Towards high throughput volume electron microscopy segmentation through deep domain adaptation*

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Abstract. State-of-the-art segmentation techniques in volume electron microscopy (EM) require a substantial amount of labeled data and are very data-dependent. These techniques even underperform on similar datasets due to a domain shift. Domain adaptation (DA) techniques aim to correct this domain shift and improve performance on an unlabeled (target) dataset using existing labeled (source) datasets. In this work, we extend recently proposed regularization-based classification DA techniques to an encoder-decoder segmentation layout. Secondly, we propose a new reconstruction-based architecture (Y-Net) which is easy to implement and end-to-end trainable. The results show that the regularization-based DA approaches improve segmentation quality in the target domain over classical finetuning. Additionally, we validated that our proposed method outperforms the former on FIB-SEM and TEM data.

Keywords: Electron microscopy · Segmentation · Domain adaptation.

1 Introduction

Research in automated EM segmentation has been an extremely active topic in the last years [1, 2]. Nevertheless, state-of-the-art models rely on large labeled datasets and are typically sensitive to small domain shifts, making them impractical for segmenting new datasets. In this work, we combine recent developments in domain adaptation with encoder-decoder segmentation networks to improve the practical usability of automated segmentation techniques in EM.

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2 Domain adaptation segmentation

Domain adaptation (DA) tackles the problem of building a predictive model for a target dataset with no labels (unsupervised) or a very small amount (semi-supervised) by using a relatively large labeled source dataset. The state-of-the-art in (deep) domain adaptation is focused on classification and largely based on regularization [3–5].

We consider three classification DA methods that introduce domain shift invariance using domain confusion networks (DANN) [3], correlation alignment (CORAL) [4] or distribution alignment (MMD) [5]. The activations in the encoder part of an encoder-decoder segmentation network are regularized according to the paradigm proposed in DANN, CORAL and MMD. Consequently, the source and target encoder features are aligned to a higher extent, which makes the segmentation in the decoder less domain sensitive.

Additionally, we propose a novel unsupervised DA method (Y-Net) that introduces a reconstruction decoder to the original encoder-decoder network. As the encoder features are designed for source reconstruction and segmentation and target reconstruction, we introduce relevant target segmentation features.

3 Results and discussion

We validate the discussed DA approaches on mitochondria segmentation in volume EM data. The source dataset consists of two annotated $165 \times 1024 \times 768$ CA1 hippocampus FIB-SEM acquisitions. We consider two target volumes: the first dataset (HeLa) consists of a $64 \times 512 \times 512$ annotated HeLa cell FIB-SEM block. The second dataset (Drosophila) [6] is an annotated $20 \times 1024 \times 1024$ Drosophila serial section Transmission Electron Microscopy (ssTEM) block.

	FT	MMD	CORAL	DANN	Y-NET	FT	MMD	CORAL	DANN	Y-NET
0%	0.70	12.61	29.17	36.08	**40.24**	20.52	5.41	42.78	45.17	**46.26**
10%	91.36	92.79	92.93	92.79	**93.63**	79.22	81.67	**82.60**	81.72	82.44
25%	88.96	91.29	92.27	94.00	**94.64**	79.19	80.83	78.49	81.16	**82.94**

Table 1. Segmentation performance (in terms of IoU) of the discussed DA approaches on the HeLa (left) and Drosophila (right) dataset. The first column indicates the percentage of used target labels.

We compare the regularization-based DA methods and Y-Net to the classical finetuning baseline (FT). We evaluate the target segmentation performance on the test set for variable amounts of target labels by means of the intersection-over-union (IoU) metric in Table 1. Generally speaking, all the DA approaches significantly outperform the finetuning baseline. From the regularization based methods, we observe that DANN performs best on both datasets. However, the proposed Y-Net model is able to improve the latter even further.

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