HoverNeXt

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*—Segmenting and classifying Haematoxylin Eosin stained histology images is a fundamental element in the digital pathology workflow. The automated method for nuclei identification faced a major challenge due to its large intraclass variability. The CoNIC Challenge aims to develop an algorithm for segmentation, classification, and counting of nuclei within the current largest known publicly available dataset. In our work, we present a combined Convolutional Neural Network for simultaneous nuclear segmentation and classification with the information of vertical and horizontal distance of nuclei pixels from the center of mass. These distances are also used for the segmentation process. Through a devoted up-sampling branch, the network predicts the type of nucleus for each segmented instance. Compared to other state-of-the-art models, the proposed model gives a good result.**

***Index Terms*—Convolutional Neural Network, Nuclear segmentation, Classification,**

I. Introduction

Medical image segmentation and classification become one of the essential tasks in medical diagnosis. It has been widely used by the medical analysis community. Nuclear Segmentation, classification, and quantification within haematoxylin and Eosin-stained histology images enable us to extract cellular features which can be used in the forward path in computational pathology. Manual evaluation of Haematoxylin and Eosin slide by visual assessment suffers from low throughput and may lead to intra and inter observer variability. To overcome this difficulty digital pathology technique is used where digitized Whole Slide Images(WSI) are obtained from glass slides through scanning devices. This WSI helps in efficient processing, analysis, and management of the cell tissue specimen. Each WSI contains[hover] thousands of nuclei of various type and are analysed for finding proper clinical output. Type of nuclei refers to the cell type to which it is located. Nuclear features help to identify survival diagnosing the grade and type of disease. To use nuclear features for the downstream analysis nuclear segmentation has to be done as the initial step. But this is a tedious task since nuclei are seen at a high level of heterogeneity. There is a remarkable difference in shape, size, and chromatin pattern between and within a different cell types, disease types, or even from one region to another within a single tissue sample. So normally nuclei classification is done using two disjoint models one for detecting each nucleus and then another for performing nuclear classification. The robustness of deep learning methods makes them ideal for the segmentation and classification of medical images. The proposed method presents a deep learning approach for simultaneous segmentation and classification of colon nuclei instances in histology images. The CoNIC: Colon Nuclei Identification and Counting Challenge [5] is hosted as a part of the International Symposium on Biomedical Imaging (ISBI) 2022. The main aim of the challenge is to develop algorithms that perform segmentation, classification, and counting for six different types of nuclei within the current largest known publicly available nuclei-level dataset in CPath, containing around half a million labeled nuclei. The challenge is divided into two tasks.

1) Nuclear segmentation and classification: To develop an algorithm to segment nuclei within the tissue and to classify each nuclei into one of the following categories: epithelial, neutrophil or connective tissue.
2) Prediction of cellular composition: To develop an algorithm to predict number of nuclei of each class in the given input image.

II. Material and Methods

A. Dataset

Dataset used in the challenge is Lizard Dataset, 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 from 6 different data sources. The further detail of the dataset is available in the original dataset paper. [3]. In the dataset, patches of size 256 X 256 which are generated from the original dataset is also available.

