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Adaptive thresholding of tomograms by projection distance minimization

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ABSTRACT

Segmentation is an important step to obtain quantitative information from tomographic data sets. However, it is usually not possible to obtain an accurate segmentation based on a single, global threshold. Instead, local thresholding schemes can be applied that use a varying threshold. Selecting the best local thresholds is not a straightforward task, as local image features often do not provide sufficient information for choosing a proper threshold.

Recently, the concept of *projection distance* was proposed by the authors as a new criterion for evaluating the quality of a tomogram segmentation [K.J. Batenburg, J. Sijbers, Automatic threshold selection for tomogram segmentation by reprojection of the reconstructed image, in: Computer Analysis of Images and Patterns, in: Lecture Notes in Computer Science, vol. 4673, Springer, Berlin/Heidelberg, 2007, pp. 563–570.]. In this paper, we describe how projection distance minimization (PDM) can be used to select local thresholds, based on the available projection data from which the tomogram was initially computed. The results of several experiments are presented in which our local thresholding approach is compared with alternative thresholding methods. These results demonstrate that the local thresholding approach yields segmentations that are significantly more accurate compared to previously published methods, in particular when the initial reconstruction contains artifacts.

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1. Introduction

Tomography is a powerful technique for three-dimensional imaging of physical objects, without the need to take the object apart. Projection images of the object are acquired along a range of angles, while rotating around the object [1]. An image of the object (a tomogram) is then reconstructed from the series of projection images. Besides its well-known applications in medical imaging, tomography is also an important tool in materials science, microbiology and in industrial applications. In this paper, we focus on tomography of objects that consist of a single material (or tissue, in the medical case). An example of such an object can be seen in Fig. 1, which shows a reconstructed slice of a mouse femur, where the trabecular bone has a rather complex morphology. Such images are commonly used in biomedical bone research [2–5]. Even though the bone density is not perfectly constant, it can still be approximated by a constant density fairly well. An example of an industrial application is the reconstruction of raw diamonds from X-ray projections [6]. If the diamond does not contain any impurities, it consists of a single material of constant density. In materials science, electron tomography is used to study the morphology of homogeneous nanoparticles [7,8].

* Corresponding author. *E-mail address:* joost.batenburg@ua.ac.be (K.J. Batenburg). Tomographic reconstructions, which are generally gray-scale images, are often segmented as to extract quantitative information, such as the shape or volume of image objects. Such segmentations are usually performed by global or local thresholding [2–5,7,8]. However, the process of threshold selection is often somewhat arbitrary. A variety of classical algorithms exist for selecting "optimal" thresholds with respect to various optimality measures [9]. Global thresholds are typically selected from the histogram of the image [10–13].

To our knowledge, all previously proposed thresholding methods only use the tomographic reconstruction to select the threshold, while discarding the information contained in the projection data. A reconstructed image, however, generally suffers from various reconstruction artifacts. In materials sciences, for example, where the projection images are acquired using an electron microscope, it is usually not possible to sample the full range of projection angles, which leads to so-called missing wedge artifacts in the reconstruction. Also, if the projection of the object falls outside the detector. the reconstruction will suffer from truncation artifacts. To reduce the impact of these artefacts in the selection of the thresholds, Batenburg and Sijbers proposed a new approach for global threshold selection that makes use of the available tomographic projection data [1,14]. By reprojecting the segmented volume, the norm of the difference between the projections of the current segmentation and the measured projection data, called the projection distance, can be

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Fig. 1. Reconstructed slice of a mouse femur.

computed. This yields a quantitative measure of the quality of the segmentation. By minimizing the difference between the computed and measured projections (*projection distance minimization*, or *PDM*), an optimal threshold can be computed. It was demonstrated in [1], that PDM leads to a significant improvement in segmentation accuracy, compared to histogram-based methods.

