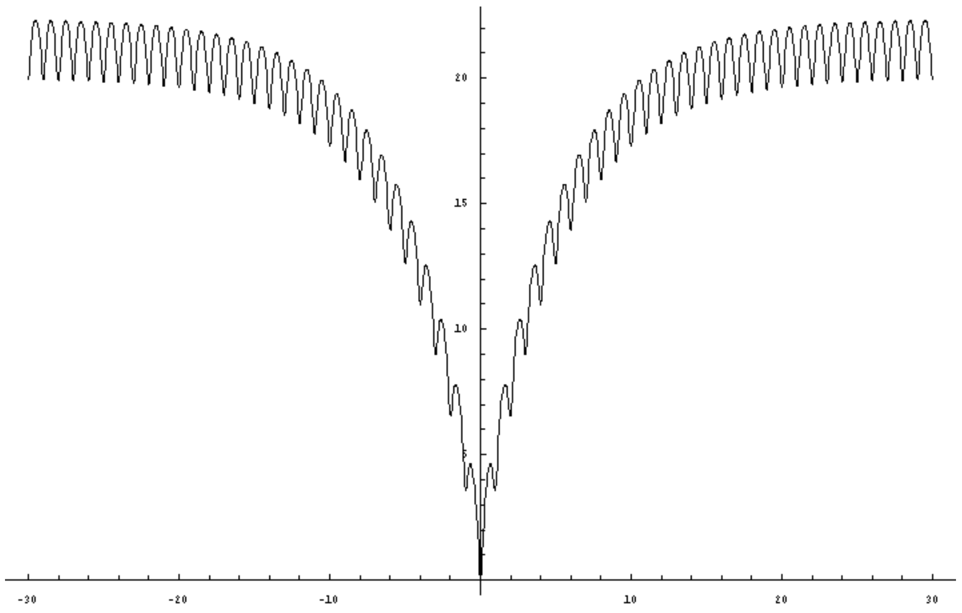


Figure 39: Ackleys function in one dimension with $x_i \in [-30, 30]$.

polynome fitness function. Ackleys function has many suboptima, but it must be realized that when we discretize the search space, we might just discretize to such an extent that we remove these suboptima. So even though less bits might seem a disadvantage because the precision of the search is diminished, less bits can also make the problem much easier as we perhaps take steps around the suboptima. For the purpose sought, the restrictions implied by our choices however will not forsake the integrity of the test. We have a precision of $\frac{60}{2^{10}} \approx 0.0585937$ for every variable x_i, which should not diminish the difficulty of the problem.

To gain a little more insight into the contents of Ackleys function, a plot is provided in figure 39. It shows that this function contains a lot of suboptima and is therefore more difficult to minimize than the polynome fitness function, even when we would only use a single dimension as shown in the graph. However, Ackleys function normally subscribes thirty dimensions and we have just chosen to use only five dimensions, which is still more than just one. To get an idea of how much more difficult the problem gets, in figure 40 Ackleys function in two dimensions is plotted. The domain has been narrowed down to $[-10, 10]$ for the two variables in the plot to keep the overview in the graph, because otherwise too many suboptima would clutter a good impression of the two dimensional view. Next to having many more suboptima, we now have blocks that are separately meaningfull, which further increases the difficulty of the function.

The most difficult of the test functions is the so called *trap functions fitness function.* Its name is in plural as the function has a fully deceptive characteristic (so it's meant to *trap* the genetic algorithm) for certain values for the parameters of the function. For other values of the parameters, the function can be easy. Since there are thus many flavours to this function, it's really a collection of functions, which is the reason for the plural aspect in the name of the function.

The function works on binary strings that are split up in building blocks of equal size, just as is the case with Ackleys function described above. Each of these building blocks however in this case contribute a fitness values themselves, separate of the other values. For every block the fitness can be computed in the same way (when uniformly scaled). When we set n to be the length of a building block, m the amount of building blocks in one string (thus the length of one binary string is mn), $o(x)$ the amount of ones in a given string x, d the so–called signal (a real value between 0

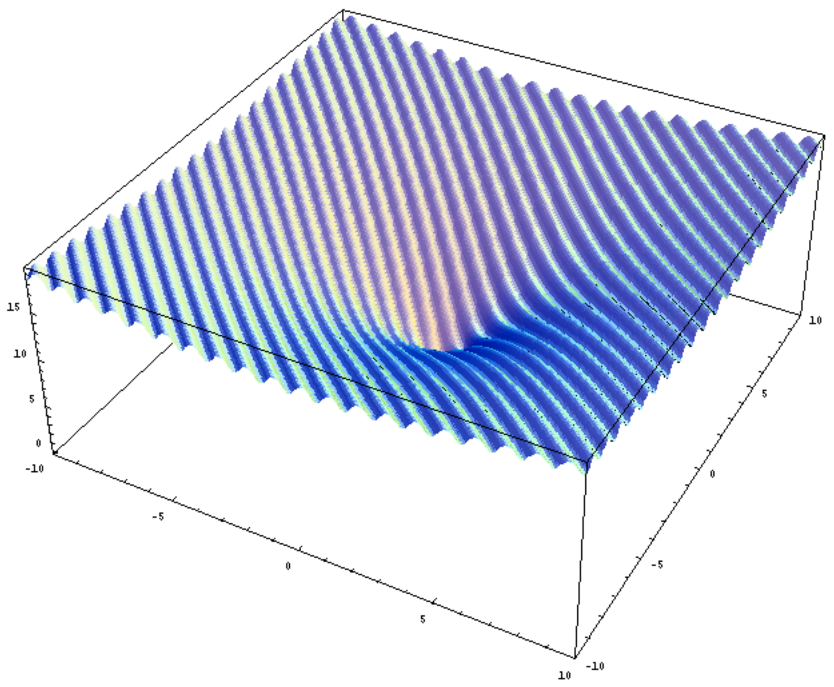


Figure 40: Ackleys function in two dimensions with $x_i \in [-10, 10]$.

and 1), the fitness evaluation of a single building block x is the following:

$$f(x) = \begin{cases} -\frac{1-d}{n-1} o(x) + 1 - d & \text{if} \quad o(x) < n \\ 1 & \text{if} \quad o(x) = n \end{cases}$$

It follows that the maximum fitness value is equal to m, which occurs when all bits are set to '1' and thus all m building blocks have a fitness contribution of 1. The fitness function for a single building block is thus dependent on the amount of '1' symbols in the input and not on some real mapping we had for the other two test functions. The fitness evaluation of a single building block is depicted in figure 41.

To close the introduction of the last test function, being the trapfunctions, we want to present some interesting information up front. The information concerns the earlier noted variable difficulty in optimizing the function. To be more precise, we want to add some information regarding the *deceptiveness* of a fitness function. Before providing this information, we refer to section 3.1.1 as a notion of schemata is required, which is given in that section.

When a fitness function is said to be *fully deceptive*, there is really only proof of the fact that a suboptimum should be the optimum for the function, except for when we have given explicitly the suboptimum and the optimum, in which case we can ofcourse distinguish the optimum from the suboptimum. Formally spoken with respect to the trapfunctions, when we regard schemata, we find that when we look at a schema for a building block of length k with only one '0' symbol, the schema–fitness will be higher than a similar schema with only one '1' symbol. When this is the case for all schemata of orders 1 up to and including $k - 1$, the fitness function is said to be *fully deceptive*. Thus, deceptiveness regards the fact that based on the schemata, it can be expected that the optimum the schemata point to is not the absolute optimum. To give an example, we look at the trapfunctions that have building block length 5 and signal $d = 0.2$. When we regard a single block only in the given problem, it doesn't matter where the don't care symbols are in the string, all that matters is that they are in the string somewhere. The data we thus achieve can be tabulated as follows:

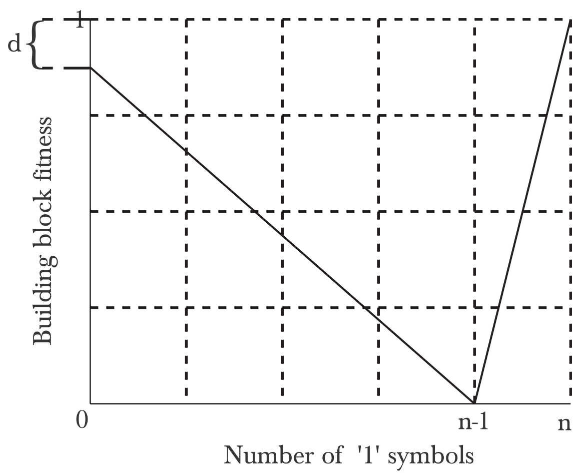


Figure 41: The fitness contribution function for a single building block.

#1	0****	1****
0	1	0
1	4	1
2	6	4
3	4	6
4	1	4
5	0	1

#1	00***	1****
0	1	0
1	3	0
2	3	1
3	1	3
4	0	3
5	0	1

#1	000**	111**
0	1	0
1	2	0
2	1	0
3	0	1
4	0	2
5	0	1

#1	0000*	1111*
0	1	0
1	1	0
2	0	0
3	0	0
4	0	1
5	0	1

Order	**0–Schema**	**1–Schema**
1	0.4	0.275
2	0.5	0.25
3	0.6	0.3
4	0.7	0.5

It follows from the table above that for any trapfunctions fitness function with building block length 5 and signal 0.2 (and exactly one building block), the function is fully deceptive since every schema with fixed '1' symbols has a lower fitness than that of the schema with the same amount of fixed '0' symbols. From the above table it follows that unless you have seen strings with only fixed symbols, you will not choose in favor of '1' symbols. This implies that the algorithm must be able to process order k relations to solve the problem. Now if we investigate another signal, namely 0.8, we get the following table of values:

Order	**0–Schema**	**1–Schema**
1	0.1	0.115625
2	0.125	0.15625
3	0.15	0.2625
4	0.175	0.5

In this case it follows not only that the function will not be fully deceptive but also that the function will be 'easy' as the values pose exactly the opposite situation of that in which the signal equals 0.2, so everything is in favor of '1' symbols. Seen to this aspect, we choose to employ two instances for the tests, namely the instance in which we have a signal of 0.2 and the instance in which we have a signal of 0.8. In both cases we will have a building block length of 5 and we shall take 4 building blocks to come to a string length of 20 bits. This will cause the optimization algorithm to have to acknowledge the existance of building blocks, which further troubles the search.

Before going to the tests, we close the introduction of the test functions by noting that especially the last test function requires a mechanism that can actually process building blocks, otherwise the search will not be powerfull enough to acknowledge that the fitness function is composite and will not most likely not find the optimum. In other words, if the linkage is learned as well as it is stated in MIMIC and the framework by Baluja and Davies, the results should be that the building block borders are acknowledged by linking bits within a single building block to mark that those bits are related.

We now investigate the results from running the tests on three different types of algorithms. For every test function, we used three different genetic algorithms. The algorithms differ only in the use of the recombination operator. The operators are the classical one–point, two–point and uniform crossover (the latter with an allele swapping probability of 0.5) and as such we are really testing classical GAs, with the only exception that we use tournament selection with a selection size of 2 instead of proportional selection, since the latter selection mechanism has some undesirable disadvantages. Furthermore we tested the use of MIMIC in three different variations as well. The difference exists in the amount of samples generated every generation. We tried generating 100, 200 and 400 samples each generation. The same has been done for the framework by Baluja and Davies. In this latter framework, we also employed a value of 1000 for c_{init} and we set the decay factor α to 0.99. These values were suggested in the paper that introduced the framework [3]. All algorithms were tested over different population sizes. It is known from genetic algorithm theory that GAs perform better when the population size increases as the initial supply of good building blocks increases and there is more good genetic material that can be directly processed. It is interesing to see in this first round of tests whether the statistical linkage frameworks are also influenced by this factor. All results are computed from values gathered over 30 runs. In the following we investigate the results per test function, going from easy to difficult in optimization level, just as we introduced them above.

The polynome $p(x) = 0.007x^5 - x^3 + 25x$
The polynome to optimize with the optimum value around 92.138 has been submitted to tests run with genetic algorithms. The results are displayed in figures 42, 43 and 44. The graph with average values shows the average fitness of the best individual found at the termination of each run out of the total of 30 runs. This value is equal to the average of the average value found at termination since the termination criterium used for the genetic algorithm has always been the equality of all genomes in the population. In other words, only when the population had completely converged did the algorithm stop. The variance value has also been computed over the 30 values from the best individuals. Finally, the graph displaying the best value (figure 44) shows the best fitness found at termination in all of the 30 runs. All graphs are drawn as a function of the population size (which is thus drawn along the horizontal axis). This general information is set out here at the beginning for now and for the remainder of the text, so we state some more global information

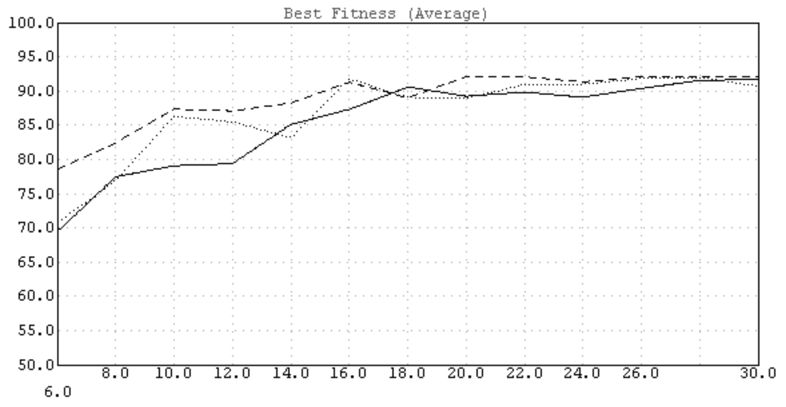


Figure 42: The average best fitness for the genetic algorithms on the polynome test function.

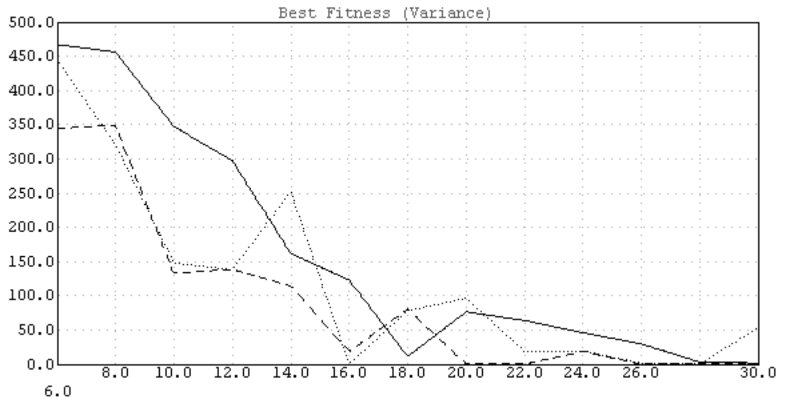


Figure 43: The variance over the best fitness for the genetic algorithms on the polynome test function.

here, making this the analysis of the first test function perhaps a bit longer than required.

Viewing the results in the graph, we can draw conclusions about the behaviour of the optimization strategy. The average values tell us how good the *expected* performance of the algorithm is in terms of optimization value (not in speed). The closer the value to the optimum, the more likely that a single run with those settings will always provide good results. The variance value is closely related to this however and we should take into account the results seen there. These values show us how much the fluctuation is with respect to the optimization results. What we strive for is to find an algorithm ofcourse that averages over 30 runs close to the optimum value and has a variance close to 0. When the variance value is 0, this means that the value found was *always* the same over the 30 runs. The variance value for a random variable X is computed as $E(X^2) - [E(X)]^2$. The well known measure *standard deviation* is the root of this value. This means that when we have a variance value of 625, the standard deviation is 25 with respect to the average value, indicating that it can be expected that any result is most likely to deviate somewhere from 0 to 25 units from the average value found, either in a positive or a negative manner. Such precise conclusions do not interest us normally however, since we are only interested to see what the characteristic of the graph is and when the variance values are either low or high. The exact value is less interesting at this time. With all of this preliminary information, presenting the legends for the graphs in this section with results for genetic algorithms, MIMIC and the framework by Baluja and Davies in graphs 45, 46 and 47 respectively, we can now actually investigate the results.

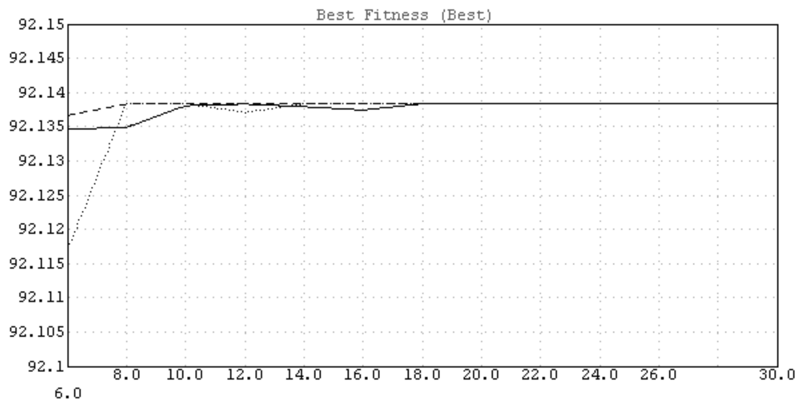


Figure 44: The best of the best fitness values for the genetic algorithms on the polynome test function.

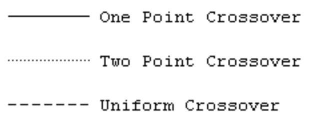


Figure 45: The legend for the graphs for genetic algorithms.

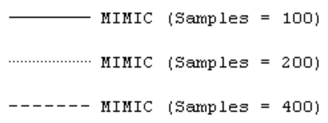


Figure 46: The legend for the graphs for MIMIC.

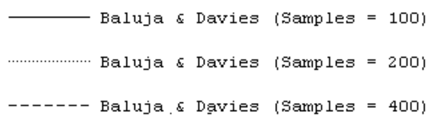

Baluja & Davies (Samples = 100)
Baluja & Davies (Samples = 200)
Baluja & Davies (Samples = 400)

Figure 47: The legend for the graphs for Baluja and Davies.

Figures 42, 43 and 44 respectively show us the average, variance and best values over the best values for the genetic algorithms upon termination over 30 runs. The graphs show results that were to be expected. As the population size increases, the algorithm becomes more steadfast in finding the optimum value in all of the 30 runs. It also shows that population sizes that are very small will not result in a genetic algorithm that will be any good. The results from one run are then unreliable as the variance graph tells us that the results tend to deviate from the average value found quite a bit. As more material to sample and work with comes around, the search will provide better results. Given the fact that the genetic algorithm removes all solutions after generating new ones, this means that the search is bought more time to investigate more points in the sample space as more room for recombination is created by increasing the amount of samples maintained at any time during the algorithm. As no mutation is used, once a bit at a certain position disappears from the entire population because of selection or because it's simply not there in the beginning because of the limitation in random initial sampling because of a small population size, it can't be introduced again. Because of the tournament selection that is used, worse individuals tend to quickly disappear, even if they have material in them that could be of great importance.

It also shows that there is a slight difference in the choice of recombination operator. The best results are achieved when uniform crossover is applied. This was once again to be expected, since building blocks are not obviously apparent in this function. What we are trying to express is the fact that there are no building blocks of adjacent members that need to be maintained. We cannot say that the building block length is equal to 1 however, since such would imply that every bit has its own fitness contribution (which is the case for instance in bitcounting). This is not the case here, but it can't be said either that certain combinations of bits are tightly linked. When the building block length would be 1, the use of uniform crossover would directly swap information across the borders of the building blocks, making it obviously the best recombination mechanism. In this case, all recombination mechanisms more of the same reliability. There is however definately a difference in performance. With smaller populations, the speed at which genetic material disappears as just noted ealier is much higher. Therefore uniform crossover especially performs better for smaller populations because it mixes that genetic material faster as well, making mixing time more in favor over pressure pushing selection. As the building blocks are however not clearly of length 1, or in other words the individual bits in the string are not unrelated, the other crossover operators quickly catch up with the performance measure.

Finally, we note how the genetic algorithm over the 30 runs is capable of finding the optimum (to within its precision) at least once already at the earliest stages of the algorithm. We should not forget however that even for a population size of ten members, $30 \cdot 10 = 300$ random strings have been generated over 30 runs. This means that by expectation we have seen at least 1 time all strings of length $\lfloor \log_2 300 \rfloor = 8$ bits. This implies that when regarding these bits to the first eight bits of the total string of length 20, we have seen strings over the domain space with precision $\frac{2^{20-8}}{2^{20}}(10 - -10) = 2^{-8} \cdot 20 = 0.078125$. So we have already been able to determine the optimum to at most within a precision of 0.078125. So it is not surprising that populations that have at least ten members are already showing best results over thirty runs equal to the optimum value.

We conclude that for the genetic algorithms this problem is fairly easy and the results show almost linear behaviour in the required size of the population to solve the problem adequately. Due to the coding there are no linkage problems and the algorithm has no problem propagating the required information in order to find the optimum value, given at least a "decent" population size.

In figures 48, 49 and 50 the performance of the MIMIC framework can be seen with respect to the polynome maximization problem. Before any comparison to the results of the genetic algorithm are made directly when looking at the graphs, the difference in the horizontal scale (population size) should be noted. The MIMIC framework was tested with population sizes 5 up to and including 25 in steps of 5 and subsequently population sizes of 50 and 100, which is much larger than the maximum size of 30 that has been tested for the genetic algorithms. The larger population sizes have been selected because of the fact that this is the first real test done with MIMIC and we

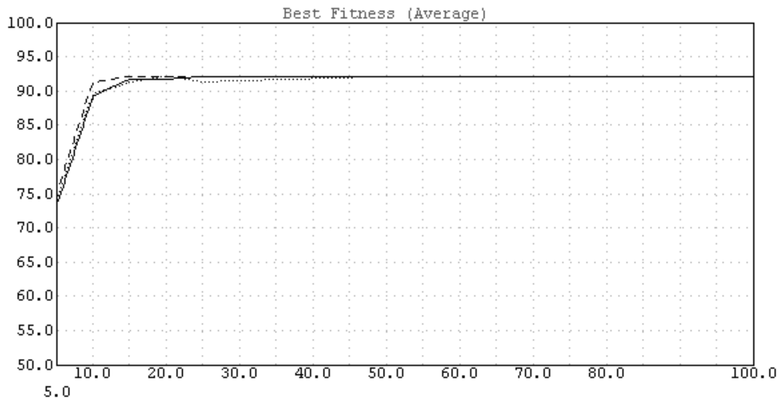


Figure 48: The average best fitness for MIMIC on the polynome test function.

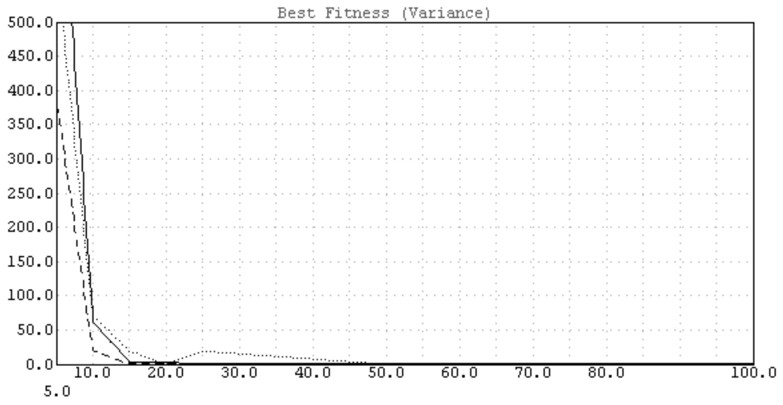


Figure 49: The variance over the best fitness for MIMIC on the polynome test function.

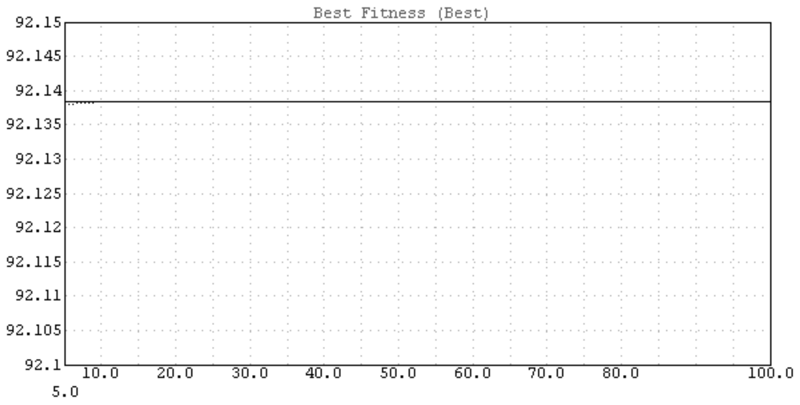


Figure 50: The best of the best fitness values for MIMIC on the polynome test function.

are better to be safe as we do not completely know what to expect. Perhaps a larger population size could even be desastrous. For genetic algorithms this will certainly not be the case. With MIMIC, the probability distribution is based upon the members of the population and as such larger populations pose also interesting test beds.

At first glance it can be noted that MIMIC seems to have little difficulty in maximizing the polynome, given however enough samples in the population to base the probability distribution on. Although the results for the average best fitness only seem to be slightly better than those in case of the best genetic algorithm, the best fitness found over the thirty runs is almost always the maximum value. We should note that at the same time the variance for small population sizes is very high, indicating that the results tend to be of a varying form in those cases. Furthermore we must not forget that MIMIC generates 100, 200 or 400 new samples *every generation*, which is a lot more than the genetic algorithm does. These new samples are ofcourse taken from some restricted space that should still contain the optimum, but the fact alone that so many samples are generated indicates that with the given derivation earlier about the precision achieved in finding the optimum by random sampling we should find anything close to the optimum already with population sizes greater than 10. Unlike with genetic algorithms, best individuals are maintained, so now the sampling really has a direct influence on the end results.

A very important note is the role of the population in the optimization algorithm. In the genetic algorithm, the population size denotes how many solutions we maintain at any given time and implicitly how many new offspring we have to evaluate each generation. This implies that for larger population sizes the running time of the GA will go up linearly with the population size. In the case of MIMIC however, the population size is of *no* influence to how many offspring[13] need to be evaluated each generation. The amount of samples that are evaluated each generation is determined directly by the amount of samples generated each generation. As this is always 100, 200 or 400, which make up our three instances of MIMIC, this remains constant over the population size. Any test results that would however plot only function evaluations as a performance term would be somewhat misleading because the function evaluations alone do not make up the running time for MIMIC. As shown before in section 3.2.1, the running time each generation is still $O(mn^2)$ with m the population size and n the string length, implying that a growing population size means also a growing running time. The running time will grow less however since indeed the amount of function evaluations will be less once the genetic algorithm population exceeds the amount of samples generated every generation. The difference will however only be a constant, unless ofcourse the amount of samples used to update the density estimator is chosen a constant itself, which would bring back the running time to $O(n^2)$. In any way, an increase in population size is somewhat less dramatic for MIMIC than it is for the genetic algorithm and it is clear that at least for the polynome problem, the MIMIC framework provides very reliable results provided a not too small population size is selected.

A burning question at this point is ofcourse whether or not MIMIC is better for this optimization problem. Given the results it's safe to say that in reliable performance (provided a large enough population size) there is no difference. An important factor is ofcourse the running time, on which there is no data provided here. However, based upon the experience of the writer, MIMIC has been seen to converge much faster to the optimum than the genetic algorithm does. The amount of generations needed is much less and the discrepancy in running time per generation is not small enough for the GA to make up for the difference.

We now look at the influence of the population size on the performance by MIMIC. It is clear from the results that a larger population benefits the MIMIC framework for this problem. As we have no further data as to be more rigorous about this (as we shall be able to with results of more difficult test functions), we can only analyse why the algorithm does not work good for smaller population sizes. The answer is not hard to find when one realizes that the new samples that are generated each generation are based on a probability density estimator which is itself in turn based

[13]To avoid confusion in the current discussion, *offspring* are called *new samples* in the MIMIC framework.

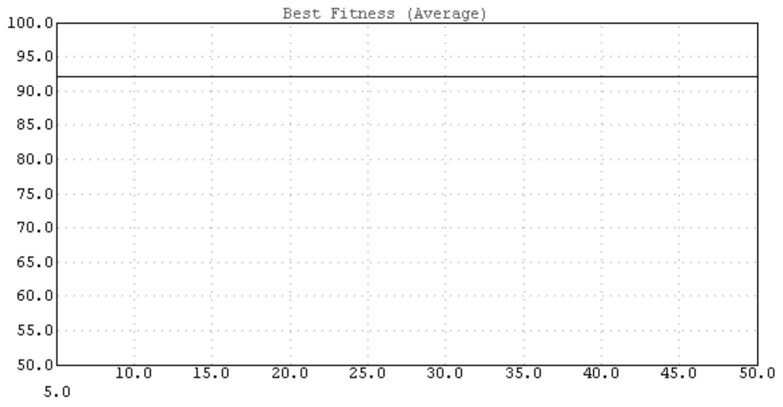


Figure 51: The average best fitness for Baluja and Davies on the polynome test function.

on only the samples in the population. A small population leaves little room for much diversity in the derivation of relations in the genetic material as it tends to be quickly overtaken by samples that are only mediocre. Furthermore, a history of better individuals is not properly maintained as there is not much room for such in a small population. All this leads to premature convergence because relations could not be properly found. In a way, this points to the same problem as found in GAs. The population must be large enough so to have enough time to process the required relations. We can therefore only conclude at this point that larger populations will slow down MIMIC, but can only benefit its performance. This must ofcourse be related to the problem type at hand, being a simple one.

