



TopoUT: Enhancing Cell Segmentation through Efficient Topological Regularization

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Abstract

Cell segmentation plays a crucial role in biological image analysis, serving as a fundamental step with downstream applications in pathology, clinical diagnosis, and drug discovery. Recent advancements in deep learning, especially the Unet architecture, have shown promising results in medical image segmentation. However, accurately segmenting cell boundaries, especially the nuclei, remains challenging due to diverse cell morphology. This paper presents a novel approach that incorporates topological data analysis methods into deep neural networks for cell segmentation. Our proposed method introduces a pair of topological regularization terms, namely loop penalty and cohesion penalty, which efficiently estimate zero- and one-dimensional topological features, respectively. To evaluate the efficacy of our model, we conduct experiments on microscopy images featuring various types of human tissue cells. By capturing rich geometric patterns, our approach outperforms baseline models, offering enhanced accuracy in segmentation. The code of this paper can be found in <https://github.com/temirlansabyrbayev/TopoUT>.

Main Contributions

This paper contribute to the usual cell segmentation framework by creating a new loss formulation for *distance-based cell segmentation*. In particular, we created a new loss that matches not only the distance of the ground truth and predicted distance to cell nucleus and boundary, but also the underlying topological and geometric structure of the distance map. We shown empirically that the improved formulation improves on some common place network formulations.

- **New loss formulation** We propose a new loss formulation for distance based cell segmentation. Unlike prescending work [4, 1], our method applies to cell image structure with a ball shaped structure instead of tubular or network structure.
- **Efficient computation of distances between diagrams** By using the special structure of persistent diagram in our case, we devised a 1-d simplification of wasserstein distances between the ground truth and predicted persistent diagram. This speeds up the computation immensely since there is a closed form for 1d wasserstein distances.
- **More accurate cell segmentation result** We show empirically that the new training loss combined with the commonly used network architecture produce cell segmentation that are consistently more accurate.

In conclusion we have proposed a new formulation for the distance based cell segmentation using persistent homology, which was an idea developed in the fields of computational topology.

Pipeline and Motivation

In this section we introduce the basic pipeline for training the segmentation model. In particular, we explain intuitively the main workflow of the distance based cell segmentation algorithm, and how our