However, the capabilities of global threshold selection methods are limited by the maximum accuracy that can be obtained using global thresholding. If the tomogram exhibits variations in the intensity of certain image features, global thresholding can never lead to an accurate segmentation. For example, thick structures typically tend to be brighter than very thin structures in a tomogram, even if both structures consist of the same material in the original object. To account for local image variations, local thresholding methods were proposed. Abutaleb developed a local thresholding method based on the joint (two-dimensional) entropy of a pixel neighborhood [15,16]. White and Rohrer developed a nonlinear, local thresholding method in which the gray value of the pixel is compared with the average of the gray values in a small neighborhood [17]. Similarly, the local thresholding method of Niblack adapts the local threshold according to the local mean and standard deviation over a sliding window [18]. Eikvil et al. developed a thresholding method in which a large window, with a small window positioned at its center, is moved across the image, and each pixel inside the small window is labeled on the basis of the clustering of the pixels inside the large window [19]. Blayvas et al. proposed an adaptive binarization method where the threshold is determined by interpolation of the image gray levels at points where the image gradient is high [20].

These adaptive thresholding methods that use a varying threshold for different regions of the image lead to better results than global thresholding in some cases. However, they suffer from the same drawback as global thresholding algorithms in the sense that no objective criterion for the segmentation quality is available if only the information from the reconstructed image is used for segmentation. Moreover, in cases where reconstruction artifacts are not negligible, most adaptive thresholding methods perform even worse than global thresholding methods since adaptive thresholding techniques are more vulnerable to local variations originating from these artifacts.

In this paper, we propose an extension of the projection-based threshold selection method from [1], that uses a locally varying threshold *field*, instead of a single global threshold. The same optimization criterion, PDM, is now used to find an "optimal" threshold field. The threshold field is represented on a square grid that is coarser than the pixel grid of the tomogram. The thresholds for pixels that do not coincide with grid points in the coarse grid are computed by bilinear interpolation. Computing the threshold field for which the projection distance is minimal appears to be computationally hard. We describe how a minimum of the projection distance can be computed efficiently for the case that the threshold is



Fig. 2. Basic setting of transmission tomography.

only allowed to vary for a single grid point in the coarse grid, while keeping the threshold values fixed for the remaining grid points. By iterating this procedure several times for all coarse grid points, a local minimum of the projection distance is reached. To avoid early convergence to a local minimum that is far away from the global minimum, a stochastic algorithm is proposed which is capable of escaping from local minima before finally converging.

This paper is structured as follows. In Section 2, the local thresholding problem for tomograms is introduced and our local thresholding approach based on PDM is described. Simulation experiments have been performed, comparing the result of local thresholding based on PDM with alternative local thresholding methods and with global thresholding based on PDM [1]. A description of these experiments and their results is given in Section 3. Section 4 concludes the paper.

2. Method

In what follows, we will assume that a reconstruction, containing noise and possible reconstruction artifacts, from an originally binary image is to be segmented. For simplicity reasons, we will restrict ourselves to two-dimensional tomograms. All concepts can be generalized to a three-dimensional setting in a straightforward manner.

2.1. Tomography setting

The gray value image that we want to segment is a tomographic reconstruction of some unknown homogenous object, which can be represented by a function $f : \mathbb{R}^2 \to \{0, 1\}$. We assume that the support of f (i.e., the set $\{(x, y) \in \mathbb{R}^2 : f(x, y) \neq 0\}$) is included in a circle of radius R. Projections are measured along lines $l_{\theta,t} = \{(x, y) \in \mathbb{R}^2 : x \cos \theta + y \sin \theta = t\}$ where θ represents the angle between the line and the *y*-axis and *t* represents the coordinate along the projection axis; see Fig. 2.

The projection function $P_{\theta} : \mathbb{R} \to \mathbb{R}$ of f for projection angle θ is defined as

$$P_{\theta,f}(t) = \int_{-\infty}^{\infty} \int_{-\infty}^{\infty} f(x, y) \delta(x \cos \theta + y \sin \theta - t) \, \mathrm{d}x \, \mathrm{d}y. \tag{1}$$

with $\delta(\cdot)$ denoting the Dirac delta function. The function $P_{\theta f}(t)$ is called the *Radon transform* of *f*. Usually, the line projections $P_{\theta f}(t)$ cannot be measured as continuous functions. Instead, the line projections are measured in a discrete set of *t*-values as well in a discrete set of projection angles θ .

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