BioSegment: Active Learning segmentation for 3D electron microscopy imaging

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Abstract. Large 3D electron microscopy images require labor-intensive segmentation for further quantitative analysis. Recent deep learning segmentation methods automate this computer vision task, but require large amounts of labeled training data. We present **BioSegment** 2.0, a turnkey platform for experts to automatically process their imaging data and fine-tune segmentation models. It provides a user-friendly annotation experience, integration with familiar microscopy annotation software and a job queue for remote GPU acceleration. Various active learning sampling strategies are incorporated, with maximum entropy selection being the default. For mitochondrial segmentation, these strategies can improve segmentation quality by 10 to 15% in terms of intersection-over-union score compared to random sampling. Additionally, a segmentation of similar quality can be achieved using 25% of the total annotation budget required for random sampling.

Keywords: Active learning · Electron microscopy · Computer vision.

1 Introduction

Volume electron microscopy (vEM or 3D EM) describes a set of high-resolution imaging techniques used in biomedical research to reveal the 3D structure of cells, tissues and small model organisms at nanometer resolution. EM techniques have emerged over the past 20 years, largely in response to the demands of the connectomics field in neuroscience, and vEM is expected to be adopted into mainstream biological imaging. Efficient training and post-processing procedures for deep learning methods in vEM constitute an active area of research [5]. For successful application, the deep learning model needs to be trained on data very similar to the data at hand, but annotated vEM training data is time-consuming to create. Various approaches try to alleviate this problem: increasing annotator efficiency using professional annotation software (*i.e.* MIB or Imaris), sparse labeling [9] or

refining model predictions using only points [1]. Additionally, model performance can increase through self-supervised learning on large unlabeled and heterogeneous data sets [4], generalizability-enhancing tricks such as data augmentation or domain adaptation [7]. In any case, additional fine-tuning on some labeled domain-specific data will improve segmentation performance and may be even required [2]. When fine-tuning, model performance can be further increased by choosing the most interesting samples to annotation using active learning [6].

Active learning is a subdomain of machine learning that aims to minimize label effort without sacrificing model performance. This is achieved by iteratively querying a batch of samples to a label providing oracle, adding them to the train set and retraining the predictor. The challenge is to come up with a smart selection criterion to query samples and maximize the steepness of the training curve [8]. In the setting of vEM segmentation, the oracle is a human imaging expert, such as a microscopist or biologist. In this human or expert-in-the-loop setting, an annotation interface will query the expert to provide labels. The total volume of EM data is considered an offline pool of unlabeled 2D training patches.

We present an update to our previous work with BioSegment 2.0. Users can upload vEM datasets and annotate mitochondria using active learning, as they did using BioSegment 1.0. Additional features includes scribble-based sparse annotation, which alleviates the cold start problem of active learning. The implementation uses MONAI Label [3], an open source image labeling and learning tool that helps researchers and clinicians to collaborate, create annotated datasets, and build AI models. It features 3D segmentation point-based refinement using 3D Slicer and active learning sample selection. We propose three new contributions since our initial paper:

1. An integration of microscopy imaging formats and the MONAI Label datastore.
2. A tool for fine-tuning existing MONAI models on vEM labelled datasets.
3. A MONAI Model Zoo contribution, suitable for the segmentation of mitochondria in vEM.

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