YoNiC

1st Devika R G
Department of Electronics and Communication
College of Engineering
Trivandrum, India
d-tve20jan020@cet.ac.in

2nd Densen Puthussery
FMS Lab
Founding Minds Software
Cochin, India
densen@foundingminds.com

3rd Hrishikesh P S
FMS Lab
Founding Minds Software
Cochin, India
hrishikesh@foundingminds.com

4th Jiji C V
Department of Electronics and Communication
College of Engineering
Trivandrum, India
jijicv@cet.ac.in

***Abstract*—Nuclear quantification of histology images with haematoxylin and eosin stains can help to extract interpretable information from cell-based features that aids in computational pathology. There exists many methods that solves the joint task of nuclear segmentation, classification and counting. This work is focused on counting the number of instances of nuclear types in whole-slide images. Specifically, we address this problem as an object detection problem where the goal is to localize the nuclei instances by finding the rectangular boxes that bounds them and then count the occurrence of each nuclei type.**

***Index Terms*—YOLO, nuclei counting, conic**

I. Introduction

The inception of deep learning has brought about huge advancements in the field of computational pathology. Specifically, the deep neural networks employing convolutional neural network (CNN) architecture has proven to be very effective in vision based tasks like medical image segmentation [2]. The type of task i.e, whether it is segmentation of background from foreground, semantic segmentation or the quantification of cell types etc. usually depends on the nature of prognosis. For example, to study the growth of specific tumor types from magnetic resonance images (MRI) or CT scans, the preferred methodology may be semantic segmentation so that one can localize the tumor cells with a pixel-level precision. In case of detecting the presence of specific types of skin lesion, one may simply resort to an object detection approach to localize the lesion to a bounding box defining the structure.

In certain cases, the problem can be further simplified to merely counting the number of occurrences of a specific cell type, like tumor cell for example for its application as a prognosis tool. In accuracy-critical applications like medical diagnosis, the availability of quality dataset is of paramount importance. One of the limiting factors in medical AI is the availability of such clean datasets. As such, the choice of methodology may also depend on the availability of such quality datasets. In this work, the problem being addressed is the quantification or counting of 6 types of nuclei in Whole-Slide Images (WSI) of colon tissue. To this end, we propose to approach the problem as an objection detection task, wherein the goal is to identify the bounding box and type of every nuclei in the image. Once the nuclei is localized, the count of each type can easily be calculated from the output tensor.

This work was done as a part of Track 2 of the Colon Nuclei Identification and Counting (CoNiC) Challenge [6] hosted as a part of the International Symposium on Biomedical Imaging (ISBI) 2022.

II. Dataset and Preprocessing

The dataset that has been used to study the problem is the Lizard dataset [3]. It consists of histology images of colon tissue with semantic segmentation annotation of six different nuclear class - epithelial cells, neutrophils, lymphocytes, plasma cells, eosinophils and connective tissue cells. There are 4981 images of the resolution 256×256 in the Lizard dataset. Of these, we split 4800 and 181 into training and validation sets. Each image is associated with an instance segmentation map and a classification map of 256×256 resolution denoting the pixel-level annotation of the nuclei instance id and the nuclei class id.

A. Label Conversion

In our approach, we propose to view the nuclei quantification task as an object detection problem. As such, the instance and class map needs to be converted into corresponding bounding box labelling format. To this end, we extracted the coordinates of the top-most, left-most, bottom-most and right-most pixels of each of the nuclei instance and extracted the centre x, y coordinates and the width and height of each bounding box. Using the corresponding class map, the class id of the bounding box was calculated and thus the segmentation annotation format was converted to bounding box annotation format. The bounding box annotations were then normalized to the range $[0, 1]$ so that it can be directly used for model training.

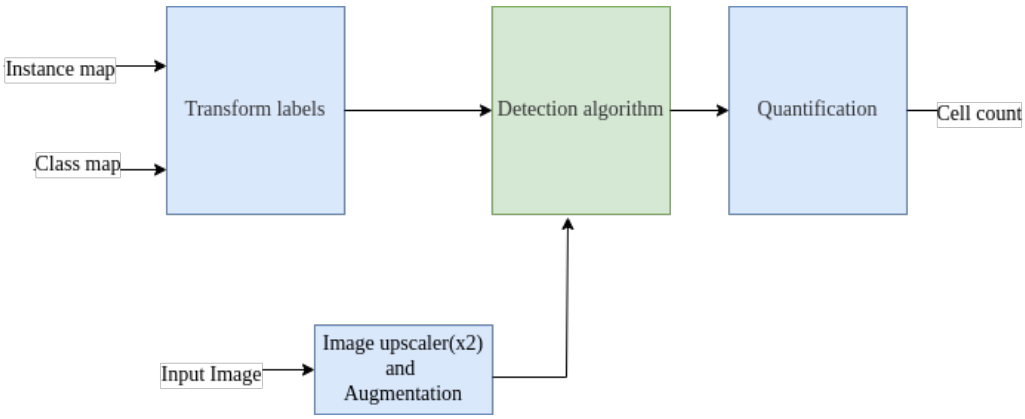

Fig. 1. Overview of Proposed Architecture

B. Data Augmentation and Pre-processing

Since the object detection algorithm we employed was a derivative of You Only Look Once (YOLO), [5] with four different stride values, the images were resized to 512×512 resolution using bi-cubic interpolation so that the features would be of reasonable resolution even at the last stride level. For better generalization, we employed multiple data augmentation strategies including random hue, random saturation, random brightness, random translation, random scaling, random shear, random flip up/down and random flip left/right.

III. Method description

For object detection task, we propose to employ YOLO which is one of the most performing algorithms in terms of mean average precision score on several benchmark datasets like MS COCO for object detection. It is an anchor based single stage object detection algorithm. In the proposed method, we are employing YOLO algorithm with upto four strides. The accuracy of anchor based detection algorithms depend on the anchor priors. Due to this reason, we calculated the most suitable anchor values using genetic algorithm so that they are a proper fit for the dataset. Similarly, other hyper-parameters like number of anchors, etc. were also found using genetic algorithm. After generating the bounding box preditions, the next strep is quantification, wherein we simplify the bounding box data into a simple tensor containing the count of different nuclei types.

IV. Result

Loss	Score
R2	0.205
MAE	4.495
MAAPE	0.412

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