The factor of the amount of samples generated each generation remains as the last issue to be discussed in the analysis of the results for the MIMIC framework and we shall turn our attention to this issue now. By merely inspecting the results in the graphs, we can derive that the results for the three variants are even closer to one another than was the case for the GAs. When thinking of the MIMIC framework in this light, it becomes clear that to some extend there will indeed be no difference in results for more or less samples per generations. From these samples the better ones are picked and put into the population. Since the creation of the samples is based on a probability density estimator, creating more samples will most likely result only in more of the same material (save for the first few generations). For instance, when the probabilities have become totally secure, or in other words the chance to set a bit conditionally is one or zero, generating one, two, five hundred or one million samples makes no difference as there can only be one string that results from these chances. It is different however in the case of a probability vector of only entries with chance 0.5 (initial phase), in which a generation of 2^n strings would only justify in full diversity this probability vector, which is intractable as enumeration is what we want to avoid in optimization. However, a collection of two genomes also justifies this probability vector (only ones and only zeros) and furthermore after only one or two generations, the probability vector will start to get a distinct form and generating 100 or 200 samples will most likely make not much of a difference anymore, especially when the probability vector is assumed to chance at a slower rate in the case of 100 samples, since two generations of 100 samples will then be somewhat equal to one generation with 200 samples. Concluding, even though it can't be denied that there is a difference in generating 100, 200 or 400 samples every generation, the perceivable results of applying these different settings will most likely be negligable for easy problems.

The results for the framework by Baluja and Davies for the polynome optimization problem are displayed in figures 51, 52 and 53. Actually there is not much to say about these results as they quite show the perfect results (to within the scope of the selected measures in the graphs). For every population size from 5 up to and including 50, the framework always finds the optimum, which can be determined by noting that the the average value is no less than the optimum value

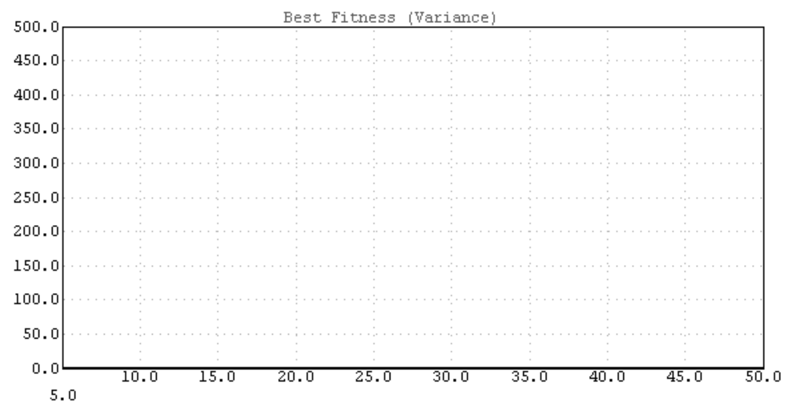


Figure 52: The variance over the best fitness for Baluja and Davies on the polynome test function.

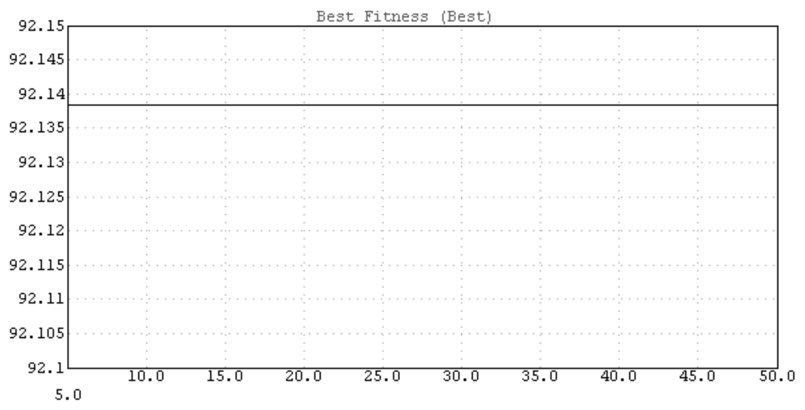


Figure 53: The best of the best fitness values for Baluja and Davies on the polynome test function.

or that the best value is the optimum and that the variance is zero. It is clear that the framework by Baluja and Davies is strong enough to solve a problem as simple as this and we shall therefore needfully postpone the drawing of any conclusions about the framework to the point where we discuss more difficult test functions. The only thing we wish to point out at this time is that the amount of time required to achieve the results is *substantially* greater than that of the other two approaches. The amount of generations required to terminate a single run in the case of a population size of 5 members and the generation of 100 samples per run is on average about 300. It should be noted however that the algorithm has been observed to spend a lot of time finetuning the results, even beyond the point where finetuning was no longer required. Also we glance a little forward in perspective a note that even though the required time seems unacceptably large, the same amount of time was required for the other test functions, with the results in all cases being virtually always the finding of the optimum with a variance of *zero* over thirty runs. . .

Ackleys function
Before we start going over the results obtained for Ackleys function, we must point out that because of the discretization applied to the search space, the best result obtainable by any algorithm is the value of 0.163 instead of 0. With this information provided on beforehand, we can now investigate the results.

First we again look at the results obtained by the classical GA. The different fitness measures are depicted in figures 54, 55 and 56. The population size range was increased because of the fact that the problem is more difficult and the GA requires time to process the building blocks that are now introduced. As was the case for the polynome optimization function, the nature of each subfunction is a real function. As such, the crossover operator that works best on such a subfunction is the uniform crossover operator. The material is then mixed the best and even though the mixing is very destructive, the exploration of the search space is done properly because the structure of the subfunctions is best explored by just taking many different samples which is best done through uniform crossover. The fact that there are multiple building blocks that require processing is not as the structure of these building blocks are all of the same type and are all explored well under uniform crossover. Hence uniform crossover works the best on the whole problem. The GA requires time to process the different subfunctions, but when provided a larger population, indeed the optimum value is found always as the variance becomes zero over thirty runs. The amount of function evaluations required can be computed as the population size times the expected amount of generations the algorithm runs with that population size before termination. Experiments have shown out that somewhat 50 generations are required on average with a population size of 140 and uniform crossover, implying that some 7000 function evaluations are required for the GA in order to solve the problem.

We can only conclude that for the genetic algorithms this problem is only slightly more difficult that the polynome optimization problem. The fact that building blocks are now playing a part in the fitness function even though we argued they are of lesser importance in the current setting, contributes to a non–linear behaviour in the required population size to solve the problem. Still, when provided a large enough population, the GA can solve the problem with any crossover operator.

Switching to MIMIC and thus the results displayed in figures 57, 58 and 59, in the line of what we saw for the polynome problem one could say that there is hardly any difference between the three approaches that generate a different amount of samples each generation. It does seem that indeed generating more samples is more advantageous, which to some extend as explained is ofcourse to be expected, but there is not much of a difference. We have already provided arguments as to why this could be the case and we shall therefore disregard the three different entries in the graph and see them as one.

Just as was the case with the polynome maximization problem, MIMIC succeeds in finding the optimum value at population sizes smaller than the GA. Also, we must again not forget that the

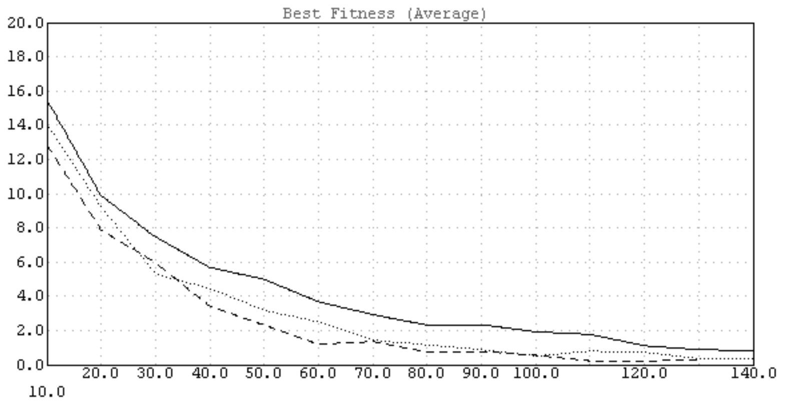


Figure 54: The average best fitness for the genetic algorithms on Ackleys function.

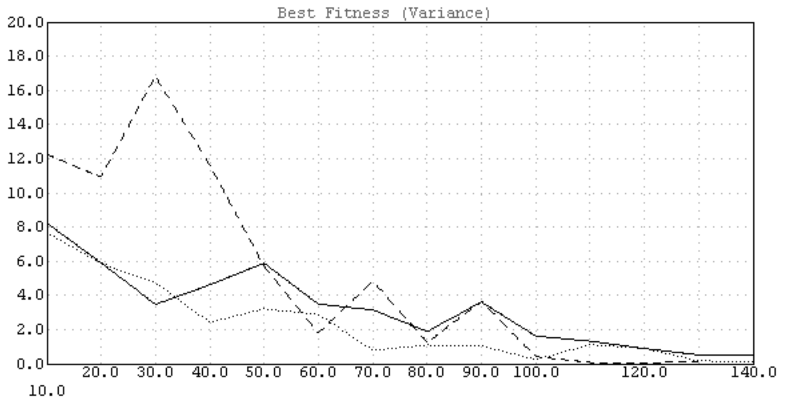


Figure 55: The variance over the best fitness for the genetic algorithms on Ackleys function.

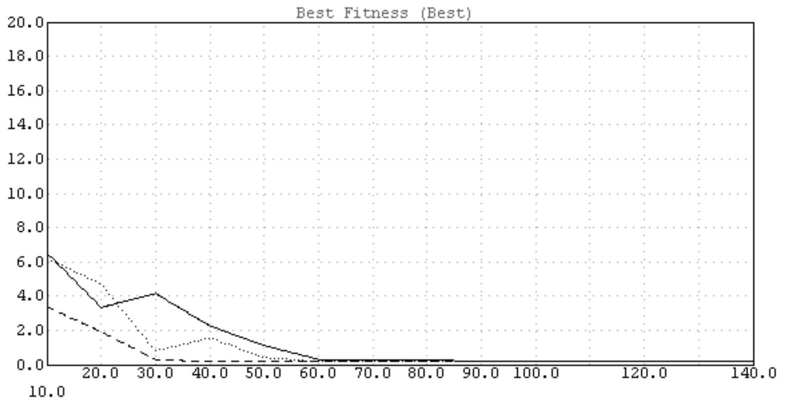


Figure 56: The best of the best fitness values for the genetic algorithms on Ackleys function.

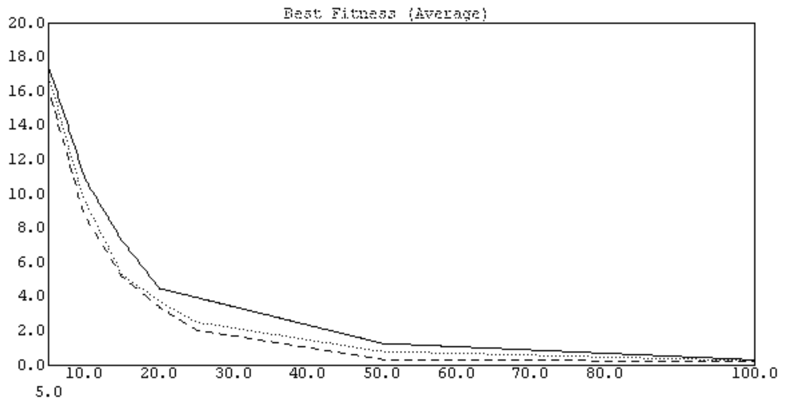


Figure 57: The average best fitness for MIMIC on Ackleys function.

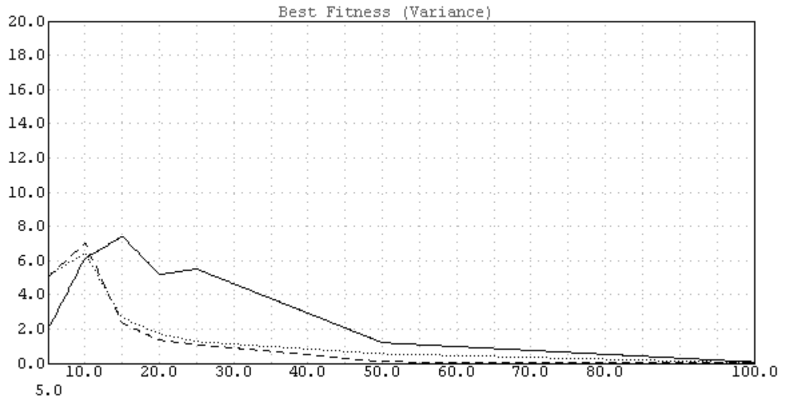


Figure 58: The variance over the best fitness for MIMIC on Ackleys function.

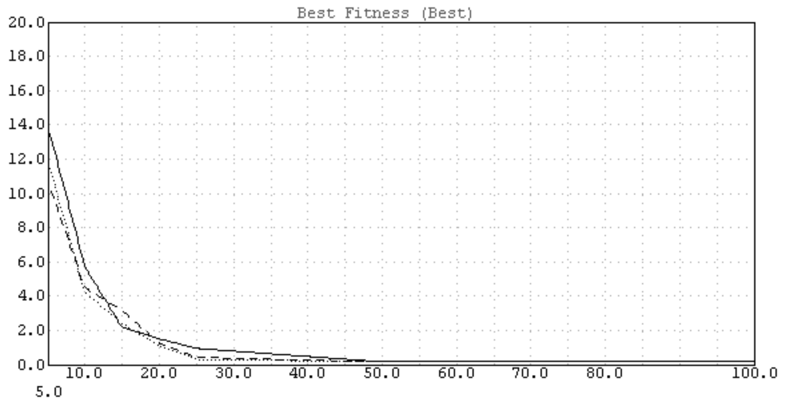


Figure 59: The best of the best fitness values for MIMIC on Ackleys function.

amount of samples generated each generation is different from the GA and the whole structure of MIMIC makes it rather unfair or meaningless to compare population sizes with the GA. The main thing to note is that once again increasing the population size is advantageous for MIMIC. For Ackleys function this becomes more apparent as the problem is more difficult and requires a larger population size in order to be solved properly and with certainty. Increasing the amount of samples per generation does not seem to help MIMIC much for this problem, but increasing the population size does. This has to do with the fact that in a larger population there is more room for deducing relations. Furthermore, the best strings yet are maintained, allowing the hopefully good relations so far to stay around and aid the search for the relations that lead to the optimum value. We can only question ourselves at this point what happens when the better strings are deceptive attractors and increasing the population size together with retaining the better individuals only brings deceptive members in the beginning and the relations deduced might be wrong? It seems that nothing will then be able to help MIMIC to still be able to find the optimum. Results to confirm or contradict this notion will most likely come from the trap functions that we shall visit shortly.

We can state that the limited version of the distribution learning structure that is the chain in MIMIC does not pose a problem for the minimization of Ackleys function. The problem is easy enough to determine the required relations adequately with such a structure. Even though the unrestrictive version incorporated in the framework by Baluja and Davies will most likely work even better, the fact that the restrictive version used in MIMIC is capable of capturing the structure also when the population size increases implies that there is no deceptive material that can misguide the creation of the chain of dependencies. Even though the population size required is greater than for the polynome optimization function, MIMIC is very much so capable of minimizing Ackleys function and thus of identifying the different variables codes as blocks of strings that determine the fitness value.

To have some means of comparison against the genetic algorithm, the amount of function evaluations needed to achieve these results is round and about 6000 as it took about 15 generations on average until termination at 400 samples per generation and a population size of 50, which taken from the graphs resulted in a succesfull minimization of Ackleys function.

It remains to observe the results obtained by the approach of Baluja and Davies. Figures 60, 61 and 62 show that the approach leaves no little doubt about what it feels to be the optimum value for the test function. Indeed, the minimum attainable value within the coding of 0.163 (rounded on 3 decimals) is obtained for every test in thirty runs with population sizes of 5, 10 and 15 with all of 100, 200 and 400 samples per generation, just as was the case for the polynome function. We can therefore based on the graphs only conclude that this approach works the best. We must however make a very strong statement at this point. The results in the graphs show now tests for population sizes over 15, which leaves doubt about the influence of the population size. The fact that no larger population sizes were tested lies within the problem of time shortage. The graphs shown are the results of tests run over seven consequtive days and nights[14]. It would take at least that long to test three more population sizes of 20, 25 and 50. Unfortunately that time was unavailable with respect to the release date of this paper. The fact that the tests took so long is mainly a result from the amount of generations required by the algorithm. Preliminary tests showed that the approach indeed was capable of finding the optimum to within the precision supplied, but because of the symmetry around the optimum value, no convergence took place. To be more precise, for a single block of 10 bits, there is no difference in fitness response between `10000000` and `0111111111` as they are evenly far away from the origin since the binary value is scaled to $[-30, 30]$ and ackley's function is symmetric around the origin as can been seen in figure 39. Therefore it was empirically established that 1000 generations suffices for the algorithm to find the optimum value and this was subsequently the maximum amount of generations allowed in the running of the tests of which we are discussing the results here. As the algorithm never terminated before reaching the 1000 generations, the time to run all the tests was as a result very

[14]The tests were run on a 120MHz Pentium with 32 Mb of RAM and no other processes than the *EA Visualizer*.

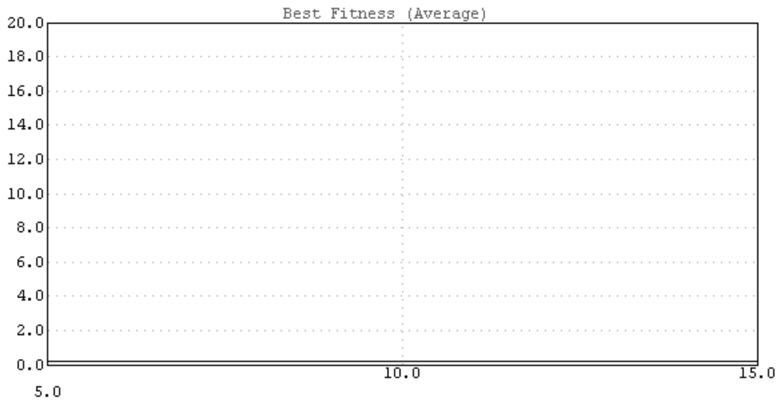


Figure 60: The average best fitness for Baluja and Davies on Ackleys function.

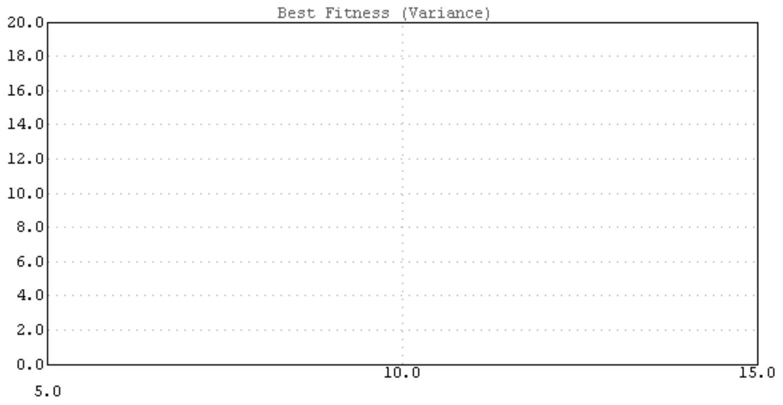


Figure 61: The variance over the best fitness for Baluja and Davies on Ackleys function.

long. Note that in the case of 200 samples per generation, the amount of function evaluations thus performed is 200000, which is over 28 times more than the GA required. As we can draw no conclusions about the results in the graphs, we shall make a note on the settings.

As proposed in the work of Baluja and Davies [3], the tests were run with a value of c_{init} of 1000 and a value of α of 0.99. At this point we should note what impact these values have on the algorithm. The two values just mentioned have a relation to the estimator array used by the framework. They represent the initial entry values and the decay factor by which the entries are multiplied every generation respectively. The c_{init} is meant to refrain the algorithm from directly drawing conclusions from the population members that are no more than randomly generated strings. This is because all entries in the estimator array are initialized to this value and the relations are based on this array through division. Information from the population is added to the array and subsequently the array is used to draw conclusions about relations through determination of conditional chances. Now when we have two entries x_0 and x_1 that we must divide and we have counted information for x_0 ten times and for x_1 four times, dividing to get simple chances for occurrence (assuming x_0 and x_1 are the only values possible) gives a chance of $\frac{10}{14} \approx 0.7142847$. When the information is initially cluttered by some initialization value, the counted information is *added* to that initial value. For instance, using the value of $c_{\text{init}} = 1000$, the values would be $x_0 = 1010$ and $x_1 = 1004$ and the chance at x_0 would be much more conservative (closer to 0.5): $\frac{1010}{2014} \approx 0.5014895$. So in fact there is a *simulated annealing* type of approach that will gradually move towards a distribution, giving the chance of recovering from bad choices by not directly

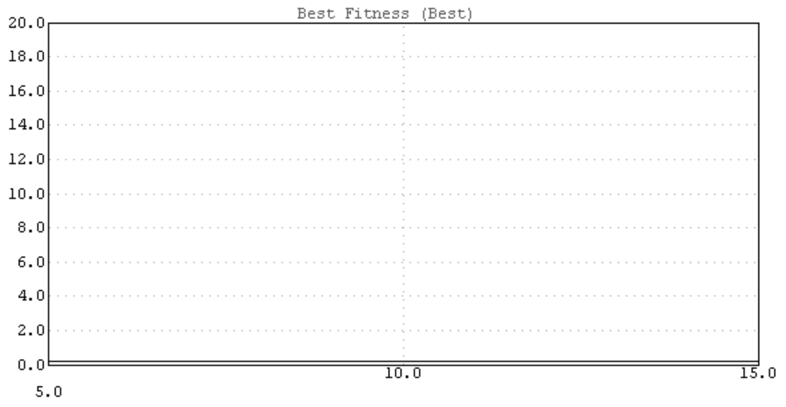


Figure 62: The best of the best fitness values for Baluja and Davies on Ackleys function.

basing all information on what is present in the population, which is the way MIMIC works. This raises the question of how important the estimator array is. Would we namely disable the estimator array by employing a decay factor $\alpha = 0$, this simulated annealing type of approach is done away with and we would be closer to the way MIMIC works, which we have seen to perform less on this problem.

Assuming that the estimator array is important, the values for c_{init} and α are of the essence. Furthermore they determine how many generations the algorithm will move along before coming close to termination because the array has become a direct estimate based on the population members. The greater c_{init}, the longer it will take before the cluttering influence of that value is undone. Also, the closer α is to one, the more time the algorithm is bought to go over decisions as the decay is much slower. With smaller values for α but larger values for c_{init}, the algorithm will more quickly move to relying on only recent population information, and thus will only shortly allow for recovering from bad decisions. In the longer view, the smaller the value for α, the less information is kept about recent generations. So indeed the parameters for the framework of Baluja and Davies seem to be very important. In the coming tests on the harder functions, we shall try out some of these settings. We should also note at this point that it is to be expected that for hard problems, the algorithm will be more likely to fail when we increase the population size. The population size is in this algorithm equal to the amount of samples used the update the estimator array. Hence, the larger the population size, the less the influence of the initial clutter value c_{init}. Therefore it would have been interesting to see what happens when the population size increases. With the settings copied from the work by Baluja and Davies [3] however, the tests took too long to investigate this for Ackleys function because of the greater string length. The tests for the harder funtions were only 20 bits, so there we were able to do tests with larger population sizes. To close the discussion, we should note that perhaps for Ackleys function the larger population size would not have mattered all too much since the problem is perhaps too easy and it is possible to solve the problem without a history in the estimator array. Finally, a larger population can in turn be remedied ofcourse by increasing the value of c_{init}. It seems therefore futile to try larger population sizes, since they will only cause the time between successive generations to increase without a decrease in required generations.

We close the discussion of the test results for Ackleys function by noting that there is a substantial difference between a GA approach and the probability density estimator approach in that the time required to step through a single generation is significantly longer. The quadratic order in computation time is not remedied by better performance on larger problems, implying that there is a substantial drawback in the new approach. Even though the approach by Baluja and Davies seems to not require a larger population size, increasing the problem length makes computation time increase much more for the density approach than for the classical GA. We must therefore also note that computation times stated in function evaluations or generations can be misleading because the actual running time depends also on the complexity per generation that is required before evaluation can yet take place. Furthermore, even though we have not yet tested influences of parameters on the approach by Baluja and Davies, we are still convinced there is a problem with the running time when the string length increases. Dropping the initial value for the estimator array as well as reducing the decay factor α will lead to quicker convergence. We have yet to see how much faster the process will go and what the implications are for the fitness results, but because the larger complexity is hidden in finding the relations, we expect the approach not to scale up tractably for larger problems.

Trap functions
After observing the results from the first two test functions and deducing information with respect to the dynamics of the probability density estimator approaches, we expect to find the most interesting results in running the trap functions as they are harder and will hopefully give us more information on the cans and can'ts of the Baluja and Davies approach. Also, results seen here will lead to confirmation on phenomena witnessed earlier and hunches about the dynamics that resulted from them. After going over the results we will set out our interests to continue the investigation with directed testing on behalf of features we wish the research further. We have posed to use two instances of the trap functions for testing and we shall therefore go over the results again by first visiting the GA, followed by MIMIC and then finally the approach by Baluja and Davies, but we shall discuss both trap functions at the same time for every algorithm to learn from the differences in performance for an easy instance and a fully deceptive instance.

Starting off by looking at the results from the genetic algorithm, figures 63 and 64 show that the genetic algorithm has more trouble optimizing these functions that was the case in the previous examples. The graphs show the percentile of building blocks correct in the population upon termination, averaged over thirty runs. A building block is correct when it has achieved the contents of `11111`. It is very obvious now that the type of crossover operator makes a difference, espcially when regarding the trap function with a signal of 0.2. It is clear that uniform crossover is unsuitable for the problem, even when the population size increases. The problem is the fact that the GA must be able to respect the building block boundaries. As uniform crossover is always applied to the parents and the chance at uniform crossover introducing a building block that is optimal is very small, the optimum substrings `11111` will very quickly disappear from the population and selection will then only drive the algorithm toward suboptima. The fact that uniform crossover has some good building blocks at all for the smallest of tested population sizes is in the most likely case a result of sheer luck that an initial population contained more than one copy of the optimal building block in one position and selection put those building blocks up against each other because of the higher fitness values they had, thus allowing the building block to survive and perhaps indeed increase its copies in the population. It is obvious that one–point and two–point crossover have more success in making the GA respect building block boundaries as the chance at disruptive crossover is much more slim. The results of the GA are almost classical and the one–point crossover variant even follows tightly the prediction model presented by Harik, Cantu–Paz, Goldberg and Miller [17].

Indeed, the GA has more trouble optimizing the trap function with the fully deceptive subfunctions as a population size of 200 does not completely suffice yet to always bring the GA to the optimal solution. We wish at this point to make no further remarks with respect to the GA dynamics as we are mainly interested in the results achieved by MIMIC and the framework by Baluja and Davies. Holding the results from the GA as comparison material, we continue to do just that.

Starting with MIMIC, figures 65, 67 and 66 show results that confirm most of the conclusions drawn on the performance of MIMIC so far. When the population size increases, the performance of MIMIC increases accordingly. Note that the population size to adequately solve the problem is just over 100, where the GA required a population of at least 160. Once again, the amount of samples per generation is rather irrelevant although for the greater populations a better difference

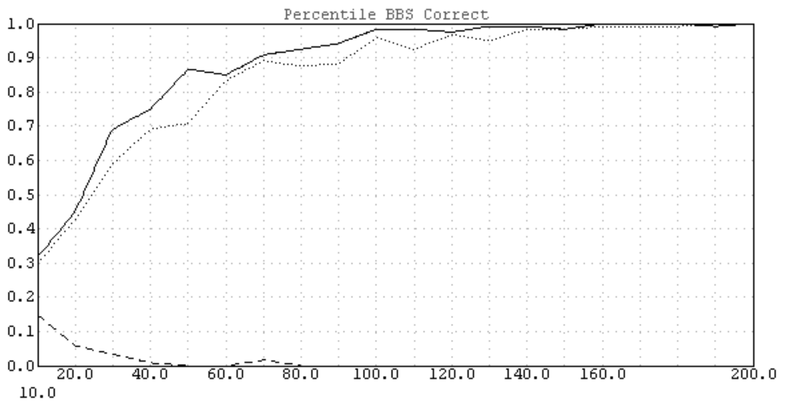


Figure 63: The percentile building blocks correct for the genetic algorithms on the trap functions with $d = 0.8$.

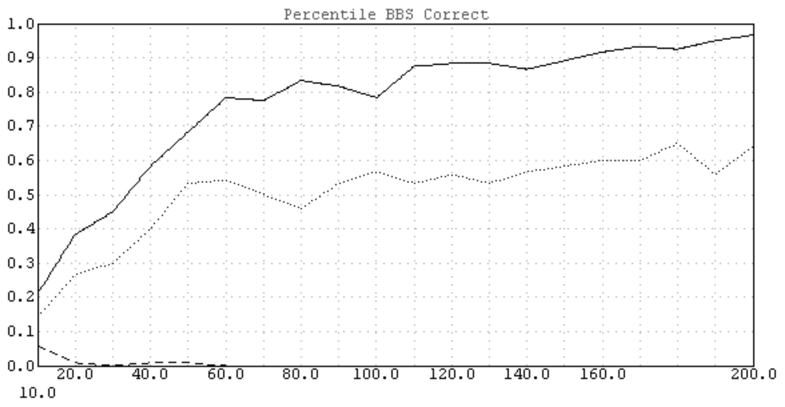


Figure 64: The percentile building blocks correct for the genetic algorithms on the trap functions with $d = 0.2$.