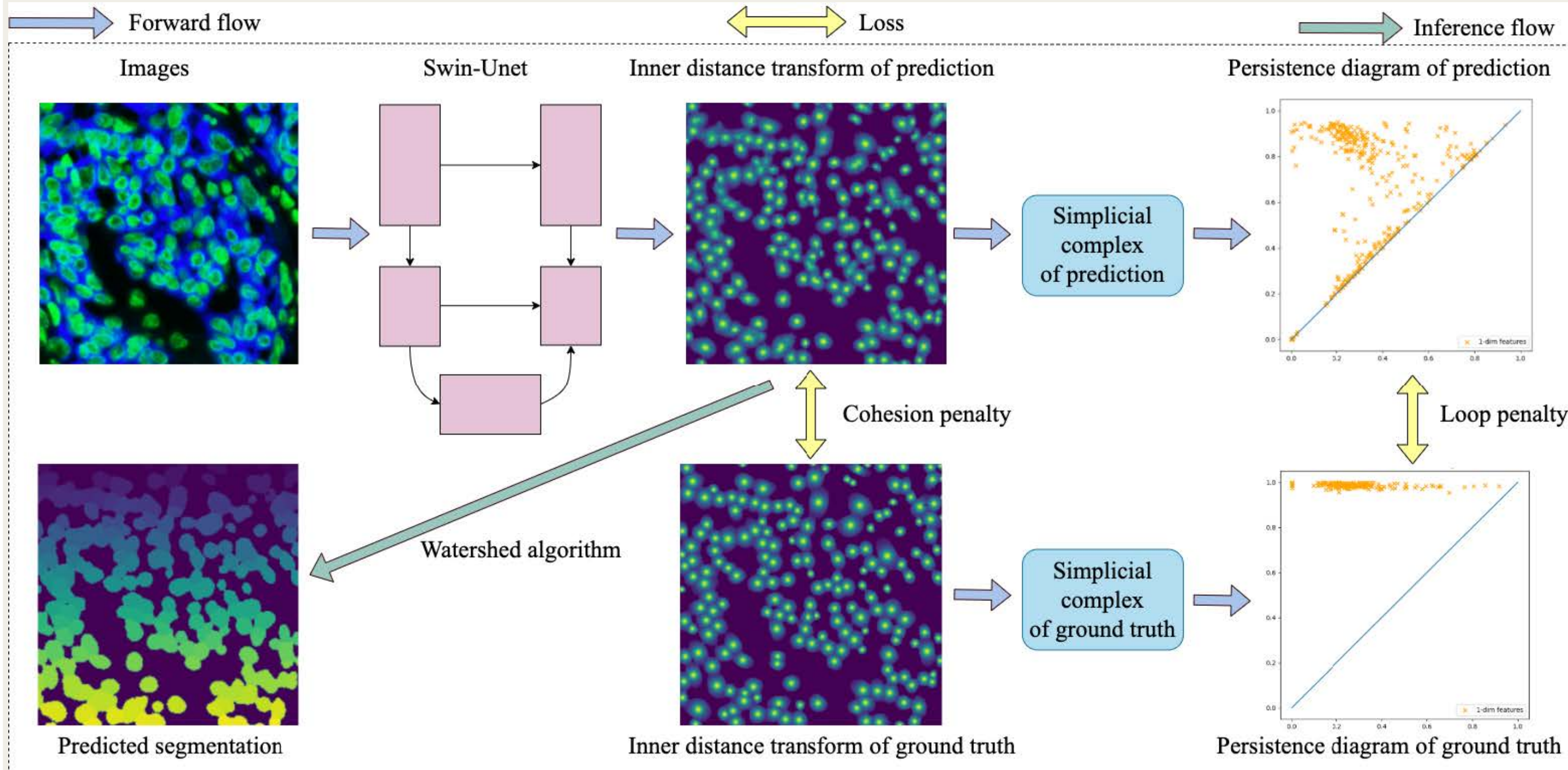


Figure 1. The pipeline of our TopoUT framework for segmentation.

We now briefly introduce the distance based cell segmentation as noted by the above diagram.

- We train the segmentation network in a supervised fashion. Given the segmentation label, we transform the label into images of distance from the boundary of the cell
- Then, we train the network to produce the distance map. The transformed distance from the label are used as the ground truth, which we run regression on.

One noticeable problem for this formulation is that the vanilla loss i.e. mean square error loss between the ground truth and the predicted distance map **does not take into consideration the structure of the distance map**.

In particular, we see that there should be a special ball-like structure to the transformed distance, whereas the commonplace training loss cannot capture.

The new network that we have considered make up for this short-coming by consider *cohesion* panelty and *loop* penalty in the two transformed distance maps.

These losses can captured the structure differences between the predicted distances and the groundtruth distance. Finally we backpropagate these distances to the network to learn. We see emprically that the distances produced are much more stable when trained on :



Figure 2. Improvement in stability of distance map given the new loss

We see in the figure, the distance transformed produced are much more stable and align with the structure of the distance map when trained on the new topologically inspired loss.

Topological Losses

The procedure to construct topological loss function learnt via backpropagation is as follows:

- We first construct lower-star filtration on the pixel values of both the predicted image and ground truth, to extract the i -dimensional topological features $\mathcal{F}_f$ and $\mathcal{F}_g$, respectively. In our implementation, we consider both $i = 1$ and $i = 0$, representing one-dimensional holes and connected components. Nevertheless, we note that current implementation of filtration is inefficient and can lead to slow training. Therefore, we design new approaches to facilitate implementations with lower computational complexity, which will be described later.
- We summarize the extracted information in their corresponding persistence diagram, $\text{Dgm}_i(\mathcal{F}_f)$ and $\text{Dgm}_i(\mathcal{F}_g)$. In both $\text{Dgm}_i(\mathcal{F}_f)$ and $\text{Dgm}_i(\mathcal{F}_g)$, each point $= (b, d) \in [0, 1]^2$ corresponds to a topological structure born at time b and die at time d , where $b < d$.

For each dimension $i = 0, 1$, we can compute:

$$L_i(f, g) \equiv d_W(\text{Dgm}_i(\mathcal{F}_f), \text{Dgm}_i(\mathcal{F}_g))$$

$$:= \inf_{\pi \in \Pi} \left[\sum_{x \in \text{Dgm}_i(\mathcal{F}_f)} x - \pi(x) \right].$$

