Optimal threshold selection for tomogram segmentation by projection distance minimization

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Abstract

Grey value thresholding is a segmentation technique commonly applied to tomographic image reconstructions. Many procedures have been proposed to optimally select the grey value thresholds based on the *tomogram data* only (e.g., using the image histogram). In this paper, a Projection Distance Minimization (PDM) method is presented that uses the tomographic *projection data* to determine optimal thresholds. These thresholds are computed by minimizing the distance between the forward projection of the segmented image and the measured projection data. An important contribution of the current paper is the efficient implementation of the forward projection method, which makes the use of the original projection data as a segmentation criterion feasible. Simulation experiments applied to various phantom images show that our proposed method obtains superior results compared to established histogram-based methods.

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Index Terms

tomography, thresholding, segmentation, forward projection, sinogram.

I. INTRODUCTION

Segmentation is a well known problem in computer vision. It refers to the classification of image pixels into distinct classes, based on similarity with respect to some characteristic. In this paper, we focus on segmentation based on the pixel grey levels. Amongst all segmentation techniques, global image thresholding is the simplest, yet often most effective segmentation method. Many algorithms have been proposed for selecting "optimal" thresholds with respect to various optimality measures [8].

Commonly, segmentation techniques employ the image histogram as a basis for determining thresholds [9], [17]–[19]. Such algorithms can be subdivided into parametric and nonparametric segmentation techniques. First, parametric approaches assume that the histogram samples can be modeled by k distributions, such as Gaussian Mixture Models [20], [25], [26]. If k is known, optimization methods such as Expectation Maximization [6] or genetic algorithms [16] can be used to estimate the parameters of the distributions. The main problem with this approach is that histogram modes are often not well modeled by Gaussian mixtures [5]. In practice, the image histogram often lacks clear modes that would allow a model based selection of threshold values. Second, non-parametric (e.g., entropy based) approaches give up any assumption on the underlying histogram distribution [4], [14], [21], [23]. More recent thresholding techniques are based on a minimum variance criterion [11] or employ the variance and intensity contrast [22] or are based on maximization of measures of similarity [3].

In this work, we focus on global threshold selection for segmentation of tomographically reconstructed images (also called *tomograms*). To the authors' knowledge, segmentation of tomograms is currently based on techniques similar to the ones described in the above paragraph [1], [2], [10], [12], [22], [24] in that tomographic images are segmented using information from the tomograms only, such as the image histogram. Although threshold selection based on the image histogram can be made fully automatic, it often lacks robustness in case clear grey value modes are absent.

In this paper, we present a novel approach for threshold selection for tomogram segmentation, which uses the information in the *projection data* instead of the tomogram data. Ideally, reconstruction algorithms for tomography should be "invertible", so that computed projections of the reconstructed image would equal the measured projection data. For Filtered Backprojection, the most common reconstruction algorithm used in practice, this assumption does not hold, mainly due to various interpolation steps involved in the algorithm. Algebraic methods, which are less commonly used, only satisfy the invertibility assumption for the case of noiseless projection data and an infinite number of iterations. As the reconstructed image does not correspond accurately with the measured projections, using the projection data for the segmentation can potentially result in a segmentation that is more faithful to the original measurements.

By minimizing the distance between the forward projection of the segmented image and the measured projection data, optimal thresholds are computed. We will refer to this method as the Projection Distance Minimization (PDM) method. In the search for optimal thresholds, many computationally expensive forward projections must be performed. An important contribution of the current paper is the efficient implementation of the forward projection method, which makes the use of the original projection data as a segmentation criterion feasible. It is shown that the proposed segmentation procedure is objective as well as repeatable. In our simulation experiments, our new method clearly outperforms established histogram-based methods.