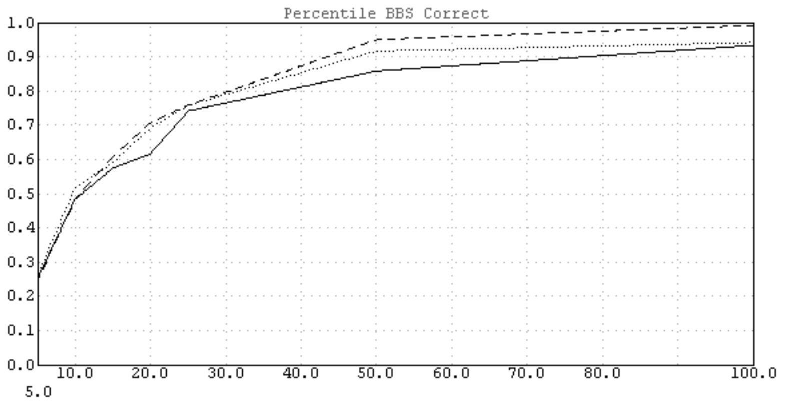


Figure 65: The percentile building blocks correct for MIMIC on the trap functions with $d = 0.8$.

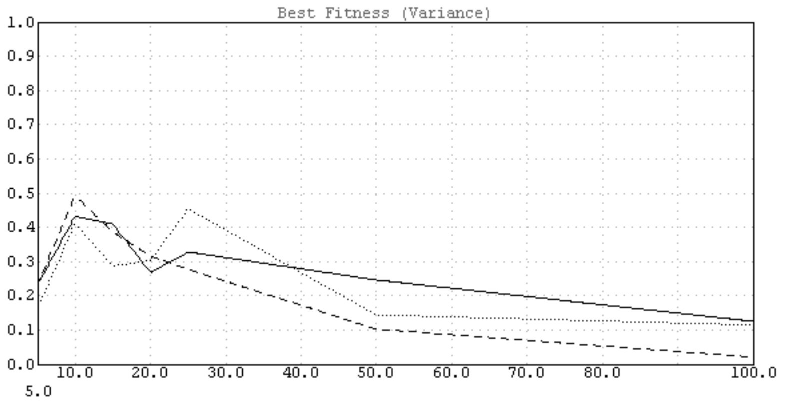


Figure 66: The variance over the best fitness for MIMIC on the trap functions with $d = 0.8$.

is shown that points to a preference for larger amounts of samples per generation. For each subfunction then as we have seen, the schema fitness for every order with 1 symbols is higher than the corresponding schema with 0 symbols. As a result, MIMIC is capable of defining relations with conditional chances that enfavor the 1 symbols even though the substrings with more 0 symbols are fitter than the ones with more 1 strings, save for the optimal one.

The results are somewhat the opposite when applying the three MIMIC algorithms to the deceptive version of the trap functions with signal $d = 0.2$ as shown in figures 68, 70 and 69. From the building blocks graph is it clear that the MIMIC approach fails to find the optimum value. The best fitness graph shows that because of the little variance and the low average of correct building blocks the algorithm is sometimes lucky and finds the optimum when the population size is small. Because of the very small percentage of building blocks correct, we can hardly say the algorithm is under those conditions reliable or competent. It would almost seem from the results that everything seen about MIMIC so far is reversed. First of all it seems that generating more samples each generation is benefitial to the algorithm and second of all an increase in the population size does in the long run not aid the algorithm, but destroys its chances completely. This behaviour tells us a lot about the MIMIC approach.

The fact that generating more samples each generation appears to benefitial to MIMIC for this test function is really nothing more than a result of the fact that when generating more samples, the amount of optimum building blocks will by expectation increase. With a smaller population

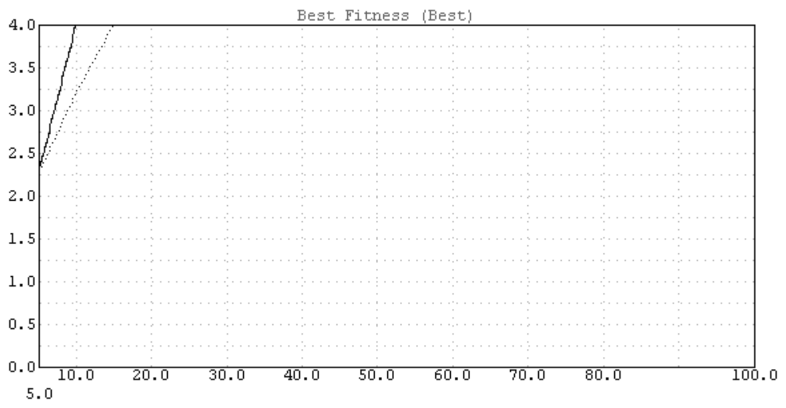


Figure 67: The best of the best fitness values for MIMIC on the trap functions with $d = 0.8$.

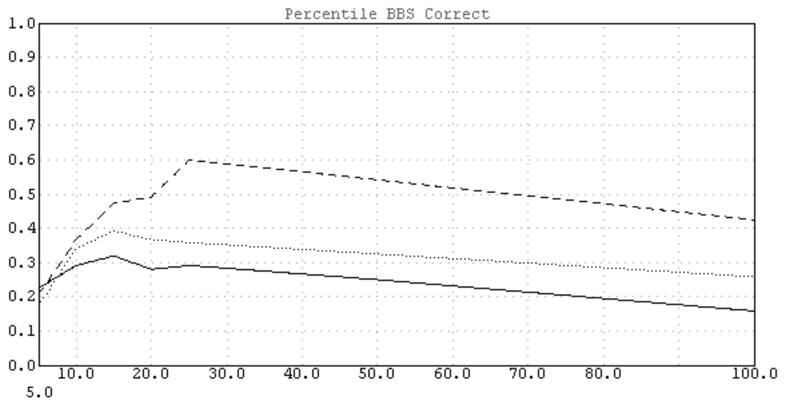


Figure 68: The percentile building blocks correct for MIMIC on the trap functions with $d = 0.2$.

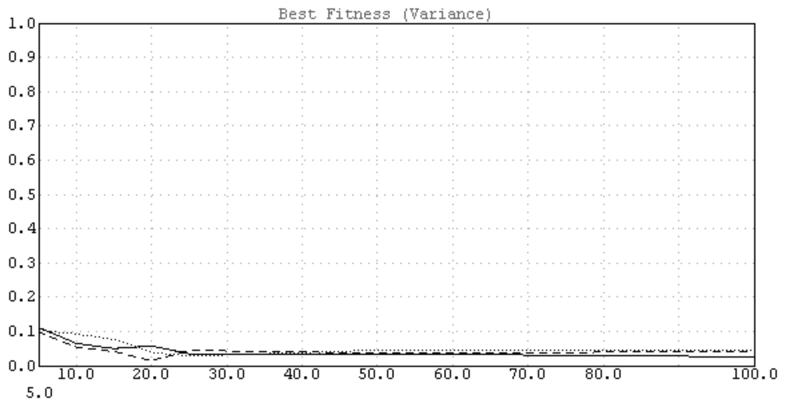


Figure 69: The variance over the best fitness for MIMIC on the trap functions with $d = 0.2$.

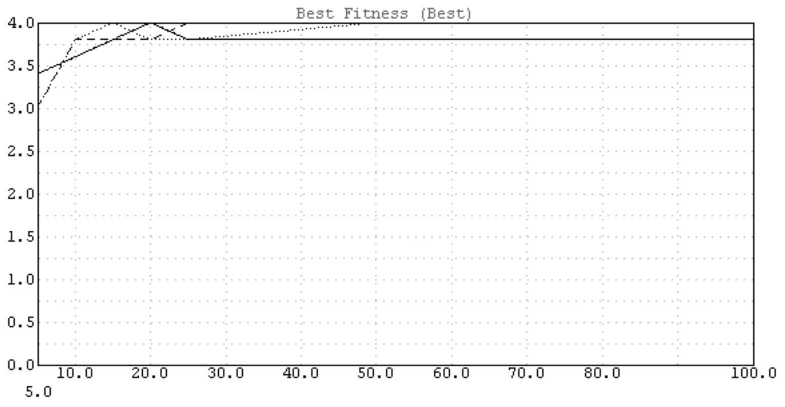


Figure 70: The best of the best fitness values for MIMIC on the trap functions with $d = 0.2$.

size, it then follows further that relatively more strings will have that optimum building block. As from an optimal building block MIMIC will learn nothing more than to make more of those optimal building blocks, the algorithm seemingly performs better by generating more samples at a very small population size. Fact of the matter is unfortunately that MIMIC is incompetent in learning the required relations with the right chances. It seems that MIMIC runs out of time to learn these relations. The population contains many blocks that aren't optimal and from those blocks, MIMIC will only learn relations that will state that it is more likely to have a `0` than a `1` symbol at a certain position, resulting in already the generation of strings that will tend to suboptimal strings. Larger populations will contain more blocks with non optimal building blocks as the selection mechanism allows more strings from the generated 100, 200 or 400 to survive in the population. The fact that things did not go wrong with the function with signal $d = 0.8$ is the fact that a large signal makes the suboptimum have a lower value. This implies again that a string with a single copy of a good building block has at least a fitness value of 1, which is never topped by a completely suboptimal string because its fitness equals $4 \cdot 0.2 = 0.8 < 1$. Thus, the selection mechanism will retain the better building blocks if they are there and will thus allow MIMIC the time to learn the right relations. As the strategy of MIMIC is to retain the best individuals, the better building blocks are preserved during the learning process and this is only stimulated in larger populations. For the trap functions with $d = 0.2$ however, a fully suboptimal string has a fitness value of $4 \cdot 0.8 = 3.2$ which is higher than many strings with one, two or even three building blocks correct. As such, retaining the better individuals is almost equal to digging a grave for MIMIC as information is kept that will only lead to bad relation deduction. Together with the fact that the learning of the relations does not happen fast enough, problems such as these cannot be solved by MIMIC.

We could thus say that MIMIC seems to run out of time in determining the required relations because the selection mechanism and the retaining of the better individuals which are mostly bad relation imposing unfortunately drives the good material out of the population too quickly as the new samples generated will only scarcely have optimal building blocks as the distribution is after the first generation equal to a random distribution. After a single generation however, consequences of the above result in a population from which relations are deduced that will result in strings with more `0` symbols, and subsequently there is no stopping the demise of the algorithm. As such, the increase in the population size will not help at all and will only make matters worse. Therefore it is very likely that a very critical aspect in the approach by Baluja and Davies is the use of their estimate array. The fact that they use an optimal dependency tree is ofcourse very interesting and less restrictive than the chain used by MIMIC, but because of the estimator array and the means of updating it, time can very well be bought to be able to assess the relations correctly. It would therefore be very interesting to see what the consequences are of extending

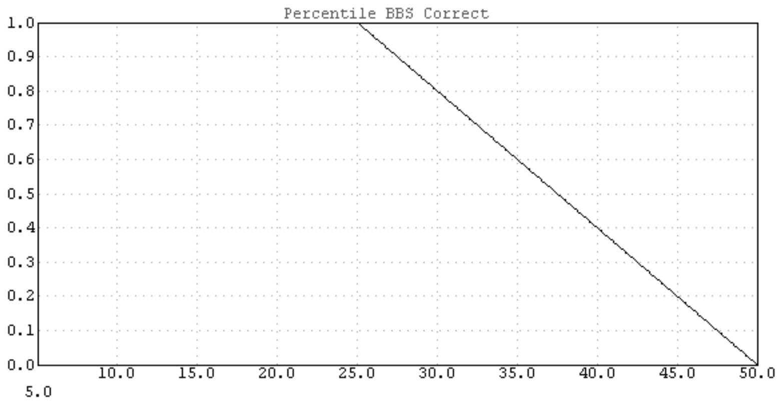


Figure 71: The percentile building blocks correct for Baluja and Davies on the trap functions with $d = 0.8$.

MIMIC with an estimator array. To place this research in a justifyable position, we should first see whether the chain that MIMIC does not impose too many restrictions. In other words, before researching the influence of the estimator array as the heart of the improvement over the MIMIC approach and determining its limitations, we should first see how the approach by Baluja and Davies performs once the estimator array is disabled there. This can very easily be established by setting $\alpha = 0$ since every generation the estimator array will be completely wiped and the relations thus based on the estimator array will stem from the filling of the array directly after the multiplication with the decay factor α, which is only the information from the current population. If we then use the *EA Visualizer* to install the same *Selector* and *Replacer* strategies as required for MIMIC, we have only the optimal dependency tree left as an improvement over MIMIC, save for the different measure in determining this relation graph which are the empirical entropies for MIMIC and the mutual information for the approach by Baluja and Davies. Having now assessed the shortcomings of MIMIC, we can conclude the batch of first round tests runs by shifting our attention towards the framework by Baluja and Davies and observing the results there obtained.

Looking first at the results for the trap functions with a signal of $d = 0.8$, figure 71 shows a difference over the previous test results as the approach fails on the test where the population size equals fifty. Figure 72 shows that the failure is complete in the sense that the approach is *always* led to the suboptimum, but such was pretty much clear because any average value that is at a maximum or minimum must have a variance of 0. The population sizes tested were once again 5, 10, 15, 20, 25 and 50. Even though it cannot be seen from the graph, it is known that only the variant generating 100 samples fails when the population size reaches 50. The variants generating 200 and 400 samples maintain finding the optimum value. As noted before, because of the way the framework by Baluja and Davies works, an increase in population size will not aid the algorithm, but more likely cause problems, especially when the nature of the problem is more difficult. The problem is that the population will contain more of the deceptive material because there is simply more of it. Basing relations on a majority of deceptive material will be the domise of the algorithm because in subsequent generations more `0` symbols are generated and the problem can no longer be overcome. Only generating more samples and thus generating more samples with correct building blocks that will replace that deceptive material in the population can remedy the problem. This is exactly what we see as a result.

Turning our attention to the deceptive version of the test function, figures 74, 75 and 73 show most interesting results that continue the trend set by the results found for the non–deceptive test function. First of all, the algorithm generating 100 samples does not always find the optimum solution anymore and cannot find anything else but the suboptimum once again when the population increases, only this time the population needs only be sized 25. The version generating 200

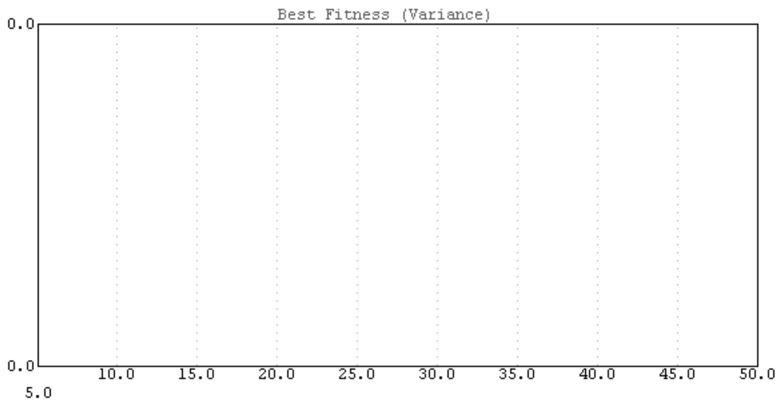


Figure 72: The variance over the best fitness for Baluja and Davies on the trap functions with $d = 0.8$.

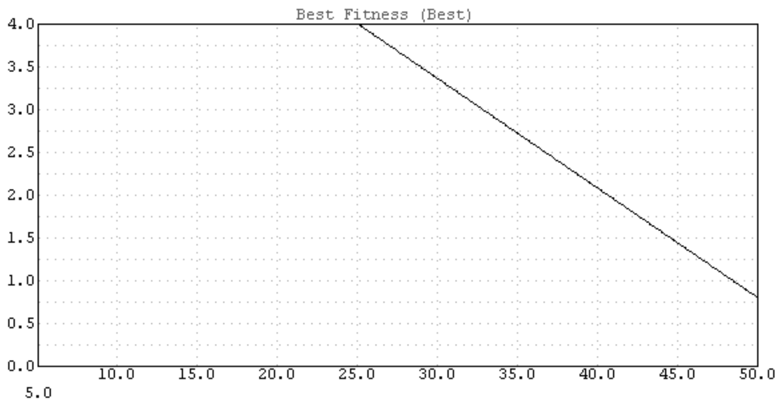


Figure 73: The variance over the best fitness for Baluja and Davies on the trap functions with $d = 0.8$.

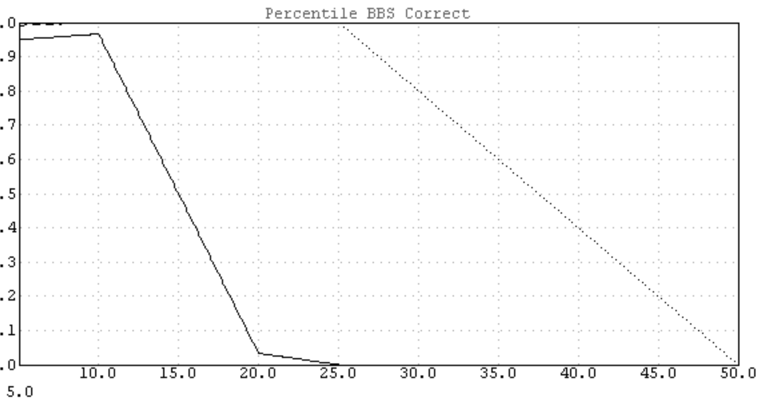


Figure 74: The percentile building blocks correct for Baluja and Davies on the trap functions with $d = 0.2$.

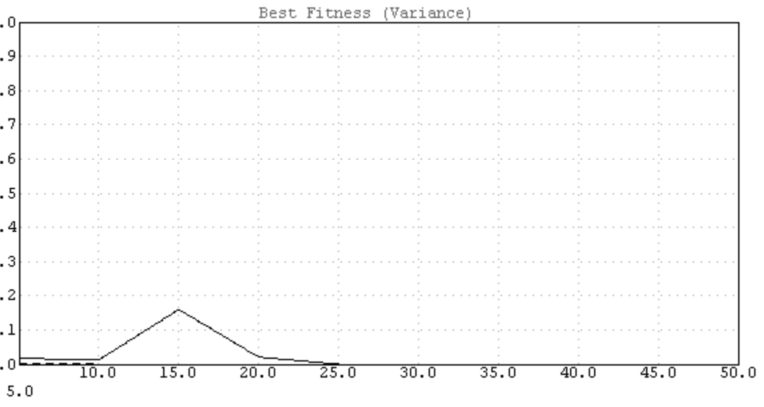


Figure 75: The variance over the best fitness for Baluja and Davies on the trap functions with $d = 0.2$.

samples is now seen to show the same problems as the version generating 100 samples already did on the trap function with $d = 0.8$ as when the population size reaches 50 it cannot find anything better than the suboptimum value. The version generating 400 samples each generation does not seem to be affected yet, but lies within the line of expectancy that when the population size reaches 100 that that variant will fail as well.

The fact that the approach fails when the population size increases we have explained and it follows from our discussion above about the performance of MIMIC on the trap functions with $d = 0.2$ that the failure does indeed come earlier at lower population sizes because of the signal. The failing of the approach at greater population sizes might very well be a problem because what happens when we have a problem that in GA terms requires a larger population size to be solved? Increasing the population does very much so not help as we have seen. For instance, increasing the problem length and thus adding building blocks might very well pose a problem that the variant generating 100 samples each generation cannot overcome when the problem length perhaps reaches already five or six building blocks. Moreover, when we scale the building blocks exponentially, meaning that the building blocks from left to right (or from right to left, depends on the implementation) have a contributing fitness that is multiplied by a number that is exponentially scaled in the building block number in the string (for instance when the base is taken to be 2, the leftmost building block is multiplied by 1 and the rightmost building block is multiplied by

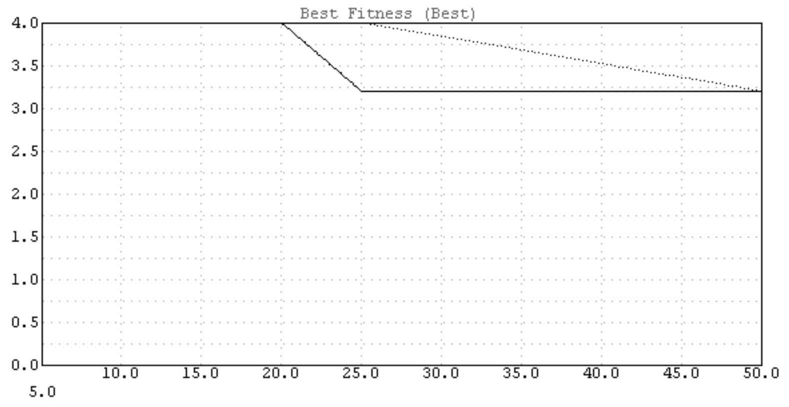


Figure 76: The best of the best fitness values for Baluja and Davies on the trap functions with $d = 0.2$.

2^m with m the amount of building blocks in a string), the significance of the rightmost building block is so strong that selection will quickly disregard the information the lesser scaled blocks. This problem can be overcome by increasing the population size so that the required material in those blocks is longer maintained and can be searched as soon as the most significant building block has converged. If increasing the population size doesn't help, such problems may very well be unsolvable by probability density estimator approaches. The only remedy might be increasing the amount of samples generated every generations, but this is likely not to be a solution either.

Topics for further directed research
After the research on the first results on the presented test functions and gaining essential insight on the dynamics of the new approaches, we can now state what the interesting topics are for further research that can now be directed toward a goal. The topics fall into three different categories:

1. What makes the approach work when it works
2. What is the influence of the parameter settings and what parameter settings are required to solve what problems
3. What are the limitations of the approach

Topics in the line of point 1 are twofold and have been pointed out during the research of the results earlier at some point. The idea is that it follows from the test results that the approaches work for some test functions. We have also seen cases in which one of the two approaches works better than the other or when the one of the two doesn't work at all (Ackleys function, trap functions with $d = 0.2$). The approaches differ in two things, namely the usage of an estimator array and the structure of the dependency tree. Finding out what makes the most important difference and thus what makes the approach actually work is then finding out what the results are when employing only one of those differences at a time. This means that we can either degrade the framework by Baluja and Davies to remove parts or add them to MIMIC. Having done this, we know what the most important ingredients are for the probability density estimator approach. In section 3.2.4 we will investigate exactly this.

Regarding point 2, the research in that direction is more that of the classical research done on GAs as well, trying to figure out what parameters are required for what problems and how the parameters influence the quality of the solution and the running time. We have given some insights for both the frameworks during the discussion of the results above and even though research in this field is interesting and important to gain insight into the strength of the approach and its computationability, we shall refrain from doing so because of limitations in time with respect to the release of this paper. As such, this topic can be stated as possible future research.

The final point stated as a topic for further directed research is directly in the line of the remarks made about the framework by Baluja and Davies and its results of the trap functions with $d = 0.2$. It would be interesting to see if indeed the approach fails when the problems are such that an increase in population size is really required, but such a remedy only means the domise of the algorithm because of its nature and dynamics. Thus, this would amount to finding the limitations of the approach and then concluding that even though there is certain power in the new approach, there is also a boundary to its applicability. Again because of time restrictions we shall not elaborate on this topic further.

3.2.4 Boundaries and differences

After the first round of tests of which the results were discussed in section 3.2.3, in this section we continue running tests, but now move on to a more specific level of testing so as to investigate only a certain part of the probability density estimator approach. As mentioned at the end of section 3.2.3, one of the things that is interesting to take a closer look at is finding out what makes the approach by Baluja and Davies better than the approach that is MIMIC. The approach by Baluja and Davies differs in some points from MIMIC. By looking at hybrid forms that employ parts from both strategies we are able to find out what the influences are of what parts that are different in the two approaches. Using results of this type, the opposite of this research being the part this is similar in both approaches can then be investigated in the light of what works and what advantages it gives in an investigation with respect to the limitations of the probability density estimator approach. Even though the latter subject is most interesting, we shall refrain from that in this section as well as the remainder of this paper because of unfortunate time restrictions. However, in the research that follows we shall see that we can yet to some extent draw conclusions about what the boundaries are of the probability density estimator approach.

The main point in this section is thus the pointing out of the differences between the approach suggested by Baluja and Davies and MIMIC. The framework by Baluja and Davies was posed to be an improvement over MIMIC and from the results seen in section 3.2.3 we can say that on the functions tested indeed its results are better. There are however three differences between the two frameworks, making it difficult to see what the influence is of which difference. It is therefore our goal in this section to investigate the influence of some of the differences individually to see how they make the framework by Baluja and Davies be an improvement over MIMIC. To this end we first point out what the three differences are:

1. The framework by Baluja and Davies uses a less restricted form for the probability distribution and in fact uses a structure that actually minimizes the Kullback–Liebler divergence that is in MIMIC only *approximately* minimized through a greedy algorithm
2. The framework by Baluja and Davies uses an estimator array to base the probability distribution on. This estimator array is updated by a selection of the samples generated based on the contents of the estimator array in the previous generation. In MIMIC the contents of a population is used to find the probability distribution in which the best n individuals are kept choosing from the new samples and the contents of the population in the previous generation.
3. The framework by Baluja and Davies uses a different measure for expressing the relation between individual bits. The measure used in MIMIC is based on conditional entropies, which is a non–symmetrical measure whereas the framework by Baluja and Davies uses the mutual information measure which is a symmetrical measure[15].

[15]A symmetrical measure means that $M(X, Y) = M(Y, X)$ with $M()$ the measure function and X and Y the

As was noted when going over the results of the first round of tests in section 3.2.3, the estimator array is most likely a very important difference as it poses a different approach to learning information because of the difference in storing information from previous generations. Also the less restricted form for finding the second order probability distribution might be very important because of the fact that learning relations might be quick and strong enough to overcome the quick loss of good blocks in the population. The item of using a different measure for finding related bits seems not too much of a point because the measures are fairly identical. As noted however, the measure used in the framework by Baluja and Davies in symmetrical, which might very well be an important difference with respect to the non–symmtrical measure used in MIMIC. In the light of achievable results in the time that remains to write this section, we restrict ourselves mainly to the first two points as we shall see that testing them together is no more difficult than one of them.

To investigate the influence of the difference in probability distribution structure as well as of the estimator array, we implement a new type of *Recombinator* in the *EA Visualizer* that is of a hybrid form. To be precise, the new *Recombinator* is restricted to the chain structure as used in MIMIC, but also has the estimator array as well as the symmetrical measure used in the framework by Baluja and Davies. In this way we can actually take along the influence of the relation measure as well. To see this, we note that disabling the estimator array by employing a decay factor $\alpha = 0$ and using the `Add Offspring To Population` *Replacer*, we have the same structure of basing the probability distribution on the population and updating that population through taking the better individuals from the population from the previous generation and the new samples of this generation, as is used in MIMIC. This means that using just these settings in the new hybrid operator, we actually have MIMIC save for the symmetrical relation measure[16]. Also, we have all differences except for the estimator array by using again those settings but now with the *Recombinator* that implements the approach by Baluja and Davies. Thus, if we test the hybrid approach with the estimator array disabled as well as enabled and the approach by Baluja and Davies with a disabled estimator array, we have all the differences layed out separately as we have given the results for MIMIC and Baluja and Davies in section 3.2.3. The graphs for the different approaches in this section show again three lines, namely one solid, one dotted and one striped line. These once again stand for 100, 200 and 400 samples per generation respectively. The whole setup with respect to the tests we have just discussed to be using does ofcourse imply that we use a subset of the same test functions as used in section 3.2.3. As we have seen that the two most interesting test functions are the two instances of the trap functions we shall only use these to investigate the differences and come to conclusions in the following.

We start off by inspecting the results obtained by the hybrid approach with the same parameter values as used in the tests in the first round in section 3.2.3, meaning a decay factor of $\alpha = 0.99$ and an estimator initialization of $c_{\text{init}} = 1000$. The results with respect to the percentile of building blocks correct over 30 runs for the trap functions with signals $d = 0.8$ and $d = 0.2$ are depicted in figures 77 and 78 respectively. The characteristic decay that occurs when the population size increases is found here as well as with the original approach by Baluja and Davies. On a first note this tells us that the structure of the probability distribution is of no influence on the behaviour that for problems such as these trapfunctions an increasing population size is desastrous. At this point it is ofcourse interesting to search for the reason why this decay is observed. We shall do so shortly, but first we extract from the graphs what we set out to extract, namely the influence of the difference between the approach by Baluja and Davies and the hybrid approach, that thus only differs in the structure of the probability distribution. Comparing the results in percentile building blocks correct, the difference is best noticable for the trap functions with $d = 0.2$. As noted, the occurence of the decay is a fact for both approaches, but for the hybrid approach the decay comes earlier. This implies that indeed the chain structure is more restrictive and this shows in practice. Using the chain finds the relations at a slower rate. The tree structure is capable

discrete variables. Non–symmetrical measures have $M(X, Y) \neq M(Y, X)$ in the general case.

[16]A minor detail is that MIMIC uses the minimal unconditional entropy to find the tail of the chain, whereas the hybrid form just as the framework by Baluja and Davies uses a random bit.