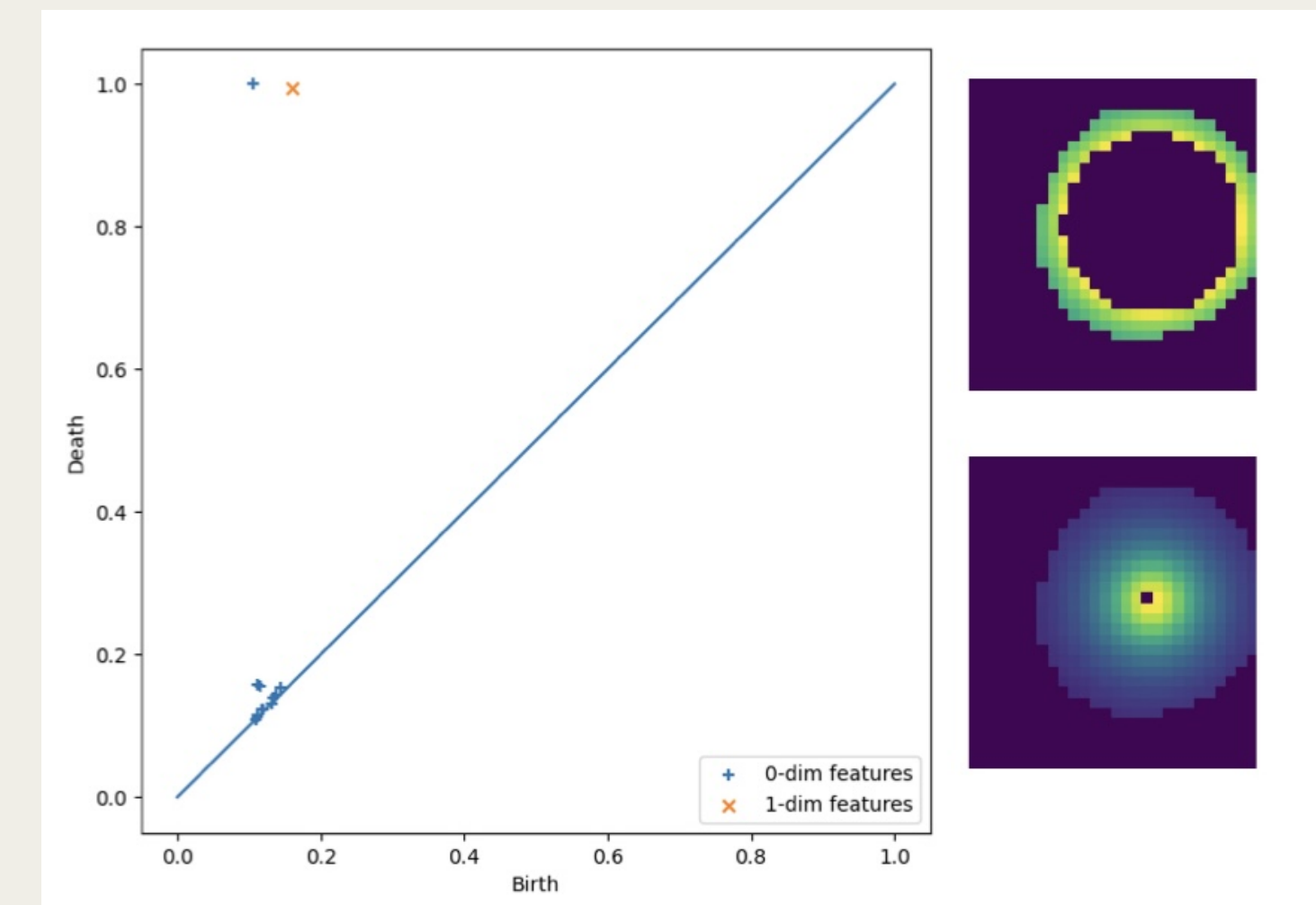


Figure 3. Intuition behind the topological loss

In summary, our loss can be formulated as:

$$L_{\text{topo}}(g, f) = \lambda_0 L_0 + \lambda_1 L_1$$

In particular, an approximation is applied to reduce the time complexity:

$$L_1(f, g) \approx d_W(\text{Birth}_f, \text{Birth}_g),$$

$$L_0(f, g) = \sum_{i, j} \{ (f(i, j) - \tau)(g(i, j) - \tau) \leq 0 \},$$

Results

We use a Swin-Unet composed of 4 encoder blocks and 4 decoder blocks with a window size of 8. We use AdamW [3] optimizer to train the network, with a batch size of 32 and a learning rate of 0.001. The training process include 250 epochs, 50 for pretraining and 200 for fine-tuning. We compare our TopoUT model with other commonly used networks, and topological autoencoder (TAE) [2] with a Swin-Unet backbone.

Model	IoU	F1-score	Recall	Precision
Mesmer	0.8460	0.7332	0.6685	0.8117
Unet++	0.7406	0.7098	0.6394	0.7975
TAE	0.8686	0.7821	0.7486	0.8188
TopoUT	0.8742	0.8086	0.7830	0.8360

The results clearly demonstrate the superiority of TopoUT over models that are either customly designed for TissueNet or widely used. Furthermore, our topological regularization method surpasses topological autoencoders, underscoring the efficacy of the proposed topological features.

Summary and Discussion

We have proposed and validated a new loss for instance based cell segmentation. We show empirically its superiority over other common methods.

We note that there could be plentiful interesting future direction. For example an uncertainty quantification of the topological structure using techniques from causal inference could be fruitful. One might also investigate the robustness of this technique using topological methods.

References

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