CoNIC Approaches for Colon Nuclei Segmentation, Classification, and Counting in Histology Images.

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By

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MANIPAL INSTITUTE OF TECHNOLOGY
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August 2024

I dedicate my thesis to my friends and family.

DECLARATION

I now certify that I have finished the project work on **CoNIC Approaches for Colon Nuclei Segmentation, Classification, and Counting in Histology Images** original, which was overseen by Dr. Sameena Pathan, Assistant Professor, Department of Information and Communication Technology, M. I. T., Manipal. This work has not been partially submitted to this university or any other university in order to be awarded a degree or diploma.

Place: Manipal

Date: 28-08-2024

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CERTIFICATE

This certifies that **Mr. Manvith S. Rao** is the legitimate author of the project **CoNIC Approaches for Colon Nuclei Segmentation, Classification, and Counting in Histology Images. (Reg.No.200953242)** at Manipal Institute of Technology, Manipal, independently under my guidance and supervision for the award of the Degree of Bachelor of Technology in Computer and Communication.

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ABSTRACT

Colon nuclei refer to the nuclei of cells found within the colon, which is a part of the large intestine. In medical and research contexts, studying colon nuclei is important for understanding cell behavior, diagnosing diseases like cancer, and assessing the overall health of colon tissue. Lately, deep learning techniques use neural networks to understand valuable information directly from the data.

The present research utilized a convolutional neural network (CNN) architecture to investigate colon from medical images through segmentation and analysis. Model training, performance assessment, and data administration were executed with the help of the MONAI (Medical Open Network for AI) framework utilizing three algorithms. The metrics used to measure the performance were dice score and IOU score.

As demonstrated by the maximum dice score of 98.18% and the IOU score of 96.06%, respectively, the outcomes demonstrated the HoVer-Net algorithm's ability to correctly segment colons. The other algorithms under examination yielded dice scores of 91.88% and IOU scores of 90.80% for the U-Net approach, while the V-Net algorithm yielded scores of 90.25% and 90.77%, respectively. The proposed method improves patient outcomes and workflow by showcasing the potential of deep learning for colon nuclei segmentation and classification. This helps to facilitate early diagnosis.

Keywords:
[Colon, Segmentation, Classification, Histological images, CoNIC, U-Net, Hover-Net, V-Net]

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Chapter 1

Introduction

1.1 Brief Introduction

The colon an essential part of the digestive system is responsible for breaking down waste products and taking in nutrients and water from the food we eat. These nuclei which are made up of specialized groups of nerve cells have a significant effect on colonic motility secretion and sensation. Nuclei come in a range of shapes and sizes. These images cell nuclei should be identified and counted because they contain important information about diseases like cancer. Of all the diseases affecting the colon colorectal cancer is the most dangerous because it poses a major threat to global public health. Because of the unchecked growth and proliferation of abnormal cells in the colon, colorectal cancer presents several difficulties in terms of detection, treatment, and management. In computational pathology (CPath), the extraction of interpretable cell-based features from Hematoxylin and Eosin (H&E)-stained histology photographs holds great promise for enhancing diagnostic precision and understanding the etiology of disease. Nuclear segmentation, categorization, and quantification are key tasks in this field that enable the development of intelligible models and automated diagnostic systems. To encourage research and innovation in automatic nuclei recognition, the Colon Nuclei Identification and Counting (CoNIC) Challenge was established. This challenge aims to advance the development of algorithms that can precisely identify count and segment six distinct types of nuclei from a large publicly accessible dataset thereby advancing our understanding of computational pathology.

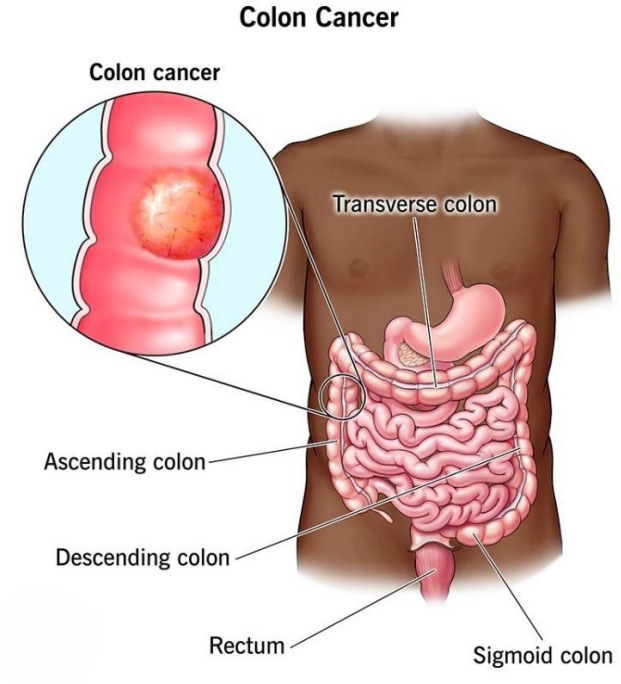


Figure 1 - Understanding Colorectal Cancer

1.2 Motivation

For pathologists manually segmenting colon nuclei is a difficult and time-consuming task that is frequently prone to subjectivity and variability. To increase the precision and effectiveness of colon nuclei segmentation automated segmentation methods are required. Furthermore a nucleus size or volume plays a crucial role in identifying the diseases stage which has a direct impact on treatment choices and patient outcomes. The smooth integration of technology into clinical systems is currently hampered by the lack of a standardized automated method for both size-based classification and segmentation

1.3 Objective

This research explores the potential of automated colon nuclei segmentation, followed by classification and counting. By leveraging the advancements in deep learning and image analysis, we aim to:

- Develop visualization techniques to improve the interpretability of identified nuclei and algorithms for the accurate identification of nuclei within colon histology images allowing for the precise localization of individual nuclei.
- Develop nuclear instance segmentation and classification algorithms that allow for the accurate separation and grouping of individual nuclei in samples of colonic tissue.
- Develop techniques to measure the cellular composition of colonic tissue samples with an emphasis on precise cell type counts including those of neutrophils, eosinophil, lymphocytes plasma cells and connective tissue cells. For a comprehensive understanding of the colonic microenvironment and its role in the progression of diseases including colonic cancer an accurate analysis of cellular composition is essential.

