

# ALEXANDER SCHÖNHUTH

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## EDUCATION, QUALIFICATIONS

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APPOINTMENT: FULL PROFESSOR  
10/2017

**Faculty of Science, University Utrecht**

TENURE  
09/2014

**Centrum Wiskunde & Informatica, Amsterdam**  
One year ahead of schedule

HABILITATION EQUIVALENT  
FRANCE 2010

French Qualification for **Professor of Computer Science**  
“Qualification Professeur des Universités”, Section 27

DOKTORARBEIT (PHD)  
09/2002 - 05/2006

**University Cologne**, Applied Mathematics  
Supervisor: Prof. Dr. Ulrich Faigle (Discrete Mathematics)  
Co-Supervisor: Prof. Dr. Herbert Jaeger (Machine Learning)

DIPLOMA (MSc)  
10/1992 - 05/1999

**University of Cologne**, Pure Mathematics  
Supervisor: Prof. Dr. Uwe Jannsen (Algebraic Geometry)

ABITUR (HIGH SCHOOL)  
08-1981-06/1990

Deutschorden-Gymnasium Bad Mergentheim  
Final grade: 1.2

## POSITIONS HELD

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FACULTY OF SCIENCE,  
UNIVERSITEIT UTRECHT,  
SINCE 10/2017

**Full Professor** (part time appointment)  
“Genome Data Science / Algorithmic Bioinformatics”

CENTRUM WISKUNDE &  
INFORMATICA, SINCE 09/2010

**Senior Researcher**  
Group: “Computational Genomics / Genome Data Science”

NETHERLANDS INSTITUTE FOR  
SYSTEMS BIOLOGY, SINCE 2010

**Principal Investigator**

UC BERKELEY  
DEPARTMENT OF MATHEMATICS  
08/2009 - 08/2010

**Postdoctoral Fellow**, Supervisors:  
Lior Pachter (Computational Biology)  
Bernd Sturmfels (Algebraic Statistics / Computational Biology)

SIMON FRASER UNIVERSITY  
SCHOOL OF COMPUTING SCIENCE  
09/2007 - 08/2009

**Postdoctoral Fellow**, Supervisors:  
Martin Ester (Data Mining)  
Cenk Sahinalp (Computational Biology)

SIMON FRASER UNIVERSITY  
SCHOOL OF COMPUTING SCIENCE  
09/2007 - 12/2007

**Teaching Instructor**  
Lecture: “Algorithms for Computational Biology”  
(CMPT 441/889)

UNIVERSITY COLOGNE, CENTER  
FOR APPLIED COMPUTER SCIENCE  
2002 - 2007

**Scientific Assistant**

LEAVE OF ABSENCE  
2000 - 2002

for health reasons

UNIVERSITY COLOGNE, CENTER  
FOR APPLIED COMPUTER SCIENCE  
1999 - 2000

**Scientific Assistant**  
PhD Studies in collaboration with University Edinburgh, Biocomputing Research Unit, Scotland (unfinished for health reasons)

UNIVERSITY COLOGNE  
DEPARTMENT OF MATHEMATICS  
1995 - 1999

**Teaching Assistant**  
Lectures on Pure Mathematics

## OTHER RESEARCH STAYS

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INSTITUTE FOR PURE AND APPLIED MATHEMATICS  
UNIVERSITY OF CALIFORNIA AT LOS ANGELES  
09-12/2011

Fall Semester Program  
“Mathematical and Computational Approaches  
in High-Throughput Genomics”

MAX PLANCK INSTITUTE FOR MOLECULAR  
GENETICS, 2002/3/4/5 (SEVERAL TIMES)

Studies on Gene Expression Time Course Analysis

JACOBS-UNIVERSITY BREMEN  
08-09/2004

Studies on “Observable Operator Models” (Machine Learning)

UNIVERSITY EDINBURGH  
03-04/2000

School of Informatics, Biocomputing Unit  
Doctoral Studies  
“Machine Learning for 2D-Gel-Electrophoresis”

## AWARDS AND NOMINATIONS

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BEST TALK AWARD  
2017

“De Novo Viral Quasispecies Assembly using Overlap Graphs”  
awarded at the **ISMB-HitSeq 2017**

PAPER AWARD  
2013

“CLEVER: Clique-Enumerating Variant Finder”  
recognized by the **Faculty of 1000**

HIGH SCHOOL AWARD  
1990

by the Foundation of German Chemical Industry  
for outstanding high school performance in chemistry

1980

Skipped the Second Grade of Elementary School

## GRANTS AND FELLOWSHIPS

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“BETER GEZOND” PROJECT GRANT 09/2018 - 08/2022	Title: “Homogeneous subgroup identification in fatigue management across chronic immune diseases through single subject research design” provided by <i>Health Holland</i> <b>361,000 EUR</b> (own part; overall project grant: 1,885,540 EUR)
PHD STUDENT GRANT 09/2018 - 08/2022	Title: “Deep Learning for Assessment of Immunotherapy as a Treatment Option in Metastatic Cancer” Chinese Scholarship Council (for Xiao Luo) <b>60,000 EUR</b>
WORKSHOP GRANT 06/2018 LORENTZ CENTER, LEIDEN (MAIN ORGANIZER)	Title: “Single Cell Data Science” Netherlands Science Organisation (NWO), Royal Dutch Academy of Sciences (KNAW) <b>13,500 EUR</b> (NWO), <b>6,000 EUR</b> (KNAW)
“VERNIEUWINGSIMPULS VIDI” 09/2013 - 08/2018	“Computational Variant Discovery in the <i>Genome of the Netherlands</i> ” Netherlands Science Organisation (NWO) <b>771,221 EUR</b>
SUMMER SEMESTER STIPENDS 07/2016, 07/2017, 07/2018	“Computational Genomics Summer Institute”, Institute for Pure and Applied Mathematics, UCLA approx. <b>9,000 USD</b>
WORKSHOP GRANT 06/2015 LORENTZ CENTER, LEIDEN (MAIN ORGANIZER)	Title: “Future Perspectives in Computational Pan-Genomics” Netherlands Science Organisation (NWO), Royal Dutch Academy of Sciences (KNAW), Sponsors from Industry <b>13,500 EUR</b> (NWO), <b>6,000 EUR</b> (KNAW), <b>3,000 EUR</b> (Sponsors)
SEMESTER STIPEND 09-12/2011 + 06/2013	“Mathematical and Computational Approaches in High-Throughput Genomics”, Institute for Pure and Applied Mathematics, UCLA approx. <b>13,000 USD</b> , including reunion retreats
PRIVATE DONATION 2009-2010	Mathematical and Computational Biology, UC Berkeley David des Jardins, Google Inc. <b>60,000 USD</b>
POSTDOCTORAL FELLOWSHIP 2007-2009	School of Computing Science, Simon Fraser University Pacific Institute for the Mathematical Sciences (PIMS) <b>40,000 CAD</b>
PER-DIEM ALLOWANCE 2008	“Workshop on Algebraic Statistics” Mathematical Sciences Research Institute (MSRI), Berkeley approx. <b>500 USD</b>
TRAVEL FELLOWSHIP 2008	“International Symposium on Information Theory and Applications” von: Society for Information Theory and Applications (SITA) approx. <b>500 EUR</b>

