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Biomedisa: The Biomedical Image Segmentation App

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Summary: The Biomedical Image Segmentation App (Biomedisa) was developed as a semi-automatic tool for improving and accelerating the tedious manual segmentation of computed x-ray tomographic images. It is based on a parameter-free and highly scalable diffusion algorithm, making it easy to use and facilitating the analysis of even large tomographic data sets in a reasonable time.

1. INTRODUCTION

X-ray microtomography (μCT) has become established as a tool for the investigation of morphological questions and studies of the internal structures of materials [1, 2]. However, with the analysis of the data and the ever-increasing amount of data, we are constantly facing new boundaries. In particular, the segmentation of tomographic images remains one of the most challenging tasks in computer vision. In many cases manual segmentation is still considered as the "gold standard".

The web application Biomedisa (https://biomedisa.de) is based on a parameter-free and highly scalable diffusion algorithm. The segmentation is done using weighted random walks. Starting from a few, manually labeled reference slices, the random walks extrapolate the information contained in the reference slices to the remaining volume (Fig. 1). The weights are defined without the use of hyperparameters. Thus, it is not necessary to search for proper values, which saves an elaborate and tedious configuration. Due to their independence, the calculation of the random walks is highly scalable. This allows one to use massive parallel computing architectures such as graphics processors and thus an evaluation of even large image data in a short time. In addition, a quick and easy correction of the segmentation results is possible by adding additional reference slices.

This semi-automatic approach has already proven to be extremely effective within the ASTOR project. Since the input data can be created with any common segmentation software, such as Amira or ImageJ, the users can continue to work in their familiar environment. However, the segmentation process itself is significantly accelerated and the quality of the resulting segmentation is improved. In order to provide users with the necessary computing power, the web application Biomedisa was set up. Users can upload their tomograms and labeled slices, run the segmentation process, and visualize both the image data and the results using 3D rendering software and a 2D slice viewer.

2. METHOD

According to [3], let V be a set of vertices in $\mathbb{R}^n$. For $x, y \in V$ we write $x \sim y$ if x is adjacent to y. Let $I(x)$ be the image data, i.e. I maps x to a gray-value. Further, let x_0 be the starting point of a random walk and σ_{x_0} the standard deviation from x_0 in a local area of x_0, then we set

$$\mu_{x_0}(y) = \frac{1}{\sqrt{2\pi\sigma_{x_0}^2}} \exp\left(-\frac{(I(x_0) - I(y))^2}{2\sigma_{x_0}^2}\right) \quad \text{for all } y \in V, \tag{1}$$

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and

$$\mu(x) = \sum_{y \in V, y \sim x} \mu_{x_0}(y) \quad \text{for all } x \in V. \tag{2}$$

The function μ induces a Markov kernel

$$P_{x_0}(y,x) = \begin{cases} \frac{\mu_{x_0}(y)}{\mu(x)} & \text{if } y \sim x \\ 0 & \text{else,} \end{cases} \tag{3}$$

where $P_{x_0}(y,x)$ is the conditional probability of a random walk moving from x to y given its position x. This means, P is the weight of the edge between two nodes x and y. Due to this definition, the random walks tend to remain in an area similar to their starting area.

Starting several random walks in pre-labeled reference slices (Fig. 1), the voxels are hit by numerous random walks over time. By the respective number of hits, one can approximatively determine the probability that a voxel can be assigned to one particular segment. Thus, the segmentation can be done by assigning each voxel to the region from which most hits were made.

All variables in (1), (2) and (3) are clearly defined, so it is not necessary to manually set the value of any parameter. Further, since the random walks are independent of each other, their computation can be easily parallelized. Therefore, the diffusion process is highly scalable and predestined to be calculated on GPUs.

3. RESULTS

Fig. 1 (b) shows a comparison of the manual segmentation (A, C) and the automatic segmentation (B, D) using the example of the ptychoid mite *Euphthiracarus reticulatus* [1]. The size of the volume is 698 × 766 × 1088 voxels. The automatic segmentation is based on the manual labeling of each 50th slice. That is, 22 slices were labeled, which took about an hour. In contrast, the manual segmentation of all slices takes approximately 50 hours. The automatic segmentation needed 13 minutes on 6 GPUs. The largest error is seen in the hairs of the mite. This is due to the selection of equidistant reference slices. Increasing the number of reference slices or an adaptive selection of the pre-labeled slices would increase the accuracy of the results. Because of the lack of hyperparameters, the short calculation time, and the easy and fast adaptation of the results by adding further reference slices, it is recommended to start with some pre-labeled slices and add additional slices if needed. The algorithm was developed within the framework of the projects ASTOR & NOVA funded by the BMBF.

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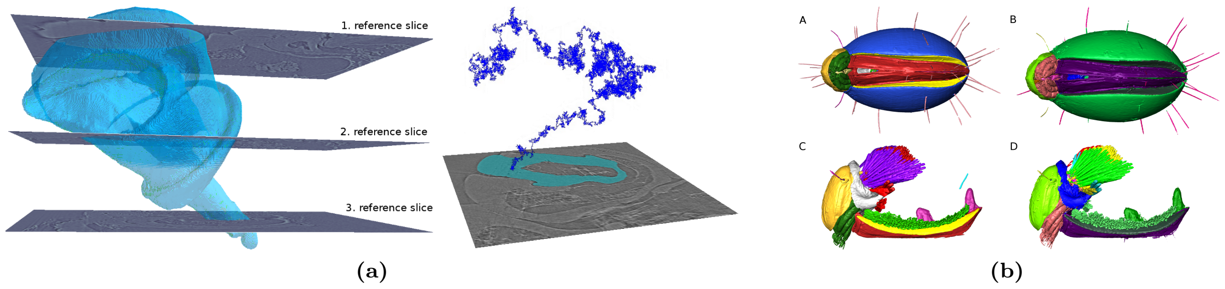

(a)

(b)

Figure 1: (a) *Left* Final segmentation of a beetle's hip joint [2] based on three pre-labeled reference slices. *Right* Weighted random walk starting in a reference slice. (b) Comparison of manual segmentation (A, C) and automatic segmenation (B, D) based on the manual labeling of each 50th slice.