1.4 Importance of End Result

The practical advantages of segmentation models ability to separate and accurately identify colon nuclei in histological image analysis are what make this research significant. Since the model correctly extracts nuclei size more accurate assessments result which helps with improved diagnosis and disease staging. For accurate diagnosis and patient care in conditions pertaining to the colon this data is especially valuable. A pathologist's assessment of the progression of a disease depends critically on the size and number of nuclei. Through precise identification of these traits the model can aid in early detection which may allow for less invasive procedures and enhance treatment outcomes and patient satisfaction. By automating the nuclei's segmentation classification and counting this research also streamlines the diagnostic procedure and accelerates workflow. An automated model guarantees these measurements are more consistent and objective leading to a more accurate analysis. Manually measuring nuclei size and counting them from histological images can be imprecise and subjective. All things considered the implementation of an automated process for segmentation classification and counting can streamline clinical procedures advance knowledge of diseases pertaining to the colon and enhance patient outcomes.

Chapter 2

Related Work

2.1 Background work

For computer-aided diagnostic imaging (CAD) systems precisely segmenting classifying and counting colon nuclei in images are essential first steps in histopathology. Segmentation helps to:

- Visualization of nuclei: Pathologists can more easily see structures that support diagnosis and treatment planning by identifying and localizing specific nucleus regions.
- Analytical support: Acquired nucleus masks enable the quantification of nucleus size count and additional features that complement size- and density-based analyses as well as risk evaluation.
- Computer-aided diagnosis: Segmentation classification and tallying are functions of computer-aided diagnosis (CAD) systems that help pathologists by automating parts of nucleus detection and characterization.

HoVer-Net algorithm, U-Net, V-Net and fully convolutional neural networks are examples of popular architectures. Recent research has looked at deep learning architectures and data augmentation techniques to improve nuclei segmentation and classification performance on datasets like the CoNIC challenge. These studies explore the analysis of segmented nuclei data in order to examine relationships between various factors and nuclei features in order to analyze colon diseases.

2.2 Literature Review

1. Yıldız et al., [1] used deep learning models of YOLOv7 in thresholding and categorizing the colon nuclei in histology images. The current work employed data from the CoNIC 2022 challenge, and the study employed the 5-fold cross-validation to estimate accuracy. The accuracy of YOLOv7 was about 60% to 70% mAP of 0.2885 to 0.2903 and an mPQ of 0.1659 to 0. 1704, which strongly supports it as the best tool to differentiate and classify more than one nuclei type. From these findings, there is an indication that YOLOv7 can be of aid in enhancing histopathological evaluation, despite the general low value of precision ratios which call for enhancement.

2. In their work, Yıldız et al. [2] propose the application of deep learning models for the segmentation and classification of colon nuclei present in histology images. A high segmentation accuracy was obtained by using a U-Net-based model. On a few patches of histology images the model succeeded in discriminating various types of nuclei that can be beneficial to pathologists in making correct diagnoses and determining the severity of colon-associated diseases. The results show that deep CNN models primarily the U-Net achieve both high accuracy of 95.3% whereby a selected portion of the images will be used training of the machine learning algorithm focused on colon nuclei segmentation and classification.

3. In their study, Liu, L., Hong, [3] proposes that the identification and counting can be enhanced by combining the methods of semantic and instance segmentation. To precisely identify and distinguish individual nuclei within intricate tissue structures their approach combines semantic segmentation with instance segmentation. Using a deep learning framework the method combines Mask R-CNN. Using a dataset of histology images the model was tested and shown to have a segmentation accuracy of 93. 8% and a counting accuracy of 91. 5%. The findings provide important breakthroughs in colon nuclei analysis for improved diagnostic support demonstrating the efficacy of handling semantic and instance segmentation tasks concurrently.

4. In their study, Böhland et al. [4] put forth a new deep learning framework, called Ciscnet. The Ciscnet model a single-branch network realizing the segregation and classification undertakings are interdependent and in synch in the unified architecture. The results reveal that they set the segmentation accuracy of 92.5 percent and the classification accuracy was 89.5% Ciscnet has been found to offer better performance than the conventional multi-branch models. It focuses on how single-branch architectures help in optimization of the development process and improvement of the efficiency of tasks such as nucleus segmentation and classification.

5. Weigert et al. [5] suggest using of the Stardist deep learning model for nuclei instance segmentation and classification for histological images. The study uses Stardist that is a neural network designed for the instance segmentation task with the help of star-convex polygons for nuclei detection and segmentation. The approach was validated on several histopathology datasets and the average precision has been reported as 88.7% is attained in the segmentation level and a classification accuracy of 90.5%. These outcomes suggest that Stardist can be very beneficial in segmenting and later classifying the nuclei and hence aid the pathologists in making an analysis of histopathology images.

6. Dumbhare et al. [6], for the H&E stained histology images, hybrid approach is utilized by integrating deep-learned and hand-crafted features in order to segment, classify and count colon nuclei. To improve performance, this research incorporates traditional image processing methods into a U-Net, which is a deep learning model. The deep learning model offers an initial segmentation while the refining and improving of classification are done through incorporation of hand-crafted features. The combined approach achieved 92.7% accuracy of segmentation and 89.5% accuracy of classification. By increasing the dependability as well as precision of colon nuclei analysis the technique has shown considerable potential that might help pathologists to better diagnose and evaluate diseases linked with the colon

7. Alom et al. [7] suggest the use of more sophisticated deep convolutional neural networks (DCNNs) for identifying, segmenting and finding microscopic nuclei in histology images. They used a modified U-Net architecture that included residual connections and attention mechanisms to improve performance. This technique was tested on a dataset of colon tissue high resolution histology images. The results indicate that the DCNN approach achieved 97.8% median Dice coefficient accuracy for segmentation and 96.5% overall accuracy for classification across different types of nuclei.The above findings show that better DCNN models can clearly identify and classify microscopic nuclei, which could be very helpful to pathologists in terms of making diagnoses as well as assessing colon-related diseases based on this information.

