Domain adaptation for cell image segmentation in different tissues

Shun Obikane¹
Yuki Kazayama²
Ryo Yamazaki²
Yoshimitsu Aoki¹

¹ Keio University, Japan
² Konica Minolta, INC. Japan

Abstract

Biomedical image segmentation plays an important role in supporting medical applications. Convolutional neural networks (CNNs) contribute to image semantic segmentation. In general, however, difference in distribution between training data and test data lead to accuracy gaps in machine and deep learning. There are many variations in accuracy among data domains. This may be solved through supervision and making a new training model. However, that is tedious and is associated with a high cost of labor in semantic segmentation. In addition to it, usually it needs some experts. The domain adaptation method was applied to solve these problems. Most of previous works focused on target accuracy Previous works think only targetd accuracy. Our experiments show that improve both accuracy in difference of organs. Thus, in the situation in which datasets from an organ are not thorough for learning, training the network on a different organ’s dataset could be sufficient for it to predict accurately in both set.

Keywords: domain adaptation, cell image segmentation

1. Introduction

Convolutional neural networks (CNNs) contributed greatly to semantic segmentation tasks, and have been applied in many medical analyses (Mohseni Salehi et al., 2017), (Fakhry et al., 2017). However, they require a large number of pixel-level annotations, and generally trained models are unable to satisfactorily predict unseen images because of the differences in distribution (domain gaps). This is especially salient in medical settings because of the variations in domain gaps (e.g., type of organs, locality, and amount of data). When new target data arrives from another domain, it must be annotated and the network must be trained for the new model, which is fatiguing. In addition, in medical applications, an expert is frequently required. Domain adaptation methods address these issues. Using source data (fully annotated) and target data (not annotated or rarely annotated), models are able to learn common representations of data and reduce domain shifts between the source and target domains. Previous studies (Hoffman et al., 2018), (Tzeng et al., 2017) focus on synthetic-to-real contexts, so the accuracy of the source is not an aspect to consider. However, in medical applications, source accuracy is also valued. We validated our domain adaptation so that it could be used in cell image segmentation for biomedical applications,
such as with cells. In this work, we treated difference of cancerous organs as a domain gaps, which has the shape of each cells and the condition of staining condition. Experiments demonstrated that our domain adaptation method performed well on target and source domains in such domain gap. Therefore, our research demonstrated that when new data was used (i.e., from a different cancerous organ), the accuracy of networks could be improved without annotating new data. In scenarios in which target datasets are not large enough to learn from, the network is able to make predictions in target and source datasets without annotating target data.

2. Method

Recently, in many studies (e.g., (Ganin and Lempitsky, 2015) (Chen et al., 2017), (Tsai et al., 2018)) domain adaptation method are based on adversarial learning methods and they show its effectiveness. This work adopted this method (Tsai et al., 2018), which is simple and appropriate for medical applications. Figure 1 shows an overview of networks that we adopted. This structure had two modules: segmentation network $G$ and discriminator $D$. Source images $I_s \in \mathbb{R}^{(H \times W \times 3)}$ have full annotations by $Y_s \in \mathbb{R}^{(H \times W)}$ and target images, $I_t \in \mathbb{R}^{(H \times W \times 3)}$ have no annotations. Using their segmentation softmax output $P = G(I) \in \mathbb{R}^{(H \times W \times C)}$ ($C$ is the number of categories) as inputs, the discriminator predicts the domain from which the input data was sourced. $L_{seg}$ is the cross-entropy loss with source data, $L_D$ is discriminator loss which aim to adapt the distribution of target predictions so that it is similar to the source predictions. So, we optimize the min-max criterion and obtained a common representation between the source and target as see blow.

$$\max_D \min_G L(I_s, I_t)$$

$$L(I_s, I_t) = L_{seg}(G(I_s)) + \gamma L_D(D(P))$$

U-net (Ronneberger et al., 2015) is usually used as biomedical segmentation networks. However, in medical applications, we have to consider the consumption of memory and guarantee that it will be accurate. Thus, we adopted DRN-C-26 (Yu et al., 2017).

3. Experiments

Cancer cell images were provided from our own datasets, which were obtained from Konica Minolta. This dataset has 3 classes: tumor cell nuclei and background. The source data was
Table 1: Experimental results (mIoU)

<table>
<thead>
<tr>
<th>Source Model</th>
<th>Target Model</th>
<th>Domain Adaptation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Source (Pancreas, Lung)</td>
<td>0.6127</td>
<td>-</td>
</tr>
<tr>
<td>Target (Bowel)</td>
<td>0.5850</td>
<td>0.5870</td>
</tr>
</tbody>
</table>

Figure 2: Output results (target: bowel)

4. Conclusion

In this paper, we showed that domain adaptation is useful for predicting unseen cancer types. Experimental results showed that domain adaptation improved the network in the contexts of source and target data. Thus, when a domain gap is present in typing cancerous cells, only the source data must be annotated and accuracy must be ensured. However, there are numerous domain gaps in networks that are used for medical applications. Our future work aims to verify whether domain adaptations are effective when the network has difficulty with different camera, various cancer types or type of staining condition.

Acknowledgments

This experiments data was supported by Konica Minolta, INC.
References