TRAVEL FELLOWSHIP  
2003 + 2004

“Intelligent Systems for Molecular Biology” 2003 + 2004  
von: International Society for Computational Biology (ISCB)  
approx. **2 200 Euro**

TRAVEL FELLOWSHIP  
2000

“CIME School on Mathematical Methods for Protein Structure Analysis and Design” 2000  
by Deutsche Forschungsgemeinschaft (DFG)  
approx. **1,500 DM**

## PUBLICATIONS

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\* Joint first authorship, † joint last authorship, ◊ joint corresponding authors

(**P**) is for peer-reviewed (journal/conferences), (**PR** for peer-reviewed review, (**PE**) for peer-reviewed extended abstract, (**I**) is for invited contribution, (**T**) is for thesis, (**B**) is for (peer-reviewed) book contribution, (**X**) archived preprint (e.g. arXiv, bioRxiv), (**CR**) for conference report, (**Pop**) for popular writing.

(**GoNL**): Genome of the Netherlands consortium: implicit authorship

See glossary (appendix) for conference shorthands.

### 2018

1. R. Chikhi, **A. Schönhuth** **P**  
*Dualities in tree representations*  
**Symposium on Combinatorial Pattern Matching (CPM)**  
<https://arxiv.org/abs/1804.04263>
2. J. Baaijens, B. van der Roest, J. Köster, L. Stougie, **A. Schönhuth** **P**  
*Full-length de novo viral quasispecies assembly through variation graph construction*  
**RECOMB Satellite on Massively Parallel Sequencing (RECOMB-Seq)**  
<https://www.biorxiv.org/content/early/2018/03/23/287177>
3. B. Yin, M. Balvert, D. Zambrano, **A. Schönhuth**<sup>†</sup>, S. Bohte<sup>†</sup> **P**  
*An image representation based convolutional network for DNA classification*  
**International Conference on Learning Representations (ICLR)**  
<https://arxiv.org/abs/1806.04931>
4. B. Ibrahim, K. Arkhipova, ... (14 authors) ..., **A. Schönhuth**<sup>†</sup>, B. Dutilh<sup>†</sup>, M. Marz<sup>†</sup> **CR**  
*Bioinformatics Meets Virology: The European Virus Bioinformatics Center  
Second Annual Meeting*  
**Viruses**, 10(5), 256
5. J. Baaijens, **A. Schönhuth** **X**  
*Overlap graph-based generation of haplotigs for diploids and polyploids*  
<https://www.biorxiv.org/content/early/2018/07/27/378356>

2017

6. J. Baaijens, A.Z. El Aabidine, E. Rivals, **A. Schönhuth** P  
*De novo viral quasispecies assembly using overlap graphs*  
 Presented at the **BioSB 2017**  
 Presented at the **ISMB 2017**  
**Genome Research**, 27(5), 835-848; **IF: 11.322**
7. J. Dröge, **A. Schönhuth**, A.C. McHardy P  
*A probabilistic model to recover individual genomes from metagenomes*  
**PeerJ Computer Science**, 3, e117; **IF: TBD**
8. J. Ebler, **A. Schönhuth**, T. Marschall P  
*Genotyping Inversions and Tandem Duplications*  
 Presented at **ISMB-HitSeq 2016**  
**Bioinformatics**, 33(24), 4015-4023; **IF: 7.307**
9. L. Francioli, M. Cretu-Stancu, ... (3 authors) ..., P/GoNL  
**The Genome of the Netherlands Consortium**, ... (5 authors) ..., P.I.W. de Bakker  
*A framework for the detection of de novo mutations in family-based sequencing data*  
**European Journal of Human Genetics**, 25(2), 227-233; **IF: 4.287**
10. L.J. Dijkstra, J. Köster, T. Marschall, **A. Schönhuth** X  
*Enhancing Sensitivity And Controlling False Discovery Rate  
 In Somatic Indel Discovery Using A Latent Variable Model*  
<http://biorxiv.org/content/early/2017/03/29/121954>

2016

11. J. Hehir-Kwa\*, T. Marschall\*, W. Kloosterman\*, ... (21 authors) ..., P  
**A. Schönhuth**<sup>†</sup>, Kai Ye<sup>†</sup>, Victor Guryev<sup>†</sup>  
*A high-quality reference panel reveals the complexity and distribution of  
 structural genome changes in a human population*  
**Nature Communications**, 7: 12989; **IF: 12.124**
12. T. Marschall, M. Marz, T. Abeel, L.J. Dijkstra, B.E. Dutilh, A. Ghaffaari, P. Kersey, PR  
 W.P. Kloosterman, V. Mäkinen, A. Novak, B. Paten, D. Porubsky, E. Rivals,  
 ... (40 authors) ..., V. Guryev, F. Vandin, K. Ye, **A. Schönhuth**  
*Computational Pan-Genomics: Status, Promises and Challenges*  
**Briefings in Bioinformatics**, 19(1), 118-135
13. I. Gregor, **A. Schönhuth**<sup>†</sup>, A.C. McHardy<sup>†</sup> P  
*Snowball: Strain aware gene assembly of metagenomes*  
 Proceedings of the **ECCB 2016**  
**Bioinformatics**, 32(17), i649-i657; **IF: 7.307**
14. T. Marschall, **A. Schönhuth** B  
*Discovery and Genotyping of “Twilight Zone” Deletions*  
 In **Computational Methods for Next Generation Sequencing Data Analysis**  
 I. Mandoiu and A. Zelikovsky (eds.), John Wiley & Sons
15. L.J. Dijkstra, J. Köster, T. Marschall, **A.Schönhuth** PE  
*A Latent Variable Model for Somatic Indel Discovery*  
 Presented at **ISMB-HitSeq 2016**
16. **A. Schönhuth**, T. Marschall Pop  
*Eliminating Blind Spots in Genetic Variant Discovery*  
**ERCIM News**, 104, 20-21

17. M. Martin, M. Patterson, S. Garg, S.O. Fischer, N. Pisanti, G.W. Klau, **A. Schönhuth**, T. Marschall X  
*WhatsHap: fast and accurate read-based phasing*  
<http://biorxiv.org/content/early/2016/11/14/085050>  
 See 22 for method article.

