

Automation of Nuclei Identification and Counting In Colon Histology Images

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Abstract—Accurate nuclear detection and quantification has an essential role in the field of nuclear image quantitative analysis. Application of machine learning algorithms in automation of nuclei segmentation and classification tasks showed superior results, specifically in overcoming the challenges such as variability of nuclei types and overlapped shapes of nuclei. Following CoNIC 2022 challenge [6] guidelines, we designed a framework to perform nuclei segmentation, classification and quantification in a dataset of H&E stained colon nuclei images (Lizard dataset [5]). We utilized hovernet model [1] as the backbone of the framework, which has been presented as a top performing algorithm for nuclei detection and classification previously. In our work, we improved the framework functionality by enhancing the data processing pipeline, as well as training and test prediction by extracting overlapped patches, applying color normalization and implementing test-time augmentation. We trained hovernet model over Lizard dataset and showed increased prediction accuracy for both segmentation and classification and cell counting tasks.

1. Introduction

Recently, deep learning methods showed their superior performance in computational pathology tasks such as nuclear instance detection and quantification. Efficient and accurate detection of nuclei can contribute in understanding how tissue component contributes to diseases. These tasks are challenging to perform manually, due to variability in shape and type of nuclei. There are various deep learning based networks presented to do automatic nuclear segmentation and/or classification of nuclei such as Mask-RCNN [10], Triple U-Net [3] and pointNuNet [7]. Evaluating the performance of such networks, shows the high capability of automated deep learning based models in performing nuclei segmentation and classification. Hovernet is the state-of-the-art network, which is introduced to perform simultaneous nuclei detection and quantification tasks within one network.

In our work, we present a framework for simultaneous segmentation, classification and quantification of nuclear instances in histology images. The framework is based on hovernet model [1]. The hovernet architecture uses the prediction of horizontal and vertical distances of nuclear pixels

to their centres of mass, which are subsequently leveraged to separate clustered nuclei. For each segmented instance, the nuclear type is subsequently determined via a dedicated up-sampling branch.

2. Dataset

We utilized Lizard dataset [5], which is the dataset for nuclear instance segmentation and classification, consisting of annotated H&E stained colon tissue nuclei with their class labels. In our work, we generated a training dataset of 256x256 overlapped patches from original images, with 64 and 128 step-size. We implemented 10 fold cross validation to train and test on different partitions of dataset to increase robustness of the model. We trained and test the hovernet model and evaluated the results.

3. Methodology

In this section, we present our framework and utilized deep learning model architecture, as well as other modules we applied in data processing and test phases.

3.1. Model Architecture

For performing both tasks, classification and segmentation of nuclei and cell counting, we utilized hovernet architecture. The Hovernet architecture consists of an encoder which is shared and three branches assigned for three tasks of classification, segmentation and cell counting. The shared encoder has the advantage sharing feature information for multiple tasks and there the whole hovernet model enables an end-to-end training for all tasks. The encoder branch of the network is a preactivated residual network with 50 layers (Preact-ResNet50). The Preact-ResNet50 network showed its superior performance and robustness for feature extraction in segmentation and classification tasks and robustness. Following Preact-ResNet50, there are three separate branches to perform nearest neighbour upsampling. Each branch is designed to do a specific task. Nuclear pixel (NP) branch predicts whether or not a pixel belongs to the nuclei or background. The hover branch predicts the horizontal and

vertical distances of nuclear pixels to their centres of mass. Finally, nuclear classification (NC) branch predicts the type of nucleus for each pixel. The NP and hover branches jointly perform nuclear instance segmentation and the NC branch predicts the type of each nucleus. All three branches have the same architectural units, a stacked series of up-sampling operations and densely connected blocks.

3.2. Test-Time Augmentation

Augmentation methods are applied over the training and test sets to train more robust machine learning models and improve prediction accuracy. When performing the prediction, if the prediction over original and augmented images are merged, this is called test-time augmentation. We implemented test-time augmentation for both training and test phases. In our implementation, given an input train or test image, the model averages the networks predictions over multiple transformations as an ensemble. This method shows superior performance in increasing prediction accuracy. During train phase, we applied affine augmentation such as rotate, shear and scale, elastic transformation, color jittering and Gaussian noise addition. In test phase, we applied only rotate and flip augmentation in different degrees and then de-augment the transformations.

3.3. H&E Stain Color Normalization

Substantial color variations exist in digital histopathology images due to variations in tissue preparation, staining procedures, or digitization scanners. Color variations may affect the performance of Artificial Intelligence (AI) and Machine Learning (ML) algorithms applied to images from different sources. Color normalization techniques have been developed [8] to reduce color variations in datasets prior to quantitative analysis with AI/ML algorithms. In our research, we color normalized the histology images of Lizard dataset, using Vahadane algorithm and investigated the training and inference performance. Applying Vahadane method with a random chosen template image, we couldn't see a great performance change in final results.

4. Metrics

For the metrics, we used the announced metrics by the challenge organizers for both tasks. For nuclear instance segmentation and classification, we calculated multi-class panoptic quality (PQ) [9] to evaluate instance segmentation and classification performance. For cellular composition, we calculated multi-class coefficient of determination (R2) to find the correlation between the predicted and true cell counts.

5. Baseline Results

Our model training was implemented in pytorch on a GPU node with 32GB V100 GPUs. A training and test

	Number of Patches			PQ	Multi PQ+	Multi R2
	Train	Valid	Inference			
256x256 Patches step-size=256	3963	1018	1018	0.614856	0.499754	0.858565
256x256 Patches step-size=128	11624	3008	1018	0.627457	0.558854	0.881924
256x256 Patches step-size=64	39645	10229	1018	0.690917	0.612478	0.556432
256x256 patches color normalized	39645	10229	1018	0.682467	0.597062	0.791553

Figure 1. Training and testing results

dataset consist of 256x256 patches were extracted from original images with different overlapping steps. we trained the model 50 epochs using 2 GPUs simultaneously. We listed our training result and in figure 1 1.

6. Conclusion

Our preliminary experiment results shows the effectiveness of our framework to generate favorable results for the task of simultaneous classification, segmentation and quantification of nuclei images. The prediction results using test-time augmentation, suggesting further investigation into ensemble models and corresponding loss functions.

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