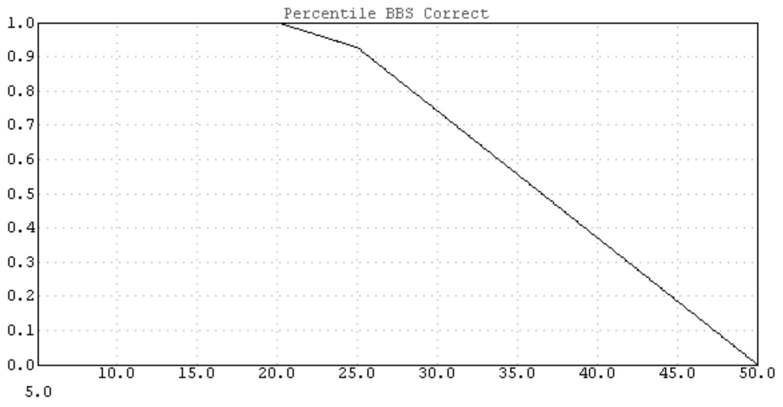


Figure 77: The percentile building blocks correct for the hybrid approach on the trap functions with $d = 0.8$.

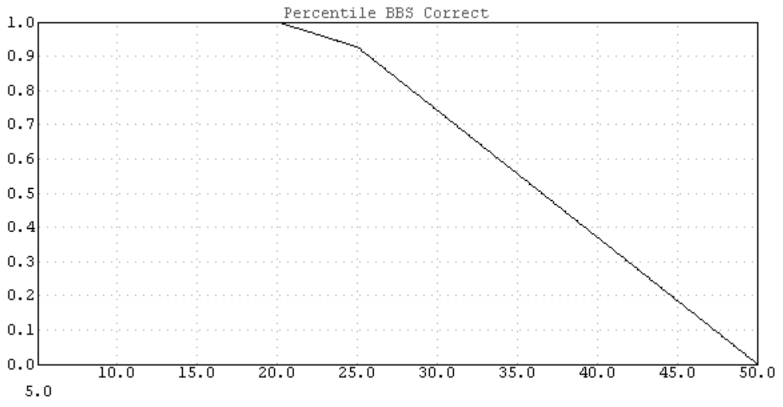


Figure 78: The percentile building blocks correct for the hybrid approach on the trap functions with $d = 0.2$.

of learning the relations faster, which results in finding the optimum at greater populations than the chain structure when the search is apparently more difficult. A first conclusion at this point could be that using the chain structure for probability distributions is less powerful than using the tree structure, but we have only seen its advantage coming from the approach by Baluja and Davies and narrowing that down. We shall be confident about this conclusion no sooner than that we observe that when augmenting MIMIC to incorporate the tree structure instead of the chain structure leads to better (and quicker learning) results as well. This will become apparent from the next tests, but first we turn to finding an answer so as to why the Baluja and Davies approach with the estimator array fails when the population size increases for the trapfunctions and what implications this has.

In order to find the explanation, we should first realise what increasing the population size means for the approaches. Both approaches use the estimator array but differ in probability distribution structure. The genomes in the population are used to update that array. Thus increasing the population size means increasing the amount of genomes that is used each generation to update the estimator array upon which the probability distribution, the conditional chances and the mutual information measure are based. To make thinking about the issue easier, imagine the fitness function to be only a single building block and not four placed one after the other. There are $2^5 = 32$ different combinations of bits for one such block, out of which only one is optimal.

This means that a random population of 32 members is expected to have one copy of the optimal block as the chance at that block appearing is obviously $\frac{1}{32}$. At this point we should remember that the new samples each generation are created and have nothing to do with the population size. The population size is merely the amount of genomes that is used from the total amount of samples generated each generation to update the array. In other words, we have for instance tested with 100 samples per generation. This means that in such a population, we have on average $\frac{1}{32} \cdot 100 \approx 3$ optimal blocks when we are generating them at random which is initially the case. Now if we select the five *best* strings of the population the update the array, we expect to update that array with three strings containing the optimal block of only ones and two strings containing the suboptimal block of only zeros. These are the two fitmost strings and we expect to have just about three copies of both of them when generating 100 samples at random. Relations learned from this will most likely be of the form that specifies that when a bit is `1`, every bit that is linked to it must also be `1` and when a bit is `0`, every bit that is linked to it must be `0` as such is the only evidence in the population. Furthermore, in this constructed example, the chance at a `1` symbol is greater as we have three strings with only ones and only two strings with only zeros, so the algorithm will most definately be driven to generate more strings with only 1 symbols and the solution is easily found. Now imagine having a population of size 50 on the same problem. Intially once again nothing else than random strings are generated and thus there we expect again to have the three optimal strings and the three suboptimal strings. Ofcourse, these are once again placed in the population. However, we now still have $50 - 6 = 44$ population members left to choose from the randomly generated strings. As the 44 remaining best are selected, there will be more strings with zero symbols than we have strings with one symbols because those have a higher fitness. As the chance for instance at generating a block with a single 1 symbol is $\frac{5}{32}$, we expect to have $\frac{5}{32} \cdot 100 \approx 15$ of such strings which are all fitter than strings with more one symbols and thus these will be in the population as well. Thus the population is filled with more information that leads to the suboptimum and any learned relation will most likely generate strings for which the root bit is more likely to be a zero symbol and thus make linked bits most likely be more zero symbols. Pushing the population size further, we get to the cases in which we have a larger population size than we generate samples, which in turn is larger than the search space. This will make the population contain by expectancy the same amount of one symbols as zero symbols in the same type of combinations. The outcome is then expected to be undefined as the relations extracted will be nothing more than random since the conditional chances are themselves identical to the unconditional chances and equal to $\frac{1}{2}$. We must not forget that even though we have clearly explained why failure occurs when the population increases for a problem with only a single building block, we must not forget we are working with a multiple of building blocks. Counting the amount of optimal blocks generated on expectation does not change however for each block seperately when generating at random. For each block we expect to have three optimal copies when generating 100 samples. It is now however not definative that they will be selected to be part of the population because for instance a single optimal block with the remainder of the string only blocks that contribute a fitness value of 0 loses over a string that has two blocks that contain three zeros and two ones and two blocks that contain two zeros and three ones in the case that $d = 0.2$ as the fitness of such a string is then is then $0.2 \cdot 2 + 0.4 \cdot 1.2 > 1$. This is not the case when $d = 0.8$ which explains why a larger population size is destructive for larger values than for the trap functions with $d = 0.2$ because such strings (which are most common in a randomly generated population) are then *not* fitter and optimal building blocks will be selected, allowing the algorithm to perhaps yet learn the required relations. It would be interesting to mathematically establish the amount of individuals in the population beyond which the framework fails, but we shall leave this for further investigation at this point. We shall note however that when we generate more samples, for instance twice as many, we have by expectance twice as many good (and bad) building blocks, making it twice as easy to learn the right relations, postponing the decay by a factor of two. This is indeed the behaviour seen in the graphs for $d = 0.2$. Note that the population sizes tested where 5, 10, 15, 20, 25 and 50, so the graph for 200 samples will probably have shown that the hybrid approach completely fails at a population size of 30 already, being exactly twice as large as the population size of 15 that was required for the 100 samples per generation variant to fail.

The amount of samples generated was for these test functions always more than the search space of a single building block as the lenghts of the blocks was no more than 5, implying a search space of $2^5 = 32$ for a single block. Even though such problems are amongst the special class of order k delineable problems with $k = 5$ here and assumed to be the type of problem we are likely to encounter in optimization where groups of k bits at most are important blocks in the search space, it is most interesting to see what will happen when k increases. In order to create a similar situation, we must generate an amount of samples in the same ratio to the population size as before. This would imply however an increase in the amount of samples per generation growing as $O(2^k)$, which is exponential. However, this is the case for *every* linkage learning algorithm we have seen so far as can be read in section 3.1. It is to be expected that the framework will in such cases still find the optimum in the same manner as is the case here for smaller values of k, so this is not a boundary for the approach.

Increasing the amount of blocks is another factor that makes the problem more difficult. We have not investigated anything to this end. To only thing we can mention is the fact that the running time increases because the string length increases. However, this running time is very much so dependent on the amount of strings that is used every generation to update the estimate array. As we have seen that this amount is best to be small, the increase should be of a lesser concern. For very large string lengths then again, problems might very well occur because of the n^2 component in the running time that depends on the string length.

We close the discussion of the hybrid approach as a downfall seen from the Baluja and Davies framework by noting that we have not included the influence of the estimator array together with its decay factor and initialization value at all. As mentioned before, increasing the decay factor makes the decision making with respect to relation finding less direct as strings from previous generations have a more of an impact. Relation finding is therefore slower but also less prone to coincedental behaviour. Furthermore increasing the initialization value for the estimator array makes the process have a more random like behaviour in the beginning, allowing it to slowly stabilize with respect to relations found instead of finding relations only from population material directly from the start. In the light of the arguments placed above, these values are very important, but most likely the greatest impact lies within those arguments. We shall shortly see what the results are of totally disabling the estimator array and leave its impact in the light of the arguments above for later research. Also, the boundaries imposed because of the increase in population that results in destructive behaviour are are topic of later research, especially since it can be placed in a much better light once more mathematically and precise the above notions are layed out. We now continue with investigating further the impact of the differences between MIMIC and the approach by Baluja and Davies.

Having seen an approach similar to Baluja and Davies in that the results are of the same form, an approach more similar to MIMIC will be found when the estimator array is disabled in the hybrid approach. The only difference then left between such a hybrid approach and MIMIC is the measure used to find the probability distribution. The structure for the distribution is in both cases the chain, only the root of the chain is selected at random in the hybrid approach and taken to be the bit with the lowest entropy in the population in MIMIC. We expect the results of the two approaches to be similar. Figures 79, 80 and 81 show the results of the hybrid approach with the same selection structure as MIMIC and no estimator array on the trap functions with $d = 0.8$. Comparing these with the results by MIMIC in figures 65, 66 and 67 from section 3.2.3, we indeed see very similar results. Even the variance values show the same form. If any preference on one of the two algorithms is to be pronounced, it would be in favor of MIMIC as for smaller population sizes it seems to slightly outperform the hybrid approach in both correct building blocks upon termination as well as variance values and finding the optimum at all at least once over thirty runs. Furthermore it seems that the results for MIMIC are slightly worse than those of the hybrid approach for larger population sizes when inspecting the variants that produce 100 and 200 samples per generation. We can however draw no conclusions at this point other than

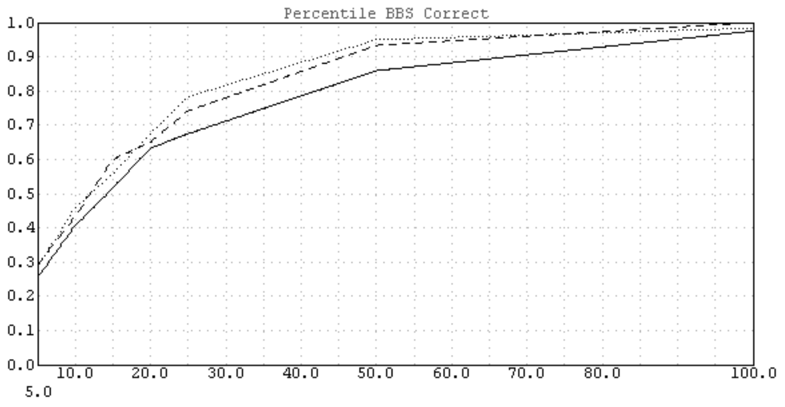


Figure 79: The percentile building blocks correct for the hybrid approach without estimator array on the trap functions with $d = 0.8$.

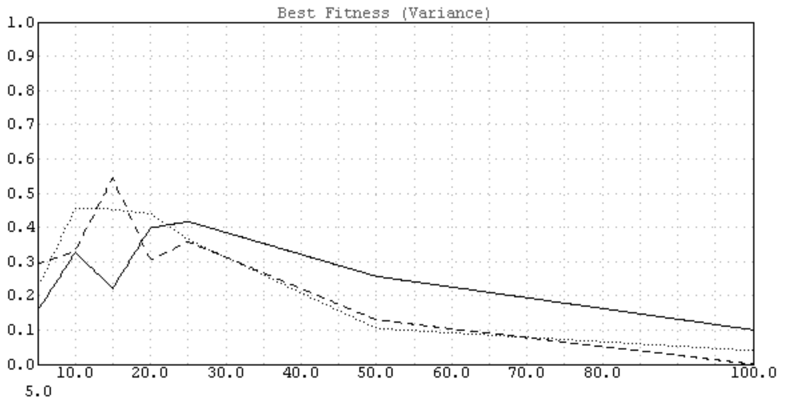


Figure 80: The variance over the best fitness for the hybrid approach without estimator array on the trap functions with $d = 0.8$.

that any difference is negligable. We must remember however that this function is the easy variant and we shall therefore before actually stating that we are sure of this argument first look at the results for the harder version of the problem where the signal equals $d = 0.2$.

Looking at the results for the hybrid approach with disabled estimator array on the trap functions as depicted in the graphs in figures 82, 83 and 84 and comparing them to the results obtained by MIMIC as depicted in the graphs in figures 68, 69 and 70 respectively in section 3.2.3, a completely different result in the field of the difference between the two approaches is to be observed.

Whereas MIMIC fails to be a competent approach that finds the optimum value at an increasing population size as is obvious from figure 68 that shows how the MIMIC approach declines in performance at an increasing population size, the hybrid approach with disabled estimator array that is thus analogous to MIMIC does not decline in performance as is depicted in figure 82. Even when the population sizes are further increased, no decline is noted further along the way. Even though there are no graph results, additional tests have shown the percentile of correct building blocks to increase over increasing population sizes. The values measured over 30 runs at 200 samples per generation are as follows:

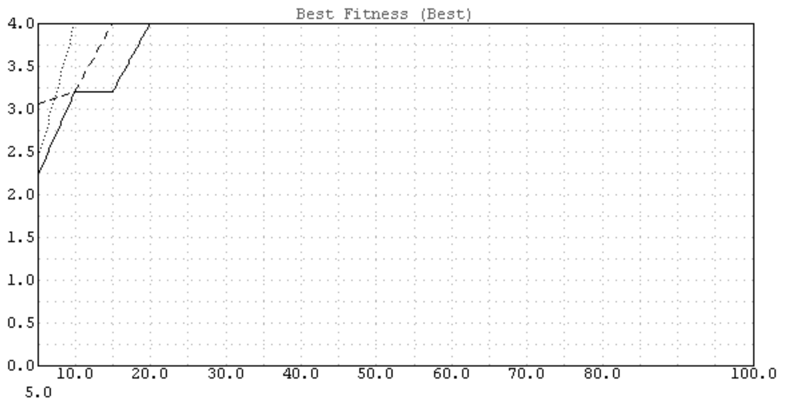


Figure 81: The best of the best fitness values for the hybrid approach without estimator array on the trap functions with $d = 0.8$.

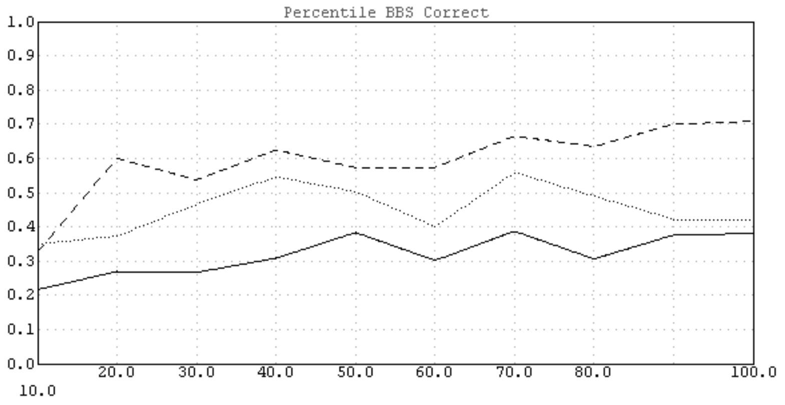


Figure 82: The percentile building blocks correct for the hybrid approach without estimator array on the trap functions with $d = 0.2$.

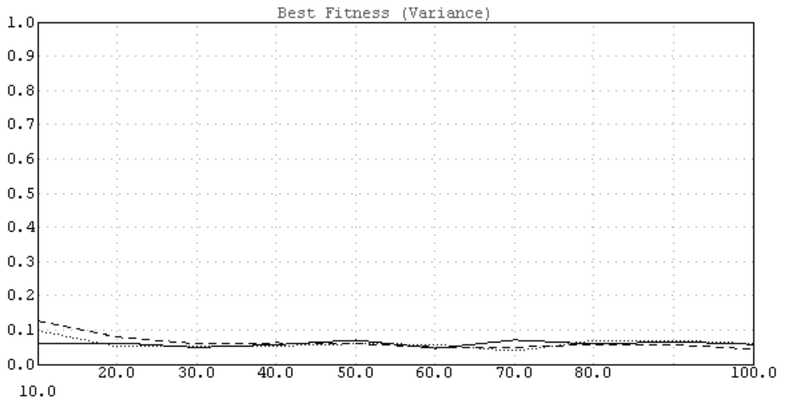


Figure 83: The variance over the best fitness for the hybrid approach without estimator array on the trap functions with $d = 0.2$.

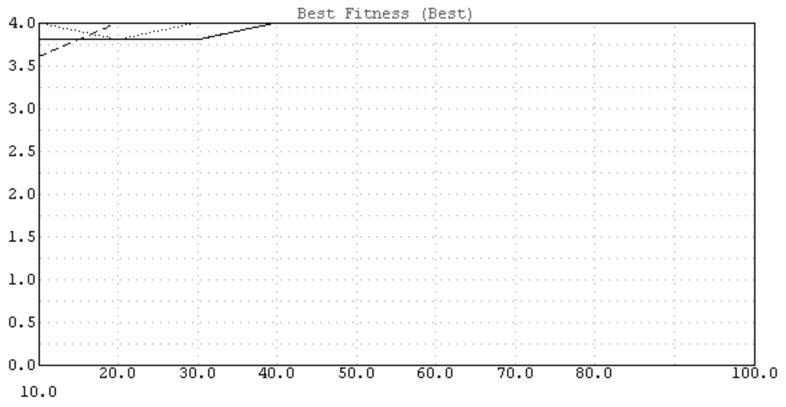


Figure 84: The best of the best fitness values for the hybrid approach without estimator array on the trap functions with $d = 0.2$.

Population size	**Percentile**
200	0.5
300	0.51
400	0.59
500	0.71

These results show that it is to be expected that eventually the optimum value will be found at a good confidence factor. Extrapolating however based solely on the results for population sizes from 200 to 500, results in a population of some 1400 genomes to find the optimum solution for sure. The problem is that termination doesn't happen very quickly at such large population sizes and 500 generations are easily required, leading to 100000 function evaluations, which is much larger than the somewhat 10000 function evaluations required by the GA. We can therefore only conclude that the MIMIC approach is inferior to the approach by Baluja and Davies which uses the estimator array. Furthermore, based on the difference that we are actually inspecting here, namely the influence of the measure and the slight variant of the greedy algorithm that determine the probability distribution, we can *not* say that the impact is negligable.

The only aspect in which the hybrid approach differs from MIMIC is the greedy algorithm that determines the chain. The bit i_n is not determined as being the bit that minimizes the entropy value but chosed at random. Furthermore, the measure used to find the bit i_k that is linked to i_{k+1} is the mutual information measure which is symmetrical as opposed to the conditional entropy measure used by MIMIC which is non–symmetrical. Even though unfortunately a precise analysis of the impact of the difference that caused this discrepancy violates our time bounds for this paper and is thus moved to further research, the *EA Visualizer* has given insight in the dynamics of the approaches and as such what we *can* do at this point is give a clue so as to where to look when this is to be investigated at a later point in time. To this end, we first describe how the general approach has been found to be by the selection–replacement strategy as found in MIMIC and does not use an estimator array. First the relations are established fully and then the population is flooded to all equal genomes according the those relations. For the current problem this means that MIMIC finds a chain of probabilities saying that when a bit is `1`, the bit linked to it must also be `1` and when a bit is `0` the bit linked to it must also be `0`. For large enough populations, these relations are unmistakeable and correct over all bits. For smaller populations the results are that for some bits those chances are exactly the opposite and it is only true for a subset of the bits. As the combinations of `0` bits are suboptimal and are thus the next best thing under the combinations of `1` bits and because of the majority of `0` bits in direct selection as follows from the above discussion on the working *with* the estimator array, the population mostly first works up to a content that has only few entries that contain the optimal building blocks and the remainder of the population contains strings with only `0` symbols. Because of the fact that the best genomes are selected from both the current population and the new samples, the string with some good building blocks *never* leaves such a population unless a better string is found. Such will not be the case however based upon the population contents just described. What will happen is that the population will gradually be flooded with the right material for as much as it is available in those few strings with the good blocks. Lets say there is exactly one such string with the first two blocks optimal and the rest suboptimal. As this is the *only* string in the entire population with these blocks (all other strings contain only suboptimal blocks), the chance at generating a `1` symbol is very small as the probabilities that are used for generating new samples are based on the current material in the population. The chance is however *not* zero and thus there will come a time when indeed a `1` symbol is generated, causing the new sample to have the same remaining structure as that one string with more good material. This string is then immediately incorporated in the population and the result is more of the strings with the good material, as they are never lost until something better comes along. The chance at generating a `1` in subsequent generations ofcourse then increases in a monotone fashion, growing more rapidly each step as more strings with that good material (and the exact same material) are generated. The algorithm should then terminate when the entire contents has thus driven out the suboptimal strings and left us with the better strings only.

For the hybrid approach and the approach by Baluja and Davies, both in which the estimator array is disabled, the above dynamics work out properly. However, for MIMIC there is a slight problem as the approach seems to learn relations less proper. Whereas the other approaches are indeed capable of isolating and indentifying the blocks still at larger population sizes, MIMIC has trouble doing this neatly. The approach is seen to have more clutter in the population during evolving stages to the point where there are more bits left here and there along with the bits that make up a few optimal blocks. These bits just here and there are a result from learning not good enough the relations and finding the blocks that really cohere in better solutions. Not being able to do so unfortunately is destructive with respect to the given function as for instance having a string with a single optimal block and two blocks that are suboptimal save for a single bit, such a string has a lesser fitness than a fully suboptimal string. In such a case, the string is pushed from the population by the forces of selection and the above final stage cannot be commenced. In greater populations more of this clutter is introduced and more often the good blocks completely disappear from the population, which is why MIMIC fails on this harder test function. The only way to overcome the problem is to increase the amount of samples per generation, but this will probably not scale up with the problem size. The reason why MIMIC didn't fail on the easier problems and seemingly even outperformed the hybrid approach is that those problems were simply not difficult enough to cause these problems. For instance, when $d = 0.8$ for the trap functions, the above situation does not turn into a problem because of the fact that the string with the good block is more fit than a fully suboptimal string and therefore the good material can be propagated yet. To give the reader a feel for the arguments described above, the population contents over typical runs for both the hybrid approach and the approach by Baluja and Davies, both with disabled estimator array and MIMIC are depicted in figure 85. The snapshots from the population contents were taken every generation, the amount of samples per generation was 200 and the population size was also 200. Every red dot means a `1` symbol in the population and every blue dot means a `0` symbol. We can only conclude from the results seen that the measure that determines the probability distribution is yet of importance for properly learning the relations. What causes the more clutter to stay behind in MIMIC and subsequently makes it fail on deceptive functions such as the trap functions with $d = 0.2$ is yet to be established in a more formal fashion in the future.

It remains to investigate the influence the difference in tree structure has with respect to the chain structure when starting from MIMIC and expanding that framework by employing the tree structure instead of the chain structure. This is the opposite from what we did in the beginning of this section where we degraded the approach by Baluja and Davies by dropping out the tree

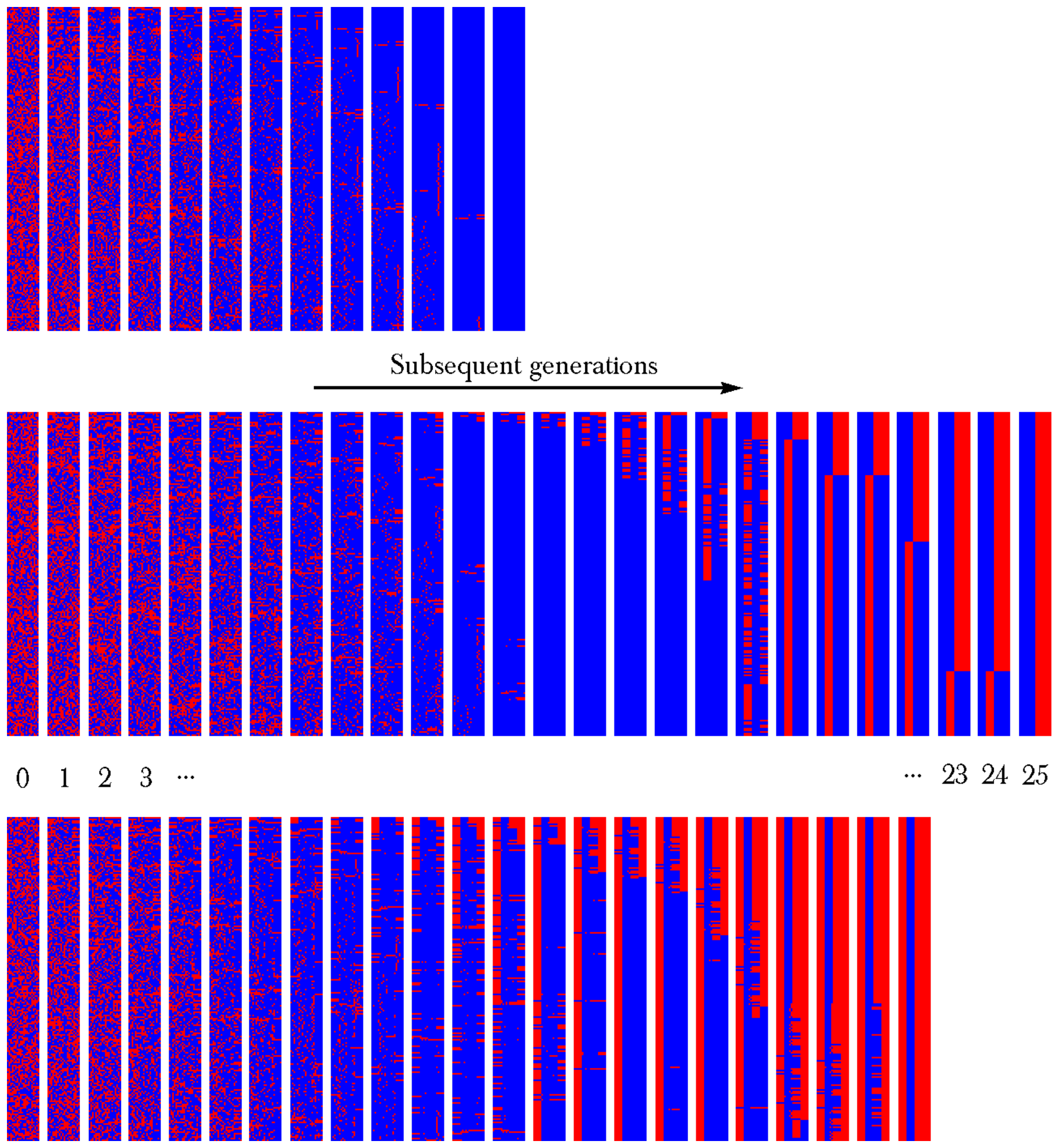


Figure 85: Population contents in typical runs for the three approaches on the trap functions with $d = 0.2$. At the top is MIMIC, the center shows the hybrid approach and the bottom Baluja and Davies (the latter two without estimator array.)

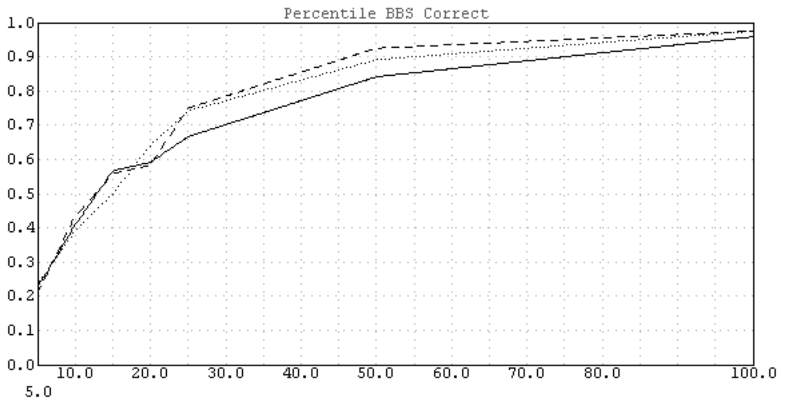


Figure 86: The percentile building blocks correct for the Baluja and Davies approach with disabled estimator array on the trap functions with $d = 0.8$.

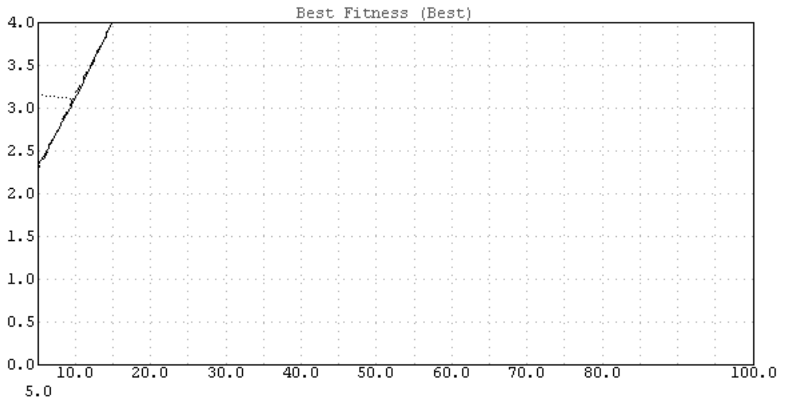


Figure 87: The best of the best fitness values for the Baluja and Davies approach with disabled estimator array on the trap functions with $d = 0.8$.

and incorporating the chain. To make sure the tree is an improvement over the chain, the results will have to point out exactly that under these circumstances as well. As noted in section 3.2.3, in order to get the tree in the MIMIC approach, we simply employ the same selection–replacing strategy that is used in MIMIC, but use the Baluja and Davies *Recombinator* in which we set α to 0 and thereby disable the estimator array, just as we did for the new hybrid *Recombinator* in the tests just discussed.