II. GREY LEVEL ESTIMATION

Without loss of generality, we will restrict ourselves to the segmentation of a 2-dimensional image, which is represented on a rectangular grid of width w and height h. Hence, the total number of pixels is given by n = wh. The grey-scale image $x \in \mathbb{R}^n$ that we want to segment is a tomographic reconstruction of some physical object, of which projections were acquired using a tomographic scanner. Our method can be used for any scanning geometry, e.g., parallel beam, fan beam and, in 3D, cone beam. Projections are measured as sets of detector values for various angles, rotating around the object. Let m denote the total number of measured detector values (for all angles) and let $p \in \mathbb{R}^m$ denote the measured data. The physical projection process in tomography can be modeled as a linear operator W that maps

the image x (representing the object) to the vector p of measured data:

$$Wx = p \quad . \tag{1}$$

For parallel projection data, the operator W is a discretized version of the well-known *Radontransform*. We represent W by an $m \times n$ matrix. Note that for each projection angle, every pixel *i* will only project onto a few detector pixels, so the matrix W is very sparse. Exploiting this sparsity forms an essential part of our method. The matrix representation of the projection operator is commonly used in *algebraic reconstruction algorithms*. We refer to Chapter 7 of [13] for details.

From this point on, we assume that an image x has been computed that approximately satisfies Eq. (1). Our approach does not depend on the reconstruction algorithm that was used to compute x, e.g., Filtered Backprojection or ART. The image x now has to be segmented using global thresholding of the grey levels. The main motivation of using thresholding in general, is that pixels representing the same "material" in the scanned object should have approximately the same grey values in the tomogram. We rely strongly on the assumption that the scanned object consists of only a few different materials. Our segmentation approach first assigns a real-valued grey level to each of the segmentation classes. Using these grey levels, the projections of the segmented image are then computed. The computed forward projections are compared to the measured projection data, which provides a measure for the quality of the segmentation (along with the chosen grey levels). This quality measure can also be used for other segmentation techniques than thresholding.

We first consider the problem of determining grey levels for each of the segmentation classes of a segmented image. We can consider a segmentation of an image into ℓ classes as a *partition* of the set of pixels, consisting of ℓ subsets. Let $S = \{S_1, \ldots, S_\ell\}$ be a partition of $\{1, \ldots, n\}$. We label each set by its index t: S_t . Each pixel j is contained in exactly one set $S_t \subset S$, denoted by $s(j) \in \{1, \ldots, \ell\}$. To each set S_t , a grey level $\rho_t \in \mathbb{R}$ is assigned, which induces an assignment of grey levels to the pixels $1 \leq j \leq n$, where pixel j is assigned the grey level $\rho_{s(j)}$. Let $\rho = (\rho_t) \in \mathbb{R}^\ell$ represent the vector of gray levels of the segmented

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image and define

$$\boldsymbol{r}_{\mathcal{S}}(\boldsymbol{\rho}) = \begin{pmatrix} \rho_{s(1)} & \dots & \rho_{s(n)} \end{pmatrix}^T, \tag{2}$$

where the symbol T denotes transposition. The vector $r_{\mathcal{S}}(\rho) \in \mathbb{R}^n$ contains, for each pixel j, the corresponding grey level of that pixel.

Our goal is to determine "optimal" grey values ρ for the given partition S. The quality of a vector ρ is determined by computing the projections of the segmented image, using the grey levels from ρ , and comparing the computed projections to the measured projections p. More formally, we define the problem of finding optimal grey values for a given partition as follows:

Problem 1: Let $\mathbf{W} = (w_{ij}) \in \mathbb{R}^{m \times n}$ be a given projection matrix, let $S = \{S_1, \ldots, S_\ell\}$ be a partition of $\{1, \ldots, n\}$ and let $\mathbf{p} \in \mathbb{R}^m$ be a vector of measured projection data. Find $\mathbf{\rho} \in \mathbb{R}^\ell$ such that $|\mathbf{W}\mathbf{r}_S(\mathbf{\rho}) - \mathbf{p}|_2$ is minimal, where $|\cdot|_2$ denotes the Euclidean norm.

The term $|Wr_{\mathcal{S}}(\rho) - p|_2$ is called the *projection distance*. We will start by deriving the equations for solving Problem 1 for a fixed partition \mathcal{S} . Subsequently, we describe how the optimal set of grey values can be re-computed efficiently, each time the partition \mathcal{S} has been modified by moving a single pixel from one class to another class. This fast update computation allows us to design efficient algorithms that combine the search for a segmentation \mathcal{S} and the corresponding grey values ρ , such that the projection distance is minimal.

