

MF-Hovernet: An Extension of Hovernet for CoNiC Challenge

Vi Thi-Tuong Vo

Department of AI Convergence
Chonnam National University
Gwangju, South of Korea
vothituongvi.cnu@gmail.com

Soo-Hyung Kim

Department of AI Convergence
Chonnam National University
Gwangju, South of Korea
shkim@jnu.ac.kr

Taebum Lee

Department of Pathology
Chonnam National University Medical School
Gwangju, South of Korea
follyman@daum.net

Abstract—Nuclei Identification and Counting is the most important morphological feature of cancers especially in colon. Many deep learning-based methods have been proposed to deal with this problem. In this work, we construct an extension of Hovernet for nuclei identification and counting to address the problem named MF-Hovernet. Our proposed model is the combination of multiple filter block to Hovernet architecture.

Index Terms—Nuclear segmentation, nuclear classification, computational pathology, deep learning.

I. INTRODUCTION

Nuclear segmentation, classification and quantification within Haematoxylin Eosin stained histology images enables the extraction of interpretable cell-based features that can be used in downstream explainable models in computational pathology. The Colon Nuclei Identification and Counting (CoNiC) Challenge [2] requires to develop algorithms that perform segmentation, classification and counting of 6 different types of nuclei: epithelial, lymphocyte, plasma, eosinophil, neutrophil or connective tissue.

This challenge includes two tasks. The first task requires participants to segment nuclei within the tissue, while also classifying each nucleus into one of the above categories. The second task is regression task. The output of this task is how many nuclei of each class are present in each input image.

II. METHODOLOGY

A. MF-Hovernet

In order to solve the problem, a method is adopted, which is combining the multiple filter block and Hovernet model [5] named MF-Hovernet.

The multi-filter block is a stack of 3 convolution layers with different kernel size: 1×1 , 3×3 and 5×5 . The first convolution kernel has a filter size of 1×1 . We apply this convolution to reduces the size of the input vector as well as extract local feature. While small kernels extract small complex features, the large kernel extract simpler features. Therefore, the next convolutional layer was set to 3×3 convolution kernel and uses a down-sampling size of 2 to obtain the global features. The last convolutional layer has a kernel size of 5×5 and a down-sampling size of 2. Each filter learns

different features. Therefore, the multi-filter block is used to deal with the issue by increasing the filter size instead of iteratively alleviating the image size. The combining multiple convolution layers is to yield a better result.

III. EXPERIMENTS

A. Datasets

For the challenge, the Lizard dataset [1] was used, which is the current largest known publicly available dataset for instance segmentation in Computational Pathology. The dataset consists of Haematoxylin and Eosin stained histology images at 20x objective magnification (0.5 microns/pixel) from 6 different data sources. For each image, an instance segmentation and a classification mask is provided. Within the dataset, each nucleus is assigned to one of the following categories: Epithelial, Lymphocyte, Plasma, Eosinophil, Neutrophil, Connective tissue.

The dataset contains 4,981 non-overlapping patch images of size 256×256 provided in the following format: RGB images, Segmentation classification maps, Nuclei counts. The RGB images and segmentation/classification maps are each stored as a single numpy array. The RGB image array has dimensions $4981 \times 256 \times 256 \times 3$, whereas the segmentation classification map array has dimensions $4981 \times 256 \times 256 \times 2$. Here, the first channel is the instance segmentation map and the second channel is the classification map. For the nuclei counts, we provide a single csv file, where each row corresponds to a given patch and the columns determine the counts for each type of nucleus. The row ordering is in line with the order of patches within the numpy files [1].

B. Evaluation

The multi-class panoptic quality (mPQ) in (1) is used to determine the performance of nuclear instance segmentation and classification. For each type t , the PQ is defined as (2).

$$mPQ = \frac{1}{T} \sum_1 PQ_t \quad (1)$$

where

$$PQ_t = \frac{|TP_t|}{TP_t + \frac{1}{2}|FP_t| + \frac{1}{2}|FN_t|} \times \frac{\sum_{(x_t, y_t) \in TP} IOU(x_t, y_t)}{|TP_t|} \quad (2)$$

The R_t^2 is used for regression task as shown in (3).

$$R_t^2 = 1 - \frac{RSS_t}{TSS_t} \quad (3)$$

Here, RSS stands for the sum of squares of residuals and TSS stands for the total sum of squares.

C. Experiment setup

The small patches of size 256x256 pixels was used as input to the MF-Hovernet model. The Adam optimizer [4] is used as the optimization method for model training. The initial learning rate is set to 0.0001, with a total of 100 training epochs. The min-batch size is set as 4. All models are implemented using the PyTorch framework [3].

D. Experiment result

REFERENCES

- [1] Graham, S., Jahanifar, M., Azam, A., Nimir, M., Tsang, Y. W., Dodd, K., ... Rajpoot, N. M. (2021). Lizard: A Large-Scale Dataset for Colonic Nuclear Instance Segmentation and Classification. In Proceedings of the IEEE/CVF International Conference on Computer Vision (pp. 684-693).
- [2] Graham, S., Jahanifar, M., Vu, Q. D., Hadjigeorgiou, G., Leech, T., Snead, D., ... Rajpoot, N. (2021). CoNIC: Colon Nuclei Identification and Counting Challenge 2022. arXiv preprint arXiv:2111.14485.
- [3] Paszke, A., Gross, S., Chintala, S., Chanan, G., Yang, E., DeVito, Z., ... Lerer, A. (2017). Automatic differentiation in pytorch.
- [4] Kingma, D. P., Ba, J. (2014). Adam: A method for stochastic optimization. arXiv preprint arXiv:1412.6980.
- [5] Graham, S., Vu, Q. D., Raza, S. E. A., Azam, A., Tsang, Y. W., Kwak, J. T., Rajpoot, N. (2019). Hover-net: Simultaneous segmentation and classification of nuclei in multi-tissue histology images. Medical Image Analysis, 58, 101563.