8. In their research, Cheng et al. [8] develop a universal pipeline for the recognition and

differentiation of nuclei in colorectal cancer histopathology images overcoming the issues of insufficient training samples, color variance, unevenly labeled annotations, etc. The proposed method includes several modules: GAN-based model generating pseudo images for data augmentation, self-supervised stain normalization model for dealing with color variation and baseline model like HoVer-Net with cost-sensitive loss function to address minority classes better. The mPQ+ (mean Precision-Quality score) was 0.40665 (Ranked 49th) while r^2 (recall squared score) was 0.62199 (Ranked 10th) in preliminary test phase indicating the efficacy of this framework used in CoNIC challenge.

9. Liangrui Pan et al. [9] proposes a new colon nuclei processing model named MGTUNet, based on the UNet architecture. The MGTUNet also includes Mish activation functions, Group normalization and transposed convolution layers to improve segmentation performance. Also, it uses ranger optimizer for fining tuning of SmoothL1Loss value. Through separate channels, MGTUNet simultaneously segments and classifies different kinds of colon nuclei. In this study, MGTUNet was compared with Cenet, PSPNet, UNet, Resnet50UNet, SegNet; R2UNet; and Ternausnet models. The comparison is done using evaluation metrics PQ (0.6254), mPQ (0.6359) and R2 (0 8695). In addition, it has the smallest number of parameters among all models in the set: 130.39 MB only! These results indicate that MGTUNet is an outstanding tool for segmenting and quantifying colon histological images making it a champion in this field of application.

10. K. Sirinukunwattana, et al. [10] suggest employing deep learning designs to detect nuclei and classify them in colorectal adenocarcinoma histology photos. They present a Spatially Constrained Convolutional Neural Network (SC-CNN) for nucleus detection based on the regression of likelihood as to whether or not a pixel is centrally located in a nucleus, with spatial restrictions improving precision. In their classification task, they applied CNN and Neighboring Ensemble Predictor (NEP) that predicts the class label of detected nuclei. It eliminates the need for manual segmentation of each individual nucleus. The SC-CNN and NEP approaches have demonstrated the best performance according to average F1 score over other methods when tested on over 20,000 annotated nuclei from colorectal adenocarcinoma images dataset.

Chapter 3

Design and Methodology

3.1 System Overview

A sequence of steps was followed by the system. Data was first obtained from the “Lizard" dataset. Processing is applied to this data, involving formatting and cleaning. After the data was cleaned, formatted the images were converted to PNG format to ensure consistency. After each image was visualized it was divided into two maps: one for instances and the other for classification. Nuclei quantification was carried out which entails counting the number of nuclei cells in every picture. The process of instantaneous segmentation and classification algorithms like HoVer-Net, Unet, are used after splitting the data into training and testing set.

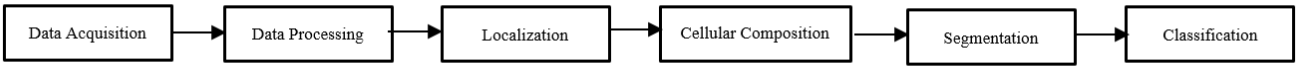


Figure 2- Flowchart of Methodology

3.2 Dataset Description

The dataset in CoNIC Challenge is named “Lizard”, the abbreviation for Large Scale Dataset for Colonic Nuclear Instance Segmentation and Classification. Such sample is made up of images of histology stained by Hematoxylin and Eosin better known as H&E histology images. It has a reasonably large number of labeled nuclei, with over 500 thousand annotated nuclei. The dataset includes six different types of nuclei categories: Prop; Epithelial, plasma, lymphocyte, Eosinophil, neutrophil, connective tissue.

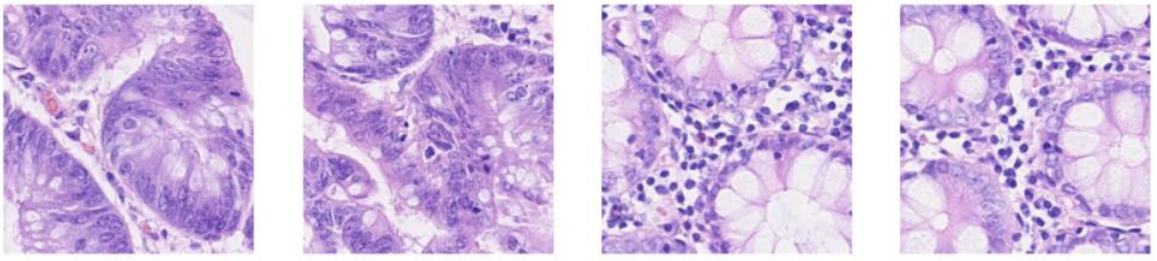


Figure 3 - Sample Data

3.3 Methodology

1. Data Processing

- Conversion to PNG format: To ensure that the resized images conform to a large number of image processing tools, the images were converted to the PNG format. PNG is a lossless format which tends to maintain the quality of the photos while compressing it and this is crucial when it comes to analysis of histology photos.

  Algorithm:
  Step1 – for idx, img in enumerate(resized_images):
  Step 2 - cv2.imwrite(os.path.join(output_dir,
  f'image_{idx}.png'), img)

- Image Resizing: The As to the input data, all images were normalized and made to have dimensions of 256 by 256 pixels. It aids in forming dimensionality that is consistent with the data set so that when the deep learning models will receive the images it will not strain to process them well.