Define $\boldsymbol{A} = (a_{it}) \in \mathbb{R}^{m imes \ell}$ by

$$a_{it} = \sum_{j: \ s(j)=t} w_{ij} \quad . \tag{3}$$

The value a_{it} equals the total area of pixels from the set S_t that contribute to detector value i, which is related to the partial projection data of set S_t (cfr. Figure 1). We denote the $\ell \times 1$ row vectors of A by $a_i = A_{.t}$. Clearly, we have

$$[\boldsymbol{W}\boldsymbol{r}_{\mathcal{S}}(\boldsymbol{\rho})]_{i} = \sum_{t=1}^{\ell} a_{it}\rho_{t} \quad .$$
(4)

Define the projection difference $d \in \mathbb{R}^m$ by

$$d = Wr_{\mathcal{S}}(\rho) - p = A\rho - p \quad . \tag{5}$$

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Fig. 1: Projections of the sets S_t , represented by the rows of A.

Furthermore, define the squared projection distance by

$$|\boldsymbol{d}|^{2} = |\boldsymbol{A}\boldsymbol{\rho} - \boldsymbol{p}|^{2} = \sum_{i=1}^{m} (\boldsymbol{a}_{i}^{T}\boldsymbol{\rho} - p_{i})^{2} = \sum_{i=1}^{m} \left(\boldsymbol{\rho}^{T}\left(\boldsymbol{a}_{i}\boldsymbol{a}_{i}^{T}\right)\boldsymbol{\rho} - 2p_{i}\boldsymbol{a}_{i}^{T}\boldsymbol{\rho} + p_{i}^{2}\right) \quad .$$
(6)

Denoting $c_i = -2p_i a_i$, $Q_i = a_i a_i^T$, we have:

$$|\boldsymbol{d}|^{2} = \sum_{i=1}^{m} (\boldsymbol{\rho}^{T} \boldsymbol{Q}_{i} \boldsymbol{\rho} + \boldsymbol{c}_{i}^{T} \boldsymbol{\rho} + p_{i}^{2}) = \boldsymbol{\rho}^{T} \bar{\boldsymbol{Q}} \boldsymbol{\rho} + \bar{\boldsymbol{c}}^{T} \boldsymbol{\rho} + |\boldsymbol{p}|^{2} \quad , \tag{7}$$

where $\bar{c} = \sum_{i=1}^{m} c_i$, $\bar{Q} = \sum_{i=1}^{m} Q_i$. Since neither \bar{c} nor \bar{Q} depends on ρ , the vector ρ that minimizes the projection difference |d| can be computed by setting the derivatives of $|d|^2$ with respect to $\rho_1, \ldots, \rho_\ell$ to 0, obtaining the system

$$2\bar{\boldsymbol{Q}}\boldsymbol{\rho} = -\bar{\boldsymbol{c}} \quad , \tag{8}$$

and solving for ρ .

In some practical thresholding problems, the grey level ρ_t for one or more of the sets S_t is already known in advance. In tomography, for example, we can usually assume that the background, surrounding the object of interest, must be 0.

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We now derive a version of Eq. (8) where one grey level is held constant. Without loss of generality, we assume that the grey level for S_1 is fixed at $\rho_1 = \alpha$.

Put
$$\tilde{\boldsymbol{\rho}} = \begin{pmatrix} \rho_2 & \dots & \rho_\ell \end{pmatrix}^T$$
, $\tilde{\boldsymbol{c}} = \begin{pmatrix} c_2 & \dots & c_\ell \end{pmatrix}^T$, $\tilde{\boldsymbol{v}} = \begin{pmatrix} q_{12} & \dots & q_{1\ell} \end{pmatrix}$ and
 $\tilde{\boldsymbol{Q}} = \begin{pmatrix} q_{22} & \cdots & q_{2\ell} \\ \vdots & \ddots & \vdots \\ q_{\ell 2} & \cdots & q_{\ell\ell} \end{pmatrix}$.
(9)

Setting $\rho_1 = \alpha$ in Eq. (7) yields

$$|\boldsymbol{d}|^{2} = \tilde{\boldsymbol{\rho}}^{T} \tilde{\boldsymbol{Q}} \tilde{\boldsymbol{\rho}} + (\tilde{\boldsymbol{c}}^{T} + 2\alpha \tilde{\boldsymbol{v}}^{T}) \tilde{\boldsymbol{\rho}} + q_{11}\alpha^{2} + c_{1}\alpha + |\boldsymbol{p}|^{2} \quad , \tag{10}$$

so that the equivalent of Eq. (8) now becomes

$$2\tilde{\boldsymbol{Q}}\tilde{\boldsymbol{\rho}} = -\tilde{\boldsymbol{c}} - 2\alpha\tilde{\boldsymbol{v}} \quad . \tag{11}$$

If more than one of the densities has a constant value, Eq. (8) can be adapted similarly.

