



Research paper

## Variational-based segmentation of bio-pores in tomographic images

Benjamin Bauer<sup>a</sup>, Xiaohao Cai<sup>b</sup>, Stephan Peth<sup>c</sup>, Katja Schladitz<sup>a,\*</sup>, Gabriele Steidl<sup>d</sup><sup>a</sup> Fraunhofer ITWM, Department of Image Processing, Kaiserslautern, Germany<sup>b</sup> University of Cambridge, Department of Plant Sciences, and Department of Applied Mathematics and Theoretical Physics, UK<sup>c</sup> University of Kassel, Department of Soil Science, Germany<sup>d</sup> University of Kaiserslautern, Department of Mathematics, Germany

## ARTICLE INFO

## Keywords:

3D image segmentation

Bio-pores

Root system

Variational segmentation

Total variation minimization

Gray value thresholding

Morphological segmentation

## ABSTRACT

X-ray computed tomography (CT) combined with a quantitative analysis of the resulting volume images is a fruitful technique in soil science. However, the variations in X-ray attenuation due to different soil components keep the segmentation of single components within these highly heterogeneous samples a challenging problem. Particularly demanding are bio-pores due to their elongated shape and the low gray value difference to the surrounding soil structure.

Recently, variational models in connection with algorithms from convex optimization were successfully applied for image segmentation. In this paper we apply these methods for the first time for the segmentation of bio-pores in CT images of soil samples. We introduce a novel convex model which enforces smooth boundaries of bio-pores and takes the varying attenuation values in the depth into account. Segmentation results are reported for different real-world 3D data sets as well as for simulated data. These results are compared with two gray value thresholding methods, namely indicator kriging and a global thresholding procedure, and with a morphological approach. Pros and cons of the methods are assessed by considering geometric features of the segmented bio-pore systems. The variational approach features well-connected smooth pores while not detecting smaller or shallower pores. This is an advantage in cases where the main bio-pores network is of interest and where infillings, e.g., excrements of earthworms, would result in losing pore connections as observed for the other thresholding methods.

## 1. Introduction

Computed tomography (CT) is an efficient tool for non-destructive imaging and the subsequent analysis of the structure of plant roots, see Mooney (2002), Tracy et al. (2010) and the references therein. Although the quality of CT images in soil science has rapidly improved in recent years, the segmentation of bio-pores remains a challenging problem. This is mainly due to the overlap of the X-ray attenuation values between bio-pores and soil caused by organic materials, and the elongated shape of the pores. Especially it appears if the pores contain partly decomposed root fragments or earthworm linings. Such features are only temporarily occupying the bio-pores and it may be desired to omit them from the segmented bio-pore network for a separate analysis. Fig. 1(a) shows exemplary a three-dimensional (3D) CT image of soil with bio-pores.

The accurate segmentation of the bio-pores is of substantial interest since the appropriate segmentation is a key determinant for the quality of the subsequent structural analysis. For example, disconnecting bio-pores due to poor segmentation can influence the subsequent analysis

of the bio-pore network dramatically. It may also be of interest to exclude temporal features such as earthworm infillings from the segmented images to be able to analyse bio-pore features such as surface to volume ratios or network geometries independently.

In Pagenkemper et al. (2013), CT was used to investigate the effects of root-induced bio-pores on the pore space of soil samples. These pore spaces are made up of a variety of different pore types showing structural heterogeneity in size, shape, and orientation. Methods relying on local or global gray value thresholds have been successfully applied to segment different pore systems as, e.g., Oh's and Lindquist's indicator kriging (Oh and Lindquist, 1999) in Pagenkemper et al. (2013) or a refined version of the double thresholding (Vogel and Kretzschmar, 1996) in Schlüter et al. (2010). For a comparison of these and some other methods for the segmentation of porous materials we refer to Iassonov et al. (2009) and for those of (multiphase) soil images with macro-pores, organic matter and rocks to Schlüter et al. (2014).

In this paper, we suggest a novel variational model for segmenting large root channels. It consists of two ingredients: a *data term* which includes a threshold depending on the depth (*z*-direction) of the given

\* Corresponding author.

