Classification and Segmentation of Vulvovaginal Candidiasis in Microscopic Leucorrhea Images Based on Combined Deep Learning Model

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Abstract

Vulvovaginal Candidiasis (VVC) is a common and serious gynecological disease. Early diagnosis and treatment are of great significance to women's health. However, most hospitals still use manual diagnosis method, which is not only inefficient but also unstable. This paper proposes a VVC image classification and recognition method based on computer vision and deep learning. Our models can greatly reduce the workload of doctors and improve detection efficiency and stability.After testing on 480 samples, our model has reached 92% accuracy, 93% recall and 97%AUC with 23M parameters. The overall performance is superior to the best baseline model that we obtain 93% accuracy, 92% recall and 96%AUC with 56M parameters. Besides, we are the first known paper to propose detection targets for pathogenic bacteria, using different colored rectangles to encircle different types of bacteria.

Keywords: Microscopic Image Classification, Bacterial Object Detection, Computer Vision

1. Introduction

Vulvovaginal Candidiasis (VVC) is one of the most serious vaginal diseases in gynecology, which can increase the incidence of HPV, PCOS and even infertility. At present, the main detection method in the hospital is manual inspection and it's inefficient as well as unstable.

Some scholars tried to introduce deep learning into the field of leucorrhea. (Du et al., 2019) detected trichomonas in leucorrhea based on VIBE method and the accuracy was 88%. (Ju et al., 2020) detected white blood cells in leucorrhea based on Faster R-CNN, with an accuracy of 90.6%. However, we only find one paper using deep learning for VVC classification. (Peng et al., 2021) used an end-to-end method to train the model and the overall accuracy was 93%.

In this paper, we apply a two-process model based on computer vision and deep learning. Our model can used for VVC classification and main pathogenic bacteria detection. Firstly, we focus on the implementation of Transfer Learning with ResNet50 to improve the accuracy of VVC classification. After that, we use Mask R-CNN to achieve mycelium and spore contouring.

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2. Method

Classification Model

The classification model aims to achieve VVC positive-negative classification of pathological images through end-to-end training. We chose ResNet50, one of the most robust residual network, as backbone network. We also found that fine tuning the pre-trained CNN network can improve the accuracy of classification. Therefore, we chose ResNet50, which was pre-trained on ImageNet consisting of 1.2 million images, as the model and ensured that the model was suitable for the classification task in this paper by fine-tuning its fully connected layer. We fine-tune the tail layer of the model, and the last three layers in the pre-trained model: full connection layer fc1000, fc1000 softmax and classification layer fc1000 are replaced with our customized new layer.

Object Detection Model

Object Detection Model aims to identify mycelium and spores in pathological images, which are two common modes of presence of the VVC causative agent Pseudomonas albicans. In this paper, the backbone network of combination type Resnet50+FPN is used for multi-scale feature extraction of mycelium and spores in microscopic images. The region suggestion network, consistent with Faster R-CNN, is responsible for integrating the feature extraction results and generating suggested target regions. The head branch classifies the generated suggested regions and regresses the bounding boxes to increase the model segmentation accuracy. In the model of this paper, there are two categories of targets, mycelium and spores, so the head branch finally needs to dichotomize the extracted targets and display them separately by different colored boxes.

3. Result

Classification Model Result

We divided the data into training set, validation set and test set according to the ratio of 8:1:1. After expanding 790 positive images, 3160 positive training data were obtained. At the same time, 3050 negative training data were randomly under-sampled to prevent low detection rate of positive features.

First, we collect the probability predicted by the model for each test data and analyze the data to obtain important metrics such as ROC and AUC. After adjusting the parameters and thresholds, the final model accuracy was 91.9% and the recall rate was 92.9%.(TP=92, FN=7, FP=32, TN=349)Table 1 shows the comparison of the performance of our method and existing methods.

Object Detection Model Result

For general segmentation tasks, an important measure of model accuracy is the mean average precision(mAP), which is the intersection of the model-predicted region A and the correct region B compared to the concatenation. However, in the identification of VVC positives, there may be 0-30 spores or mycelium in a single image with different morphologies, obscuration, overlap and other complications. As shown in Figure 1, it is difficult and unnecessary for the annotator to accurately annotate all suspected targets in the data preparation stage. Instead, it's enough for the doctor to find only one spore or mycelium.

Table 1: Comparison with different methods

Methods	Backbone	Epoch	Accuracy	Recall	AUC	Params
(Peng et al., 2021)	Inception	100	93%	93%	96%	56M
(BohuaLou, 2019)	VGG-Net	1320000	78%	Not Given	Not Given	138M
Proposed Model	ResNet	35	92%	93%	97%	23M

Therefore, we reasonably relaxed the model prediction requirements: it was considered correct for positive data as long as at least one target was accurately marked during the testing phase, and for negative data as long as no region was marked. Figure 2 shows the effect of model labeling in the form of bbox, and it can be seen that the model identified 24 suspicious targets and used green boxes to indicate mycelium and red boxes to indicate spores. The model can correctly label 88.5% of the accuracy and 96.9% of the recall rate.
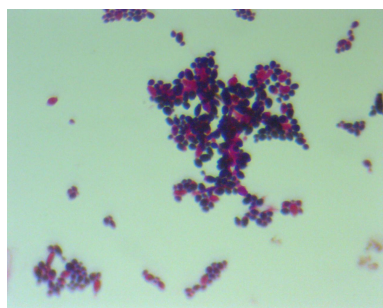

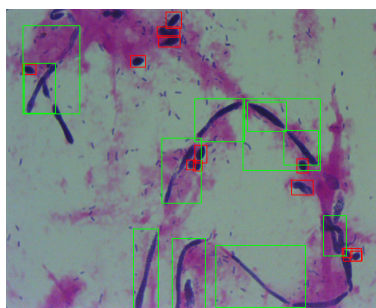Figure 1: Too many spores in one image

Figure 2: Performance of our method

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