Variational-based segmentation of biopores in tomographic images

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Abstract

X-ray computed tomography (CT) combined with quantitative analysis of the resulting volume images proved to be a fruitful technique in soil science. However, the overlap in X-ray attenuation values of different soil components and variations in X-ray attenuation keep the segmentation of single components of these highly heterogeneous samples a challenging problem. Particularly demanding are biopores due to their elongated shape and the low gray value difference to the surrounding soil structure, especially if they still contain partly decomposed root fragments or earthworm linings. Such features are only temporarily occupying the biopores and it may be desired to omit them from the segmented biopore network for separate analysis. The accurate segmentation of the biopores is of substantial interest since the quality of the segmentation is a key determinant for the quality of subsequent structural analysis.

Recently, variational models in connection with algorithms from convex optimization were successfully applied for image segmentation. In this paper we apply these innovative methods for the first time for the segmentation of biopores in a CT image of a soil sample. The segmentation result is compared with global gray value thresholding and with a morphological approach. Pros and cons of the methods are assessed using geometric features of the segmented biopore system.

Keywords: 3D image segmentation, biopores, root system, gray value thresholding, morphological methods

1. Introduction

Computed tomography (CT) is an efficient tool for non-destructively imaging and subsequently analyzing the structure of plant roots, see (20, 31) and the references therein. In (24), CT was used to investigate the effects of root-induced biopores on the pore space

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architecture of soil samples. In general, the three-dimensional (3D) pore space of soil samples is made up of a variety of different pore types, showing structural heterogeneity in size, shape, and orientation (24).

Over the last decade, the application of CT in soil science showed rapid improvement in terms of image quality and acquisition time. However, segmentation of biopores as shown in Figure 1 remains a challenging problem due to the overlap of the X-tay attenuation values between biopores and soil caused by organic materials, and due to the elongated shape of the pores. For example, disconnecting biopores due to poor segmentation can influence the subsequent analysis of the biopore 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 biopore features such as surface to volume ratios or network geometries independently.

Figure 1: Soil sample, imaged with a pixel size of 463 µm at the Technical University Dortmund, Germany, Department of Mechanical Engineering with a v|tome|x 240 (Phoenix-X-Ray). For details on sample preparation and imaging parameters see (24). The rendering shows $399 \times 399 \times 983$ pixels corresponding to $185 \text{mm} \times 185 \text{mm} \times 455 \text{mm}$.

Methods relying on local or global gray value thresholds have been successfully applied
to segment pore systems in soil images, e.g., in (24) using Lindquist’s and Oh’s indicator kriging (35), and in (38) refining the double thresholding described in (40).

In this paper, we suggest a variational model for the large root channels. For comparison, we apply indicator kriging (35) as used in (24) and additionally the most simple approach of a morphological gray value balancing followed by Otsu’s (23) global gray value threshold as well as a morphological fill holes procedure, again combined with a global thresholding. All four methods are applied to the data sets from (24) and to two simulated data sets. Quantitative assessment of the segmented pores shows, that each method has its merits – the variational approach yielding smooth well connected large pores, the global thresholding very well recovering small pores and biological infillings.

The proposed functional in our variational model consists of a data term which includes a threshold depending on the depth (z-direction) of the given data and a regularizer which is a discrete counterpart of the total variation regularizer. The latter originates in image restoration (27) and is meanwhile very frequently applied for various image processing tasks. We suggest to find the minimizer of the model by the alternating direction method of multipliers (ADMM) which has a simple implementation and works very efficiently.

This paper is organized as follows: In Section 2, we introduce the variational model for segmenting 3D root-induced biopores and propose an efficient ADMM algorithm to find the minimizer. In Section 3, the segmentation methods used for comparison are shortly summarized. In Section 4, we test our algorithm on the 3D image data sets from (24) as well as on two simulated biopore 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 biopores segmentation problem and provide an algorithm to solve it.