## 2015

18. R. Cijvat, S. Manegold, M. Kersten, G.W. Klau, **A. Schönhuth**, T. Marschall, Y. Zhang P  
*Genome Sequence Analysis with MonetDB*  
**Datenbank-Spektrum**, 15(3), 185-191; **IF: 0.55**
19. R. Wittler, T. Marschall, **A. Schönhuth**<sup>†</sup>, V. Mäkinen<sup>†</sup> P  
*Repeat- and Error-Aware Comparison of Deletions*  
**Bioinformatics**, 31(18), 2947-2954; **IF: 5.766**
20. W. Kloosterman, L. Francioli, F. Hormozdiari, T. Marschall, ... (24 authors) ..., **A. Schönhuth**, E. Eichler, P.W.I. de Bakker, K. Ye, V. Guryev P  
*Characteristics of De Novo Structural Changes in the Human Genome*  
**Genome Research**, 25, 792-801; **IF: 11.351**
21. W. Leung, T. Marschall, Y. Paudel, L. Falquet, H. Mei, **A. Schönhuth**, T.Y. Maoz P  
*SV-AUTOPILOT: optimized, automated construction of structural variation discovery and benchmarking pipelines*  
**BMC Genomics**, 16(1), 238; **IF: 3.867**
22. M. Patterson, T. Marschall, N. Pisanti, L. van Iersel, L. Stougie, G.W. Klau<sup>†</sup>, **A. Schönhuth**<sup>†</sup> P  
*WHATSHAP: Weighted Haplotype Assembly for Future-Generation Sequencing Reads*  
**Journal of Computational Biology**, 22(6), 498-509; **IF: 1.537**  
 See 17 for software.
23. T. Bellitto, T. Marschall, **A. Schönhuth**, G.W. Klau P  
*Next-Generation Cluster Editing*  
 Proceedings of the **GCB 2015**  
<http://arxiv.org/abs/1310.3353>
24. E.M. van Leeuwen, ..., J.J. Hottenga, **The Genome of the Netherlands Consortium** P/GoNL  
*Population-specific genotype imputations using minimac or IMPUTE2*  
**Nature Protocols**, 9, 1285-1296; **IF: 9.646**
25. E.M. van Leeuwen, ..., **The Genome of the Netherlands Consortium**, ..., C. Duijn P/GoNL  
*Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels*  
**Nature Communications**, 6:6065; **IF: 11.329**
26. L. Francioli, ..., S.R. Sunyaev, **The Genome of the Netherlands Consortium** P/GoNL  
*Genome-wide patterns and properties of de novo mutations in humans*  
**Nature Genetics**, 47(7), 822-826; **IF: 31.616**
27. P.F. Palamara, ..., A.L. Price, **The Genome of the Netherlands Consortium** P/GoNL  
*Leveraging distant relatedness to quantify human mutation and gene-conversion*  
**The American Journal of Human Genetics**, 97(6), 775-789; **IF: 10.794**
28. R. Cijvat, S. Manegold, M. Kersten, G.W. Klau, **A. Schönhuth**, T. Marschall, Y. Zhang PE  
*Genome sequencing analysis with MonetDB: a case study on Ebola virus diversity*  
 Proceedings of the **BTW 2015**, GI-Edition Lecture Notes in Informatics P-242, 143-150  
 see 18 for journal contribution

29. U. Faigle, **A. Schönhuth** X  
*On Hidden States in Quantum Random Walks*  
<http://arxiv.org/abs/1601.02882>

## 2014

30. **The Genome of the Netherlands Consortium\*\*** P  
*Whole-genome Sequence Variation, Population Structure and Demographic History of the Netherlands*  
**Nature Genetics**, 46, 818-825; **IF: 29.352**  
 \*\*I am considered an explicit author due to decisive contributions
31. A. Töpfer, T. Marschall, R.A. Bull, F. Luciani, **A. Schönhuth**<sup>†</sup>, N. Beerenwinkel<sup>†</sup> P  
*Viral Quasispecies Assembly via Maximal Clique Enumeration*  
 Proceedings of the **RECOMB 2014**, 309-310  
**PLoS Computational Biology**, 10(3): e1003515; **IF: 4.587**
32. M. Patterson, T. Marschall, N. Pisanti, L. van Iersel, L. Stougie, G.W. Klau<sup>†</sup>, **A. Schönhuth**<sup>†</sup> P  
*WHATSHAP: Haplotype Assembly for Future-Generation Sequencing Reads*  
 Proceedings of the **RECOMB 2014**, 237-249  
 See 22 for journal contribution and 17 for software.
33. **A. Schönhuth** P  
*Generic Identification of Binary-valued Hidden Markov Processes*  
**Journal of Algebraic Statistics**, 5(1), 72-99
34. P. Deelen, ..., **The Genome of the Netherlands Consortium**, ..., M.A. Swertz P/GoNL  
*Improved imputation quality of low-frequency and rare variants in European samples using the Genome of The Netherlands*  
**European Journal of Human Genetics**, 22, 1321-1326; **IF: 4.349**
35. L.J. Dijkstra, **A. Schönhuth** PE  
*Testing 2x2 Association with Uncertain Classification*  
 Proceedings of **SMPGD 2014**, 41-42

## 2013

36. T. Marschall, I. Hajirasouliha, **A. Schönhuth** P  
*Mendelian-Inheritance-Aware Discovery and Genotyping of Midsize and Long Indels*  
 Proceedings of the **ISMB-HitSeq 2013**  
**Bioinformatics**, 29(24), 3143-3150
37. M. El-Kebir\*, T. Marschall\*, I. Wohlers\*, M. Patterson, J. Heringa, **A. Schönhuth**<sup>†</sup>, G.W. Klau<sup>†</sup> P  
*Mapping Proteins in the Presence of Paralogs using Units of Coevolution*  
 Proceedings of the **RECOMB-CG 2013**  
**BMC Bioinformatics**, 14(Suppl 15):S18
38. M. Allhoff, **A. Schönhuth**, M. Martin, I.G. Costa, S. Rahmann, T. Marschall P  
*Discovering Motifs that Induce Sequencing Errors*  
 Proceedings of the **RECOMB-Seq 2013**  
**BMC Bioinformatics**, 14(Suppl 5): S1
39. U. Faigle, **A. Schönhuth** PE  
*Observation and Evolution of Finite-dimensional Markov Systems*  
 Proceedings of the **CTW 2013**, 93-97