So far, we have assumed that the partition S was fixed. Suppose that we have computed \bar{c} and \bar{Q} for the partition S. We now change S into a new partition S', by changing s(j) for a single pixel j.

The only rows of A that are affected by this transition are the rows i for which $w_{ij} \neq 0$. This means that the new vector \bar{c}' and matrix \bar{Q}' can be computed by the following updates:

$$\bar{\boldsymbol{c}}' = \bar{\boldsymbol{c}} + \sum_{i:w_{ij}\neq 0} (\boldsymbol{c}'_i - \boldsymbol{c}_i) \tag{12}$$

and

$$\bar{\boldsymbol{Q}}' = \bar{\boldsymbol{Q}} + \sum_{i:w_{ij}\neq 0} (\boldsymbol{Q}'_i - \boldsymbol{Q}_i) \quad .$$
⁽¹³⁾

The fact that \bar{c}' and \bar{Q}' can be computed by applying updates for only a few of the terms c_i and Q_i respectively, means that the optimal grey values for the entire image can be recomputed efficiently. This property allows us to develop algorithms for simultaneous segmentation and grey level estimation. Any segmentation algorithm that moves pixels from one class into another class, one at a time, can efficiently keep track of the optimal grey levels. Once the optimal grey levels are known, the projection distance can be computed from Eq. (7). In the next section, we first demonstrate this approach for a simple thresholding algorithm, finding both the optimal thresholds and grey values in a single pass. Subsequently, a PDM algorithm is proposed that can be used if multiple threshold levels are required for segmentation.

III. THRESHOLDING WITH SIMULTANEOUS GREY LEVEL ESTIMATION

The concepts in the previous section apply to any partition S of the pixels. We will now restrict ourselves to a specific type of partitions, that are induced by a thresholding scheme. Our starting point is a grey level image $x \in \mathbb{R}^n$, that has been computed by any continuous tomographic reconstruction algorithm, e.g., Filtered Back Projection. The image x now needs to be segmented by means of thresholding, using a fixed number of ℓ classes for the pixels.

Every pixel *i* is assigned a class according to a thresholding scheme using thresholds $\tau_1 < \tau_2 < \ldots < \tau_{\ell-1}$. Put $\boldsymbol{\tau} = (\tau_1 \ldots \tau_{\ell-1})^T$. Define the *threshold function* by

$$s(i, \boldsymbol{\tau}) = \begin{cases} 1 & (x_i < \tau_1) \\ 2 & (\tau_1 \le x_i < \tau_2) \\ \dots & \\ \ell & (\tau_{\ell-1} \le x_i) \end{cases}$$
(14)

The threshold function induces a partition S_{τ} of the set $\{1, \ldots, n\}$. Define

$$\boldsymbol{r}(\boldsymbol{\tau},\boldsymbol{\rho}) = \begin{pmatrix} \rho_{s(1,\boldsymbol{\tau})} & \dots & \rho_{s(n,\boldsymbol{\tau})} \end{pmatrix}^T$$
 (15)

Similar to Section II, we define the quality of a set of thresholds τ and grey values ρ as the total squared projection distance for the corresponding segmentation. We now consider the problem of simultaneously finding thresholds and grey values, such that the total squared projection difference is minimal:

Problem 2: Let $W \in \mathbb{R}^{m \times n}$ be a given projection matrix, let $x \in \mathbb{R}^n$ be a grey scale image and let $p \in \mathbb{R}^m$ be a vector of measured projection data. Find $\tau \in \mathbb{R}^{\ell-1}$ with $\tau_1 < \ldots < \tau_{\ell-1}$ and $\rho \in \mathbb{R}^{\ell}$, such that $|Wr(\tau, \rho) - p|_2$ is minimal.