E-mail address: [katja.schladitz@itwm.fraunhofer.de](mailto:katja.schladitz@itwm.fraunhofer.de) (K. Schladitz).

data and takes the illumination/attenuation changes in this direction into account, and a *regularizing term* which is a discrete counterpart of the total variation function (Rudin et al., 1992) and takes care of smooth boundaries of the bio-pores.

Approaches for the denoising and segmentation of images based on the calculus of variation have been applied very successfully in recent years. Among the most influential examples are the Rudin-Osher-Fatemi total-variation based image denoising model (Rudin et al., 1992) and the Mumford-Shah (MS) model image segmentation model (Mumford and Shah, 1989). The MS model supports smooth image segments with small boundary lengths. Since the MS model is neither convex nor smooth, it is hard to find a global minimizer numerically. The simpler piecewise constant MS model focuses on piecewise constant segments. For the two phase segmentation this model is actually the active contour model of Chan and Vese (2001) which is still non convex. Several convex relaxations of the piecewise constant supervised model were proposed in the literature, also for multiphase case, see, e.g., Lellmann et al. (2009), Nikolova et al. (2006), Pock et al. (2009), Zach et al. (2008). These models have the advantage that they have only global minima which can be computed by standard convex minimization schemes. For the two phase segmentation it was shown in Nikolova et al. (2006) that the above convex relaxed approaches find the global minimum of the original non convex model. Our proposed model can be considered as a modification of these convex approaches which takes illumination changes via a special data term into account. For a very recent comprehensive study of energy minimizing methods for the segmentation of natural images we refer to Kappes et al. (2015).

We suggest to find the global minimizer of our convex model by the alternating direction method of multipliers (ADMM) (Boyd et al., 2011; Gabay, 1983) which has a simple implementation and works very efficiently.

We compare our variational method with three other usual segmentation approaches. More precisely, we apply indicator kriging (Oh and Lindquist, 1999) as used in Pagenkemper et al. (2013), a global gray value thresholding (Otsu, 1979), and a morphological extract holes procedure combined with a global thresholding. All these methods require, in contrast to the variational method, some pre- and postprocessing steps described in Section 3 which handle in particular the illumination changes in the  $z$ -direction. All four methods are applied to four data sets from Pagenkemper et al. (2013) and to two simulated data sets. Quantitative assessment of the segmented pores shows that each method has its merits. The variational approach yields smooth well-connected large pores. Non detection of smaller or shallower pores can be an advantage in cases where the main bio-pores network is of interest. Moreover, the smooth surface eases subsequent skeletonization as artificial branches due to local surface roughness are avoided. On the other hand, morphological correction of global gray value fluctuations followed by a simple global gray value thresholding according to Otsu (1979) very well recovers small pores and biological infillings.

This paper is organized as follows: In Section 2, we introduce our variational model for segmenting 3D root-induced bio-pores and propose an efficient ADMM algorithm to find the global minimizer. The segmentation methods used for the comparison are shortly summarized in Section 3. In Section 4, we test our algorithm on four 3D image data sets from Pagenkemper et al. (2013) as well as on two simulated bio-pore systems and compare it to the segmentation algorithms introduced in the previous section. Conclusions are given in Section 5.

## 2. Variational segmentation model

In this section, we introduce our model for tackling the root-induced bio-pores segmentation problem and provide an algorithm to solve it.

Let  $\Omega := \{1, \dots, N_1\} \times \{1, \dots, N_2\} \times \{1, \dots, N_3\}$  be the image grid. For

fixed  $z \in \{1, \dots, N_3\}$ , let  $\Omega_z := \{(x, y, z) : (x, y) \in \{1, \dots, N_1\} \times \{1, \dots, N_2\}\}$  be the horizontal (discrete) plane through  $z$ . By  $f: \Omega \rightarrow [0, 1]$  we denote the given 3D CT gray-value image. Let  $\nabla_x$  be the forward difference operator in  $x$ -direction (and similarly in  $y$ - and  $z$ -direction), i.e.,

$$\nabla_x f(x, y, z) := f(x + 1, y, z) - f(x, y, z),$$

where we suppose mirror boundary conditions. For fixed  $z \in \{1, \dots, N_3\}$  and given  $\varepsilon > 0$  we define the edge set  $\mathcal{E}_z(\varepsilon) \in \Omega_z$  by

$$\mathcal{E}_z(\varepsilon) := \{(x, y) \in \Omega_z : \sqrt{(\nabla_x f(x, y, z))^2 + (\nabla_y f(x, y, z))^2} > \varepsilon\}.$$