40. T. Marschall, **A. Schönhuth** X  
*Sensitive Long-Indel-Aware Alignment of Sequencing Reads*  
<http://arxiv.org/abs/1303.3520>

## 2012

41. T. Marschall, I. Costa, S. Canzar, M. Bauer, G. Klau, A. Schliep, **A. Schönhuth** P  
*CLEVER: Clique-Enumerating Variant Finder*  
Proceedings of the **RECOMB-Seq 2012**  
Proceedings of the **ISMB-HitSeq 2012**  
**Bioinformatics**, 28(22), 2875-2882  
Award: “Faculty of 1000”
42. I. Hajirasouliha\*, **A. Schönhuth\***, D. Juan, A. Valencia, S.C. Sahinalp P  
*Mirroring Co-evolving Trees in the Light of Their Topologies*  
**Bioinformatics**, 28(9), 1202-1208

## 2011

43. M. Singer\*, A. Engström\*, **A. Schönhuth<sup>†,◇</sup>**, L. Pachter<sup>†,◇</sup> P  
*Determining Coding CpG Islands by Identifying Regions Significant for Pattern Statistics on Markov Chains*  
**Statistical Applications in Genetics and Molecular Biology**, 10(1):43
44. C. Hafemeister, I. Costa, **A. Schönhuth**, A. Schliep P  
*Classifying short gene expression time-courses with Bayesian estimation of piecewise constant functions*  
**Bioinformatics**, 27(7), 946-952
45. U. Faigle, **A. Schönhuth** P  
*Efficient tests for equivalence of hidden Markov processes and quantum random walks*  
**IEEE Transactions on Information Theory**, 57(3), 1746-1753
46. U. Faigle, **A. Schönhuth** PE  
*Representations of Power Series over Word Algebras*  
Proceedings of the **CTW 2011**, 154-157
47. U. Faigle, **A. Schönhuth** X  
*A Markovian Model for Joint Observations, Bell's Inequality and Hidden States*  
<http://arxiv.org/abs/1011.1295>

## 2010

48. P. Dao, R. Colak, R. Salari, F. Moser, **A. Schönhuth<sup>†,◇</sup>**, M. Ester<sup>†,◇</sup> P  
*Inferring Cancer Subnetwork Markers using Density-Constrained Biclustering*  
Proceedings of the **ECCB 2010**  
**Bioinformatics** 26(18), i625-631
49. R. Colak, F. Moser, J. Shu, **A. Schönhuth<sup>†</sup>**, N. Chen<sup>†</sup>, M. Ester<sup>†</sup> P  
*Module Discovery by Exhaustive Search for Densely Connected, Co-expressed Regions in Biomolecular Interaction Networks*  
**PLoS One**, 5(10): e13348



50. M. Singer, D. Boffelli, J. Dhabhi, **A. Schönhuth**, G.P. Schroth, D.I.K. Martin, L. Pachter **P**  
*MetMap Enables Genome-scale Methylation for Determining Methylation States in Populations*  
**PLoS Computational Biology**, 6(8): e1000888
51. **A. Schönhuth\***, R. Salari\*, F. Hormozdiari, A. Cherkasov, S.C. Sahinalp **P**  
*Towards improved assessment of functional similarity in large-scale screens: an indel study*  
**Journal of Computational Biology**, 17(1), 1-20
52. **A. Schönhuth**, R. Salari, S.C. Sahinalp **P**  
*Pair HMM Based Gap Statistics for Re-evaluation of Indels in Alignments with Affine Gap Penalties*  
 Proceedings of the **WABI 2010**, LNCS 6293, 350-361

## 2009

53. I. Costa, **A. Schönhuth**, C. Hafemeister, A. Schliep **P**  
*Constrained Mixture Estimation for Analysis and Robust Classification of Clinical Time Series*  
 Proceedings of the **ISMB/ECCB 2009**  
**Bioinformatics**, 25(12) i6-i14
54. **A. Schönhuth**, H. Jaeger **P**  
*Characterization of Ergodic Hidden Markov Sources*  
**IEEE Transactions on Information Theory**, 55(5), 2107-2118
55. **A. Schönhuth** **P**  
*On Analytic Properties of Entropy Rate*  
**IEEE Transactions on Information Theory**, 55(5), 2119-2127
56. F. Hormozdiari, M. Hsing, R. Salari, **A. Schönhuth**, S. Chan, S.C. Sahinalp, A. Cherkasov **P**  
*The Effect of Insertions and Deletions (Indels) on Wirings in Protein Interaction Networks: a Large Scale Study*  
 Proceedings of the **RECOMB-SysBio 2008**  
**Journal of Computational Biology**, 16(2), 159-167
57. P. Dao, **A. Schönhuth**, F. Hormozdiari, I. Hajirasouliha, S.C. Sahinalp, M. Ester **P**  
*Quantifying Systemic Evolutionary Changes by Color Coding Confidence-scored PPI Networks*  
 Proceedings of the **WABI 2009**, LNCS 5724, 37-48
58. R. Colak\*, F. Hormozdiari\*, F. Moser\*, **A. Schönhuth\***, J. Holman, M. Ester, S.C. Sahinalp **P**  
*Dense Graphlet Statistics of Protein Interaction Networks and Random Networks*  
 Proceedings of the **PSB 2009**, 14, 190-202
59. **A. Schönhuth**, I. Costa, A. Schliep **B**  
*Semi-supervised Clustering of Yeast Gene Expression Data*  
 A. Okada et al. (eds.), **Cooperation in Classification and Data Analysis**  
 Studies in Classification, Data Analysis and Knowledge Organization, 151-159, Springer-Verlag

## 2008

60. **A. Schönhuth** **P**  
*A Simple and Efficient Solution of the Identifiability Problem for Hidden Markov Sources and Quantum Random Walks*  
 Proceedings of the **ISITA 2008**

61. R. Salari\*, **A. Schönhuth\***, F. Hormozdiari, A. Cherkasov, S.C. Sahinalp **P**  
*The Relation Between Indel Length and Functional Divergence: a Formal Study*  
 Proceedings of the **WABI 2008**, LNCS 5251, 330-341
62. **A. Schönhuth** **I**  
*Equations for Hidden Markov Models*  
**Workshop on Algebraic Statistics**, MSRI, Berkeley  
 See <http://arxiv.org/abs/0901.3749>
63. **A. Schönhuth** **X**  
*The Ergodic Decomposition of Asymptotically Mean Stationary Sources*  
 See <http://arxiv.org/abs/0804.2487>