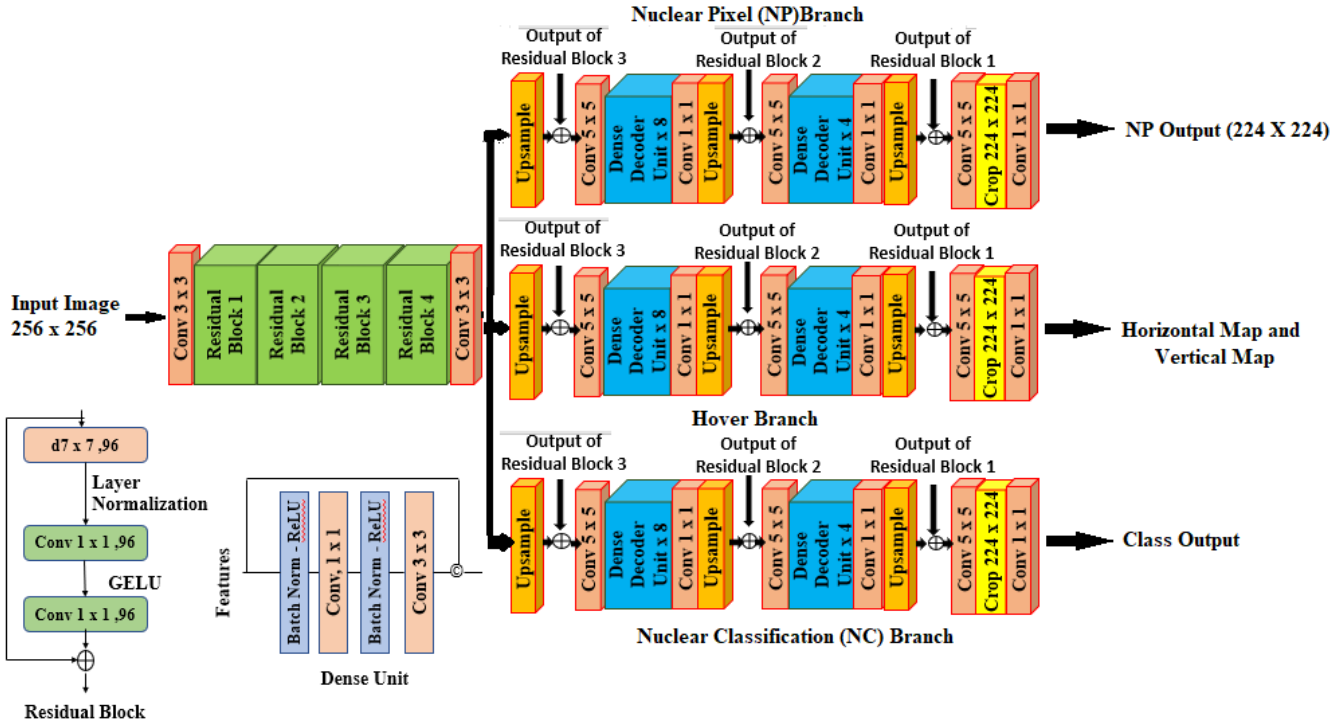

Fig. 1. Overview of Proposed Architecture

B. Methodology

Deep neural networks are used to extract prominent features of the cell tissue. The detailed architecture of the whole network is as shown inFig 1.

C. Encoder

The encoder block is used as a feature extraction network.The feature extraction network is the modified form of ConvNeXt model. [1]. Modified form ConvNeXt consists of a stem block and four residual blocks. The detail of the output size and operation of each residual block in the encoder is shown in the Fig 2. Each Residual block consists of a layer normalization and two 1 X 1 Convolution layer.

D. Decoder

Following the encoder block nearest neighbour upsampling is performed via three distinct branches to obtain accurate nuclear segmentation and classification. The three distinct branches are (i) nuclear pixel (NP) branch, (ii) Hover Branch, and (iii) nuclear classification branch. The NP branch predicts whether the pixel belongs to nuclei or background, whereas the Hover branch predicts the horizontal and vertical distances of nuclei pixels to their center of mass. The NC branch predicts the type of nucleus for each pixel.

E. Losses

There are 3 main outputs from the decoder (i) nuclear pixel (NP), (ii) prediction of horizontal and vertical maps(iii) nuclear classification output. For nuclear pixel and nuclear classification we use binary and multi-class focal loss [4] along with dice loss. For the horizontal and vertical map outputs mean squared error(MSE) loss is used.

	Output Size	ConvNeXt -T
Stem	256 X 256	3 X 3, 96, Stride 1
Res1	256 X 256	[d7 x 7, 96; 1 X 1, 384; 1 X 1, 96] X 1
Res2	128 X128	[d7 x 7, 192; 1 X 1, 768; 1 X 1, 192] X 1
Res3	64 X 64	[d7 x 7, 384; 1 X 1, 1536; 1 X 1, 384] X 1
Res4	32 X 32	[d7 x 7, 768; 1 X 1, 3072; 1 X 1, 768] X 1

Fig. 2. Detailed Architecture of ConvNeXt

III. Network Training

The proposed encoder-decoder architecture was trained for 50 epochs with batch size 4 on a 16 GB Tesla-V100 GPU. A lower batch-size was used because of the restricted availability of hardware resources. For optimization Adam optimizer was used with a learning rate of 1e-4 and a decay rate based on Cosine Annealing was used.

IV. Evaluation and Result

Each task of the challenge is evaluated based on a single metric. For evaluating the nuclear instance segmentation and classification a multiclass panoptic quantity(PQ) is used as the metric. The metric PQ is calculated per image and the image level results are averaged. For the second task, a multiclass coefficient of determination is used to determine the correlation between the predicted and true counts.

Metric	Score
PQ	0.402
PQ+	0.399
mPQ+	0.252

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