A. Two grey levels

The simplest case of Problem 2 occurs when the image x is segmented into two classes, using a single threshold τ . In that case, an exhaustive search over all possible thresholds can

be performed efficiently: first, a list of all pixels is computed, sorted in ascending order of grey level in the continuous reconstruction x. The initial segmentation is formed by setting the threshold τ at a very high value, so all pixels will be in the segmentation class S_1 . The threshold τ is now gradually decreased, each time moving pixels from S_1 to S_2 . By using the update operation from Section II, it is possible to keep track of the optimal grey values and the projection difference by applying only small update steps. Figure 2 shows the steps of the segmentation algorithm. For each pixel j, the time complexity of the update computation is $O(u(j)\ell^2)$, where $u(j) = \#\{i : w_{ij} \neq 0\}$. Each pixel is moved from S_1 to S_2 only once. Therefore, the total time complexity of the algorithm is $O(U\ell^2)$, where U denotes the total number of nonzero elements in the projection matrix W. Note that for fixed ℓ , this means that the time complexity of finding the optimal threshold is O(U), which is the same as the complexity of computing a single forward projection of an image x for each projection angle.

B. More than two grey levels

If there are more than two segmentation classes, computing the total squared projection error for each possible set of candidate thresholds will take a very long computation time, due to the vast number of candidate thresholds. However, using the update operation from Section II, it is possible to compute a *local minimum* of the projection error in reasonable time.

A simple algorithm for this case is the following: first, determine initial thresholds τ_0 , possibly using another automated procedure, such as fitting Gaussian functions to the histogram. Next, compute A, \bar{Q} and \bar{c} . In an iteratively loop, compute for each thresholds the effect of a small increase and a small decrease of that threshold on the total projection distance. Among all these possible steps, select the one that results in the largest decrease of the total projection error. The algorithm terminates if no step can be found that decreases the total error.

Although this approach works well in some cases, it often gets stuck in a local minimum, far away from the global minimum. This is because the projection distance landscape, although smooth at a coarse level, is irregular at a fine scale. Hence, if a threshold is increased or decreased only by a small amount in each step, it may be impossible to escape from a local Make a list L containing all elements $j \in \{1, ..., n\}$, sorted in ascending order of x_j ; $\tau := x_{L(n)} + 1; \quad S_1 := \{1, \dots, n\}; \quad S_2 := \emptyset;$ For i = 1, ..., m: $a_{i1} := \sum_{j=1}^{m} w_{ij}; a_{i2} := 0;$ compute c_i and Q_i ; Compute \bar{c} and \bar{Q} ; $S_1 := \emptyset; \quad S_2 = \{1, \dots, n\}; \quad k := n + 1;$ $d_{\text{opt}} := \text{FLOAT}_MAX$; (keeps track of the optimal projection distance found by the algorithm) while k > 1 do begin $k := k - 1; \quad \tau := x_{L(k)};$ while $(k \ge 1)$ and $(x_{L(k)} = \tau)$ do begin $k := k - 1; \quad j := L(k); \quad S_1 := S_1 - \{j\}; \quad S_2 := S_2 \cup \{j\};$ for each *i* such that $w_{ij} \neq 0$: update c_i , Q_i , \bar{c} and \bar{Q} ; end Compute the minimizer ρ of $|d|^2 = |\mathbf{p}|^2 + \bar{\mathbf{c}}^T \rho + \rho^T \bar{\mathbf{Q}} \rho$; if $(d < d_{opt})$ then $d_{\text{opt}} := d; \quad \boldsymbol{\rho}_{\text{opt}} := \boldsymbol{\rho}; \quad \tau_{\text{opt}} := \tau;$ end

Fig. 2: basic steps of the algorithm for solving Problem 2 in the case $\ell = 2$.

minimum in a single step, whereas this problem does not occur if larger step sizes are used to update the thresholds.

Figure 4(a) shows a grey-scale tomogram that must be segmented using three segmentation classes. In Figure 4(b), the projection distance is plotted as a function of the two thresholds, τ_1 and τ_2 . The example illustrates that the projection distance is typically a rather smooth

function of the thresholds that has a clear global minimum. However, when we zoom in on the surface of the graph (shown in Figure 4(c)), we see that the projection distance graph can have many local minima, which are very close to the surface of the global graph. Figure 4(d) shows a plot of the phantom error as a function of both thresholds, i.e., the number of misclassified pixels with respect to the original phantom image. In this example, the global minimum of the phantom error and the projection distance nearly coincide.