**before 2008**

64. U. Faigle, **A. Schönhuth (2007)** **P**  
*Asymptotic Mean Stationarity of Sources with Finite Evolution Dimension*  
**IEEE Transactions on Information Theory**, 53(7), 2342-2348
65. U. Faigle, **A. Schönhuth (2006)** **P**  
*Quantum Predictor Models*  
**Electronic Notes in Discrete Mathematics** 25, 149-155
66. **A. Schönhuth (2006)** **T**  
*Diskretwertige stochastische Vektorräume (German)*  
**Doktorarbeit (PhD Thesis)**, University Cologne
67. A. Schliep, I. Costa, C. Steinhoff, **A. Schönhuth (2005)** **P**  
*Analyzing Gene Expression Time Courses*  
**IEEE/ACM Transactions on Computational Biology and Bioinformatics**, 2(3), 179-193
68. M. Leber, L. Kaderali, **A. Schönhuth**, R. Schrader **(2005)** **P**  
*A fractional programming approach to efficient DNA melting temperature calculation*  
**Bioinformatics**, 21, 2375-2382
69. I. Costa, **A. Schönhuth**, A. Schliep **(2005)** **P**  
*The Graphical Query Language: a tool for analysis of gene expression time-courses*  
**Bioinformatics**, 21, 2544-2545
70. U. Faigle, **A. Schönhuth (2005)** **I**  
*Note on Negative Probabilities and Observable Processes*  
**Dagstuhl Seminar Proceedings** 05031, 108, 1-14  
 S. Albers, R. Moehring, C. Pflug, R. Schultz (eds.)
71. A. Schliep, C. Steinhoff, **A. Schönhuth (2004)** **P**  
*Robust Inference of Groups in Gene Expression Time-courses using Mixtures of HMMs*  
 Proceedings of the **ISMB/ECCB 2004**  
**Bioinformatics**, 20, Supp.1, 283-289
72. A. Schliep, B. Georgi, W. Rungtarityotin, I. Costa, **A. Schönhuth (2004)** **B**  
*The General Hidden Markov Model Library: Analyzing Systems with Unobservable States*  
 In: K. Kremer, V. Macho (eds.)  
**Forschung und Wissenschaftliches Rechnen 2004** GWDG-Bericht 68, 121-136
73. A. Schliep, **A. Schönhuth**, C. Steinhoff **(2003)** **P**  
*Using Hidden Markov Models to Analyze Gene Expression Time Course Data*  
 Proceedings of the **ISMB 2003**  
**Bioinformatics**, 19, Supp. 1, 255-263

74. P. Pipenbacher, A. Schliep, S. Schneckener, **A. Schönhuth**, D. Schomburg, R. Schrader (2002) **P**  
*ProClust: Improved Clustering of Protein Sequences with an Extended Graph-based Approach*  
 Proceedings of the **ECCB 2002**  
**Bioinformatics**, 18, Supp. 2, 182-192
75. **A. Schönhuth** (1999) **T**  
*Milnor-K-Homologie and Homotopieinvarianz (German)*  
**Diplomarbeit (MSc Thesis)**, University Cologne

### In Preparation

76. D. Laehnemann\*, **A.Schönhuth\***, J. Köster, M. Gombert, A. Borkhardt, U. Fischer, A.C. McHardy  
*ProSolo: Calling Genetic Variants in Single Cells Using a Latent Variable Model*  
 Poster, presented at “Statistical Challenges in Single Cell Genomics”, Ascona 2017  
 Manuscript in preparation

## CONFERENCE GLOSSARY

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BIOSB	Dutch Conference on Bioinformatics and Systems Biology
BTW	Conference on Database Systems for Business, Web and Technology
CTW	Cologne-Twente-Workshop
ECCB	European Conference on Computational Biology
GCB	German Conference on Bioinformatics
ISITA	International Symposium on Information Theory and Applications
ISMB	Intelligent Systems on Molecular Biology
ISMB-HITSEQ	ISMB Special Interest Group on High-Throughput-Sequencing
NBIC	Netherlands Bioinformatics Conference
PSB	Pacific Symposium on Biocomputing
RECOMB	Research in Computational Molecular Biology
RECOMB-SEQ	RECOMB Satellite on Massively Parallel Sequencing
RECOMB-SysBio	RECOMB Satellite on Systems Biology
RECOMB-CG	RECOMB Satellite on Comparative Genomics
SMPGD	Statistical Methods for Post-Genomic Data
WABI	Workshop on Algorithms in Bioinformatics

## MEMBERSHIPS, SERVICES

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- CONSORTIA
- “Structural Variant Consortium”, Hartwig Medical Foundation, since 2018
  - “Project MinE”, since 2016
  - “Computational Pangenomics” (founding member), since 2015
  - “Genome of the Netherlands” (GoNL), since 2012

## CONFERENCES

- **Steering Committee Member**  
RECOMB Satellite on Massively Parallel Sequencing, since 2018
- **Publicity Chair**  
Research on Computational Biology (RECOMB), Hongkong, May 2017
- **Program Faculty**  
Computational Genomics Summer Institute, UCLA, 2016, 2017, 2018
- **Program Committee Chair**  
RECOMB Satellite on Massively Parallel Sequencing, 2016
- **Main Organizer**  
Workshop, Lorentz Center, Leiden, Juni 2018
- **Organizer**  
European Virus Bioinformatics Center Annual Meeting,  
Utrecht University, April 2018
- **Main Organizer**  
Data Structures in Bioinformatics, Amsterdam, February 2017
- **Main Organizer**  
Workshop, Lorentz Center, Leiden, Juni 2015
- **Session Organizer**  
International Symposium on Mathematical Programming 2012
- **Session Chair**  
RECOMB 2018
- **Session Chair**  
International Symposium on Information Theory and Applications 2008
- **Session Chair**  
RECOMB Satellite on Next-Generation-Sequencing 2012
- **Session Chair**  
International Symposium on Mathematical Programming 2012
- **Session Chair**  
Bertinoro Computational Biology 2013, 2015, 2017

## MEMBERSHIPS

- IEEE, Information Theory Society, since 2007
- International Society for Computational Biology, since 2003