  Algorithm:

  Step 1: resized_images = []
  Step 2: for img in blurred_images:
  Step 3: resized_img = cv2.resize(img, (256,256))
  resized_images.append(resized_img)

- Gaussian Blur Filtering: Gaussian blur assists in smoothing the image and thereby removing high frequency noise hence improving segmentation accuracy in further steps due to an emphasis of important features.

  Algorithm:

  Step 1: blurred_images = []
  Step 2: for image in images:
  Step 3: blurred = cv2.GaussianBlur(image, (5, 5), 0) #
  Kernel size of 5x5
  blurred_images.append(blurred)
  Step 4: blurred_images = np.array(blurred_images)

2. Localization

Identify the specific positions or regions within an image where nuclei are present. In the context of colon histology images, localization is crucial because it allows us to pinpoint the exact areas where nuclei of different cell types are located. This process ensures that the analysis is focused on relevant structures within the tissue.

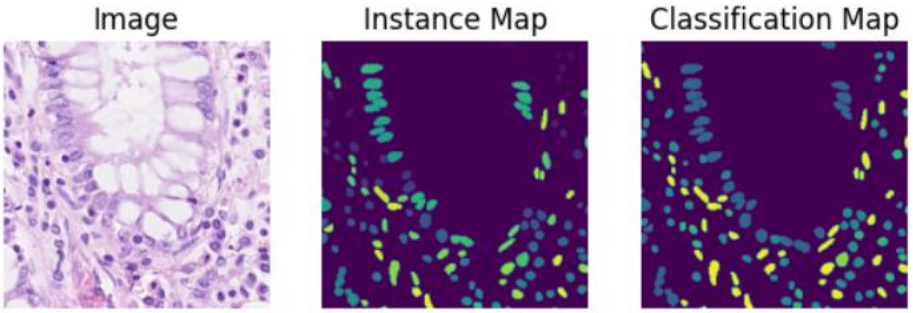


Figure 4 – Instance Map and Classification Map.

As can be seen above, the instance map uniquely labels each nucleus and the classification map labels each nucleus according the category it belongs to. In particular, the class mapping of values in the classification map is as follows:

0: background
1: neutrophil
2: epithelial
3: lymphocyte
4: plasma
5: eosinophil
6: connective

Connective tissue cells is a category that encompasses fibroblasts, muscle cells and endothelial cells. Below, we can transform the instance map and classification map so that we have 6 instance maps- one for each class map uniquely labels each nucleus and the classification map labels each nucleus according the category it belongs to.

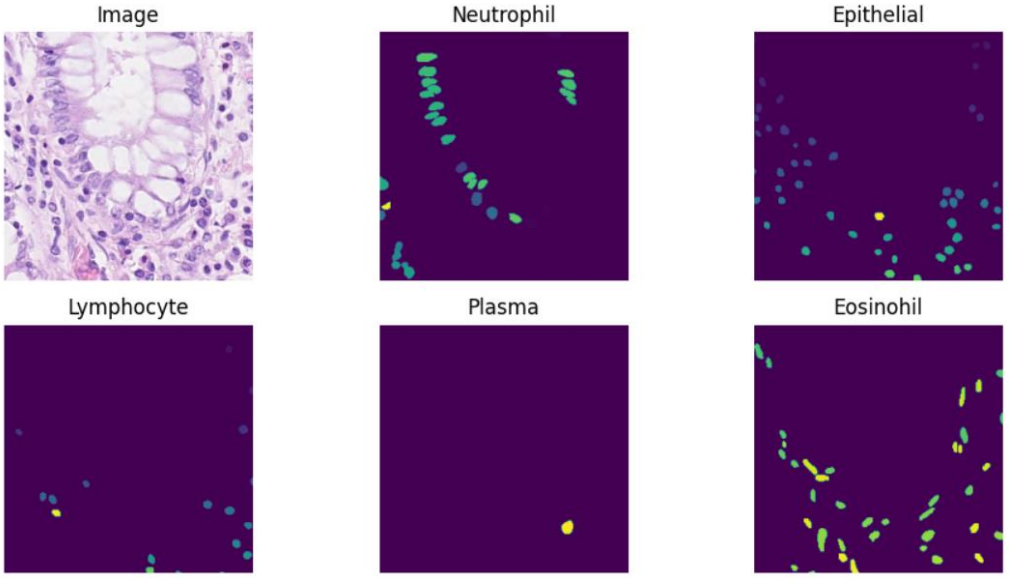
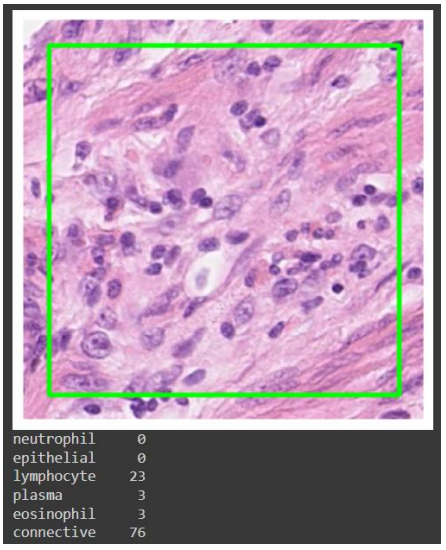


Figure 5 – Six Instance maps uniquely identifying each nucleus.

For counting, we only consider the central 224x224 region. This is so that we only consider nuclei for counting if they are entirely within the image. To show this, we plot the central region as a green box overlaid on top of the patch.