Figures 86 and 87 show the results for the adapted Baluja and Davies approach on the trap functions with $d = 0.8$. There are no noticable improvements over the results by MIMIC or the hybrid approach with disabled estimator array. This could imply that chain is sufficient to capture the required structure as the good material is present in large enough quantities and that thus the tree cannot impose an advantage here. It could also mean that the tree is less of an advantage than expected based on the results with the estimator array at the beginning of this section. To find out which of these two options is the right one, we take a look at the results from the deceptive version of the test function with $d = 0.2$.

Figures 88 and 89 show the results for the trap functions with $d = 0.2$. As the hybrid approach had shown to require larger populations, the approach was tested directly with larger populations, up to and including 500. The sizes tested were 5, 10, 15, 20, 25, 50, 75, 100, 200, 300, 400 and 500. Up

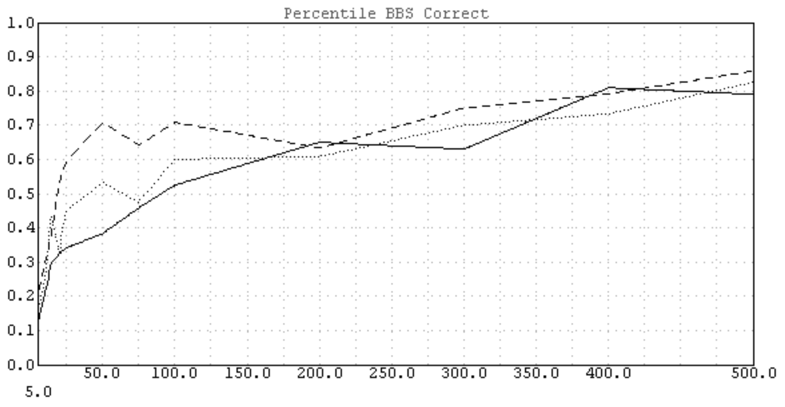


Figure 88: The percentile building blocks correct for the Baluja and Davies approach with disabled estimator array on the trap functions with $d = 0.2$.

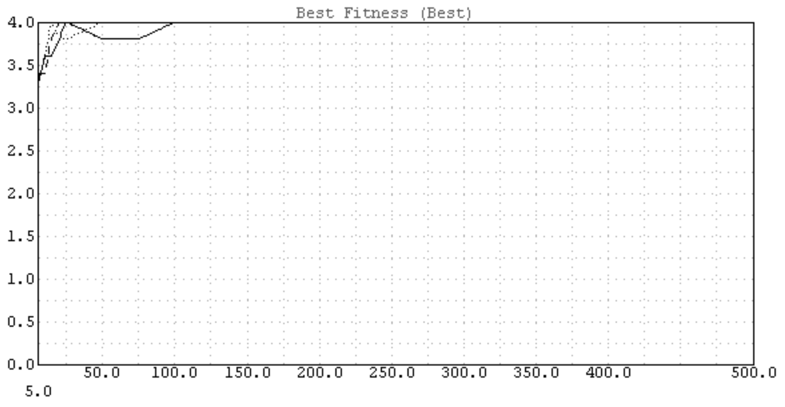


Figure 89: The best of the best fitness values for the Baluja and Davies approach with disabled estimator array on the trap functions with $d = 0.2$.

to population sizes of 100 again no improvements are found for the tree approach over the hybrid approach that uses only the chain, but judging from the larger populations, the graph entry for 200 samples per generation shows a clear improvement over the tabulated data of the additional testing for the hybrid approach. Even though it is clear that the dynamics of the algorithm are identical, indeed the tree makes the relation learning quicker and thus it outperforms the chain and finds the optimum sooner with increasing population sizes. We therefore conclude that the tree approach that actually minimized the Kullback–Liebler divergence is indeed an improvement over the chain based approach.

The last thing that is very interesting to note at this point is that the graph entries in figure 88 lie very close together at the larger population sizes. It is therefore most likely that an increase in the amount of samples per generation is much more benefitial for the algorithm, keeping the population size stable and relatively small, than is increasing the population size as the influence of the latter is seemingly too small to solve the problem adequately. A final conclusion is therefore that on the one side generating more samples is benefitial to MIMIC like approaches but on the other side the exact influence of this on the performance as well as its comparison to the influence of an increasing population size requires further research.

3.2.5 Possible future extensions

In section 3.2.4 we have investigated in a specific manner subjects on the probability density estimator approaches that are MIMIC and the framework by Baluja and Davies. These subjects followed from initial research found in section 3.2.3. Even though some sides of the new approaches have been researched, many topics can yet be further investigated as they can unfortunately in the light of this work be no more looked into. We state some of these topics in the following.

We have noted in section 3.2.4 that we can go quite far in using mathematical terms to describe the dynamics of the new approaches. By doing so, the limitations and requirements will become much more evident and the required settings will then become clearer. At this point the settings that are required to solve a certain problem are unclear and a relation is needed that specifies in some way how the parameters should change when the characteristics and difficulty of the problem change. By forming a mathematical description of the dynamics of the approaches, points such as these are most likely made clearer.

Tests with approaches using the estimator array showed that for the trap functions an increasing population size meant a downfall in performance when using an estimator array. The implications of this must be investigated so that it becomes whether there are limitations to the type of function that can be optimized. Testing functions that in GA terms require larger populations in order to solve them (such as exponentially scaled trap functions) might point out that there is a bottleneck in the approaches. A natural question is then whether these problems can be overcome by increasing the amount of samples per generation.

Directly in the light of this, it is most interesting to research how large the influence is of using more samples per generation and whether there are limitations to its goodness as influence. Furthermore, we have seen in the approaches that do no use an estimator array that the increasing population size does make the algorithm perform better, but the progress is very slight in this. Inrementing the amount of samples per generation seems to have a greater effect on the performance. As this is not enlightened enough and is an important topic, this is a seperate topic of research. Finding that mathematical framework however will already aid very much so in researching this topic.

So far we have only compared the result to a classical GA and to variants of the same type of approach. We gave an overview of the history of linkage learning and the GAs that followed from research to this aspect. As they are the more GA like approach to relation processing, direct comparisons to results from these methods (such as fmGA, GEMGA and LLGA) would tells us much more about the advantages and disadvantages of the new approaches.

The amount of test functions used is very limited, even though we have theoretic grounds which make it possible to draw conclusions on as we did in the progress of the research in section 3.2.4. Different types of test functions would however only broaden information on performance and dynamics of the new approaches and serve to improve our confidence and stress our theories that we have come up with so far. As MIMIC and the approach by Baluja and Davies use second order statistics and a second order probability distribution to find the optimum, it would be very interesting to see what happens when we have higher forms of interaction between bits in test functions, specifying that the value for certain bits is dependent on more bits than just one other.

It cannot be denied that there is a difference because of the information measure used together with the greedy algorithm (more likely the latter) for finding the chain that is the probability distribution. As seen, the results are less clean identifications of the structures amongst the bits for the MIMIC approach that uses conditional entropies. Further research can point out the exact influence this difference has and a more formal framework can make this explicit.

As MIMIC for has been seen to under certain circumstances not be quick enough in learning relations and as a result has to do with less clean blocks which are its domise in more difficult test functions, it would be interesting to see what type of effect the addition of crowding would have on such an approach that allows to keep the diversity longer and in that way buy more time to learn the relations. Perhaps a scheme in which crowding is used for some time and then gradually or immediately taken out allows for much better relation processing.

Finally, but certainly not the least important, nothing of the research so far has been directed towards an investigation of the scalability of the approaches. We have at several occasions noted that the new approaches have a running time that is of a higher order in the amount of bits than does the classical GA for instance and it would be interesting to see whether running times and performances scale up for larger problems.

Summarizing the above, the following topics require further research directly in the light of the research done so far in this paper:

- A mathematical approach that lays out the fundamental parts both for the MIMIC type of approach as well as the Baluja and Davies type of approach that uses an estimator array
- Boundaries in the approach because of a downfall in performance with increasing population sizes when using an estimator array and possible solutions by increasing the amount of samples per generation
- The advantages of more samples per generation and its relation to the performances under an increasing population size
- Direct comparison to linkage learning type of GAs
- Using test functions that require higher forms of linkage and might not be fit by second order statistics only
- Explicit difference in information measure used for the probability distribution
- The influence of crowding like schemes that maintain the population diversity longer so as to perhaps have more time to learn relations
- Scalability of the approaches

3.3 Research conclusions

Even though the research on the recent algorithms MIMIC and the framework by Baluja and Davies has not been very deep, the *EA Visualizer* aided in getting good insights in their dynamics. It is based on these insights that we summarize in a conclusive manner the result found in the research.

Frameworks such as MIMIC that base probability distributions on genomes in the current population and update this population through truncation selection on the newly generated samples and the current population contents together, can only benefit from larger populations when the problem is easy even though it will slow the algorithm down. The notion of easy is perceived as problems that may be difficult to the extend in which blocks have to be processed, but the optimal blocks that are thus to be found must not be require a strict notion of presence in that a good building block together with some noise on the other building blocks has a worse fitness than a string with more suboptimal blocks, as the MIMIC approach has been found to be a bit noisy and thereby being unable to optimize problems that have this characteristic. MIMIC runs out of time to learn the correct relations with respect to the pressure of selection.

For easy problems again the the difference in generating more or much more samples is negligable whereas generating more samples for difficult problems is more advantageous to both of the new approaches.

For the approaches using the estimator array as introduced by Baluja and Davies [3], for larger values of c_{init} it will take longer before the randomization like influence is undone whereas the close the decay factor α is to one, the more time the algorithm is bought to go over decisions as the decay is slower. A larger population should be accompanied by a larger value of c_{init} when the random like behaviour the beginning of the algorithm is required.

The structure of the probability distribution and the algorithm used to fill in that distribution is important and the tree approach by Baluja and Davies with the optimal algorithm for that structure is stronger than the chain approach used in MIMIC. However, for problems such as the trapfunctions with a deceptive characteristic, the structure of the probability distribution is of no influence on the bahaviour that for these problems an increasing population size leads the algorithm to a suboptimum.

The measure used to find the probability distribution is of importance for the properness and the speed at which relations are learned. The mutual information measure used in the approach by Baluja and Davies has been found to work better than the conditional entropies used in MIMIC.

4 Conclusions

In this graduation paper an extensive description of a new system for evolutionary algorithms that has been implemented in JAVA. The modelling of the system has been such that decisions have been made in the first place to enfavor expressional power with respect to the evolutionary algorithms that can be composed and run. Directly in second place, the design has been set up so that the entire process of visualizing information after installing an EA is user friendly through the use of graphical user interfaces and the presence of a system–complete help system. Furthermore, the user is guarded from direct contact with unnecessary details in the implementation structure of the *EA Visualizer*, even when the system has to be extended.

The resulting system has been automated and the release version (version `1.3`) is completely self–contained and ready to be used in different types of applications, be they educational or in research. Insight in dynamics of evolutionary algorithms is stimulated by the powerfull tool that is the *EA Visualizer* because of its interactive visualization mechanism.

The possibilities of the system and strength of the decomposition have been found to be great. Every algorithm encountered both in a more classical sense of evolutionary algorithms as well as new type of approaches have either been implemented using the decomposition or shown how to fit in the system according to the decomposition. All of these fittings have been explained to be of a natural form as long as the general meaning of the components is understood.

Within the restricted amount of time, the insight gained in recent algorithms in the evolutionary field as researched in this paper has been vast. On the one side, the implementation of the new algorithms is proof of the competence of the system and on the other side the insight quickly gained is proof of the value of the tool that is the *EA Visualizer* in using it in evolutionary computation.

Concluding, the *EA Visualizer* is a program built that fullfills the requirements made at the outset and has even gone beyond those requirements to become a complete system that can withstand the test of time because of its expandability and unique interactive mechnanism for visualizing information on evolutionary algorithms that can for any person interested in the field of evolutionary computation be a most valuable asset.

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A The EA Visualizer as an automated system

In section 2.3.5 the model of the editor version of the system was presented. Furthermore in section 2.3.2 insights were given to the automation of the system through the usage of a central name system and creator classes. The original setup of the *EA Visualizer* did not account for an editor that would make the system easily expandable. As a result, any user that wanted to expand the system would have to understand the structure of the system and know how and where to add lines of code in order to notify the system of the fact that additions have been made. Steps to this end included adding methods to creator classes in accordance with rules set so as to keep the contents of the creator class neat. Whereas there first was no name system either, names had to be stored directly within the creator classes as well as in the added components or views, which accounted for further problems and lack of transparancy. Defining parameter components and dependencies had to be done according to strict rules which only required more of a programmers guide type of description which made expansion of the system not too much fun. The main point to note is that this approach only calls for problems as the user can only forget stages in the expansion process or perform them wrongly or in a slob fashion which would make subsequent expansions more difficult.

Thus an editor version makes a big difference because all the administrative operations are taken care of by the system. The fact that most things had to be done according to strict rules only confirms the idea that creating an editor is feasible as addition of code has a clear structure. This doesn't mean however that such automation of the system that makes the system easier to use and to keep on using, is easy. An automated structure requires tight rules that specify how which parts of the system are read and written and where what information can be found. Furthermore, with the structure of the *EA Visualizer* that allows for highly parametrized algorithms and the specification of dependencies, actually implementing this struture is not trivial. In this appendix we go into full detail (including low level source code excerpts) to show how this is done in the *EA Visualizer* to give the reader an impression of the complexity as well as a more thorough understanding of the implementation of the system. Even though the system contains many more details, this part has been selected to be described in more detail as it is more away from evolutionary algorithms and it shows that more is required than just a simple implementation of evolutionary dynamics. Before we continue with the details we note that parts of source code that are incorporated here are directly taken from the actual program. At some points additional newlines might have been introduced however to make the code fit on the page.

A.1 Creator classes

In section 2.3.2 we already noted the need for creator classes in the system. We also shortly described their contents. We now take a closer look at these special classes, starting with the component creator. The component creator, which is the class `EAComponentCreator` in the system, creates the `EAComponent` objects that are used for the evolutionary algorithms. This creator class is especially designed for the data administration of components in the system and is thus automatically generated:

```
/**
 * Automatically Generated File By The EA Visualizer Editor<BR>
 * Created on: Wed Jul 22 19:47:59 CEST 1998
```

The above is a part of the comment in the file `EAComponentCreator.java` that is automatically generated by the editor every time the system is synchronized. All the information about the structure of the system that is in the administration of the editor is then written out amongst others to this file. As this file is automatically generated, the contents of it must be of a strict structure so it can be generated according to rules. We shall take a look at how this is established and how every component is incorporated separately into the component creator so that the system can call upon the creator to provide an instance (object) of the component.

The following variables are used in the creator class:

```
public final class EAComponentCreator
{
  private MessageFrame     mf;
  private VisualPackage    vp;
  private NameSystem       ns;
  private BinaryDictionary dict;
  private String           name;
  private Vector           gen, sim, rec, fit, mut, sel, mat, rep,
                           hyb, ter, pop, prn;

  private static boolean first = true;
```

The variables are all declared `private` because no other class should be able to touch these variables. The class is declared `final` because we do not wish anyone to create subclasses of this specialized class. For the first time, we see here the actual appearance of the `MessageFrame` and `VisualPackage` objects that were introduced in section 2.3.2. The `NameSystem` is included so as to establish the uniformity in the usage of names. As the creator class will have be able to tell the system what components are present and will have to call the components by name, the name system is required to find out what these names are. A binary dictionary is used for method access as we shall see later. The name of the component creator is known by the name system as all names are stored there, so we want to find out the name of the component creator and then store this information for once and for all. A number of `Vector` objects are declared which will contain the names of the components that are present in the system so that these names can be provided when needed in $O(1)$ time, implying we use memory in favor of running time here. Finally, a `static boolean` variable is declared that will help the component creator to make sure that only one instance is created by the system so that no addition to the system will hack in such a way that the creator can be used in places in shouldn't be usable.

The latter statement implies that on construction of the component creator, we require to fill all the vectors with the names. This is exactly what is done in the constructor of the class as we shall see.

```
  public EAComponentCreator( MessageFrame mf, VisualPackage vp, NameSystem ns )
  {
    int    i, sz;
    Method methods[];
    Vector dummy;
```

The constructor of the component creator is executed using the variables declared above. The only interesting part is the `methods` variable which is an array of `Method` objects. The `Method` class is the JAVA runtime equivalent of the method as written out when defining a class. This means that methods like `public double getX()` for a `Point` class are just as dynamically available as the object that results after instantiating a class using the `new` operation. As `new` creates a new object that is an instance of a class, every object is a subclass of `Object` which supports the method `getClass()` which returns the runtime equivalent of the class that you have written out. This means that the class that is thus returned is a `Class` *object* which inherently must again be an `Object`. For any `Class` object, there is a method named `getDeclaredMethods()` that returns an array of methods as objects being the runtime equivalent `Method` as mentioned. These methods are required because we want to dynamically be able to find the right method that will during the running of the system create a new object. Indeed, the `Method` objects can be invoked, implying that we can actually pass methods as objects and invoke them just as is the case in C for instance where adresses of functions can be passed on. This implies that if we construct a data structure on beforehand with all the methods of the current class in it and we have made sure on beforehand that the names of the methods are created systematically, we can find the desired method by querying this data structure and we can then invoke the method. Why this is what we require follows from the fact that for every component in the system we need to be able to create a new instance for it, return its parameter components and its dependencies. Whereas we would still be able to perform some of the former with the exception of the creation by placing the results in the data structure directly (in other words `Vector` objects that contain strings or other unalterable objects), for others would not be able to do so. For instance the creation of new instances of components would require to have an object that can be cloned as whenever a new instance is created, it is done so to be used and altered in the future (imagine for instance the binary string genotype which is subsequently constantly altered). The same goes for the parameter components which contain the values that are entered in them and are thus also changed after they have been returned by the creator. The latter would imply that we are only capable of using a data structure with only objects as data hooked to keys, when we ensure that a *cloning* mechanism is available. The fact of the matter is that JAVA indeed has such a mechanism, but using this would imply that the user always has to define a cloning method for every new object he or she creates. This problem is directly undone by using the indirection through method access as described above as we are actually taking care of writing *every* possible `clone()` method. It has proven however that this is exactly what makes the browser version as an applet fail as the `SecurityManager` in JAVA prohibits the invoking of methods that have to do with runtime classes, methods and so on. This is ofcourse done so that code is protected over the web and so that classes cannot be taken apart by a simple JAVA program on the WWW. On the other hand, it renders a very usefull tool obsolete. In the following we shall show how the usage of `Method` and `Class` runtime objects allows for the systematic structure of the component creator.

The constructor of the component creator starts by checking if any one but the *EA Visualizer* is attempting to create an instance of this class:

```
if( !first )
  Halter.halt( "Attempt to create second EAComponentCreator." );
```

The `Halter` is a special class that is capable of stopping the system. The user sees this as a large red window that appears informing the user of the nature of the problem that has caused the system to halt. The initialization then continues:

```
first   = false;
this.mf = mf;
this.vp = vp;
this.ns = ns;
name    = ns.findActualName( this );
```

The administration of the `MessageFrame` and the `VisualPackage` is done so that in the future these objects can be used. The same is done for the `NameSystem` object. As mentioned, the name system contains *all* names for all parts of the *EA Visualizer*, so also for the component creator, so the component creator requests its name from the name system. This name is required so that when warning or error message need to be reported on the message frame, the name of the creator can be specified so that the user will know where the problem originated. Then follows the actual administration of the methods of the class:

```
methods = (this.getClass()).getDeclaredMethods();
dummy   = new Vector( methods.length );
for( i = 0; i < methods.length; i++ )
  dummy.addElement( new Pair( ""+methods[i], methods[i] ) );

dict = new BinaryDictionary( dummy );
```

As noted before, the runtime versions of all methods in the class are collectable in an array of `Method` objects by using the method `getDeclaredMethods()`. A new `Vector` is then created to store (*name*, *object*) pairs for every `Method` object and thus for every method in the component creator class. This vector is after the collecting of all these pairs used to create a new binary dictionary. When we discussed the class variables, we mentioned that this data structure was used for method access. We now know the intention of this data structure. A dictionary contains (*key*, *value*) pairs. The idea is that when given a *key*, the *value* is retrieved as quickly as possible. In this case, the keys are the unique runtime method strings and the objects are the runtime methods themselves. This implies that when we require a method, we use the dictionary by specifying the string of the method we require and requesting the *value* entry for the thus given *key*. The dictionary will return the `Method` object and we are able to use the runtime system of JAVA to actually invoke the method dynamically as we shall see shortly. The binary dictionary is a data structure that allows for querying in $O(\log n)$ time with n the amount of data entries in the dictionary. This query time is achieved by keeping the data entries sorted and using binary search for querying. Incrementally constructing the data structure costs $O(n^2)$ time, which is exactly why in the above piece of code the pairs are constructed first and not directly added to the dictionary. Constructing the dictionary given the n entries on beforehand namely costs $O(n \log n)$ time.

The constructor method of the component creator finishes with the creation of the name vectors for the different components:

```
    createGenotype();
    createSimilarity();
    createRecombinator();
    createFitness();
    createMutator();
    createSelector();
    createMater();
    createReplacer();
    createHybrid();
    createTerminator();
    createPopulation();
    createPrng();
  }
```

All these methods have the exact same functionality. They differ in the fact that they take care of different components. A single example is therefore enough:

```
  private void createGenotype()
  {
    BinaryDictionary dummy;
    Vector           dummy2;

    dummy2 = new Vector();
    dummy2.addElement( new Pair( ns.findActualName(
                                 "eavmodel.genotype.BinStringGenotype" ), null ) );
    dummy2.addElement( new Pair( ns.findActualName(
                                 "eavmodel.genotype.ESGenotype" ), null ) );
    dummy2.addElement( new Pair( ns.findActualName(
                                 "eavmodel.genotype.TSPNumberedListGenotype" ), null ) );
    dummy2.addElement( new Pair( ns.findActualName(
                                 "eavmodel.genotype.MultiValuedAlleleStringGenotype" ), null ) );

    dummy = new BinaryDictionary( dummy2 );
    gen = dummy.getAllKeys();
  }
```

To create the name vector, all the components in the form of classes that are known to the system are written out in complete and unique class name form and then submitted to the name system to find the actual name for the class such as `"Binary String"`. All these entries are put in a temporary binary dictionary, from which all keys are subsequently subtracted. This is actually nothing more than a way to sort the keys as the binary dictionary will sort the pairs provided on the keys in $O(n \log n)$ time. Collecting all keys from the dictionary then thus results in a sorted sequence of the *actual* names so that the user in the end is presented with a sorted list which makes it easier to find entries.

It is now clear that the available genotypes for instance can be collected from the component creator through a method as simple as the following:

```
public Vector genotypeEAComponentStrings()
{
  return( (Vector) gen.clone() );
}
```

The main functionality of the component creator is however the creation of components. Given the actual name for a component[17] and instances for the parameters for the component, an `EAComponent` object needs to be returned. The parameters can be filled in since the user is required to fill in the parameters through the parameter components in the system (see section 2.3.2). We shall see later on how the parameter components for a component can be collected through the component creator as well as the dependencies, right now we concentrate on the actual creation of components which is thus done when parameter components and dependencies have already been retrieved and used elsewhere to make sure the settings are done by the user without system violations. The creation of a new `EAComponent` is established as follows:

```
public EAComponent create( String str, Vector parameters )
{
  EAComponent eacomponent;

  eacomponent = construct( str );

  if( eacomponent != null )
  {
    if( parameters != null )
      eacomponent.setParameters( parameters );
    eacomponent.setParameterComponentNames( parameterComponentsNames( str ) );
    eacomponent.setMessageFrame( mf );
    eacomponent.setName( str );
  }
  else
  {
    mf.addMessage( name + ": Requested EAComponent " + str + " not found for creation.");
    mf.addMessage( AdditionalString.spacesInstead( name ) + "  null returned.");
  }

  return( eacomponent );
}
```

The component object is first actually created by calling the method `construct()` that we shall see shortly. If the requested component was creatable, the `eacomponent` will not be a `null` reference and the parameters for that component can be set. The `EAComponent` class has a method `setParameters` to establish this. Other administrative goals are carried out subsequently such as the setting of the parameter component names for which a `final` method is incorporated in the `EAComponent` class. As a result of this, the system can get the parameter components names and in a similar fashion it has been established that the system can get the actual parameter components for every component in the system so that at any time the parameters can be investigated (in for instance a view that provides an overview of all settings for all installed components). Finally,

[17]The actual name is used since the users selects from a list of actual names.

the message frame is set as well as the name for the component. If the component was not creatable, the component creator places a message that will appear in the system messages window below the main window of the *EA Visualizer*. All of the former is really not much more than data administration and the question remains how the components are actually created. This is established through the construct method:

```
private EAComponent construct( String str )
{
  Class       clazz;
  EAComponent result;

  clazz  = ns.findClass( str );
  result = null;
  if( clazz != null )
    try
    {
      result = (EAComponent) clazz.newInstance();
    }
    catch( Exception e )
    {
      mf.addMessage( name + ": Requested EAComponent " + str +
                     " not creatable, Internal Error!!!");
      mf.addMessage( AdditionalString.spacesInstead( name ) + "  null returned.");
    }

  return( result );
}
```

The name system is first consulted to find the runtime `Class` object for the component specified through the string which is the actual name for the component. As we shall see later, the namesystem holds two binary dictionaries that allow for $O(\log n)$ querying with an actual name as well as a classname or object. In this case, the string is an actual name and we use the method `findClass()` to find the actual `Class` runtime object that was stored when the `NameSystem` object was created. If the entry is known to the name system, the result will not be a `null` reference and we create a new instance of the class as normally would be done by using the `new` construction. We are now writing dynamic code however and using runtime classes, so we shall have to use the runtime equivalent which is the method `newInstance()`. This method throws a number of exceptions however which have to with security and other aspects in the creatability of the new instance. If anything goes wrong, a message is displayed to the user in the system messages window.

Now we know how the new components can be created, which is essential to the creation of a new evolutionary algorithm in the system, we still require to know how we can find the parameter components for a component so that before the actual creation of a component occurs the parameters for that component can be set. Returning the parameter components is done in two phases just as was the case for the creation of the components. First the parameter components are actually created and then the names for the parameter components are retrieved. These results are then zipped together, meaning that every parameter component is assigned its name. Subsequently, data such as the message frame and the visual package is transferred to every parameter component. Requesting the parameter components from the component creator is done by using the following method:

```
public Vector parameterComponents( String str )
```

The string `str` is once again the actual name of the component to retrieve the information for. As noted, this method first calls another method to actually retrieve the objects that are the parameter components and then administers data for each and every one of them. The method called is `getParameterComponents()` which is a `private` method and can thus only be called by the component creator itself:

```
private Vector getParameterComponents( String str )
{
  return( invoker( "ParameterComponents", str ) );
}
```

As is obvious, the above method is not too complicated as the method only calls yet another method. The idea is that the `invoker` contains the functionality required as other methods will require the same structure. An example is the internal retrieval of the names for the parameter components:

```
private Vector getParameterComponentsNames( String str )
{
  return( invoker( "ParameterComponentsNames", str ) );
}
```

The same structure is required for the four methods that return the names of the dependency imposing components for a specified component. The main idea is that for every component that can be created through the component creator a few methods are created with names that are based on the full class name of the component. For instance, the class that implements the trap functions is placed in the package `eavmodel.fitness` and is called `TrapFunctionsFitnessFunction`. As a result, the following methods are written in the component creator by the system:

```
private Vector eavmodelfitnessTrapFunctionsFitnessFunctionParameterComponentsNames()
private Vector eavmodelfitnessTrapFunctionsFitnessFunctionParameterComponents()
private Vector eavmodelfitnessTrapFunctionsFitnessFunctionGenotypes()
private Vector eavmodelfitnessTrapFunctionsFitnessFunctionFitnessFunctions()
private Vector eavmodelfitnessTrapFunctionsFitnessFunctionSimilarities()
private Vector eavmodelfitnessTrapFunctionsFitnessFunctionPopulations()
```

The prefix to every method is the full class name without dots as dots are not allowed in method names. Note that because the dots are always placed in the same position, removing the dots does not harm the uniqueness of the names used. For *every* `EAComponent` that is creatable in the system, these `private` methods are incorporated in the component creator. The contents of these methods is based on what the user enters in the editor. For instance the `ParameterComponentsNames` variant of the above methods returns a vector with the names for the parameter components that were entered in the editor. Note that thus the specification of the method names is very systematic:

1. The methods are `private`
2. The methods return a `Vector`
3. The methods have the full classname without dots as a prefix to the method name
4. The suffix of the method name is one of the following:
   (a) `ParameterComponentsNames`
   (b) `ParameterComponents`
   (c) `Genotypes`
   (d) `FitnessFunctions`
   (e) `Similarities`
   (f) `Populations`
5. The methods have no parameters

This list of characteristics for the methods implies that when given the string that specifies the suffix of the method name and the string that specifies which class is to be used, a string can be created that is exactly the header of the method required. Recall at this point that the global and `private` class variable `dict` was a binary dictionary created when the component creator itself was created and contains as keys the string representations of the methods and values the `Method` runtime objects. The string representations of the methods are indeed exactly the headers (be it specified slightly more exact as we shall see below), implying that we can create the header of the method required and find through the binary dictionary `dict` the runtime `Method` object that is exactly the method we wish to invoke. This is exactly what the `invoker` method in the component creator does:

```
private Vector invoker( String type, String str )
{
  Class  clazz;
  Method method;
  String cname;
  Vector result;

  clazz  = ns.findClass( str );
  if( clazz != null )
  {
    cname  = "private java.util.Vector eavmodel.EAComponentCreator." +
             AdditionalString.toStrippedString( clazz.getName() ) + type + "()";
    method = (Method) ((Pair) dict.find( cname )).getFirst();
    if( method == null )
    {
      mf.addMessage( name + ": Can't find method for " + type + ", Internal Error!!!");
      mf.addMessage( AdditionalString.spacesInstead( name ) + "  Not found: " + cname );
      mf.addMessage( AdditionalString.spacesInstead( name ) + "  null returned.");
    }
    else
    {
      result = null;
      try
      {
        result = (Vector) method.invoke( this, null );
      }
      catch( Exception e )
      {
        mf.addMessage( name + ": Error at invoking method for " + type + ", Internal Error!!!");
        mf.addMessage( AdditionalString.spacesInstead( name ) + "  Method: " + cname );
        mf.addMessage( AdditionalString.spacesInstead( name ) + "  null returned.");
      }
      return( result );
    }
  }
  else
  {
    mf.addMessage( name + ": Requested EAComponent " + str + " not found for " + type + ".");
    mf.addMessage( AdditionalString.spacesInstead( name ) + "  null returned.");
  }

  return( null );
}
```

The above method has as its parameters the type of method that is to be invoked or in other words the suffix to the method name and the actual name of the component that the method is to refer to. The name system is used to find the runtime `Class` object for the component referred to by the string containing the actual name for the component. If the component string is valid, the returned object is not a `null` reference and the exact header for the method sought can be constructed. In the actual header used by the Java runtime environment, all classes are referred to through the unique name that results from specifying the complete package reference. As noted before, the dictionary dict can then be used to find the Method required and when all is right, the reference will not be null reference, allowing us to use the invoke method of the JAVA runtime environment to actually run the method and gather the results which we know to be a Vector. The JAVA invoke method on the runtime Method requires as parameters the object to invoke the method on, which is ofcourse the component creator itself, along with instances for the parameters which is ofcourse null because we saw earlier that all the methods we automatically constructed have no parameters.