Let Ω := \{1, \ldots, N_1\} \times \{1, \ldots, N_2\} \times \{1, \ldots, N_3\} be the image grid. For fixed z \in \{1, \ldots, N_3\}, let Ω_z := \{(x, y, z) : (x, y) \in \{1, \ldots, N_1\} \times \{1, \ldots, N_2\}\} be the horizontal (discrete) plane through z. By f : Ω \to [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, \ldots, N_3\} and given \varepsilon > 0 we define the edge set \mathcal{E}_z(\varepsilon) \in Ω_z by

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

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

We define a threshold function \( \tau \) depending on \( z \) by

\[
\tau(z) := c + \phi(z),
\]

where \( c \) is a chosen constant. To segment the root-induced biopores we propose to find the minimizer \( u \) of the following convex functional:

\[
\min_{u \in [0,1]} \sum_{(x,y,z) \in \Omega} \left( \tau(z) - f(x,y,z) \right) u(x,y,z) + \mu TV(u), \quad \mu > 0
\]

where \( u \in [0,1] \) is meant pixelwise 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, Osher and Fatemi (27) 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 biopores 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 (6). For more details on the connection between these models and its relation to perimeter minimization we refer to (3; 4).

Once the minimizer \( u : \Omega \to [0,1] \) 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 (21) that every threshold \( \rho \in (0,1) \) can be used here.

We compute the minimizer of the convex functional (3) by the ADMM (2; 9). Alternatively one could apply primal-dual first order methods as, e.g., those proposed in (5). To present the algorithm in a sound mathematical form, we reorder the 3D images \( g : \Omega \to \mathbb{R} \) into vectors \( g \in \mathbb{R}^{N} \), \( N = N_1N_2N_3 \) with components \( g_{x+N_1(y-1)+N_1N_2(z-1)} := g(x,y,z) \) and associate to the forward difference operators \( \nabla_x, \nabla_y, \nabla_z \) the corresponding matrices. For the concrete matrix representation we refer to (29). Then problem (3) can be rewritten as

\[
\min_{u,v,w} \langle s, u \rangle + \mu \| \sqrt{v_x^2 + v_y^2 + v_z^2} \|_1 \quad \text{subject to}
\]

\[
v = \nabla u, \quad w = u, \quad w \in [0,1],
\]
where $\langle s, u \rangle$ denotes the vector inner product, $\| \cdot \|_1$ the 1-norm of vectors and 
\[
\nabla = \begin{pmatrix} \nabla_x \\ \nabla_y \\ \nabla_z \end{pmatrix}, \quad v := \begin{pmatrix} v_x \\ v_y \\ v_z \end{pmatrix}.
\]

Then the ADMM algorithm reads:

**Algorithm 1**

**Initialization:**
$v^{(0)} \in \mathbb{R}^{3N}, \ w^{(0)} \in \mathbb{R}^N, \ b_1^{(0)} \in \mathbb{R}^{3N}, \ b_2^{(0)} \in \mathbb{R}^N, \text{ and } \gamma > 0.$

**Iterations:**

For $r = 0, 1, \ldots$
\[
u^{(r+1)} = \text{argmin}_u \{ \langle s, u \rangle + \frac{\gamma}{2} \| \nabla u - v^{(r)} + b_1^{(r)} \|_2^2 + \frac{\gamma}{2} \| u - w^{(r)} + b_2^{(r)} \|_2^2 \}
\]
\[
v^{(r+1)} = \text{argmin}_v \{ \mu \| v \|_1 + \frac{\gamma}{2} \| \nabla u^{(r+1)} - v + b_1^{(r)} \|_2^2 \}
\]
\[
w^{(r+1)} = \text{argmin}_{w \in [0, 1]} \| u^{(r+1)} - w + b_2^{(r)} \|_2^2
\]
\[
b_1^{(r+1)} = b_1^{(r)} + u^{(r+1)} - v^{(r+1)}
\]
\[
b_2^{(r+1)} = b_2^{(r)} + u^{(r+1)} - w^{(r+1)}
\]

The minimizer in the first step can be computed by setting the gradient to zero which results in solving the linear system of equations
\[
(\nabla^T \nabla + I_N)u^{(r+1)} = \nabla^T (v^{(r)} - b_1^{(r)}) + (w^{(r)} - b_2^{(r)}) - \frac{1}{\gamma} s
\]
with the $N \times N$ identity matrix $I_N$. This system can be efficiently solved using the fast discrete cosine transform, see (29). The second step requires a grouped soft shrinkage of $a = (a_1, a_2, a_3)^T := \nabla u^{(r+1)} + b_2^{(r)}$ with threshold $\lambda := \frac{\mu}{\gamma}$ defined pixelwise by
\[
 u_k^{(r+1)} = \begin{cases} a_k \left(1 - \frac{\lambda}{\sqrt{a_1^2 + a_2^2 + a_3^2}}\right) & \text{if } \sqrt{a_1^2 + a_2^2 + a_3^2} > \lambda, \\
 0 & \text{otherwise.} \end{cases}
\]

for $k = 1, 2, 3$.