Algorithm:

Step 1: Select Random Patch

```
rand_idx = np.random.randint(0, images.shape[0])
patch_img = images[rand_idx]
patch_lab = labels[rand_idx]
```

Step 2: Separate Instance and Classification Map

```
viz_dict = {"Image": patch_img, "Instance Map":
patch_inst_map, "Classification Map":
patch_class_map} fig = plt.figure(figsize=(7,10)) for
count, (img_name, img) in enumerate(viz_dict.items(),
1): ax = plt.subplot(1, 3, count) plt.imshow(img)
plt.title(img_name) plt.axis("off")
```

Step 3: Visualize Class Specific Instance Maps

```
class_names = ["Neutrophil", "Epithelial", "Lymphocyte", "Plasma", "Eosinophil",
"Connective"]
fig = plt.figure(figsize=(10, 5))
for idx in range(7):
    ax = plt.subplot(2, 4, idx + 1)
    if idx == 0:
        plt.imshow(patch_img)
        plt.title("Image")
    else:
        plt.imshow(patch_inst_map_perclass[..., idx - 1])
        plt.title(class_names[idx - 1])
    plt.axis("off")
```

Step 4: Count Nuclei Per Class

```
patch_counts = counts.iloc[rand_idx] # Get count data for
the patch print(patch_counts)
```

3. Cellular Composition

Methodology:

To identify the nuclei and categorize them, we used deep learning algorithms in the colon histological images. Using instance maps and classification maps, we were able to uniquely identify and categorize each nucleus into one of six classes:

Neutrophils
Epithelial cells
Lymphocytes
Plasma cells
Eosinophil
Connective tissue cells

We first calculated the total number of nuclei across all image patches in the dataset. This involved counting unique nuclei instances identified in the instance maps, separated by class using the classification map.

Total Nuclei: 569,861
Neutrophils: 5,082
Epithelial cells: 282,082
Lymphocytes: 120,933
Plasma cells: 31,965
Eosinophil: 3,849
Connective tissue cells: 125,950

Next we consider only the central 224x224 region of each image patch for counting. This region was chosen to avoid partial nuclei at the edges, ensuring more accurate counts.

Total Nuclei Counted: 446,216
Neutrophils: 4,012
Epithelial cells: 222,017
Lymphocytes: 93,612
Plasma cells: 24,793
Eosinophil: 2,999
Connective tissue cells: 98,783
To visualize thee distribution of different cell types, we plotted the number of nuclei per class based on the counts obtained from the central regions.

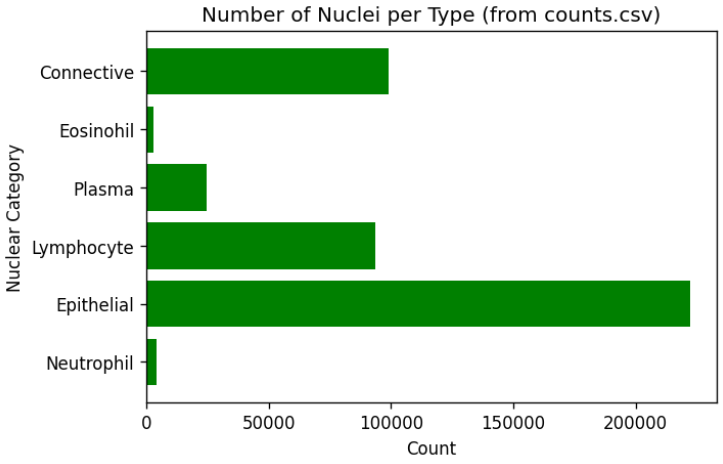


Figure 6 – Horizontal Histogram of Cellular Composition

4. Segmentation and Classification

The chosen deep learning architecture colon segmentation were HoVer-Net, U-Net and V-NET models which are all built upon the Convolutional Neural Network (CNN) model.

I. HoVer-Net Model:

HoVer-Net is a model for simultaneous segmentation and classification of nuclei in multi-tissue histology images. The network architecture of HoVer-Net comprises of Encoder-Decoder architecture.

1. Encoder Block:
   - The purpose of encoder block in a segmentation model is to perform feature extraction on the input image.
   - The encoder processes the input image through a series of convolution layers, down sampling the spatial dimensions while increasing the number of feature channels

2. Decoder Block:
   - In this case, the decoder utilizes the maps that are produced by the encoder to obtain the final mask for segmentation.
   - The Decoder block helps in expanding the Encoder Block features.
   - There are three branches under which all these tasks fall; Nuclear Pixel (Segmentation of Nuclei), HoVer Branch (Generation of Horizontal and Vertical Feature Maps) used for detection of overlapping nuclei, Nuclear Classification (Assigns class label to segmented nuclei).

