

Using Multi-scale SwinTransformer-HTC with Data augmentation in CoNIC Challenge

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Abstract—Colorectal cancer is one of the most common cancers worldwide, so early pathological examination is very important. However, it is time-consuming and labor-intensive to identify the number and type of cells on H&E images in clinical. Therefore, automatic segmentation and classification task and counting the cellular composition of H&E images from pathological sections is proposed by CoNIC Challenge 2022. We proposed a multi-scale Swin transformer with HTC for this challenge, and also applied the known normalization methods to generate more augmentation data. Finally, our strategy showed that the multi-scale played a crucial role to identify different scale features and the augmentation arose the recognition of model.

Index Terms—Colorectal cancer, H&E images, Segmentation, Classification, Counting, Deep Learning

I. INTRODUCTION

The age of colorectal cancer is 60 to 70 years old, and the recovery rate of stage I colorectal cancer can reach more than 90 percent. If detected and treated early, the cure rate is very high [1]. At present, most clinical pathologists used Haematoxylin & Eosin (H&E) images to interpret the type and number of cells when diagnosing whether a patient has colorectal cancer. However, this task is subjective and time-consuming for clinicians and pathologists, so CoNIC challenge 2022 [2] required researcher to develop algorithms that perform segmentation, classification and counting of 6 different types of nuclei within the Lizard dataset [3]. The CoNIC challenge had of two tasks. First, Task 1 is Nuclear segmentation and classification which required participants to segment cells and classify cells into six type of classes such as epithelial, lymphocyte, plasma, eosinophil, neutrophil or connective tissue. Task 2 is Prediction of cellular composition, which required participants to predict how many nuclei of each class are present in each input image.

In the past, many studies have used image processing technology on pathological sections to extract quantitative information such as the number and type of cells for various clinical purposes. Therefore, we review traditional algorithms and deep learning methods for cell segmentation and cell classification. In a previous study, Wang et al. [4] and Yoshida et al. [5] used the classifier to extract features of cell nuclei.

Although the above studies have stated the effectiveness of traditional algorithms, the high resolution of H&E images easily consumes computing resources and time. Most machine learning methods also required a large number of parameter settings, so it is difficult to obtain fast and accurate cell segmentation and classification results in traditional algorithms.

Currently, there are many deep learning methods aid in different cancers or tumor interpretation. Graham et al. [6] developed a deep learning model robust to staining changes in H&E images, and introduced a weighted loss function sensitive to H&E intensity in images to improve the accuracy of nuclei segmentation. Khoshdeli et al. [7] exploited contour prediction as input to a further network for segmentation, and used the fusion of convolutional networks to overcome the complexity of nuclear phenotypes, as well as the problem of overlapping cells. Naylor et al. [8] proposed a deep learning method for cell boundary detection by regressing the nucleus distance map, which also avoids the prediction of regions with blurred contours. In addition, a regression task using distance maps from H&E histopathology images using a fully convolutional network was also used to address the problem of segmenting contact nuclei. To perform a better algorithm in CoNIC challenge, we combined the detection and segmentation backbone, namely Swin-Transformer [9] and Hybrid Task Cascade (HTC)[10]. Swin-Transformer performed better than previous SOTA on COCO, which also succeed for the object detection task, so we choose its detector to be part of our detection backbone. Due to the H&E images containing much representation, we employed Hybrid Task Cascade (HTC) for instance segmentation. HTC adopted a fully convolutional branch to provide spatial context, which may distinguish lots of features on the high representation data. Therefore, we took the advantage of Swin Transformer and HTC to be our algorithm.

II. METHOD

While H&E images with contained lots of cells and issues, our goal is to accurately segment and classify the targets into six categories, as shown in Fig. 1. Hence, we proposed a multi-scale deep learning method, and the general workflow of our method is as follows (Fig. 2).