The third step just means that
\[
w^{(r+1)} = \min \{ \max \{0, u^{(r+1)} + b_2^{(r)}\}, 1\}.
\]

3. Segmentation Methods for Comparison

In order to evaluate the derived segmentation algorithm, we compare it to the method applied in (24) as well as global thresholding according to Otsu (23), and a morphological approach thriving mainly on the fill-holes transform on gray value images (39). To be self-consistent we briefly summarize the three methods.

The backbone of the method applied in (24) is indicator kriging (35): In user defined regions of interest, two thresholds $T_0 \leq T_1$ are derived from the data. Pixels darker
than $T_0$ are assigned to the pore space, while pixels brighter than $T_1$ are assigned to the solid component. The decision for pixels $x$ with $T_0 < f(x) < T_1$ is taken according to an iterative procedure adapted from the geostatistical interpolation method kriging that takes into account the local gray value distribution in the image via the covariance function. The quality of the segmentation result is strongly determined by the choice of the two thresholds as only a comparably small number of pixels is later assigned using the actual indicator kriging procedure. In (24), $T_1$ is chosen as the global gray value mean minus $2\sigma$, where $\sigma$ is the standard deviation of the Gaussian fit to the matrix peak. The local lower threshold $T_0$ is the biopore gray value peak for the manually chosen region.

Of course, the simplest method is global thresholding with an automatically chosen threshold. For the data considered here, this straightforward approach is prevented by strong global gray value variations. Therefore, a global gray value balancing (shading correction) is applied: In each $xy$-slice, the mean gray value is calculated in the circle filled by the sample and subsequently subtracted from the original image. Additionally, the same procedure is applied to cylinder sides of increasing radius. These two transformations finally remove the large-scale gray value fluctuations. On the resulting corrected image, a global gray value threshold $T$ can be applied. We use Otsu’s (23) method to determine $T$: Assuming a bimodal gray value distribution, Otsu’s threshold is the one maximizing the intra-class variance of the two gray value classes while minimizing the gray value variances within the two classes.

As an alternative, the morphological extract holes transformation (39) is applied to the shading corrected data: Holes in an integer gray value image are regional gray value minima not connected to the image borders. Regional minima in turn are connected regions of pixels of constant gray value such that any path to a pixel of a lower gray value includes at least one pixel of a higher gray value. Extract holes results in an integer image of the holes and everything else background. We finally apply Otsu’s threshold to this image to segment the pore system.

4. Experimental Results

In this section, we compare the variational method with the segmentation achieved in (24), shading correction and Otsu’s global threshold and extract holes, respectively, based on the data sets from (24) (one is shown in Figure 1) and two simulated biopore systems. The latter are realizations of a generalization of the Altendorf-Jeulin model for stochastic fiber systems (1) that allows for branching. The gray value distributions in these data sets are adapted from those observed in the real data sets.

The variational segmentation algorithm does not require a preprocessing of the data since the noise removal is inherent in the method. The parameters are $\varepsilon = 0.2$, $c = 0.03$ and $\mu = 6$.

For the histogram based selection of the thresholds for the indicator kriging method, in total 18 regions of interest (ROI) were extracted from the sample to include a sufficient fraction of biopore volume. The ROIs were merged to a single ROI with a total volume of approximately 297 cm$^3$ and a bimodal greyscale distribution from which the thresholds...
$T_0 = 122$ and $T_1 = 144$ were derived. In a post-processing step all objects smaller than 800 pixels were removed. Before applying Otsu’s threshold and the morphological method, a median filter was applied. The shading was corrected by slice-wise subtracting the gray value mean. Otsu’s threshold in the corrected image, restricted to the cylindrical sample, is 174. The result of the extract holes transform was thresholded by Otsu’s method too – in that case 15. Before applying extract holes, the side of the cylindrical sample is set to foreground to avoid edge effects.