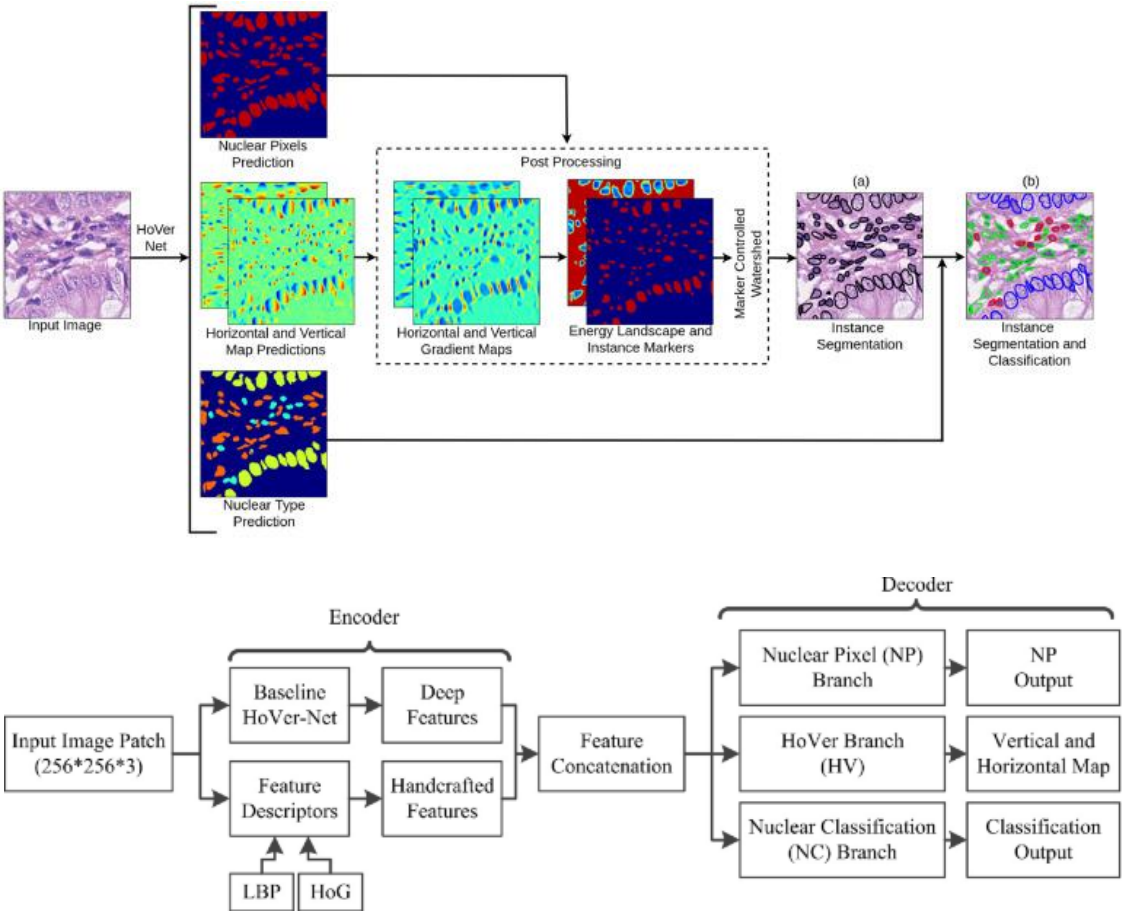


Figure 7 – HoVer-Net Architecture for 3D segmentation model.

II. The U-Net model was developed for biomedical image segmentation utilizing masks, a goal similar to that of the HoVer-Net. Still, the task of generating categorization masks is where this model excels the most. The primary benefits of this model over other segmentation and classification models are its low weight and quick training and inference times.

1. Contracting Path (Encoder):
   It Processes the input image through a series of convolutional and pooling layers. Each layer extracts features and reduces the spatial resolution (width and height) while increasing the number of channels (feature maps). This results in capturing high-level semantic information while reducing image size.

2. Expansive Path (Decoder):
   It up samples the feature maps from the contracting path using techniques like transposed convolutions (de-convolutions). It combines up sampled features with corresponding features from the contracting path at the same scale through skip connections. Skip connections help preserve spatial information lost during down sampling and improve localization accuracy in the segmentation output. Each layer in the decoder increases the spatial resolution while decreasing the number of channels.

3. Output Layer:
   It applies a final convolutional layer with the desired number of output channels. It produces a segmentation mask where each pixel is assigned a class label based on the predicted probability.

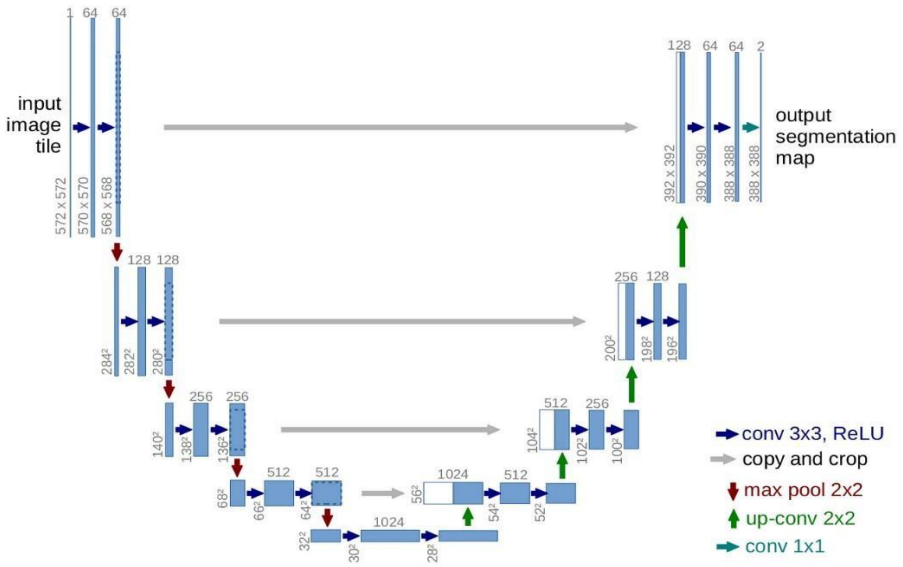


Figure 8 – U-net Architecture for 3D segmentation model.

III. V-Net (Volumetric Convolutional Neural Network) is another popular architecture for 3D medical image segmentation tasks. It shares some core principles with U-Net but incorporates specific design choices to potentially improve performance. Here's a detailed explanation:

1. Contracting Path (Encoder):
Similar to U-Net, V-Net uses a contracting path to process the input image via several layers of pooling and convolution. Functions like as feature extraction, which uses convolutional filters to extract pertinent information from the input image, such as edges, textures, and intensity patterns, are carried out by each layer. Reducing spatial dimensionality is another aspect of it: By decreasing the breadth and height of the feature maps, pooling layers (such as max pooling) down sample the data. This lessens the computing load while assisting in the acquisition of higher-level semantic information. Increasing Feature Channels: As you get farther into the network, you usually find that there are more channels in the feature maps. This allows for the representation of a growing number of extracted features.

2. Dense Block:
V-Net introduces a key difference in its contracting path by incorporating dense blocks. These blocks connect all previous feature maps within the contracting path to the current layer. This dense connectivity allows for better feature propagation and potentially improves the utilization of extracted information throughout the network.

3. Expansive Path (Decoder):
Up sampling Feature maps are up sampled using techniques like transposed convolutions to recover spatial resolution. Skip Connections directly concatenate features from the contracting path (at the same scale) with the up sampled features in the decoder. This crucial step preserves spatial details lost during down sampling and allows for more precise localization in the segmentation output. Decreasing feature channels, as you move up the decoder, the number of channels in the feature maps typically decreases.