A. Data preprocessing and Data augmentation

We used the patch-level datasets provided by the challenge, the format of which contained 4,981 non-overlapping images of size 256x256. The datasets were split roughly by 4:1:0.1 for training, validation, testing and we also made sure that the 6 types of cell classes were roughly separated in data distribution. In the beginning, we used random flip, random rotate, resize and normalizing as our preprocessing method. To reduce the influence of inconsistent staining images, we used the skill described in this paper [11] to normalize the H&E images. In addition, we adjusted the parameters recommended in the paper based on our data. The normalized data were used to be our augmentation.

B. Training procedure

In this challenge, we used Swin-Transformer with Hybrid Task Cascade (HTC) model to identify 6 types of cells in the H&E images. Objects in H&E images possess various representations and high complexity, so the input size was set to 256 x 256, 512 x 512, 800 x 800, 1024 x 1024, 1152 x 1152. The Adam warm-up optimizer used in the training of networks. There were two loss functions applied in this algorithm, respectively containing cross entropy loss and smooth L1 loss. We trained the proposed method for 40 epochs and the learning rate was set to 0.0001.

C. Post processing

After training, we used the ensemble method to collect the prediction from 5 different scale which mentioned in above. In our testing stage, we found that small scale could catch the bigger cells, on the other hand, the big scale could search much more small features and cells in the H&E images.

III. EXPERIMENTAL RESULT

In the testing stage, the organizers of the CoNIC challenge used two kinds of evaluation metrics for Task 1 and Task 2 [6]. The Task 1: Nuclear segmentation and classification used the multi-class panoptic quality (mPQ) to determine the performance which contained DQ and SQ. DQ was Detection Quality considered whether the prediction had been detected or not, and finally sum of the TP, FP and FN were calculated in per image. SQ was Segmentation Quality which calculated the IoU and number of TP. In Task 2: Prediction of cellular composition, the official evaluation metric used multi-class coefficient of determination R^2 to determine the correlation between the predicted and true counts is used. The results of the preliminary test of our proposed method were that mPQ was 0.40585 and R^2 was 0.42771, which was showed in Table I.

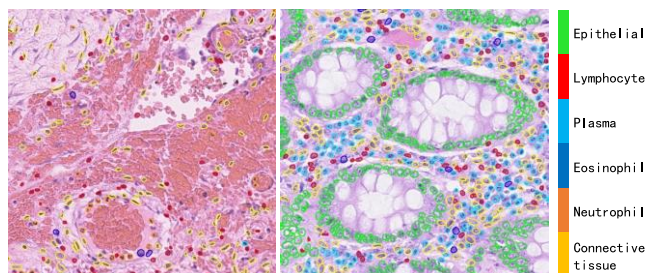


Fig. 1. The examples of dataset provided by CoNIC challenge.

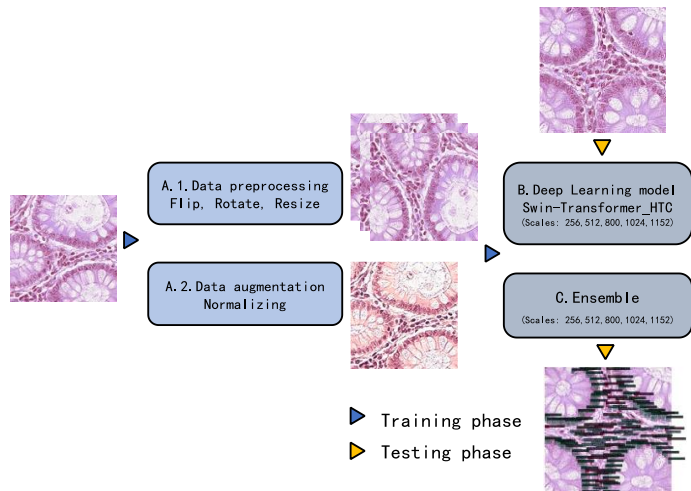


Fig. 2. The workflow of our proposed algorithm.

TABLE I

Performance	Conic challenge	
	Task 1 (mPQ+)	Task 2 (R^2)
proposed	0.40585	0.42771

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