## PROGRAM COMMITTEES

- Research on Computational Biology (RECOMB), 2016, 2017, 2018
- Intelligent Systems on Molecular Biology (ISMB), 2013, 2014, 2016, 2017, 2018
- European Conference on Computational Biology (ECCB), 2016, 2018
- High-Throughput Sequencing Algorithms and Applications (HitSeq), 2016
- German Conference on Bioinformatics (GCB), 2015, 2016, 2017, 2018
- RECOMB Satellite on Massively Parallel Sequencing (RECOMB-Seq), 2015, 2016
- Asian-Pacific Bioinformatics Conference (APBC), 2013
- Benelux Bioinformatics Conference (BCB), 2012, 2015
- ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB), 2012, 2017

## GRANT REFEREEING

Dutch Science Organization (NWO), Dutch Technology Foundation (STW), Wellcome Trust/ DBT India Alliance, Genome Canada, United States - Israel Binational Science Foundation (BSF)

REFEREING JOUR- NALS (SELECTION)	Nature Communications, Genome Biology, SIAM Journal on Computing, Nucleic Acids Research, PLoS Computational Biology, Bioinformatics, IEEE Transactions on Knowledge and Data Engineering, IEEE/ACM Transactions on Bioinformatics and Computational Biology, BMC Bioinformatics, PLoS One, Bernoulli, IEEE Transactions on Information Theory, IEEE Signal Processing Letters, Zentralblatt MATH
REFEREING CON- FERENCES (SELECTION)	Intelligent Systems on Molecular Biology (ISMB), Combinatorial Pattern Matching (CPM), Research in Computational Molecular Biology (RECOMB), European Conference on Computational Biology (ECCB), Workshop on Algorithms in Bioinformatics (WABI), Asian-Pacific Bioinformatics Conference (APBC), ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB)
EDITORIAL BOARDS	<ul style="list-style-type: none"> <li>◦ 'Handbook of Research on Computational and Systems Biology: Interdisciplinary Applications', IGI-Global, 2010</li> <li>◦ New Journal of Science, Bioinformatics Section Hindawi Publishing Corporation, Cairo, New York</li> </ul>

## INVITED / REFEREED LECTURES

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**K** = keynote, **I** = invited, **R** = refereed

2017	<ul style="list-style-type: none"> <li>◦ <i>Institut für Informatik</i>, Universität Augsburg, 27/11 <b>I</b></li> <li>◦ <i>INRIA Evaluation</i>, Paris, 12/10 <b>I</b></li> <li>◦ <i>Bertinoro Computational Biology Conference</i>, Bertinoro, 04/10 <b>I</b></li> <li>◦ <i>German Conference of Bioinformatics</i>, Tübingen, 19/09 <b>R</b></li> <li>◦ <i>Laboratoire de Biometrie et Biologie Evolutive</i>, INRIA Lyon, 22/08 <b>I</b></li> <li>◦ <i>Computational Genomics Summer Institute</i>, IPAM, UCLA, 11/07 <b>I</b></li> <li>◦ <i>Department of Computer Science</i>, University Helsinki, 09/05 <b>I</b></li> <li>◦ <i>Institut für Informatik</i>, University Bonn, 02/05 <b>I</b></li> </ul>
2016	<ul style="list-style-type: none"> <li>◦ <i>Amsterdam Data Science Highlight Presentation</i>, Amsterdam, 09/12 <b>I</b></li> <li>◦ <i>Workshop on Graph Assembly Algorithms for Omics Data</i>, Milano, 18/11 <b>I</b></li> <li>◦ <i>European Conference on Computational Biology (ECCB)</i>, The Hague, 07/09 <b>R</b></li> <li>◦ <i>Recent Advances on Computational Metagenomics (ECCB Workshop)</i>, The Hague, 04/09 <b>K</b></li> <li>◦ <i>Computational Genomics Summer Institute</i>, IPAM, UCLA, 20/07 <b>I</b> Topic: <i>Big Uncertain Genome Data</i></li> <li>◦ <i>Computational Genomics Summer Institute</i>, IPAM, UCLA, 19/07 <b>I</b> Topic: <i>Snakemake Tutorial</i></li> </ul>

2016	○ <i>Medizinische Fakultät, Universität Bonn, 15/06</i>	I
(CONT.)	○ <i>International Symposium on Bioinformatics Research and Applications (ISBRA) Minsk, 08/06</i>	K
	○ <i>Institut für Informatik, Universität zu Köln, 29/04</i>	I
	○ <i>Medizinische Fakultät, Universität zu Köln, 01/03</i>	I
	○ <i>Fachbereich Mathematik und Informatik, Phillips-Universität Marburg, 04/02</i>	I
	○ <i>INRIA, Cristal, Lille, 06/01</i>	I
2015	○ <i>German Conference of Bioinformatics, Dortmund, 29/09</i>	R
	○ <i>Heinrich-Heine-Universität, Düsseldorf, 17/08</i>	I
	○ <i>Bertinoro Computational Biology Conference, Bertinoro, 16/06</i>	I
	○ <i>Genscale INRIA, Rennes, 30/04</i>	I
	○ <i>Helmholtz Center for Infektion Research, Braunschweig, 26/03</i>	I
	○ <i>CeBiTec-Symposium, Universität Bielefeld, 23/03</i>	I
	○ <i>Institut für Biophysik (Mosig), Ruhr-Universität Bochum, 23/02</i>	I
	○ <i>Utrecht Bioinformatics Center, Utrecht University, 18/02</i>	I
	○ <i>School of Computing Science, Simon Fraser University, 26/01</i>	I
2014	○ <i>Workshop on Data Structures in Bioinformatics, LIRMM, Montpellier, 9/12</i>	I
	○ <i>Institut für Informatik, TechFak Bielefeld, 12/11</i>	I
	○ <i>Amsterdam Institute for Molecules, Medicines and Systems, VU Amsterdam, 29/09</i>	I
	○ <i>Cancer Research UK, Cambridge University, 22/09</i>	I
	○ <i>Bioinformatics Lab, TU Delft, 16/09</i>	I
	○ <i>Biosystems Science and Engineering, ETH Zürich, Basel, 20/08</i>	I
	○ <i>Biological Sequence Analysis and Probabilistic Models, Oxford, 17/07</i>	R
	○ <i>Institut für Mathematik und Informatik, Uni Marburg, 06/06</i>	I
	○ <i>Center for Applied Computer Science, Uni Köln, 03/06</i>	I
	○ <i>Netherlands Bioinformatics Conference, Lunteren, 08/04</i>	R
2013	○ <i>Leiden University Medical Center, Leiden, 18/11</i>	I
	○ <i>RWTH Aachen, 12/11</i>	I
	○ <i>EMBL Cancer Genomics, Pre-Conference on Somatic Variant Calling, Heidelberg, 11/3</i>	I
	○ <i>Bertinoro Computational Biology Conference, Bertinoro, 9/12</i>	I
	○ <i>The Genome Institute (L. Ding), Washington University, St. Louis, 6/18</i>	I
	○ <i>IPAM Reunion Retreat, UCLA, Lake Arrowhead, 6/12</i>	I
	○ <i>Department of Computer Science (B. Raphael), Brown University, Providence, 6/7</i>	I
	○ <i>Cologne-Twente-Workshop, Enschede, 5/20</i>	R
	○ <i>Statistical Genomics and Data Integration for Personalized Medicine Workshop, Ascona, 6/17</i>	I