4. Output Layer:
   The final layer applies a convolution with the desired number of output channels, corresponding to the segmentation classes. The output is a segmentation mask with each pixel labelled based on the predicted probability.

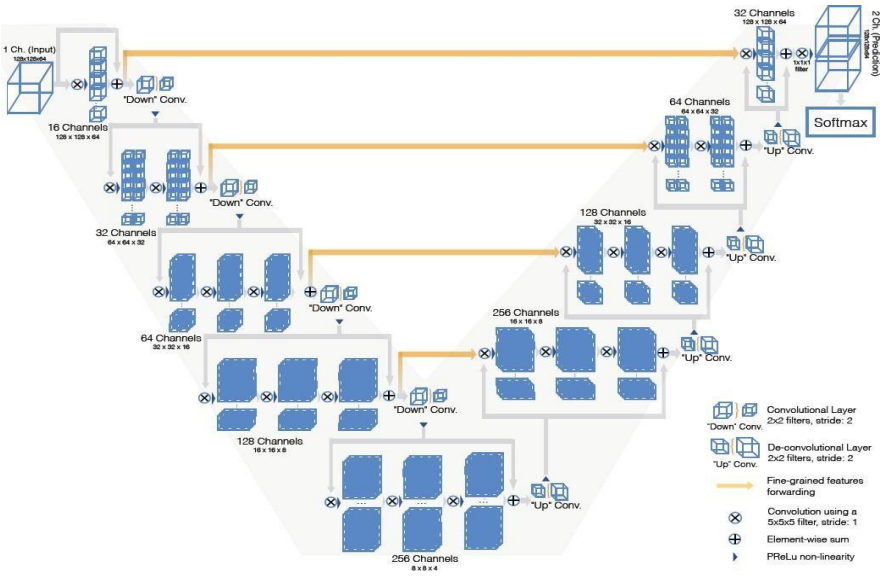


Figure 9 – V-Net Architecture

While HoVer-Net, U-Net, V-Net have specific architectural details, they share a core algorithmic structure for segmentation tasks. Below is a generalized algorithmic representation.

Algorithm:

Step 1 – Define the segmentation model

```
def segmentation_model(input_data, num_classes):
```

Step 2 – Define the encoding path

```
contracting_path_outputs=[]
 for n in num_contracting_blocks:
     x = convolutional_layer(input_data)
     x = batch_normalization(x)
      x = activation(x)
     x = downsampling_layer(x)
```

Step 3 - Define the decoding path

```
for n in num_expanding_blocks:
     x = upsampling_layer(x)
     if attention:
        x = attention_module(x, contracting_path_outputs[-(n+1)])
    x = concatenate(x, contracting_path_outputs[-(n+1)])
    x =  convolutional_layer(x)
    x = batch_normalization(x)
    x = activation(x)
```

Step 4 - Define the output layer

```
output = convolutional_layer(x, num_classes=num_classes)
output = activation(output)
```

5. Training

Train-Validation Split: We utilize 80% the number of patches for training and the remaining for validation. However, because we apply stratified sampling according to the origin, the final number of patches may not be 80/20 (each image may contain a different number of patches). Therefore, we generate a number of splits (indicated via the NUM_TRIALS variable) and select the one that has the number of patches that most closely matches with our expected ratio.

Algorithm:

Step 1- Set Up Parameters and Read Data
NUM_TRIALS = 10
TRAIN_SIZE = 0.8
VALID_SIZE = 0.2
info =pd.read_csv(f'{DATA_DIR}/patch_info.csv')
Step 2 - Initialize Stratified Shuffle Split
splitter = StratifiedShuffleSplit(
n_splits=NUM_TRIALS,
train_size=TRAIN_SIZE,
test_size=VALID_SIZE,
random_state=SEED
Step 3 - Generate Splits and Select the Optimal One
splits = [] for train_idx, valid_idx in
splitter.split(img_sources,
cohort_sources): train_names =
np.unique([f for f in file_names if
f.split('-')[0] in
img_sources[train_idx]])
valid_names = np.unique([f for f in
file_names if f.split('-')[0] in
img_sources[valid_idx]])
splits.append({'train':
[file_names.index(f) for f in
train_names], 'valid':
[file_names.index(f) for f in
valid_names]})

Chapter 4

Results

1.1 Performance metrics

1. *PQ* and mPQ+: Panoptic Quality (PQ) is used to assess the performance of nuclear instance segmentation. It is defined as follows:

PQ = DQ × SQ (EQ1)

Where *DQ* and *SQ* refer to detection quality and segmentation quality, respectively, which are given by,

$$DQ = \frac{|TP|}{|TP| + \frac{1}{2}|FP| + \frac{1}{2}|FN|} \quad \text{(EQ2)}$$

Where TP denotes true positive, FP denotes false positive, and FN denotes false negative.

$$SQ = \frac{\sum_{(x,y)\in TP} IoU(x,y)}{|TP|} \quad \text{(EQ3)}$$

Where y represents a prediction segment, x represents a ground truth segment, and IoU stands for intersection over union, which is expressed as,

$$IoU = \frac{TP}{TP + FP + FN} \quad \text{(EQ4)}$$

The mean of PQ over all classes T is therefore the definition of multi-class PQ (mPQ+).

$$mPQ^{+} = \frac{1}{T}\sum_{t} PQ_t \quad \text{(EQ5)}$$

2. R^2 : R^2 is a goodness-of-fit metric that, on a scale of 0 to 1, assesses how closely the model's forecast matches the actual data. The model is better fitted when R^2 is closer to 1. It goes by the name of coefficient of determination as well.

$$R^2 = 1 - \frac{\sum (y_i - \hat{y}_i)^2}{\sum (y_i - \bar{y})^2} \quad \text{(EQ6)}$$

3. *Mean Squared Error* (*MSE*): The mean square of the differences between the actual and model-predicted values is used to calculate it.

$$MSE = \frac{1}{D}\sum_{i=1}^{D}(x_i - y_i)^2$$

(EQ7)

4. *Dice Score*: Dice Score is an accuracy metric. It serves as a tool for segmentation model performance evaluation. It's a gauge of how similar the things are to one another.

$$Dice = \frac{2 \times TP}{(TP + FP) + (TP + FN)}$$

(EQ8)

A higher dice score denotes a better the model prediction; the dice score ranges from 0.00 to 1.00. A dice score of more than 0.8 is typically regarded as excellent.