A straightforward way to deal with this problem is to introduce a stochastic element in the minimization procedure, which allows the algorithm to change a threshold while increasing the projection distance. A disadvantage of incorporating a stochastic element is the increased computation time.

As an alternative, we propose a multi-scale algorithm. Instead of changing one of the thresholds by the minimum amount necessary to move one or more pixels to another set, we change a threshold by a fixed amount (the *stepsize*) in each update step. Each time no further improvement can be made using a single step, the step size is reduced. The algorithm terminates if the stepsize has reached a certain minimum.

Note that the computation time for each step depends on the number of pixels that are moved from one class to another class. Therefore, a large step of stepsize 10 takes the same amount of computation time as 10 small steps of stepsize 1.

Figure 3 shows the basic steps of our proposed algorithm for cases with more than two segmentation classes. The algorithm can also be used if there are only two classes, but there is no guarantee that a global minimum of the projection distance will be found, which is guaranteed for the algorithm from Section III-A.

Although our proposed algorithm is still vulnerable to local minima of the projection distance, it performs well in our simulation experiments, as described in the next section.

IV. RESULTS AND DISCUSSION

To validate our proposed threshold selection method, simulation experiments were set up. For this purpose, four phantom images were constructed: a synthetic 512×512 binary *vessel* image representing a vessel tree, a 564×564 binary *femur* image, a 554×554 grey valued *mouse leg* image, and a 512×512 grey valued *foam* image (see Figure 5a-d). The femur,

 $\boldsymbol{\tau} := \boldsymbol{\tau}_{\mathbf{0}}; \text{ For } i = 1, \dots, m: S_i := \{1 \le j \le n : \tau_{i-1} < x_j \le \tau_i\};$

For $i = 1, \ldots, m$: compute a_i, c_i and Q_i ;

Compute \bar{c} and \bar{Q} ;

stepsize := initial stepsize;

while stepsize > min_stepsize do

begin

begin

For all thresholds $i = 1, ..., \ell - 1$, compute the minimal projection distance that can be obtained if τ_i is either increased or decreased by stepsize, considering only cases where $\tau_1 < ... < \tau_{\ell-1}$;

if (an improved projection distance was found w.r.t. the current thresholds τ) then begin

update the threshold τ_i for which the minimal projection distance was obtained by adding (or subtracting) stepsize;

Update the variables a_i , c_i and Q_i accordingly, for all affected i = 1, ..., n;

end

else

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stepsize := stepsize \times F;
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end

end

Fig. 3: Basic steps of the algorithm for solving Problem 2 in the case $\ell \ge 2$. The constant F, where 0 < F < 1, refers to the factor by which the stepsize is reduced if no further improvement is found for the current stepsize.

mouse leg and foam images are based on tomograms computed from micro-CT data. These data sets were acquired with a SkyScan 1072 cone-beam micro-CT scanner. The pixel size was 4.52 micron, 6.85 micron, and 35.36 micron for the femur, mouse leg and foam images,

respectively. The object to source distance was 41.6 mm, 50.2 mm, and 121.1 mm, and the camera to source distance 216.1 mm, 202.3 mm, 161.2 mm for the femur, mouse leg, and foam image, respectively. The camera pixel size was 11.73 micron. We remark that we used a parallel beam geometry for the simulation experiments reported in this paper, but that the approach can be extended in a straightforward manner to the cone-beam geometry.

From the phantom images, CT projections were simulated as follows. First, the Radon transform of the images was computed, resulting in a sinogram for which each data point represents the line integral of attenuation coefficients. The width of a detector cell is the same as the pixel size of the phantoms. Then, (noiseless) CT projection data were generated where a mono-energetic X-ray beam was assumed¹. The projections were then polluted with Poisson distributed noise where the number of counts per detector element I_0 (flat field) was varied from $5 \times 10^3 - 6 \times 10^4$. Next, the noisy sinogram of the attenuation coefficients was obtained by dividing the CT projection data by the maximum intensity and computing the negative logarithm. In this way, simulated projection images were obtained for varying signal-to-noise ratios. Finally, the simulated, noisy CT images were reconstructed using both the Filtered Backprojection (FBP) algorithm from the Image Processing Toolbox of Matlab[®] and an SART algorithm. All reconstructions were rescaled to an intensity range of [0 - 255]. As an example, a SART reconstruction of each phantom image from 90 projections is shown in Figure 5e-h.