2012	<ul style="list-style-type: none"> <li>◦ <i>Department of Computer Science (A. McHardy)</i> Heinrich-Heine-Universität Düsseldorf, 11/23</li> <li>◦ <i>Computational Biology and Applied Algorithms (T. Lengauer)</i> Max Planck Institute for Computer Science, Saarbrücken, 11/22</li> <li>◦ <i>Stochastics and Nonlinear Dynamics in the Life Sciences</i>, Conference, Amsterdam, 11/15</li> <li>◦ <i>Delft Bioinformatics Lab (D. de Ridder)</i>, TU Delft, 9/25</li> <li>◦ <i>Intelligent Systems on Molecular Biology, High-Throughput-Sequencing SIG (ISMB-HitSeq)</i> Long Beach, 7/14</li> <li>◦ <i>Computational Biology Group (N. Beerenwinkel)</i> Department of Biosystems Science and Engineering, ETH Zürich, 6/25</li> <li>◦ <i>Science for Life Laboratory (J. Lagergren)</i>, Karolinska Institutet and School of Computer Science and Communication, KTH Stockholm, 6/4</li> <li>◦ <i>Hot Topics Meeting</i>, Netherlands Bioinformatics Centre, Utrecht, 4/16</li> <li>◦ <i>CWI Scientific Meeting</i>, Amsterdam, 3/30</li> </ul>	<p>I</p> <p>I</p> <p>I</p> <p>I</p> <p>R</p> <p>I</p> <p>I</p> <p>I</p> <p>I</p>
2011	<ul style="list-style-type: none"> <li>◦ <i>Off-Week Seminar on High-Throughput-Genomics</i> Institute of Pure and Applied Mathematics, UCLA, 11/10</li> <li>◦ <i>Department of Computer Science (A. Schliep)</i> Rutgers, The State University of New Jersey, New Brunswick, 10/12</li> <li>◦ <i>SIAM Conference on Applied Algebraic Geometry</i>, Raleigh, North Carolina, 10/9</li> <li>◦ <i>International Conference on Operations Research</i>, Zürich, 9/1</li> <li>◦ <i>Cologne-Twente Workshop</i>, Frascati, 6/16</li> <li>◦ <i>Institute for Programming Research and Algorithmics, Lentedagen</i>, Vlijmen, 4/14</li> <li>◦ <i>Korteweg-de Vries Instituut</i>, Universiteit van Amsterdam, 3/23</li> <li>◦ <i>Statistics for the Life Sciences Seminar</i>, Vrije Universiteit Amsterdam, 3/21</li> <li>◦ <i>Analytic Genomics Laboratory</i>, Universite Marie et Pierre Curie, Paris, 2/18</li> <li>◦ <i>Department of Mathematics</i>, TU Eindhoven, 2/11</li> </ul>	<p>I</p> <p>I</p> <p>I</p> <p>R</p> <p>R</p> <p>I</p> <p>I</p> <p>I</p> <p>I</p>
2010	<ul style="list-style-type: none"> <li>◦ <i>European Conference on Computational Biology (ECCB)</i>, Ghent, 9/27</li> <li>◦ <i>Workshop on Algorithms in Bioinformatics (WABI)</i>, Liverpool, 9/8</li> <li>◦ <i>Life Sciences Group</i>, Centrum Wiskunde &amp; Informatica, Amsterdam, 5/3</li> <li>◦ <i>Lehrstuhl für Bioinformatik</i>, Universität Jena, 4/29</li> <li>◦ <i>Toyota Technological Institute</i>, Chicago, 4/2</li> <li>◦ <i>Annual Meeting of the American Mathematics Society (AMS)</i>, Lexington, Kentucky, 3/28</li> <li>◦ <i>Lane Center for Computational Biology</i> School of Computer Science, Carnegie Mellon University, Pittsburgh, 2/25</li> <li>◦ <i>Division of Biostatistics</i>, University of California at San Francisco, 1/13</li> </ul>	<p>R</p> <p>R</p> <p>I</p> <p>I</p> <p>I</p> <p>I</p> <p>I</p>
2009	<ul style="list-style-type: none"> <li>◦ <i>Institute for Human Genetics</i>, UC San Francisco, 11/10</li> <li>◦ <i>Symposium on Biomedical Computation</i>, Stanford University, 11/7</li> <li>◦ <i>SIAM Conference on Mathematics for Industry</i>, San Francisco, 10/10</li> <li>◦ <i>Genome Informatics Group</i>, Universität Bielefeld, 3/30</li> <li>◦ <i>Seminar on Discrete Mathematics</i>, University of British Columbia, 2/24</li> </ul>	<p>I</p> <p>R</p> <p>I</p> <p>I</p> <p>I</p>

2008	◦ <i>Workshop on Algebraic Statistics</i> , MSRI, UC Berkeley, 12/16	I
	◦ <i>International Symposium on Information Theory and Applications</i> , Auckland, 12/8	R
	◦ <i>RECOMB Satellite on Systems Biology</i> , MIT, Cambridge, Massachusetts, 10/31	R
	◦ <i>Workshop on Algorithms in Bioinformatics (WABI)</i> , Karlsruhe, 9/15	R
BEFORE	◦ <i>Cologne-Twente-Workshop</i> , Lambrecht, 6/9/2006	R
2008	◦ <i>Software Presentation at ISMB/ECCB</i> , Glasgow, 8/4/2004	R
	◦ <i>“Hidden Markov Models: A Tutorial”</i> , University Cologne, 1/15/2003	I