In other words,  $\mathcal{E}_z(\varepsilon)$  contains the voxels located around the boundaries in  $\Omega_z$ . Then

$$\phi(z) := \frac{1}{|\mathcal{E}_z(\varepsilon)|} \sum_{(x,y) \in \mathcal{E}_z(\varepsilon)} f(x, y, z) \quad (1)$$

can be considered as average gray value of the voxels located around the boundaries in  $\Omega_z$ . We define a threshold function  $\tau$  depending on  $z$  by

$$\tau(z) := c + \phi(z), \quad (2)$$

where  $c$  is a chosen constant. To segment the root-induced bio-pores we propose to find the minimizer  $u$  of the convex functional

$$\min_{u \in [0,1]} \sum_{(x,y,z) \in \Omega} \underbrace{(\tau(z) - f(x, y, z))}_{s(x,y,z)} u(x, y, z) + \mu TV(u), \quad \mu > 0, \quad (3)$$

where  $u \in [0, 1]$  is meant voxelwise and

$$TV(u) := \sum_{(x,y,z) \in \Omega} \sqrt{(\nabla_x u(x, y, z))^2 + (\nabla_y u(x, y, z))^2 + (\nabla_z u(x, y, z))^2}.$$

The first term of model (3) is a data term. If  $f(x, y, z)$  is larger or equal than the threshold  $\tau(z)$ , then a large  $u(x, y, z) \approx 1$  is not penalized. Conversely, if  $f(x, y, z)$  is below the threshold, then the data term becomes small for  $u(x, y, z) \approx 0$ . The second term is the regularization term which imposes smooth boundaries. In particular small image details (artifacts) are neglected. This well-known regularizing term was first introduced by Rudin et al. (1992) for image restoration tasks, The data and the regularization terms are coupled by the regularization parameter  $\mu$  which steers the influence of the different terms to the solution. Note that due to the attenuation values between bio-pores at different  $z$  layers, a layer adapted value  $\tau(z)$  leads to better segmentation results.

There is a close relation of model (3) (for constant  $\tau$ ) to the Chan-Vese segmentation model (Chan and Vese, 2001). For more details on the connection between these models and its relation to perimeter minimization we refer to Cai and Steidl (2013), Chambolle et al. (2010).

Once the minimizer  $u: \Omega \rightarrow [0, 1]$  of (3) is found, we can apply a thresholding procedure with a threshold  $\rho \in (0, 1)$  to find the two desired segments of  $u$ . Fortunately it was proved in Nikolova et al. (2006) that every threshold  $\rho \in (0, 1)$  can be used here.

We compute the minimizer of the convex functional (3) by the ADMM (Boyd et al., 2011; Gabay, 1983). Alternatively one could apply primal-dual first order methods as, e.g., those proposed in Chambolle and Pock (2011). To present the algorithm in a sound mathematical form, we reorder the 3D images  $g: \Omega \rightarrow \mathbb{R}$  into vectors  $g \in \mathbb{R}^N$ ,  $N = N_1 N_2 N_3$  with components  $g_{x+N_1(y-1)+N_1 N_2(z-1)} := g(x, y, z)$  and associate to the forward difference operators  $\nabla_x, \nabla_y, \nabla_z$  the corresponding matrices. For the concrete matrix representation we refer to Shafei and Steidl (2012). Then problem (3) can be rewritten as

$$\min_{u,v,w} \langle s, u \rangle + \mu \left\| \sqrt{v_x^2 + v_y^2 + v_z^2} \right\|_1 \quad \text{subject to } v = \nabla u, \quad w = u, \quad w \in [0, 1],$$

where  $\langle s, u \rangle$  denotes the vector inner product,  $\|\cdot\|_1$  the 1-norm of vectors and

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