Our proposed PDM algorithm from Subsection III-A was used to compute thresholds for each of the reconstructions of the vessel and femur phantoms. For all reconstructions of foam and the mouse leg phantom, the PDM algorithm of Subsection III-B was used. The initial stepsize was set to 10.0, the factor F to 0.5, and the algorithm was terminated when the stepsize reached 0.01. For all PDM experiments, we have used k-means clustering to initialize the threshold values.

The proposed PDM thresholding technique was then compared to commonly applied thresh-

¹More advanced CT simulation experiments, for example, taking into account scatter and beam-hardening, could as well have been performed, but would, to our view, unnecessarily complicate the discussion of the experimental results.

olding techniques [7]. First, a parametric optimal thresholding technique was implemented where the image histogram was fitted to a Gaussian Mixture Model (GMM) from which an optimal threshold was derived [26]. Next, the commonly used iterative threshold selection scheme of Otsu was implemented [15], [20]. This is also the default thresholding method used in Matlab. As a final method, k-means clustering was applied to the image histogram. The results of the GMM, Otsu, and k-means thresholding were compared to the proposed PDM method.

For each method, as well as for FBP and SART reconstruction, the number of misclassified pixels K with respect to the original phantom image was computed. The results of the simulation experiments for the binary vessel and femur image are shown in Figure 6, where K is plotted as a function of the number of counts per detector element. Each data point denotes the average of 25 independent experiments along with its error bar. In order not to overload the figures, the results from the GMM fitting to the histogram are not shown since the GMM results were observed to be significantly worse than those of the conventional Otsu and k-means thresholding methods, especially for SART reconstructions and high SNR FBP reconstructions. This can be easily understood from the image histograms shown in Figure 7. Figure 7(b), 7(c), and 7(d) clearly show that a GMM is not suited for fitting to the histogram modes. Experimental results indeed confirmed that GMM fitting leads to thresholds for which the number of misclassified pixels K is significantly larger than for k-means or Otsu thresholding. Only for FBP reconstructions with low SNR, the gaussian mixture model yielded reasonable thresholding results (that is, comparable to those of Otsu and k-means thresholding), as may also be expected from visual inspection of Figure 7(a). However, for each case, the number of misclassified pixels K for the GMM thresholding method was always larger than that of Otsu or k-means thresholding.

From Figure 6, it is clear that the segmentation results from Otsu and k-means thresholding are very similar (Otsu thresholding leads to a slightly larger number of misclassified pixels compared to k-means clustering). Furthermore, Figure 6 reveals that the proposed PDM method leads to significantly better segmentation results in terms of the number of misclassified pixels. As an additional accuracy measure for the vessel and femur phantoms, the number of misclassified pixels K was compared to the number of misclassified pixels K_{min} of the 'optimally thresholded image'. The latter image can be found by an exhaustive search over all possible threshold values and comparing the thresholded image to the original, noiseless image ². From those numbers, a simple error measure E was computed for each segmentation method as follows:

$$E = K - K_{min} \quad . \tag{16}$$

For each method, E is evaluated as a function of I_0 , the flat field number of counts per detector element employed during simulation of the CT sinograms. The results of the simulation experiments for the vessel and femur image are shown in Figure 8, where E is plotted as a function of the number of counts per detector element.

The segmentation results of the mouse leg and foam images are shown in Figure 9. Since these images are gray valued, the PDM method could only be compared to the GMM and the k-means thresholding method. Also for these two phantoms, the segmentation of the PDM method was observed to yield significantly better segmentation results compared to the GMM and the k-means thresholding method. During the experiments with the vessel, femur and mouse leg phantoms, we noticed that the FBP reconstruction was consistently more accurate than the SART reconstruction. An important parameter in SART is the number of iterations. For the foam phantom, we increased this parameter from 10 to 40, yielding more accurate SART reconstructions. Even though the characteristics of the SART reconstruction (and its histogram) changed significantly, PDM still consistently yields more accurate segmentation results than histogram-based methods.