It now follows that when we create the editor in such a way that the required methods for every component are written out properly to the source code file of the component creator (EAComponentCreator.java), the invoker in the component creator will be able to find the required methods and the automation is complete for the components. It should be clear at this point that the way in which dependency imposing components are handled is the same in which the parameter components are taken care of. When the genotype dependency imposing components for a certain component are required, the method genotypes() is called with the actual name for the component in a string as a parameter as we already saw in section 2.3.2. The implementation of this in the component creator is ofcourse nothing other than the following:

```
public Vector genotypes( String str )
{
  return( invoker( "Genotypes", str ) );
}
```

We have now specified the complete structure of the component creator and it should be clear at this point how the view creator is constructed as there are many things similar to the component creator. The general idea is exactly the same with methods that are constructed according to some standard form, the usage of a binary dictionary to store the method names, the using of the runtime environment to create new instances of views and an invoker to allow for method invocations for methods in the view creator class EAViewCreator. There is only one fundamental difference however, which has to do with matters discussed in appendix B. The multiple runs evolutionary algorithms are of a complex nature because of the fact that they allow for multiple settings for the parameters of the components and the fact that some of these settings might be linked so as to prohibit unwanted crossproduct enumerations. Information to this end is however not only important in the internal structure of the system that is used to enumerate the settings in the proper way as is discussed in appendix B, it can also be of crucial importance to the multiple runs views or more precisely the environment that is especially constructed to be able to create a table that contain entries for different EAs and their settings. The environment we are referring to is the EAInfoEnvironment which can be used to distuinguish between different EAs and their settings as the environment creates a table based on the components and the settings for these components in an EA based on the information in an EAInfo object. It might be so however that the environment should neglect differences in different settings. For instance, it might be desirable to not distinguish between two EAs based on their population size because we want to make a plot as a function of the population size. The environment should then map EAs with only a different population size to the same table entry, whereas other differences (such as for instance different recombinator) should map to another table entry. In order to specify what it is that should be neglected, a parameter component named the EAInfoEnvironmentParameterComponent is created in which these settings can be made. However, these settings are dependent on the settings made when the multiple runs EA was created. We cannot specify what parameters of what recombinators to neglect if we don't know what recombinators have been installed. To this end the vector AllSelLin, which stands for *All Selected & Linked*, that results from the EAMultipleMultipleRunsInterface and contains all information about the selected and linked components and parameters is passed on through the invoker in the view creator as an addition to what we saw in the component creator above because the parameter components might need this vector. Furthermore in just a general fashion as the parameter components and the dependency components, recall from section 2.3.2 that a method isMultipleRunsView() is required to find out whether a view is a multiple runs view.

Creating methods for this all over the view creator implies that the result of the methods is not always a `Vector` as the result of `isMultipleRunsView()` clearly has to be a `boolean` and it would be a waste of space to use a `Vector` to wrap the `Boolean` wrapper class in that in turn wraps the actually required value. So the result of the `invoker` method can either be a `Boolean` or a `Vector`, which alters the `invoker` method in the view creator further. All in all, calling the invoker now thus requires specifying the result type of the method required, the vector `allSelLin` and as before the suffix for the method as well as the actual name for the view. Here's an example from the `EAViewCreator` class:

```
private Vector getParameterComponents( String str, Vector allSelLin )
{
  return( (Vector) invoker( "java.util.Vector", "ParameterComponents", str, allSelLin ) );
}
```

To make the discussion complete, the invoker in the `EAViewCreator` is the following:

```
private Object invoker( String restype, String type, String str, Vector allSelLin )
{
  Class  clazz;
  Method method;
  String cname;
  Object result, params[];

  clazz  = ns.findClass( str );
  if( clazz != null )
  {
    cname  = "private " + restype + " eavview.EAViewCreator." +
             AdditionalString.toStrippedString( clazz.getName() ) + type;
    if( type.equals( "ParameterComponents" ) )
      cname += "(java.util.Vector)";
    else
      cname += "()";
    method = (Method) ((Pair) dict.find( cname )).getFirst();
    if( method == null )
    {
      mf.addMessage( name + ": Can't find method for " + type + ", Internal Error!!!");
      mf.addMessage( AdditionalString.spacesInstead( name ) + "  Not found: " + cname );
      mf.addMessage( AdditionalString.spacesInstead( name ) + "  null returned.");
    }
    else
    {
      result = null;
      try
      {
        if( type.equals( "ParameterComponents" ) )
        {
          params    = new Object[1];
          params[0] = allSelLin;
          result    = method.invoke( this, params );
        }
        else
          result = method.invoke( this, null );
      }
      catch( Exception e )
      {
        mf.addMessage( name + ": Error at invoking method for " + type + ", Internal Error!!!");
        mf.addMessage( AdditionalString.spacesInstead( name ) + "  Method: " + cname );
        mf.addMessage( AdditionalString.spacesInstead( name ) + "  null returned.");
      }
      return( result );
    }
  }
  else
  {
    mf.addMessage( name + ": Requested EAView " + str + " not found for " + type + ".");
    mf.addMessage( AdditionalString.spacesInstead( name ) + "  null returned.");
  }

  return( null );
}
```

A.2 Name system

The third and final automated class in the system is the name system. As noted in section 2.3.2 having a single class that defines the actual names for the components prohibits errors when a name has be repeated somewhere and any changes to the actual name only have to be taken care of in a single place, allowing for the editor to update the name system without any harm done to the rest of the system. As noted earlier in this appendix, the name system is not much more than a binary dictionary. In fact it holds two binary dictionaries to allow to find the class that belongs to a certain actual name but also to find the actual name for a class. The contents of the name system is determined by the editor as it generates the name system. In turn, the editor is dependent on the user. As a result anything the user specifies for names ends up neatly in the name system in a proper fashion. Creating the name system is not so difficult:

```
  public NameSystem( MessageFrame mf )
  {
    Vector classToNamesVector, namesToClassVector;

    if( !first )
      Halter.halt( "Attempt to create second NameSystem." );

    first              = false;
    this.mf            = mf;
    classToNamesVector = new Vector();
    namesToClassVector = new Vector();
    create( classToNamesVector, namesToClassVector );

    classToNames       = new BinaryDictionary( classToNamesVector );
    namesToClass       = new BinaryDictionary( namesToClassVector );
  }
```

Just as was the case for the creator classes, only a single copy of the name system is allowed to be created in the system. Two vectors are created by the name system that store in the one case the class names as the key and the actual names as the value in the dictionary and in the other case the other way around. The contents of these vectors are then subsequently used to in $O(n \log n)$ time generate the binary dictionaries. The actual contents of the dictionaries is determined by the method `create()` that fills the vectors that are subsequently used to generate the dictionaries. This method contains nothing more than a whole lot of lines that fill the vectors will all the components in the system, both for the `EAComponent` classes as well as the `EAView` classes, but also interfaces in the system and all other parts that may be of interest to the user so that they placed in the help system. Furthermore, the `NameSystem` class contains the required query methods:

```
  public String findActualName( Object obj )
  public String findActualName( String str )
  public Class  findClass( String str )
```

The first two methods are actually the same and the first is even redundant as for any object `obj` the first method call could be replaced by a method call using the second method:

```
    findActualName( (obj.getClass()).getName() );
```

So actually all the functionality expressed by the three methods above is exactly what is required, namely the finding of the runtime `Class` object for each actual name and the finding of the actual name given the full string specification of the class. Especially for the help system, the name system contains a method that returns all names in the system so that an index page can be made in the help system:

```
public Vector getAllClassNames()
```

Thus the name system really holds no new interesting items or complexity that requires explanation. What *is* still very much so interesting at this point however is how the three above classes are actually generated and kept updated. This requires a closer look at the editor version of the system.

A.3 The *EA Visualizer* editor

Observing the editor however is not a very fascinating experience as it is really only a lot of mambo jambo–ing with interfaces and the handling of data that belongs to those interfaces. For instance the name of a component is controlled through either a `NameEditor` or a `NameBrowser` interface, depending on whether we are editing or browsing a class. Any changes in the name through the editor are put through to the system by looking up an entry in some data structure and changing the field for the name. Even though the implementation is far from trivial, it is more of the same and only complex because of its size. Incorporating details to this end here would however add too much to still be of interest to the reader. The part of the editor that is interesting and that we are looking for is the creation of the three classes above which is what we shall adress in the following.

First and foremost, upon creating the editor version of the program, three data files are read, decrypted and parsed:

```
  startup.addMessage("  Reading encrypted file with EAComponent definitions.");
  components  = readComponents();
  if( components == null )
    Halter.halt( "Error reading definitions for EA Components" );

  startup.addMessage("  Reading encrypted file with EAView definitions.");
  views = readViews();
  if( views == null )
    Halter.halt( "Error reading definitions for EA Views" );

  startup.addMessage("  Reading encrypted file with NameSystem definitions.");
  names = readNames();
  if( names == null )
    Halter.halt( "Error reading definitions for names" );
```

For each of the files it is first checked if the result is okay, otherwise the system is halted. The reading of one file consists of decrypting it and subsequently parsing the results:

```
private Vector readComponents()
{
  DynIntValues string;

  string = definitions.readFile( "components" );

  if( string != null )
    return( parseComponents( string ) );

  return( null );
}
```

The `definitions` variable is an `RSA` object that allows us to deal with encrypted files. A file is seen as subsequent characters which are in the *EA Visualizer* interpreted as `int` values. The `DynIntValues` is an equivalent of the `Vector` in JAVA, only there are no wrapper classes required as the array that the `DynIntValues` class works on is an integer array. The parsing of the components is done according to the structure of the file. The structure is not specified here to ensure the safety of the data in the encrypted files but what is in these files is ofcourse the data required for components, views and names such as name of a component or view, the parameter components and their names and the dependency imposing components for a component or view. Once the results are parsed and stored in some way in a `Vector`, the `EAVisualizerEditor` maintains this information as the current system data. Any changes in these `Vector` objects will cause the user to have to synchronize the system in order to keep what is on disk consistent with what is in memory.

As mentioned earlier, the handling of the data is really a very extensive juggling with interfaces and data wich in the end all leads back to the information in the tree `Vector` objects that are exactly used for the component creator, view creator and name system. The main idea is thus that the data required is stored in an encrypted version on disk and is read into the *EA Visualizer* when the editor is started up and maintained in memory as the current version of the system. When then requested after editing, the editor is capable of writing the information to disk to synchronize the system:

```
private void synchronizeSystem()
{
  disableMenus();

  modified = false;

  addMessage("Updating system files, please wait...");

  plusMessage("  Generating EAComponentCreator.java...");
  writeComponents();
  addMessage(" Compiling...");
  compile( "eavmodel/EAComponentCreator.java" );

  plusMessage("  Generating EAViewCreator.java...");
  writeViews();
  addMessage(" Compiling...");
  compile( "eavview/EAViewCreator.java" );

  plusMessage("  Generating NameSystem.java...");
  writeNames();
  addMessage(" Compiling...");
  compile( "eavview/EAViewCreator.java" );

  addMessage("  Writing encrypted file with EAComponent definitions.");
  writeComponentsDefinitions();

  addMessage("  Writing encrypted file with EAView definitions.");
  writeViewsDefinitions();

  addMessage("  Writing encrypted file with NameSystem definitions.");
  writeNamesDefinitions();

  if( !modified )
  {
    setTitle( normalTitle );
    ((menubar.getMenu( 2 )).getItem( 3 )).disable();
  }

  addMessage("System synchronized.");

  enableMenus();
}
```

From the above it is clear how the system is synchronized. First of all the three classes are generated based on the current information in the memory of the editor. Generating the classes is however ofcourse not enough because the source code has to be compiled in order to be used by the system the next time it is started. To this end the method `compile` is called to use the `javac` executable in the operating system to compile the files. When this is done, the information in memory is written to disk in the encrypted files to not only synchronize the system itself with the latest changes, but also the editor so the latest changes by the user are not lost after all. We shall not go into the writing of the files just as much as we didn't specify how the contents of the encrypted files are parsed as this will harm the security of the data. It is really of no importance anyhow. The only thing that matters is the fact that the required data is somehow formatted and written to disk in encrypted form. The thing that is ofcourse important to complete the description of the creator classes and the basis of the automation of the system, is the actual creation of the three classes described above. The basic idea is that the file is formatted in text in a neat way or in other words pretty printed in blocks. The header information comes first which is always the same, followed by the variable data, followed by the footer information which is again always the same.

For the component creator for instance, the vectors that contain the information about the different component classes are created in methods such as `createGenotype()` which thus have to be generated anew with information about all classes that are genotypes as is stored in the internal memory of the editor. The creation of these methods is thus done as follows:

```
private void writeComponentsCreators()
{
  int    i, j, sz, sz2;
  char   c;
  Vector vector, vector2, names;
  Triple t;
  String name, name2;

  vector = compdict.getAllValues();
  names  = compdict.getAllKeys();
  sz     = vector.size();
  for( i = 0; i < sz; i++ )
  {
    name = (String) names.elementAt( i );
    c    = (char) (name.charAt( 0 ) - 'a' + 'A');

    writeString( "" );
    writeString( "  /**" );
    writeString( "   * Sets up information for creating." );
    writeString( "   */" );
    writeString( "  private void create" + c + name.substring( 1, name.length() ) + "()" );
    writeString( "  {" );
    writeString( "    BinaryDictionary dummy;" );
    writeString( "    Vector           dummy2;" );
    writeString( "" );
    writeString( "    dummy2 = new Vector();" );

    vector2 = (Vector) vector.elementAt( i );
    sz2     = vector2.size();
    for( j = 0; j < sz2; j++ )
    {
      t     = (Triple) vector2.elementAt( j );
      name2 = (String) t.getFirst();
      writeString( "    dummy2.addElement( new Pair( ns.findActualName( \"" +
                   name2 + "\" ),
      null ) );" );
    }

    writeString( "" );
    writeString( "    dummy = new BinaryDictionary( dummy2 );" );
    writeString( "    " + name.substring( 0, 3 ) + " = dummy.getAllKeys();" );
```

```
      writeString( "  }" );
    }
  }
```

The writing of code is done for every component type that is known to the system and is stored in the `compdict` vector. These types are exactly the types introduced in the decomposition in section 2.2. First the header of the method is written using a few `writeString` statements that are caught by the editor and prepared for encryption. Next, all actual components are looped and written to be added to the `Vector` in the component creator that is used to build the binary dictionary and subsequently used to get all the keys out of to be stored in the especially used `Vector` that we saw earlier to contain all components on creation, which are vectors that are named following the first three letters of the component type that is being processed. In a similar matter methods are written for each component according to the method headers we discussed earlier. To give an example, we show an excerpt from the method that writes this information to disk:

```
        /* ParameterComponents */
        writeString( "" );
        writeString( "  private Vector " + name + "ParameterComponents()" );
        writeString( "  {" );
        sz3 = pcs.size();
        if( sz3 == 0 )
          writeString( "    return( null );" );
        else
        {
          writeString( "    Vector result;" );
          writeString( "" );
          writeString( "    result = new Vector(" + sz3 + ");" );
          for( k = 0; k < sz3; k++ )
            writeString( "    result.addElement( new " + ((Pair) pcs.elementAt( k )).getFirst() +
                         " );" );
          writeString( "" );
          writeString( "    return( result );" );
        }
        writeString( "  }" );
```

The parameter components method is written by the above code. First the header of the method that is being written is stated. Then depending on the size of the parameter components vector, either `null` is returned or a `Vector` is constructed with all the parameter components which is subsequently returned. Note that the larger difficulty in writing and understanding code such as this is to realize that you are writing (or reading) a JAVA program that is itself writing a JAVA program. So actually you are programming two JAVA programs at the same time in the same file.

The only thing that is left worth looking at in this appendix is how the files are actually compiled into the system so as to complete the update making the user able to use the new or altered components the next time the *EA Visualizer* is started. This is done as noted before through a `compile` method that compiles a JAVA file:

```
  private void compile( String filename )
  {
    Process      p;
    DynIntValues values;
    String       input, toExec;

    input  = filename.replace( '/', File.separatorChar );
    toExec = "javac -nowarn " + input;
    try
    {
      p = (Runtime.getRuntime()).exec( toExec );
      try
      {
        p.waitFor();
        values = readInputStream( p.getErrorStream() );
        if( values != null )
        {
          if( values.size() > 0 )
          {
            addMessage("Compile unsuccesfull:");
            addMessage( values.toString() );
            modified = true;
          }
        }
      }
      catch( InterruptedException e )
      {
        p.destroy();
        addMessage( "Compile interrupted. " + e);
      }
    }
    catch( IOException e )
    {
      addMessage( "Can't run compiler javac, I/O error." + e);
      addMessage( "Did nothing.");
    }
  }
```

As is clear from the above, the operating system is utilized to compile the file that was created. A new process is started for the system call and once again the runtime environment of JAVA is used. This time it is used in a different fashion however, reaching out to the OS instead of digging into the structure of the JAVA program itself. The system is instructed to wait for the compilation to finish and once this is done, the results are gathered by reading the input stream that is the output of the process. Finally, if there is any of such output, it means that the compiler had errors during compile, making the editor not set itself into synchronized mode, but remember that the synchronization is not complete and has to be performed again. Such compile failure can occur when for instance the user spells a parameter component wrong because the name of the parameter component is used as direct JAVA code in the creator classes. A further advanced editor could try to catch the parameter component structure in such a way that the specification of parameter components by name is no longer required either, which in turn would avoid occurence of this type of error. It is also clear at this point how the *EA Visualizer* can be started in the editor in such a way that the results are visible to the user. An updated system needs to be restarted in order to see the results, so the system will have to be restarted anew. In order to avoid having to close down the editor or to have to go about very difficult structures to redo the construction of the editor datastructures while keeping all interfaces open, the JAVA runtime system is simply used again to fork another process that starts the operational version of the *EA Visualizer* that as a result is initialized with the in the editor altered settings.

The main point to note and to conclude this appendix with is that because of the clear structure introduced in the three classes `EAComponentCreator`, `EAViewCreator` and `NameSystem` that are the fundaments of the automation in the *EA Visualizer*, the editor version could be constructed and automation could become a fact. Working systematically is therefore the key issue. Even though the editor code is complex because of its size and double JAVA program structure, the code that is actually created in the three classes is the more ingenuitive.

B Complexity of multiple runs EAs

Out of all parts in the *EA Visualizer*, the facilitation of running a multiple of runs with different evolutionary algorithms or different settings in a completely parametrized and automated fashion, is by far the most tedious and complex part of the system. It is therefore that we shed some light on the implementation of this issue in this appendix. The multiple runs EAs as they are called in the *EA Visualizer*, do not require any new programming from the user with respect to the “normal” EAs in the system. In other words, if we forget about multiple runs EAs for a second and think of the *EA Visualizer* solely based upon its decomposition, interactive visualization technique, parameter settings mechanism and so forth in the light of constructing and running a single evolutionary algorithm, what is required from the user is implementations for views, evolutionary and perhaps also parameter components. Based on all that is thus created by the user and the mechanisms within the *EA Visualizer*, the multiple runs EA is created completely by the system and is thus fully *automated*. In appendix A it has already been shown that full automation is tedious to implement and requires strict structure. As this is supposedly the case given the setup of the system that is the *EA Visualizer*, it is indeed possible to perform the automation. In section 2.3.2 a very brief description of the requirements for the implementation of the multiple runs EAs is given. The complexity of the matter has led to the not including of further details there as it would only clutter the storyline. Right here and now however we do proceed into describing the process in detail to show how this complex automation has been achieved.

The implementation of the multiple runs EAs consists basically of three different parts. The first two parts are subject to the users influence and deal with the entering of parameters as well as the specification of the links between the parameters. The last part is contained within the system and concerns the running of the multiple runs EAs. It is clear how a single evolutionary algorithm is to be run, as that is what is at the heart of the *EA Visualizer* and is performed by the `EARunner`. We are now however faced with a multiple of parameters for a multiple of components, of which we might yet again have a multiple, which can be run a multiple of times and most importantly, of which the parameters might be linked to ensure synchronized enumeration. This last part thus deals with the *enumeration* of the different evolutionary algorithms and their settings. A fourth part could be seen as the gathering of the results and the visualizing of the data. Even though writing visualizations for multiple runs EAs is likely to be difficult, this part is left out as the main lines are described in the main part of this paper in section 2.4.3 properly. To actually write code for a new view, the source code can be consulted to find examples. Here we are concerned with how the multiple runs have been facilitated within the *EA Visualizer* and we shall in the following discuss the three parts. Before we continue with the details we note that parts of source code that are incorporated here are directly taken from the actual program. At some points additional newlines might have been introduced however to make the code fit on the page.

B.1 Entering the settings

As has already become clear from section 2.3.2, the specification of settings for a multiple runs EA must be done in two steps because the dependency imposing components have to be separated from the other components as the dependency imposing components cannot be specified to have multiple instances together with multiple instances of non–dependency imposing components. To remedy this, a multiple of these restricted multiple runs EAs can be created through the `EAMultipleMultipleRunsEAInterface` class, which results in the two steps process. As the specification of each of these separate multiple runs EAs is identical, we restrict ourselves to describing only such a single restricted multiple runs EA, to be called an rmrEA in the following.

The specification of an rmrEA is done by first selecting an instance for the four dependency imposing components. This is done in a similar fashion as is done in the `EASettingsInterface` and includes the filtering of lists of components that depend on the other components. This functionality is taken care of in the `EAMultipleRunsDependencyImposingComponentsInterface` class. The parameters for the instances that are selected for the dependency imposing components are not specified here as these parameters are indeed allowed to varied contrary to the instances themselves. So the larger part of the functionality offer is done through the `EAMultipleSettingsInterface` class, where the actual parameter settings for the instances is done. As is described in section 2.3.2, the instances required for the non–dependency imposing components can be a multiple. For instance, for the *Recombinator* we can select to have both one–point and two–point crossover and in the mean time also have a multiple of instances for the *Selector* such as tournament, roulettewheel and truncation selection. Checking which component instances are allowed and which are not, is the same procedure as was the case in the single run version, so no additional complexity is required to that end. For each of the instances selected for the non–dependency imposing components, which count at least one per component, the parameters can be set. These parameters may however be a multiple of parameters as parameters can be varied. In section 2.3.2 the parameter component model to this end was described and we shall not repeat it here. We shall however at this point take a look at how the model is actually used in the implementation. To this end, we observe what happens when the `Parameters` button is pressed for an instance of the non–dependency imposing components:

```
private void handleOtherParameterButton( Button b )
{
  int                              i, index;
  String                           str;
  List                             l;
  Vector                           v;
  MultipleValuesParameterInterface pi;

  b.disable();

  for( i = 0; i < AMOUNT; i++ )
    if( b == options[i] )
      break;

  l     = components[i].getList();
  str   = l.getSelectedItem();
  index = l.getSelectedIndex();
  v     = (Vector) parameters[i].elementAt( index );
  pi    = (MultipleValuesParameterInterface) interfaces[i].elementAt( index );
  if( pi != null )
    currentInterfaces[i] = pi;
  else
  {
    currentInterfaces[i] = new MultipleValuesParameterInterface( this, v, str, vp, mf );
    interfaces[i].setElementAt( currentInterfaces[i], index );
  }
  currentInterfaces[i].show();
  backups.setElementAt( currentInterfaces[i].makeBackup(), i );
}
```

The implementation shows that first the button that was pressed is disabled. Second, it is looked up for what component the button was pressed. To this end, the buttons are stored upon creation in a global array `options`. The index `i` that denotes the button index is then used to index the `components` array that contains the list of instances for each non–dependency imposing component. The `index` of the instance that is at the point of pressing the button selected in that list is determined and used subsequently to find the parameters for that selected instance. Also, the multiple values parameter interface as introduced in section 2.3.2 is determined by in the same fashion indexing the `interfaces` array that holds all these parameter interfaces for the rmrEA. If it is the first time the parameters are set for the selected instance, the variable `pi` will be a `null` reference and a new interface is created and stored in the `currentInterfaces` array that holds all interfaces that are belong to the currently selected instance for each non–dependency imposing component as well as the `interfaces` array of all parameter interfaces for each non–dependency imposing component. The resulting interface is shown and a backup of the contents of the interface is created so as be able to set the values back when the `Cancel` button is pressed in the parameters interface. It follows that the interesting part of this matter is done when the `parameters` array is filled with the parameters for the instance, because that is where the structure of the parameter components as introduced in section 2.3.2 is utilized. The `parameters` array is ofcourse filled upon the moment that an instance is added to the list of a certain component. When the index of the component is once again determined in the `int` variable `i`, the actual name of the instance to add is stored in the `String` variable `str`, added to the right component list and the `EAComponentCreator` which is described in detail in appendix A is consulted to find the parameter components for the instance, which are directly stored in the `parameters` array:

```
(components[i].getList()).add( str );
parameters[i].addElement( creator.parameterComponents( str ) );
```

The parameter components are ofcourse those that describe the settable parameters only and not in a multiple runs fashion. These matters are handled in the `MultipleValuesParameterInterface` class. Upon creation of such a new interface, the parameter components passed in the `Vector` named `parameters`. When the parameter components are actually added to the interface, it is first checked to see if there exists a multiple runs version for the parameter component (see section 2.3.2 for a description of the parameter component structure):

```
for( i = 0; i < sz; i++ )
{
  ...
  comp    = (SingleValueParameterComponent) parameters.elementAt(i);
  mvpc    = comp.multipleValuesVersion();
  comp    = mvpc != null ? mvpc : comp;
  ...
  comp.setParent( this );
  comp.setVisualPackage( vp );
  comp.setMessageFrame( mf );
  ...
  if( comp.isSelfSufficient() )
  {
    prevs[i].disable();
    adding[i].disable();
    removing[i].disable();
    nexts[i].disable();
    counts[i].setText("    ");
  }
  ...
}
```

The `...` parts are left out as they convey no interesting details. As seen from above, for each parameter component that is as mentioned a parameter component for the single value only, it is checked if there is a multiple values version for it. If there is, the parameter component taken is the multiple values version instead of the single value version. Subsequently, administration data is set for the parameter component. Finally, when the component is found to be self sufficient for the specification of a multiple of parameters, the buttons for adding and removing a multiple of the parameter components that always guarantee the possibility of entering multiple settings, are disabled.

So far, we have seen how the parameters are set for the instances of the non–dependency components and we have described how a multiple of instances can be added for each of those components. The parameters for the dependency imposing components are not much different. On beforehand to opening the interface defined in the `EAMultipleSettingsInterface` class, the dependency imposing components are selected as we noted before. The parameters are thus all that can be varied a multiple of times and therefore the interface from the `EAMultipleSettingsInterface` class only holds four `Parameters` buttons an no instances lists for the dependency imposing components. When a `Parameters` button is pressed, it is first determined what kind of a component the button is for and then the correct parameter interface is displayed. The same is the case for the recombination and mutation chances as these can be varied as well ofcourse. The implementation of this is not much different from what has been discussed so far and we shall therefore refrain from this here as more difficult and interesting things lie ahead. Before going into those things however, we note that at all times, backups need to be created to allow for the `Cancel` button to be pressed. This involves creating data structures and storing and restoring data when required. Even though this job is very tedious and leads to a nice addition to the amount of lines of code, we do not specify the exact contents of this mechanism but note that this is definately required and makes the process quite a bit more annoying to implement.