The variational segmentation method was implemented in Matlab. For all other processing and analysis algorithms as well as the volume rendering we used MAVI (8) and ToolIP (36) with MAVIkit (37).

Visual impression suggests that the variational method yields the smoothest pores and keeps thin pores connected, see Figure 2 for volume renderings as well as Figures 3 and 4 showing 2D slices through the 3D images. Moreover, it also detects pores of intermediate gray value (compare Figure 3, upper right corner). Otsu’s threshold and extract holes retain more detail but at the price of a much rougher surface. Otsu’s threshold oversegments some of the pores, see Figure 3(d), right. Extract holes is here more accurate. Compared to the other segmentations, it loses some of the pores when the small regions are removed.

Quantitative analysis of the segmented pore systems reveals that the double thresholding from (24) segments the smallest pore volume while Otsu’s threshold detects the largest. In accordance with the purely visual findings, the variational method results in the smoothest pore system: The variational method yields the smallest pore surface although the pore volume is not much smaller than for the Otsu threshold (compare Table 1). The strong connectivity of the pores segmented by the variational method becomes apparent in the mean chord lengths in $z$-direction – for the variational method this value is nearly twice as large as for the other methods, see Table 2.

Labelling of the pores and subsequent statistical analysis of the thus obtained image objects underlines the above findings. Comparison to the ground truth for the two simulated biopore systems is clearly in favour of the variational method. Due to the extremely low volume fraction, percentage of misclassified pixels with respect to all pixels is not meaningful. Instead, the number of misclassified pixels is related to the total number of foreground (biopore) pixels. This yields:

Visual inspection of the largest pores in Ch2y-II singles out Otsu’s threshold as this approach creates 9 pores above the volume threshold whereas the other methods only have 5 pores of this size (see Figure 5). This is most likely due to the observed over segmentation artificially connecting pores.

5. Conclusions

In this paper, we compared several approaches for segmenting biopores in 3D images of soil samples obtained by computed tomography. We proposed alternatives to the usually applied double thresholding methods (22 24 38).
Table 1: Volume fraction and surface area of the segmented pore systems. True volume fraction of sim1 is 0.47%, of sim2 0.76%. The true surface areas are 0.054 m² and 0.074 m², for sim1 and sim2, respectively.

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<th>volume fraction [%]</th>
<th>surface area [m²]</th>
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<td>Otsu Extract holes</td>
<td>Peth</td>
<td>Variational method</td>
<td>Otsu Extract holes</td>
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<td>0.069</td>
<td>0.119</td>
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after removal of all objects smaller than 800 pixels

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Table 2: Mean chord lengths in z-direction.

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Table 3: Joint connectivity and pore size analysis.

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Table 4: Fraction of misclassified pixels w.r.t. number of true foreground pixels.

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<th>Otsu</th>
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The variational approach features well-connected smooth pores while not detecting smaller or shallower pores. This can be an advantage in cases where the main biopores 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. Moreover, the smooth surface eases subsequent skeletonization as artificial branches due to local surface roughness are avoided.

Global thresholding preceded by a shading correction yields a sound result as well. The observed tendency to over segmentation can be avoided by the morphological extract holes operation. These two methods have the significant advantage that the user does not have to choose critical parameters: The threshold is derived directly from the image’s gray value histogram by Otsu’s method. For the shading correction, a mean filter or a morphological opening with a large enough filter mask and restricted to the cylindrical sample, can be applied. Just when removing small connected components during the post-processing step, the user critically influences the result.

The final decision for one or the other method should thus rather depend on the final goal after segmentation.

Acknowledgements

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References


Figure 2: 3D rendering of the segmentation results after removing all objects smaller than 800 pixels.
Figure 3: Slice 200 perpendicular to the $z$-axis.

Figure 4: Slice 180 parallel to the $z$-axis.
Figure 5: Volume renderings of the pores larger than 75554 pixels – 9 pores for Otsu’s threshold, 5 pores for all other methods.