From Figures 6-8, it is clear that for the SART as well as the FBP reconstructions, the PDM method outperforms conventional thresholding techniques with respect to the error measure given in Eq. (16). For 180 and 360 projections with the binary vessel and femur images, the PDM threshold error virtually equals the minimum possible threshold error. Recall that the

²Note that, in practice, this optimally thresholded image cannot be found since the original, noiseless image is not available.

latter can only be found by an exhaustive search over all threshold values and provided the ground truth is known.

We remark that the comparison between the PDM method and alternative segmentation algorithms presented here is limited to the class of global threshold algorithms. Global thresholding is by far the most popular segmentation method because of its simplicity, and is often used as a preprocessing step for further analysis and quantification. Comparing our approach with alternative global threshold methods, as opposed to more advanced algorithms such as watershed segmentation, provides a fair comparison within this important class of segmentation methods. Nevertheless, we also believe that PDM can be used as an effective segmentation criterion for more advanced segmentation methods. We intend to explore this direction in future research.

V. CONCLUSIONS

Global grey value thresholding is a conceptually trivial, yet often used segmentation technique in tomography. However, finding the optimal grey level thresholds is far from trivial. Many procedures have been proposed to select the thresholds based on the image histogram. Although such methods can be made fully automatic, they often lack robustness in case clear grey value modes are absent. Ideally, the grey level image computed by a tomographic reconstruction algorithm should conform perfectly to the measured projection data. However, this assumption is typically not satisfied in practice.

In our paper, we have presented an innovative approach, called PDM (Projection Distance Minimization), to find the optimal threshold grey levels by exploiting the available projection data. Reprojection of the segmented image and subsequent comparison with the measured projection data, yields an objective criterion for the quality of a segmentation. Our approach aims at minimizing the projection distance. Even though the quality of the grey level reconstruction used for segmentation still imposes a limit on the quality of the segmentation, PDM can potentially find thresholds that result in more accurate segmentation than histogram-based methods.

Computing the projection distance for a single segmentation is already a computationally expensive operation. Computing the projection distance for many different threshold combinations is computationally infeasible. We have described how efficient update operations can be used to keep track of the projection distance, while changing the segmentation slightly. For binary images, this leads to an algorithm for finding the optimal global threshold, that has the same time complexity as a single projection distance computation. For images that contains more than two grey levels, we proposed an efficient algorithm for finding optimal thresholds that has guaranteed convergence, but not necessarily to a global minimum of the projection distance.

The experimental results show that if the original object consists of only a few different materials, PDM results in a small difference between the original object and the reconstruction. Simulation experiments were performed for both FBP and SART reconstructions of three phantom images, at varying noise levels. In nearly all test cases, PDM clearly results in significantly better reconstructions than classical thresholding algorithms (Gaussian Mixture Model fitting, Otsu thresholding, K-means clustering, etc). Moreover, using only the available projection data, PDM is capable of finding thresholds for which the difference between the segmented reconstruction and the original object is nearly the same as the best possible difference (computed using knowledge of the phantom).

Although we only applied PDM to global thresholding, the approach can also be used in conjunction with more advanced segmentation algorithms. In particular, the update operation that keeps track of the projection difference can be used within any segmentation algorithm that iteratively moves a few pixels from one class to another class. In future work, we will explore the use of PDM with several alternative segmentation algorithms.

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Fig. 4: Phantom and projection error landscapes for the mouse leg image as a function of the threshold values τ_1 and τ_2 .



Fig. 5: (a-c) Phantom images ; (d-f) Simulated SART reconstructions from 90 projections.



Fig. 6: Best pixel errors for the 'vessel' and 'femur' image. For each subfigure, the number of misclassified pixels K is shown as a function of the number of flat field counts per detector element.



Fig. 7: Histograms of FBP and SART 'vessel' reconstructions from 90 and 360 projections.

Fig. 8: Segmentation results for the 'vessel' and 'femur' image. For each subfigure, the error measure E is shown as a function of the number of flat field counts per detector element. DRAFT

Fig. 9: Segmentation results for the 'foam' and the 'mouse leg' image. For each subfigure, the number of misclassified pixels K is shown as a function of the number of flat field counts DRAFT per detector element.