## TEACHING

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<b>Lecture (scheduled):</b> Deep Learning Faculty of Sciences, University Utrecht	Oct-Dec 2018
<b>Lecture:</b> Analytics and Algorithms for Omics Data (BMB508218) Faculty of Sciences, University Utrecht	June 2018
<b>Project Course:</b> Python, Object-Oriented Programming (BETA-B1PYT) Faculty of Sciences, University Utrecht	March/April 2018
<b>Problem Based Learning Seminar:</b> Bioinformatics, Gene Expression Analysis Section University of British Columbia / Simon Fraser University	Spring Semester 2008
<b>Lecture:</b> Computational Biology (CMPT 441/889) School of Computing Science Simon Fraser University	Fall Semester 2007
<b>Seminar</b> (with U. Faigle): Machine Learning Center for Applied Computer Science University Cologne	Winter Semester 2006/07
<b>Lecture:</b> Object-oriented Programming (in English) Graduate Studies in Computational Biology Cologne University Bioinformatics Center	2002 - 2006
<b>Lecture:</b> Foundations of Databases (in English) Graduate Studies in Computational Biology Cologne University Bioinformatics Center	2002 - 2006
<b>Lecture:</b> Software Engineering (in English) Graduate Studies in Computational Biology Cologne University Bioinformatics Center	2002
<b>Seminar</b> (with R. Schrader): Phylogenetic Trees, Algorithms and Optimization Center for Applied Computer Science, University Cologne	Summer Semester 2000
<b>Tutoring</b> as Teaching Assistant Department of Mathematics, University Cologne	1995 - 1999



## SUPERVISION / THESIS COMMITTEES

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(M) Main Supervisor

(J) Joint Supervision

(C) Thesis Committee Membership

Mircea Cretu-Stancu <b>PhD Student</b> , Utrecht University	05/2018 (C)
Dimitrios Bountouridis <b>PhD Student</b> , Utrecht University	04/2018 (C)
Samhita Pamidimarri Naga <b>Master Student</b> , Universiteit van Amsterdam / Vrije Universiteit	since 02/2018 (M)
Mithat Kurban <b>PhD Student</b> , Hacettepe University Ankara	06/2017 - 08/2017 (J)
Marleen Balvert <b>Postdoctoral Fellow</b> , PhD University Tilburg	since 04/2017 (M)
Bastiaan van der Roest <b>Master Student</b> , Universiteit van Amsterdam	04/2017 - 10/2017 (M)
Christopher Esterhuyze <b>Bachelor Student</b> , Vrije Universiteit Amsterdam	04/2017 - 07/2017 (M)
Bojian Yin <b>Master Student</b> , Vrije Universiteit Amsterdam	since 03/2017 (M)
Johannes Köster <b>Postdoctoral Fellow</b> , PhD Uni Duisburg-Essen	05/2016 - 08/2017 (M)
Kristoffer Sahlin <b>PhD Student</b> , Karolinska Institutet Stockholm	10/2015 (C)
Johannes Dröge <b>PhD Student</b> , Helmholtz Institute for Infection Research (with Alice McHardy)	04/2016 - 12/2016 (J)
David Laehnemann <b>PhD Student</b> , Helmholtz Institute for Infection Research (with Alice McHardy)	since 09/2015 (J)
Ivan Gregor <b>PhD Student</b> , Heinrich-Heine-Universität Düsseldorf (with Alice McHardy)	since 04/2015 (J)
Yogesh Paudel <b>PhD Student</b> , Wageningen University	01/2015 (C)
Jasmijn Baaijens <b>PhD Student</b> , Master, TU Eindhoven	since 09/2014 (M)

Armin Töpfer <b>PhD Student</b> , ETH Zürich (with Niko Beerenwinkel)	04/2013 - 08/2014 (J,C)
Louis Dijkstra <b>PhD Student</b> , Master, Universiteit van Amsterdam	09/2013 - 08/2015 (M)
Murray Patterson, PhD <b>Postdoctoral Fellow</b> , ERCIM Fellow, PhD University of British Columbia	02/2013 - 02/2014 (M)
Dr. Tobias Marschall <b>Postdoctoral Fellow</b> , PhD TU Dortmund	05/2011 - 03/2014 (M)
Manuel Allhoff <b>Master Student</b> , Centrum Wiskunde & Informatica (with Dr. Tobias Marschall, Prof. Dr. Sven Rahmann)	04-10/2012 (J)
Dr. Jan Voss <b>PhD Student</b> , University Cologne, with Prof. Dr. Ulrich Faigle	till 2012 (J,C)
Iman Hajirasouliha, PhD “Algorithms for structural variation discovery and protein-protein interaction prediction” <b>PhD Student</b> , Simon Fraser University, with Prof. Dr. Cenk Sahinalp	2008 - 2012 (J)
Phuong Dao, PhD “Computational methods for discovering functional modules from protein interaction networks” <b>PhD Student</b> , Simon Fraser University, with Prof. Dr. Martin Ester	2009 - 2012 (J)
James Wagner “Gibbs sampling for gapped motif discovery” <b>Master Student</b> , Simon Fraser University, with Prof. Dr. Martin Ester	2008 (J)
Sandra Sazdovska “Self-Creating Gene Ontologies” <b>Master Student</b> , Graduate Course in Computational Biology	2006 / 2007 (M)
Pilar Soley “Statistical Evaluation of Self-Created Gene Ontologies” <b>Master Student</b> , Graduate Course in Computational Biology	2006 / 2007 (M)
Rileen Sinha “Learning Genetic Networks in Drosophila Melanogaster” <b>Master Student</b> , Graduate Course in Computational Biology	2005 / 2006 (M)
Mateus Patricio “A Bayesian Approach to Automatic Determination of Initial Model Collections” <b>Master Student</b> , Graduate Course in Computational Biology	2005 / 2006 (M)
Marcelo Reis “Integration of Transcriptional Regulation Information in Yeast Gene Expression Analysis” <b>Master Student</b> , Graduate Course in Computational Biology	2004 / 2005 (M)
Dr. Hiwot Chemu “Integration of Transcriptional Regulation Information in Yeast Gene Expression Analysis” <b>Master Student</b> , Graduate Course in Computational Biology	2004 / 2005 (M)

Dr. Olof Persson 2003 / 2004 (M)  
“Statistical Modeling of Gene Expression Experiments: Determining Initial Model Collections”  
**Master Student**, Graduate Course in Computational Biology

Xue Li 2003 / 2004 (M)  
“Hidden Markov Model Based Analysis of Gene Expression Time Course Data: Visualization of Clustering Results”  
**Master Student**, Graduate Course in Computational Biology

Markus Leber 2002 / 2003 (J)  
“Design of a Fractional Programming Algorithm for DNA Melting Temperature Determination” (with Lars Kaderali)  
**Master Student**, Graduate Course in Computational Biology

## MISCELLANEOUS

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FOREIGN                      German (native), English (fluent), Dutch (very good), French (very good), Italian  
LANGUAGES                      (good), Spanish (basic)

Amsterdam, September 2018