Before being able to close this subsection of the appendix and thus round up the description of the entering of the settings, it is important to know how we can retrieve these settings elsewhere to work with them. This is required because in the next part of the process of the creation of a rmrEA, we need to have these settings in order to allow for the user to specify links between exactly these settings. To this end a method `getAllSelections()` is written in the `EAMultipleSettingsInterface` that returns a combination of values for all the parameter components[18]. To be exact, the result of the method is a `Vector` of `Vector` objects that contain the selected parameter values as `String` objects for each instance of a component as well as its name, for both the dependency imposing as well as the non–dependency imposing as well as the recombination and mutation chances components[19]. The resulting `Vector` is named `result` and is filled by first placing the dependency imposing components in it:

```
for( i = 0; i < 4; i++ )
{
  vector3 = null;
  if( depInterfaces[i] != null )
  {
    sz      = depInterfaces[i].amountOfParameters();
    vector3 = new Vector( sz );
    for( j = 0; j < sz; j++ )
      vector3.addElement( new Pair( depInterfaces[i].parameterName( j ),
                                    depInterfaces[i].getSelectedValues( j ) ) );
  }
  else
    vector3 = new Vector(0);

  vector2 = new Vector( 1 );
  vector2.addElement( new Pair( depend.elementAt( i ), vector3 ) );
  result.addElement( new Pair( labels[i].getText(), vector2 ) );
}
```

For each dependency imposing component `i` a new `Vector` is created the size of the amount of parameters for the instance of the dependency imposing component. For each of these parameters `j` a (*name*, *value*) pair is stored with the *name* being the name of the parameter and the *value* being the `Vector` of selected values for the `j`–th multiple values parameter component. The name for the instance of the `i`–th dependency imposing component which is stored in the global vector `depend` is then paired with the thus created `Vector` of parameters. The resulting pair is placed in a `Vector` (which thus has only a single element), which in turn is paired with the name of the `i`–th dependency imposing component, which is stored in the array `labels`. Next, the non–dependency imposing components are added to `result` in a similar fashion:

```
for( i = 0; i < AMOUNT; i++ )
{
  l      = components[i].getList();
  sz     = l.countItems();
  vector = new Vector( sz );
```

[18] Actually this method is not even used by the next part, but only used as the final result when all selected and linked information is stored. However, the contents of this method is a combination of the methods `getSelectedInstances()` and `getSelectedParameters()` that *are* used by the interface of the next part.

[19] Even though the method `getAllSelections()` might seem rather involved, we note that the creation of a *backup* for the interface as well as a restore method is even more involved as more position information and such is yet required.

```
    for( j = 0; j < sz; j++ )
    {
      pi      = (MultipleValuesParameterInterface)
                             interfaces[i].elementAt( j );
      vector2 = null;
      if( pi != null )
      {
        sz2     = pi.amountOfParameters();
        vector2 = new Vector( sz2 );
        for( k = 0; k < sz2; k++ )
          vector2.addElement( new Pair( pi.parameterName( k ),
                                   pi.getSelectedValues( k ) ) );
      }
      else
        vector2 = new Vector( 0 );

      vector.addElement( new Pair( l.getItem( j ), vector2 ) );
    }

    result.addElement( new Pair( components[i].getName(), vector ) );
  }
```

For each non–dependency imposing component `i` and each instance `j` of that component that is added, all the multiple values parameter components are looped and transformed into (*name*, *value*) pairs, which are all added to a `Vector`. Each thus constructed `Vector` that thus belongs to instance `j` of component `i` is paired with the name of instance `j` of component `i` and added to another `Vector`. Each of these `Vector` objects thus created for each component `i` is paired with the name of the non–dependency imposing component and added to the result `Vector`. Finally, the recombination and mutation chances are added:

```
  /* Add Recombination */
  vector  = new Vector( 1 );
  vector2 = new Vector( 1 );
  vector3 = recChancesInterface.getSelectedValues( 0 );
  vector2.addElement( new Pair( "Recombination Chance", vector3 ) );
  vector.addElement( new Pair( "Recombination Chance", vector2 ) );
  result.addElement( new Pair( "Recombination Chance", vector ) );

  /* Add Mutation */
  vector  = new Vector( 1 );
  vector2 = new Vector( 1 );
  vector3 = mutChancesInterface.getSelectedValues( 0 );
  vector2.addElement( new Pair( "Mutation Chance", vector3 ) );
  vector.addElement( new Pair( "Mutation Chance", vector2 ) );
  result.addElement( new Pair( "Mutation Chance", vector ) );
```

Adding chances for recombination in the same structure as we did the components before, comes down to adding a `Vector` that contains a single pair with the name `Recombination Chance` and a `Vector` that contains a single pair with the name `Recombination Chance` and a `Vector` that contains a single pair with the name `Recombination Chance` and a `Vector` that contains only the result of the multiple values parameter component for the recombination chances. This latter sentence is probably more difficult yet to understand than the code above, but it follows that the structure in the `Vector` that results from the `getAllSelections()` method is the same for the mutation and recombination chances so that the entries `Vector` can be treated in a uniform fashion. The structure of the resulting `Vector` is depicted in figure 90. We conclude this section and thus the description of the entering of the instances and the parameters for a single rmrEA by concluding the method `getAllSelections()`, which is done by returning the result:

```
  return( result );
}
```

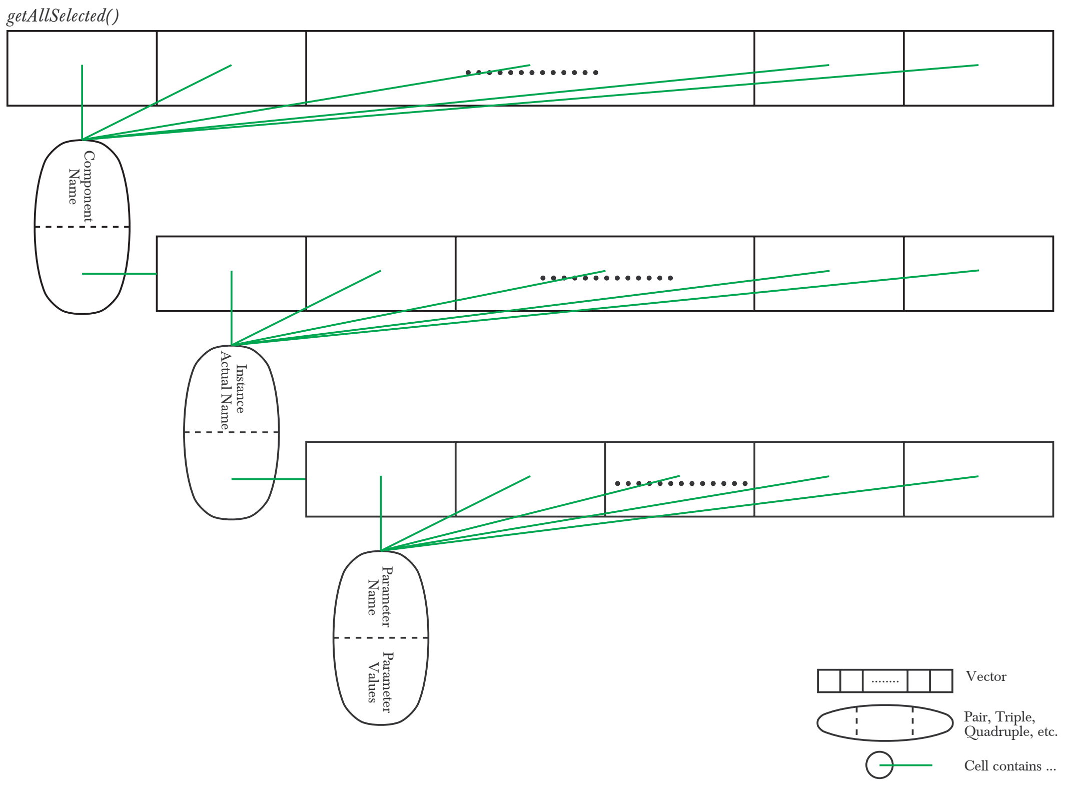

Figure 90: The structure of the resulting `Vector` from the `getAllSelections()` method.

B.2 Specifying the links

The next step in creating an rmrEA is the specification of the links. This part can ofcourse be skipped by the user, implying that all parameters will enumerated in a composite way, meaning that the crossproduct of all settings is actually taken and the resulting set of parameter combinations is used to equip a single run EA with for every combination in the set. What we mean to describe in this subsection is how the facilitation of the specification of such links is established. The implementation must be general because it should be made possible that all that is variable in an rmrEA can be linked together. For instance, as parameters can clearly be linked, it should be possible to link the population size parameters to the parameters of the selection size of the *Before Selector*. Also the instances for the *Recombinator* must be linkable for example with the instances of the *Terminator* to establish algorithms with different termination conditions with the *Recombinator* operator and moreover only three combinations instead of nine which result from the crossproduct. Also however, parameters must be linkable to instances because we might very well want to try one–point crossover with a tournament size of two, two–point crossover with a tournament size of four and uniform crossover with a tournament size of ten for instance. Then again, it is impossible to link the recombination instances with the parameters for one of the instances of the recombination operator as this has no meaning. Furthermore, it is meaningless to link the parameters of one instance to the parameters of another instance when the two instances belong to the same component as all instances for the components are always installed subsequently and never at the same time. This implies that indeed *all* combinations of linking are allowed *except* for links within a single component. Furthermore it is trivial but required for completeness to note that all participants in a link should have the same arity. In other words, five population sizes can only be linked to five selection sizes and not ten.

To establish this, the instances and their parameters are separated so that the lists thus created can be filtered. The parameters are identified by a string that specifies the name of the instance, the name of the component and the name of the parameter. The instances are simply identified by the name of the component. The contents of the class that is created for the links are highly tricky and we would only do justice to describe its contents if we were to describe *all* of its contents, otherwise it would be too vague to understand what is happening in what part. As we find it more interesting to see how the results are combined to actually enumerate the settings in the third phase and wish to elaborate more on that, we shorten the description of the functionality behind the interface for the links implemented in the class `EAMultipleRunsLinksInterface`. We shall however provide a description of how the structure in the latter class works.

The class holds a doubly linked list for all links that are defined. Every link holds information with respect to the arity as well as the contents of the link. The doubly linked list fits the way in which the different links can be viewed in the interface through the use of `Prev` and `Next` buttons. When a link is still empty, its arity is 0. Adding something to the link triggers filtering to take place on the remaining candidates for the link. First and foremost, all candidates that do not have the same arity as the candidate thus added to the link are removed from the candidate list. Furthermore, everything that belongs to the component that the candidate is related to, is removed as well. This latter filtering is the implementation of the requirement that links are not allowed within a single component. This filtering is done as well when a candidate is removed from the link. Note that this filtering must be performed not upon the current list of candidates but on the total list of candidates because otherwise candidates that were filtered out because of their relation to a component are not put back[20]. It all gets another step more complex when more than one link is defined. Candidates that were added to another link are namely not allowed to reappear in a list of candidates for the current link. Not to forget in all of this that all of these relations and filterings should be recomputed dynamically when the list is browsed through using the `Prev` and `Next` buttons. Indeed, the administration of data is tricky in the

[20]The actual implemention *does* filter the list of current candidates, but uses a method `putBackAllOfComponent` that puts back component related candidates first.

`EAMultipleRunsLinksInterface`, let alone the creation of and the restoring from backups. It is for this reason that (at this time) the contents of the link defining interface are reset at the point when the settings in the `EAMultipleSettingsInterface` are altered because checking what links are still valid and subsequently possibly restoring links or destroying them is very complicated.

To conclude the description of the specifications of the links for an rmrEA, we need to look at how to distuinguish between the different entries of a link because once the instances of a non–dependency imposing component or the values for some parameter are added, they are must be identifyable in order for them to be set back in the right place when required and to be used properly by the enumerator which we describe in the next and final section. To this end, just as was the case for the setting of the parameters, a method is required that returns all link information in some `Vector` so that this information can be used at a later stage. The information will be *heterogeneous* just as was the case for the `Vector` that resulted in the previous section, so a good and tight description is required to distuinguish between the instances and the parameters. The method `getAllLinks()` returns exactly this information. To be exact, the resulting `Vector` contains `Vector` objects that represent the different links that have been specified by the user. One such `Vector` specifies the contents of a link through a quadruple which holds exactly four objects, just as a pair holds two. The first item in the quadruple is the name of the non–dependency imposing component that entry is related with. For both the parameters as well as the instances, it is clear that such a relation always exists. The second item is the instance name that the entry is related with. When the instances of a component are to be linked, there is not relation with one such instance and thus this reference is made `null` in that case. Otherwise, the name is that of the instance of the non–dependency imposing component defined in the first item of the quadruple for which the parameter values are the current entry to the link. The third item is the name of the parameter, which is `null` again in the case of an instances entry to the link. The final item in the quadruple is an integer index which points to an entry in the parameters `Vector` that resulted from the `EAMultipleSettingsInterface`. The entry pointed to is the entry that refers to the instance entry in the link for the parameter. This way the parameter is uniquely defined. If the index was not specified, this might have not been the case because when for instance the one–point crossover operator was added twice, the triple (*recombinator*, *one–point*, *offspring arity*) does not uniquely define which of the two one–point crossover instances is added to the link. We end the link defining discussing with depicting the structure of the `Vector` that results from the `getAllLinks()` method in figure 91.

B.3 Enumerating the EAs and their settings

In order to enumerate the settings a multiple runs EA, it should be noted again at this point that a multiple runs EA is nothing more than a multiple of rmrEAs. This implies that when we are able to enumerate the settings for a single rmrEA, we can do this n times for the n rmrEAs that make up the multiple runs EA. All of the above was directed towards the rmrEA and we shall continue to do that here, but not before we now first describe how the system can run a multiple runs EA when we supposedly have an enumerator class `EAMultipleSettingsEnumerator` that when given the proper information will enumerate the settings in an rmrEA for us.

As the running of a single EA is done by the `EARunner` and is initiated and controlled by the `EAVisualizer` class itself, the running of the different rmrEAs that make up a multiple runs EA is done within the `EAVisualizer` class. Basically, whenever the `EARunner` signals termination and the runcounter has reached the total of runs the user specified to run for each combination of settings, the enumerator is asked to go to the next setting. As explained in section 2.3.2, the enumerator will directly alter these settings in the algorithm as it is an `EAInfoSetter`. When the settings are altered, the `EARunner` is signalled to reset itself and the new run is initiated. If the enumerator can no longer go to the next setting because all parameter combinations have been run, a new `EAMultipleSettingsEnumerator` is created for the next rmrEA if there is one to enumerate through the new combination of settings. Here is an excerpt from the actual implementation:

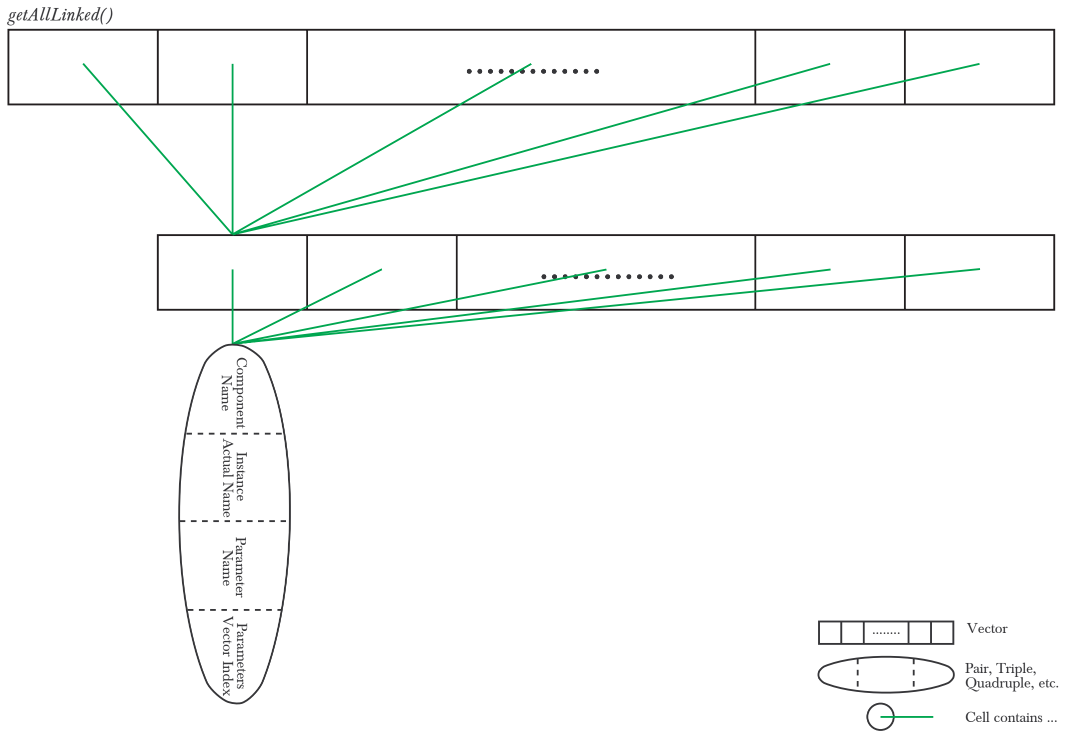

Figure 91: The structure of the resulting `Vector` from the `getAllLinks()` method.

```
    if( runcount < (earunner.getInfo()).getRuns() )
    {
      ...
      earunner.reset();
    }
    else
    {
      if( eamse.hasNext() )
      {
        ...
        eamse.setNext();
        ...
        earunner.reset();
      }
      else
      {
        count = (earunner.getInfo()).getAllCounter();
        if( count < (earunner.getInfo()).getAllTotal() )
        {
          ...
          t     = (Triple) allSelLin.elementAt( count );
          eamse = new EAMultipleSettingsEnumerator( (Vector) t.getFirst(),
                           (Vector) t.getSecond(), creator, combCount,
                           combTotal, mf );
          ...
          earunner.reset();
        }
        else
        {
          actualTermination();
          return( true );
        }
      }
    }
```

In the above code, `emse` is the `EAMultipleSettingsEnumerator`. The code exactly implements what we just described in words. The only thing that is unclear in the above is where the vector `allSelLin` came from. This vector is the result of the method `getAllSelectedAndLinked()` from the `EAMultipleMultipleRunsInterface` class. In the former we have already seen the methods `getAllSelected()` and `getAllLinks()` for one rmrEA. The vector `allSelLin` is a combination of the vectors returned by the latter two methods taken over all rmrEAs that constitute a multiple runs EA. To be precise, the vector `allSelLin` contains triples of which the first item is the result of the `getAllSelected()` method, the second item is the result of the `getAllLinked()` method and the third and last item is the amount of runs that the rmrEA should be run (note that an rmrEA is thus defined through the two vectors that are the first two items of a triple in the `Vector` that is returned by the `getAllSelectedAndLinked()` method). In figure 92 the complete structure of this very important `Vector` is depicted.

It remains to describe how the settings for one rmrEA are enumerated in the class which we turn to now, the `EAMultipleSettingsEnumerator` class. In general, all the settings are appointed to a certain counter variabele, respecting the links that were made. These counter variables are then enumerated. Each state of these counter variables corresponds to a new combination of settings for the EA, which can be retrieved through the counter relations with the settings. The creation of a new enumerator consists of two phases. The first phase deals with the setup of the data structure required for the enumeration and the second phase is a short phase that sets up the so called fast counters. This second phase is not really part of the creation phase as it is used a multiple of times during the enumeration, but the first time it is executed is indeed during the creation phase. We shall go over the two phases separately.

The first phase in the creation of the enumerator consists out of five passes over a certain data structure that is generated in the first pass. In the following we describe the different passes in detail and at the end of the fifth pass, the enumerator will be set and ready direct after the setup

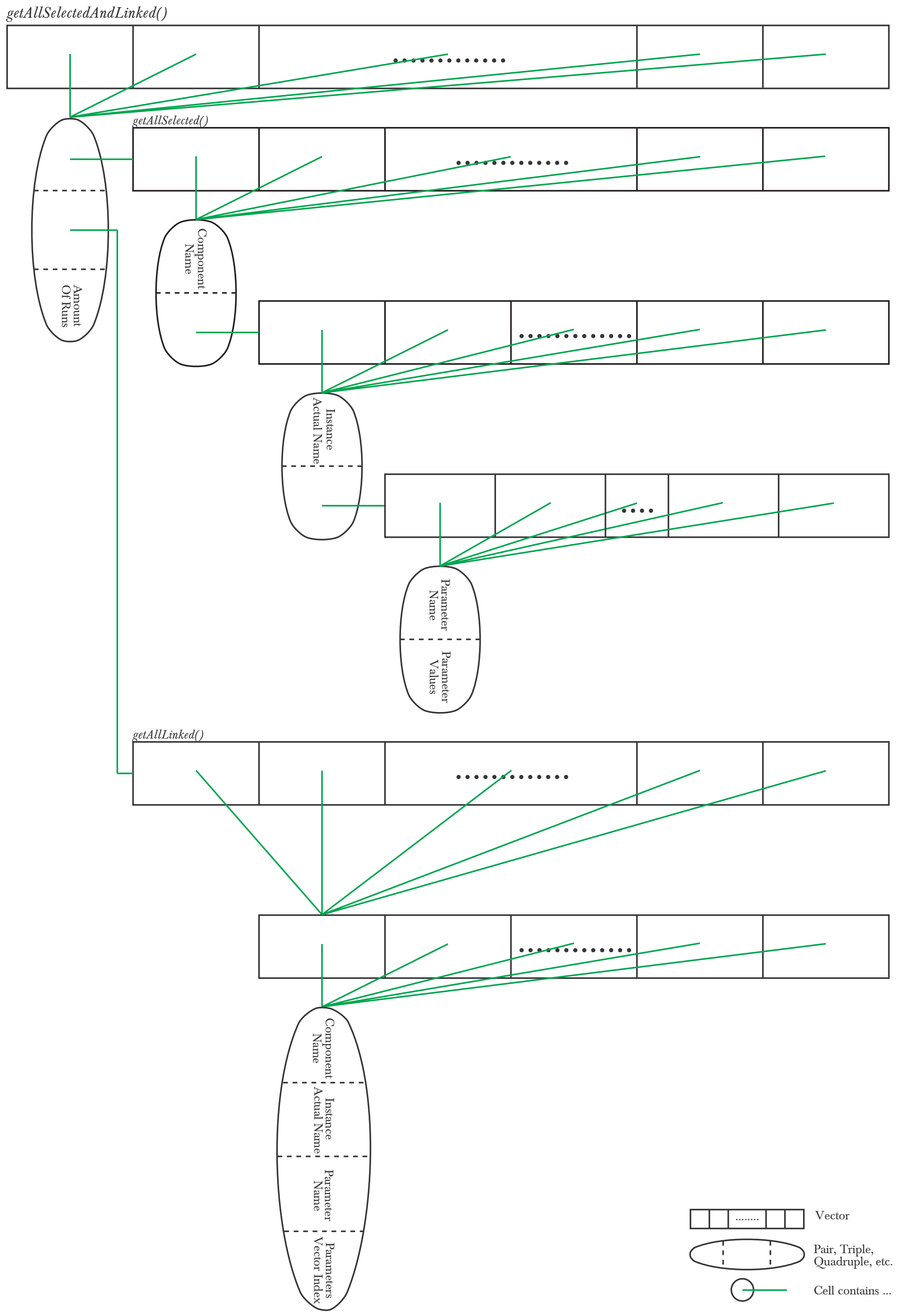

Figure 92: The structure of the resulting `Vector` from the `getAllSelectedAndLinked()` method.

of the fast counters.

First Pass: Augment the received datastructure to incorporate counters
As mentioned before, the general idea is to map every part of the settings that is enumerable to a counter and to subsequently trivially iterate the counters. After a counter update, the data structure is then traversed to see what settings have to be altered by looking at the counter a certain setting is mapped to. If the counter has changed, the setting should change. Since all the selections for the rmrEA are contained in the `Vector` that resulted from the method `getAllSelections()` we saw in the first section of this appendix and is known under the variable `selections` here, that data structure is the place to incorporate the counters. For every component there should be a counter that is meant to enumerate the different instances and for every parameter for every instance for every component there should be a counter that is meant to enumerate the different settings for the parameter. The first pass is meant to go over the data structure that is that `Vector` with all the selections and augment it so that the counters just mentioned can be incorporated. The meaning of the counters is at this point still irrelevant and therefore they are all set to -1:

```
private void makeEnumDataFirstPass( Vector selections )
{
  Integer counter;
  int     i, j, k, l, sz, sz2, sz3, sz4;
  Vector  vector, cvector, vector2, cvector2, vector3, cvector3;
  Pair    p, p2, p3;

  counter  = new Integer( -1 );
  sz       = selections.size();
  enumData = new Vector( sz );
  for( i = 0; i < sz; i++ )
  {
    p       = (Pair) selections.elementAt( i );
    vector  = (Vector) p.getSecond();
    sz2     = vector.size();
    cvector = new Vector( sz2 );
    for( j = 0; j < sz2; j++ )
    {
      p2       = (Pair) vector.elementAt( j );
      vector2  = (Vector) p2.getSecond();
      sz3      = vector2.size();
      cvector2 = new Vector( sz3 );
      for( k = 0; k < sz3; k++ )
      {
        p3       = (Pair) vector2.elementAt( k );
        vector3  = (Vector) p3.getSecond();
        sz4      = vector3.size();
        cvector3 = new Vector( sz4 );
        for( l = 0; l < sz4; l++ )
          cvector3.addElement( vector3.elementAt( l ) );
        cvector2.addElement( new Triple( p3.getFirst(), counter, cvector3 ) );
      }
      cvector.addElement( new Pair( p2.getFirst(), cvector2 ) );
    }
    enumData.addElement( new Triple( p.getFirst(), counter, cvector ) );
  }
}
```

As is clear from the above code, the augmented data structure is stored in the variable `enumData`. The augmentation is nothing more than a walk over the given data structure and copying the data, incorporating the counters at the required levels and thereby making pairs into triples. Furthermore, in order to not adapt the given datastructure, *new* `Vector` objects need to be created. In the above code this is done by creating additional `Vector` variables `cvectori` for every `vectori` where the addition of the character `c` insinuates the idea of a “copy”. Indeed, at the top level counters are incorporated as noted because for every component a counter is needed to enumerate its selected instances. The first `for` loop (over `i`) starts with getting the `i`–th pair

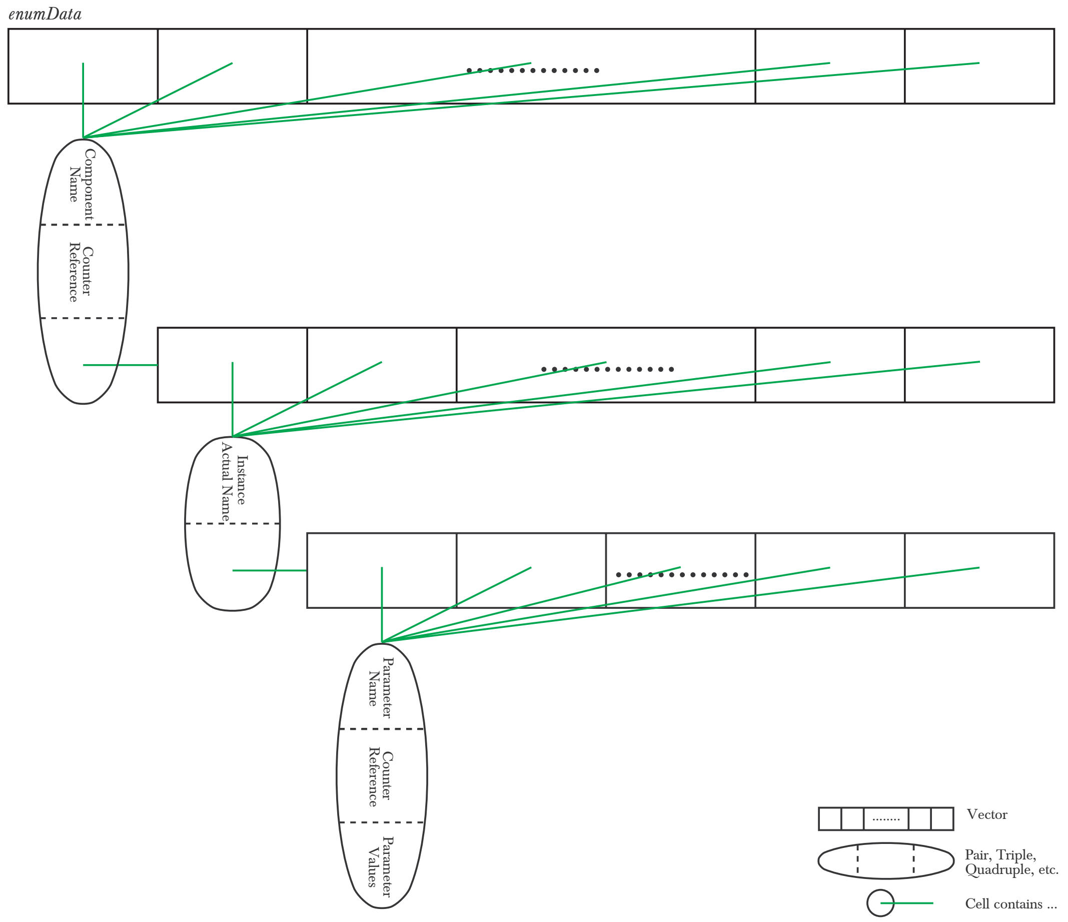

Figure 93: The augmented data structure stored in `enumData`.

out of the `selections` vector. The incorporation of the counter is seen in the last statement of the code above, which adds the `i`–th triple to the new vector `enumData` where the first item of the triple is the first item of the pair (an unchangable `String`), the second item of the triple is a counter which is set to -1 and the third item is an augmented copy of the `Vector` stored as the second item in the `i`–th pair of the `selected` vector. In a similar fashion, the other vectors are copied and at the level of the actual parameters more counters are incorporated. All in all, this leads to the augmented data structure that is depicted in figure 93 and which is thus realized in the variable `enumData` with copied information from the `selected` vector. Note that all data objects that are unchangable (such as `String` objects) are not cloned into `enumData`, which is done because we cannot do those objects any harm anyway and so we are saving time and memory.

Second Pass: Deal out counters according to links
Now that the data stored in `enumData` has room for the counter variables or better said indirections to counter variables, we can start assigning the counters to the entries in the `Vector` by going over the links and assigning the entries of those links the same counter indexes. This required going over the two datastructures looped over each other. First of all we need to enumerate the links. This we can do according to the specification given before as the links are stored in the variable `links` and the structure of that `Vector` was given earlier as the result of the `getAllLinks()` method. Thus, enumeration of that data structure initiates the second pass:

```
  private void makeEnumDataSecondPass( Vector links )
  {
    Integer   counter;
    int       i, j, k, l, m, sz, sz2, sz3, sz4, sz5, pos;
    Vector    vector, vector2, vector3;
    Pair      p;
    Triple    t2, t3;
    Quadruple q;
    String    cname, iname, pname;

    sz = links.size();
    for( i = 0; i < sz; i++ )
    {
      counter = new Integer( i );
      vector  = (Vector) links.elementAt( i );
      sz2     = vector.size();
      for( j = 0; j < sz2; j++ )
      {
        q       = (Quadruple) vector.elementAt( j );
        cname   = (String) q.getFirst();
        iname   = (String) q.getSecond();
        pname   = (String) q.getThird();
        pos     = ((Integer) q.getFourth()).intValue();
```

Recall that one entry of a link is a quadruple as can also be seen in the above code. We also specified that when the link involved the instances of a component to be linked (such as crossover operators for the *Recombinator*), the instance name which is stored as the second item in the quadruple would be a `null` reference. This allows us to check for the type of link entry we have. If the link entry is indeed the instances of a component, we only have to enumerate the top layer of the `enumData` vector as the counter we are looking for is stored within the triples that are the direct entries of `enumData` as described above. This means we enumerate the triples in `enumData` and when we find the component that matches the name of the component whose instances are part of the link, we set the counter reference to be the link number `i` which is indeed exactly the iteration variable used in the outer `for` loop to iterate the links:

```
        if( iname == null ) /* Instances of a component */
        {
          sz3 = enumData.size();
          for( k = 0; k < sz3; k++ )
          {
            t2 = (Triple) enumData.elementAt( k );
            if( cname.equals( (String) t2.getFirst() ) )
            {
              t2.setSecond( counter );
              break;
            }
          }
        }
```

If the name of the instance is not a `null` reference, it is a parameter entry in the link meaning that the parameters for some instance of some component need to be added to the link. This requires a deeper enumeration of the data stored in `enumData` however, since the counters we are now looking for are stored amongst the parameters themselves which are so to speak two levels deeper. However, the index position for the data stored in `pos` can now directly be used to skip over the different `Vectors` and only iterate the required `Vector` to find the counter entry. This is possible because the definition of the index number was the number that indexed the instance entry in an unfolded list of *all* (*instance*, *component*) pairs that are placed in substructures in `enumData`. Once the required `Vector` is located, it is iterated until the right parameter is found and then the counter indicator is placed:

```
        else /* Parameters */
        {
          sz3 = enumData.size();
          for( k = 0; k < sz3; k++ )
          {
            t2      = (Triple) enumData.elementAt( k );
            vector2 = (Vector) t2.getThird();
            sz4     = vector2.size();
            if( sz4 <= pos )
              pos -= sz4;
            else
            {
              p       = (Pair) vector2.elementAt( pos );
              vector3 = (Vector) p.getSecond();
              sz5     = vector3.size();
              for( m = 0; m < sz5; m++ )
              {
                t3 = (Triple) vector3.elementAt( m );
                if( pname.equals( (String) t3.getFirst() ) )
                {
                  t3.setSecond( counter );
                  break;
                }
              }
              break;
            }
          }
        }
      }
    }
  }
```

Third Pass: Deal out counters only for components
Now that we have processed all the link data, we could iterate the entire `enumData` structure and set all remaining counters. This would however result in an undesirable counter setting because the counters for the instances of the components would be mixed with the counters that are for the parameters only. This would mean that new instances for components would just as frequently be required as the setting new parameters for *already installed* components. The creation of new components takes significantly longer time[21] however and when this has to be done often, the delay is noticable. Therefore, the counters for the parameters are best assigned to the "fasted running counters", which would be comparable to the most significant bits in a binary string when counting from 0 to 2^{l-1} with l the string length. Concluding, it is more efficient in the result to first assign counters to all the components (thus on behalf of the enumeration of their instances) that are assigned counters yet or in other words still have their counter set as -1. The counter indirections to deal out start ofcourse at the amount of links processed in the second pass:

```
  private void makeEnumDataThirdPass( Vector selections, Vector links )
  {
    int    i, j, k, sz, sz2, sz3, index;
    Vector vector, vector2;
    Triple t, t2;
    Pair   p;

    count = links.size();
    sz    = enumData.size();
    for( i = 0; i < sz; i++ )
    {
      t      = (Triple) enumData.elementAt( i );
      index  = ((Integer) t.getSecond()).intValue();
      if( index < 0 )
      {
```

[21]In fact it doesn't take long at all and the time for a single creation operation is negligible, but over a multiple operations it shows.

```
        t.setSecond( new Integer( count ) );
        count++;
      }
    }
  }
```

Fourth Pass: Deal out counters for the rest
It is obvious that at this point, the remainder of the counters are to be set. We also know that the only counters left to be set are those of the parameters, so the data in `enumData` is to be completely iterated to get to the level that contains the counters for the parameters. In order to remember what counters are assigned to the non–linked parameters and are thus to run the fastest as explained at the third pass, the global variable `count` that has been used in the third pass to count what counter indirection to use next is frozen and another global variable is used to continue the count. This new global variable is named `total`, meaning that at the end counters `0..count-1` are used for the links (which enumerate slowest) and the remainder of the components on behalf of their instances and counters `count..total-1` are used for the parameters that aren't linked and should thus be iterated fastest. The implementation is straight forward and no more difficult that that of the third pass:

```
  private void makeEnumDataFourthPass( Vector selections )
  {
    int    i, j, k, sz, sz2, sz3, index;
    Vector vector, vector2;
    Triple t, t2;
    Pair   p;

    total = count;
    sz    = enumData.size();
    for( i = 0; i < sz; i++ )
    {
      t      = (Triple) enumData.elementAt( i );
      vector = (Vector) t.getThird();
      sz2    = vector.size();
      for( j = 0; j < sz2; j++ )
      {
        p       = (Pair) vector.elementAt( j );
        vector2 = (Vector) p.getSecond();
        sz3     = vector2.size();
        for( k = 0; k < sz3; k++ )
        {
          t2    = (Triple) vector2.elementAt( k );
          index = ((Integer) t2.getSecond()).intValue();
          if( index < 0 )
          {
            t2.setSecond( new Integer( total ) );
            total++;
          }
        }
      }
    }
  }
```

Fifth Pass: Set up the counter arrays and count the amount of combinations
All settings have been assigned a counter variable now, implying that we are ready to set up the counters and finish the creation phase by counting the amount of combinations that this enumerator is to run according the counters. For each counter, its range must be determined so that a counter array can be constructed that is similar to a binary or decimal string. The counter array differs in the fact that every counter that is part of the string has its own range, thus causing the effect known as *carry* to occur when a counter exceeds its own maximum range and not some radix range as is the case for the binary string (radix of two) and the decimal string (radix of ten) which is the way in which we write our numbers. Before we can simply create these

counters however, we must note at this point the difference between the *fast* counters and the *normal* counters.

The fast counters are given to the parameters that are not linked. As noted at the third pass, it is more efficient to differentiate between the instances of the components and the parameters for the instances as enumerable items. Above that however, the *fast* counters have now a special meaning since they are solely associated with the unlinked parameters and vice versa. The unlinked parameters are namely the source of a complication in enumeration. Imagine for instance having both one–point and two–point crossover added as the *Recombinator*. Both these instances of the *Recombinator* component have parameters. However, only *one* of the two operators is active at any given time in the enumeration. This implies that enumerating the parameters of instances of components is not allowed when the instance is not installed at the current time. This implies that whenever the components are changed, the fast counters will have fully run their cycle and must at that point be determined over since they might have changed. Note that the fast counters could have been left out and the normal counters could have been used, even with this problem, but implementing it would have become extermely tricky without any gain in computation time or easy in programming. Concluding, we can only set up the normal counters at this time and need to redetermine and reset the fast counters every time they have completely run through all their combinations.

The only thing that remains to be discussed at this point is due to the recognition of this problem. What if two parameters of instances are linked but there are a multiple of instances (note that this cannot occur within a single component as this was prohibited in the link specification). To understand the impliciations of such a selection, the meaning of it should first be questioned. It actually doesn't make a lot of sense to make such a setting as what it expresses on behalf of the user is:"I want the settings for parameter p_x for instance i_y of component c_z to be linked to parameter p_u for instance i_v of component c_w with $z \neq w$ and $y \in \{1, \ldots n\}$ and $v \in \{1, \ldots m\}$ with $n \geq 2$ and $m \geq 2$ but only for the combination of y and v, for the other combinations it doesn't matter to me...". To imagine such a setting, we would for instance want to have one–point and two–point crossover for the *Recombinator* and tournament and roulettewheel selection for the *Before Selector* and then link the parameters of one–point crossover to those of tournament selection so that when they are selected together, their parameters will be enumerated together and for the other combinations there will be crossproducts. It is highly likely that the instances for the components themselves need to be linked too, in which case such a scenario becomes very understandable again. Indeed, if the former is required anyway even though it's highly unlikely, a problem exists in that when in the former example two–point crossover and roulettewheel selection are selected, they will be run for as many times as the arity of the linked parameter between one–point crossover and tournament selection. This entire problem would have occurred many times as well when the fast counters are not investigated seperately each time a new component is installed, which is exactly what we set out to prevent as described above.

We are now ready to present the final pass in the first phase of the construction process. First of all, the arrays for the counters are made. From the previous passes it is clear that we require `count` positions for the normal counters, `total - count` positions for the fast counters and `total` positions for the mapping of the fast indexes to the right array indices since the fast counters are numbers above `count` and have to be redirected to numbers below `total - count` (note that only `total` values are required to do this in a straightforward manner). For each counter array there is also a `prev` version which is required to find out what counters have changed after one step in the iteration process that updates the counter array(s).

```
private void makeEnumDataFifthPass()
{
  int    i, j, k, sz, sz2, sz3, sz4, index, index2;
  Vector vector, vector2, vector3, vector4;
  Triple t, t2;
  Pair   p;
```

```
prevCounters     = new int[count];
counters         = new int[count];
maxVals          = new int[count];
fastCounters     = new int[total-count];
fastPrevCounters = new int[total-count];
fastMaxVals      = new int[total-count];
fastMap          = new int[total];
```

Next, we require to determine the maximum values for the counters so that they can be properly iterated. Furthermore, at this point we create and fill an array of `Vector` objects named `parameters` that shall in a later stage be used to put the current actual parameters in so that they can be actually set in the current EA in a straightforward manner. All entries of that array are now set to `null` references as the parameters are unkown at this point. Finally, we only set the normal counters at this point as the functionality for setting the fast counters will be required more often during the enumeration process, implying that we best make a seperate method for the settings of these counters. This means that only the parameter entries that have their counter redirection smaller than `count` may be used to retrieve the maximum value of the normal counter that is pointed to by their counter redirection. The maximum value for a normal counter is either the amount of instances for a component, which equals the size of the vector that contains these instances, or the amount of parameter instances for a parameter for an instance for a component, which then equals the size of the parameter instances vector:

```
sz         = enumData.size();
parameters = new Vector[sz];
for( i = 0; i < sz; i++ )
{
  t              = (Triple) enumData.elementAt( i );
  index          = ((Integer) t.getSecond()).intValue();
  vector         = (Vector) t.getThird();
  sz2            = vector.size();
  parameters[i]  = new Vector( sz2 );
  maxVals[index] = sz2;
  for( j = 0; j < sz2; j++ )
  {
    p       = (Pair) vector.elementAt( j );
    vector2 = (Vector) p.getSecond();
    sz3     = vector2.size();
    vector3 = new Vector( sz3 );
    parameters[i].addElement( vector3 );
    for( k = 0; k < sz3; k++ )
    {
      vector3.addElement( null );
      t2      = (Triple) vector2.elementAt( k );
      index2  = ((Integer) t2.getSecond()).intValue();
      vector4 = (Vector) t2.getThird();
      sz4     = vector4.size();
      if( index2 < count )
        maxVals[index2] = sz4;
    }
  }
}
```

The method continues by initializing the normal counter arrays themselves. The `prev` counters are all set to -1 and the normal counters to 0. Note that since these values are different, the method setting the components will think all counters have changed with respect to the previous setting and will thus install all new components as required:

```
for( i = 0; i < count; i++ )
{
  prevCounters[i]  = -1;
  counters[i]      = 0;
}
```

The method finishes by counting the amount of combinations and setting this information in a neat and global fashion (according to the mechanism provided because the enumerator is an implementation of EAInfoSetter). Following this count, the system–global[22] combination counter is set to 0 and all counters are again reset as the counting of the combinations alters the counters. Indeed, the counting of the combinations is done by sheer iteration because the process is quite complicated and difficult to mathematically compute because of the changing assignments of the fast counters. The fast counters are therefore created but not fully iterated because once the fast counters are determined, the amount of combinations they make is easily computed. This implies that the normal counters *are* completely iterated, which is why the they need to be reset after the counting of the combinations.

```
    countCombinations();

    combCount.setFirst( new Long( 0 ) );
    for( i = 0; i < count; i++ )
    {
      prevCounters[i]  = -1;
      counters[i]      = 0;
    }
  }
```

The second phase in the creation of the enumerator is the setting of the fast counters. At this point it should be understood by the reader why the creation phase is divided in two phases because of the functionality of the fast counters as explained above. As noted there, the fast counters are subject to changes in the installed instances for the components as they make parameters switch between active and non–active, making fast counters required or illegal respectively, implying in turn that the fast counters are dynamic in size since different instances may have a different amount of parameters. As a result, a variable fastInUse is used next to the fastCounters array that determines just how many of the counters in that array are actually in use. It follows that we require to enumerate the Vector that is enumData to reach the level of the parameters and for each parameter that isn't linked and thus has its counter redirection larger or equal to count set the fast counters information analogously to the normal counters as seen above:

```
  private void makeFastCounters()
  {
    int    i, j, sz, sz2, index;
    Vector vector;
    Triple t, t2;

    fastInUse = 0;
    sz        = enumData.size();
    for( i = 0; i < sz; i++ )
    {
      t      = (Triple) enumData.elementAt( i );
      index  = ((Integer) t.getSecond()).intValue();
      vector = (Vector) t.getThird();
      vector = (Vector) ((Pair) vector.elementAt( counters[index] )).getSecond();
      sz2    = vector.size();
      for( j = 0; j < sz2; j++ )
      {
        t2    = (Triple) vector.elementAt( j );
        index = ((Integer) t2.getSecond()).intValue();
        if( index >= count ) /* Not a linked item */
        {
          fastMap[index]         = fastInUse;
          fastMaxVals[fastInUse] = ((Vector) t2.getThird()).size();
          fastInUse++;
        }
      }
    }
```

[22]Only global to those system classes that need it.

After this setting of the fast counters, the amount of combinations is stored in the variable `fastTotalAmount` by simply multiplying all maximum values for the fast counters and once again analogously to the normal counters, the fast counter array entries and the `prev` fast counter array entries are initialized to 0 and -1 respectively:

```
    fastAmountDone  = 0;
    fastTotalAmount = 1;
    for( i = 0; i < fastInUse; i++ )
    {
      fastPrevCounters[i]  = -1;
      fastCounters[i]      = 0;
      fastTotalAmount     *= fastMaxVals[i];
    }
  }
```

Even though we have gone over a complex structure and have taken a lot of time explaining how to set up a structure for the enumeration of the settings of an rmrEA, we have indeed not done more than that yet. In other words, the actual enumeration is not even described yet. The general idea how to achieve this is at this point probably clear, so we shall be brief in describing this. We already showed how the system itself actually uses the enumerator to enumerate the different settings. It therefore suffices to describe the contents of the methods called by the system, which are `hasNext()` and `setNext()`. The method `hasNext()` returns whether there are yet more settings to enumerate and thus whether the system can call `setNext()` to make the enumerator install the new settings after updating the counters. As we have shown, the amount of combinations that result in the enumerator is computed in the fifth pass of the creation. As this information stored "gobally" through the structure offered through the `EAInfoSetter` JAVA `interface`, writing the `hasNext()` is really easy as the counter for the enumerations is updated and stored in the same way as the total amount of combinations:

```
  public boolean hasNext()
  {
    return( getLong( combCount ) < getLong( combTotal ) - 1 );
  }
```

It remains to describe how to establish the `setNext()` method. First of all, the method should protect the system in that an unfortunate additional call to this method when there are actually no more settings to enumerate should not result in an attempt to enumerate further anyhow. When there are more setting to enumerate however, there are two cases. When the fast counters can still be iterated further, this should be done by one step. Otherwise, the normal counters should be iterated one step and the fast counters recomputed as explained earlier. The updating of the fast counters is completely analogous to the updating of the normal counters, so the code that shortly follows should suffice as a description for that as well. When the iteration of the counters is completed, the updates should be transferred to the evolutionary algorithm that is to be run, which is done by calling the method `setEAInfoForCurrent()` that installs instances for the components and updates the settings according to the current contents of the counters and their previous values. After that, the enumeration has been brought one step further and thus the variable `combCount` that we just saw used in the method `hasNext()` should be updated:

```
  public void setNext()
  {
    int i;

    if( hasNext() )
    {
      if( hasNextFast() )
        setNextFastCounters();
      else
      {
        for( i = 0; i < count; i++ )
          prevCounters[i] = counters[i];

        i = count - 1;
        counters[i]++;
        while( i > 0 && counters[i] == maxVals[i] )
        {
          counters[i] = 0;
          counters[i-1]++;
          i--;
        }

        makeFastCounters();
      }

      setEAInfoForCurrent();

      combCount.setFirst( new Long( getLong( combCount ) + 1 ) );
    }
  }
```

The only part that is not clear at this point is how the contents of the current evolutionary algorithm that runs on behalf of the rmrEA that is run in turn on behalf of the multiple runs EA that the user specified, are actually set. This is done in the method `setEAInfoForCurrent()` as described above. The details of the enumerator have been exposed to quite some great detail in the above and at this point the reader should quite be able to write the contents of such a method or at least have a feel for what the contents should be like. It contains a lot of redirection using counters as the contents of the normal and fast counters needs to be redirected towards the data structures that hold the actual values for the evolutionary algorithm. To this end, the `enumData` vector must be enumerated and for each component (which lie at the top level of `enumData`) the actually installed instance should be regarded. This instance is to found by looking at the counter value that the component is directed to. When that instance is thus collected through indexing directly in the `Vector` of instances for the component, the parameters for that instance should be enumerated. For each parameter, if it is a linked parameter the normal counters should be observed and otherwise the fast counters. If the counter at the specified position in the counters array that is to be observed has changed, a new value should be installed. This can be done through a method `installNewValue()` of which we shall leave the details behind here. This method does nothing more than update the `parameters` array we saw earlier. After the enumeration of the parameters, it should be checked if the counter that is reserved for the instances of the current component has changed. If that is the case, a whole new component will need to be created and installed, to which end the method `installNewComponent()` can be called of which we shall also leave the details behind here. This method does nothing more than go over all components to see what global placeholder to update and use the component creator to actually create the new component. If a new component needed not be installed, if new values had to be installed for the component, this is actually done by calling the method `actuallyInstallNewValues()` that goes over all global component holders again but now retreives the current installed component and sets its parameters according to the `parameters` array. This actual installment is done separately from the parameter selection installment done through the `installNewValue()` method because the actualy installment is not required when a whole new component is created as the new parameters are then immediately used to initialize the new component. The resulting method for setting the current information within the EA with the tricky counter redirections is the ending of this appendix and looks like this:

```
  private void setEAInfoForCurrent()
  {
    int     i, j, sz, sz2, index, index2;
    Vector  vector;
    Triple  t, t2;
    boolean changed;

    sz = enumData.size();
    for( i = 0; i < sz; i++ )
    {
      t       = (Triple) enumData.elementAt( i );
      index   = ((Integer) t.getSecond()).intValue();
      vector  = (Vector) t.getThird();
      vector  = (Vector) ((Pair) vector.elementAt( counters[index] )).getSecond();
      changed = false;
      sz2     = vector.size();
      for( j = 0; j < sz2; j++ )
      {
        t2     = (Triple) vector.elementAt( j );
        index2 = ((Integer) t2.getSecond()).intValue();
        if( index2 < count )
        {
          if( prevCounters[index2] != counters[index2] )
          {
            installNewValue( t2, true, i, j, index, index2 );
            changed = true;
          }
        }
        else
        {
          if( fastPrevCounters[fastMap[index2]] != fastCounters[fastMap[index2]] )
          {
            installNewValue( t2, false, i, j, index, index2 );
            changed = true;
          }
        }
      }
      if( prevCounters[index] != counters[index] )
        installNewComponent( t, i, index );
      else if( changed )
        actuallyInstallNewValues( t, i, index );
    }
  }
```

C EA Visualizer specifications, dimensions and history

In this appendix we give an idea of the size of the resulting system and what it actually took to create and test it. This no theoretic information of any sort and is only meant as nice–to–know background information that is usually indicated in system descriptions by the words *for your information...*

Specifications
The EA Visualizer is both a general framework and a development environment for interactive visualisations of evolutionary algorithms and is written in JAVA. A general framework for evolutionary algorithms is defined by breaking the algorithm up into 12 components. All these components are more parts that can be edited separately using the editor version of the program. Composing evolutionary algorithms and viewing results is completely interactive. Working with the *EA Visualizer* (without expanding it) requires no knowledge of any kind of JAVA or any other programming language. Single runs in which components are directly used or multiple runs that are based upon these single runs and are automatically made available by the system can be run both. The system is highly expandable in evolutionary components as well as views, parameter components and utilities in an automated fashion as system updates are done by the system itself and require no additional operations by the user. The *EA Visualizer* can be expanded to contain many more instances for the twelve different components, but the following tables show the already available instances in the system as well as the readily available views and parameter components:

Component	**Instances**
Genotype	Binary String Evolution Strategies Multi Valued Allele String TSP Numbered List

Component	**Instances**
Similarity	Binary String - Bitwise Difference
	Binary String - Range Difference
	No Similarity
Fitness Function	Ackley's Function
	Binary String - Polynome Optimizer In [a,b]
	Binary String - Bit Counting
	Evolution Strategies - Polynome Optimizer In [a,b]
	Geometric TSP Numbered List
	String Matching
	Binary String - Trap Functions
Recombinator	Baluja & Davies Optimal Dependency-Trees
	Binary String - One Point Crossover
	Binary String - Two Point Crossover
	Binary String - Uniform Crossover
	ES Crossover
	MIMIC
	Hybrid PDE based on MIMIC & Baluja and Davies
	Multi Valued Allele String - Two Point Crossover
	Multi Valued Allele String - Uniform Crossover
	TSP Numbered List - Cycle Crossover
	TSP Numbered List - Distance Preserving Crossover
	TSP Numbered List - Edge Map Recombination
	TSP Numbered List - Order Crossover
	TSP Numbered List - Partially Mapped Crossover
Mutator	Binary String Random Mutation
	ES Mutation
	Multi Valued Allele String Random Mutator
	No Mutation
Selector	No Selection (Select All)
	Random Selection
	Roulettewheel Selection
	Tournament Selection
	Truncation Selection
Mater	Mate all genomes in one group
	Restricted Random Mating Using Clustering
	Random Mater
	Simple Mater
Replacer	Add Offspring To Population
	New Offspring Only
	Crowding
	Deterministic Crowding
	Elitist Replacing
	Preselection
Terminator	All Equal Genomes And Maximum Generations
	All Equal Genomes
	Maximum Generations
Hybrid Searcher	No Hybrid Search
	2 Opt Heuristic For The TSP
Population	Sharing Using Adaptive Clustering
	Vector Population
PRNG	Standard Java PRNG

View	**Instances**
Internal	Best & Worst Binary String Genome
	Geometric TSP Tour
	Progress Indicator For Multiple Runs
	Locations On Polynome
	Multiple Run Fitness Statistics
	Fitness Statistics
	Trap Functions % BBS Correct
	Trap Functions: Correct Building Blocks
	Best & Worst Evolution Strategies Genome
	Best & Worst Multi Valued Allele String Genome
	Binary String Population Dots
External	External Multiple Runs Overview
	External Multiple Runs Statistics
	Fitness Statistics Numbers
	Trap Functions: Correct Building Blocks Numbers
	MIMIC Distribution Numbers
	Optimal Dependency Tree For Baluja & Davies Optimal Dependency Trees

Parameter Components
Specifying A Polynome
Multiple Choices Using Checkboxes
A Real Number Within Bounds
An Integer Number Within Bounds
Multiple Choices Using A List
Specifying The Cities For A 2-D Geometric TSP
Multiple Integers Within Bounds
Multiple Real Numbers Within Bounds
An Environment To Differentiate Between Different Settings In A Multiple Runs EA
A String Without Restrictions
A Color In RGB Space
An Interval With Real Bounds

Requirements
All that is required is a system that runs JAVA `1.1` and a harddrive that has at least 6 Mb of free hard drive space. The *EA Visualizer* will run on any such system as the implementation is completely portable over all types of systems as long as JAVA is available. To run the program as an applet, an appletviewer has to be incorporated in the system, but this cannot be used to start up the editor.

Even though these are the only requirements for running the *EA Visualizer*, the recommendations are more specific. The *EA Visualizer* was developed mainly on a pentium 120 Mhz system with 32 Mb of internal memory. This makes the system run neatly, but ofcourse not fast enough. . . Less memory makes the system harder to handle as the operating system is more than likely going to swap data from and to a harddrive. It is therefore in the eyes of the author a minimum requirement to have a system comparable to a 120 Mhz pentium with 32 Mb of internal memory, 6 Mb of free harddrive space, a JAVA `1.1` system and a mouse pointing device.

Dimensions, history and system up–time
The original implementation that resides in the source directory of the author is different from the files that will be distributed once the system is ready for shipment as the main system JAVA files are not incorporated in such a version but only their compiled class equivalents. The source directory contains 235 `.java` files that each contain a single class. This means that the *EA Visualizer* consists of 235 different classes over three top level packages. The total size of these

files is in the final version generated right before the writing of this text 2058152 bytes on a DOS based system and thus in general over 2 Mb in text files only. An estimate based on extrapolation tells us this is about 65000 lines of code (but this latter measure is very much so subject to the style of the programmer). The help system is an additional 185761 Kb over 135 help files in text files only. The development root directory in total is over 9.4 Mb in size, whereas the program directory that is thus available for shipping is over 5 Mb in size. This latter size also contains the automatically generated HTML documentation files as generated by JAVADOC. A zipfile that could be used for distribution of the program only is standard just over 2 Mb. Without the HTML files such a zipfile is just over 1.4 Mb and fits (almost precisely) on a single 1.44 Mb diskette.

The history in development of the *EA Visualizer* beside the just mentioned 120 Mhz pentium PC running WINDOWS 95 is filled with many tests on silicon graphics, hewlett packard and SUN machines running UNIX variants. On these different platforms the *EA Visualizer* was initiated using JAVA `1.0.2` and subsequently developed using versions `1.1.4` and `1.1.6`. The first working version of the *EA Visualizer* was version `1.0`, was a straightforward implementation of the initial model that followed from the requirements analysis, contained a specific component generator for each component and didn't use packages yet. Version `1.1` still didn't have the single component creator and the editor version but offered multiple runs and used packages. In the first full version the structure as described in this paper was implemented and thus adapted for automation through the editor version of the program and used only a single component creator and view creator. The help system came on–line in this version `1.2` as well as the editor itself. The final version, version `1.3`, resolved some bugs reported in version `1.2`, incorporated the hybrid approach for the probability density estimators and a general graph drawer that can be used for many applications in the future of the system. Also some efficiency means were introduced by offering the user more freedom in selecting when the views are to be updated and separate from that when they are to be redrawn.

On all these machines, the *EA Visualizer* has an estimated up–time (time that the system was running) of about 5000 hours during both days and nights initiated by both the author as well as students taking the course *Evolutionaire Algoritmen* by Dr. Ir. Dirk Thierens during the spring semester of 1998 at the Utrecht University.

Project dimensions

The total time required to finish the project is estimated to be at least 1600 hours, out of which some 850 hours were used for the initial development of the program that led to version `1.2` some 250 hours were used to update the system and create the final version that is known as version `1.3`, some 50 hours were used to read about and create the historic overview of linkage learning, some additional 250 hours were used to write the remainder of this paper and create the illustrations and the remaining (at the very least) 200 hours were used for investigating and gathering results for the linkage issues, reading miscellaneous papers, writing help files, writing material for the closing talk of this graduation project, etc. Finally, the resulting graduation project directory has come to be over 125 Mb in size, starting from scratch almost completely one year ago as the graduation project was started (on a part–time basis) in september of 1997.