4.1 Result Analysis

Segmentation algorithm	PQ	mPQ+	R^2
HoVer-Net	0.6149	0.4998	0.8585
V-Net	0.6015	0.4080	0.7277
U-Net	0.6108	0.4140	0.8188

Table 1 - Results of segmentation algorithms

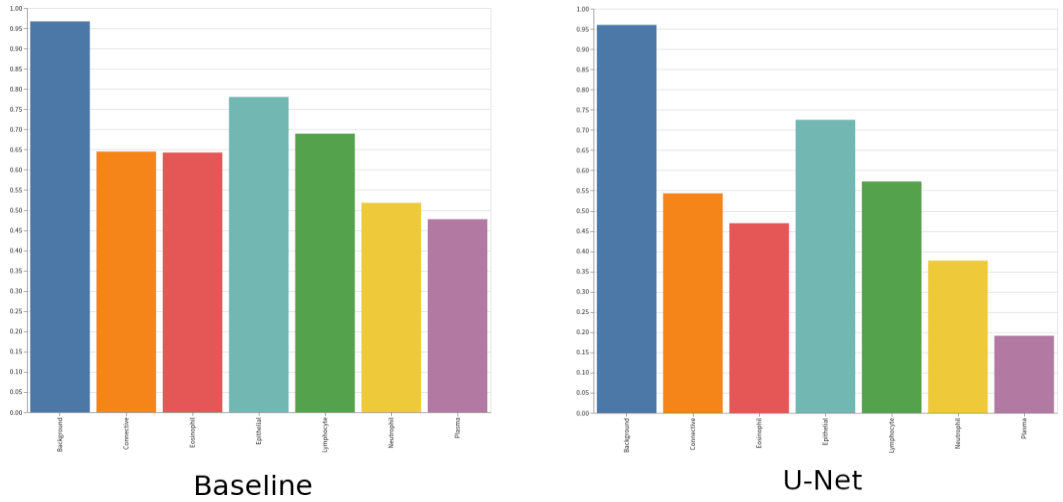


Figure 10 – Result of initial classification mask tests

Figure 10: Outcomes of the preliminary classification mask experiments. Left: HoVer-Net; right: basic U-Net. Be aware that only the validation set was used in the computation of these results. The colors are blue for the background, orange for connective tissue, red for eosinophil, light blue for epithelium, green for lymphocyte, yellow for neutrophil, and purple for plasma.

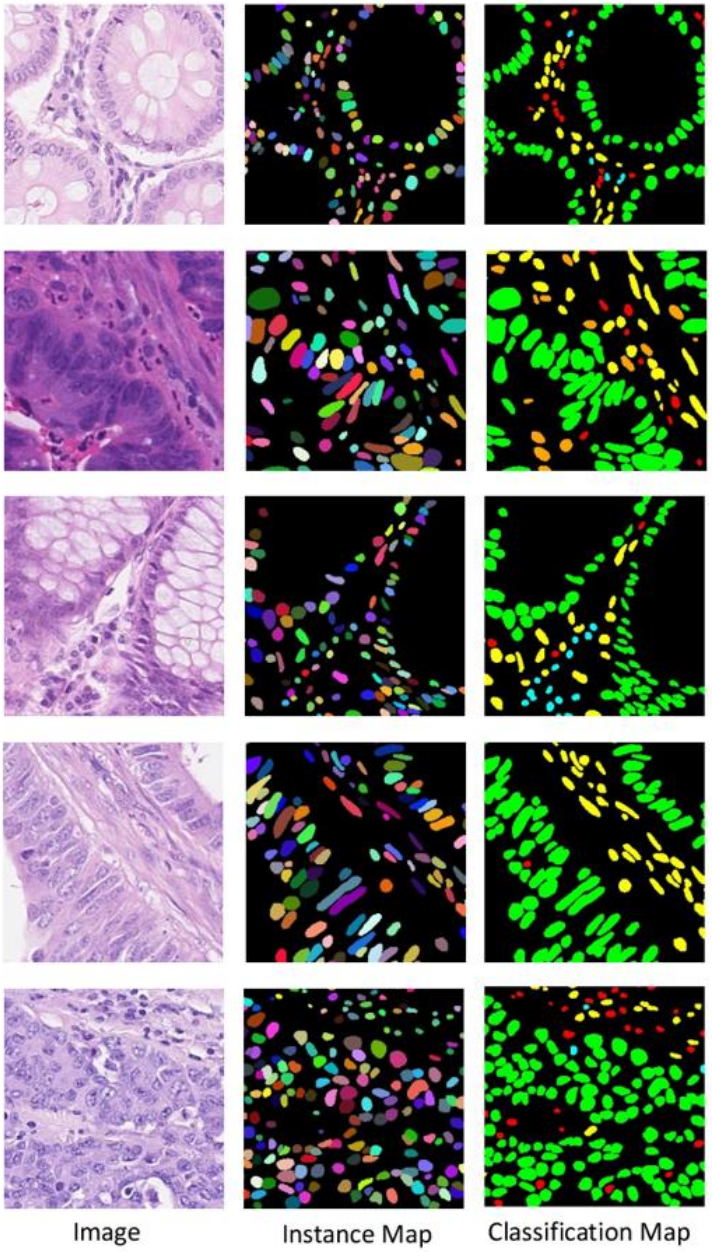
These findings reveal a fascinating finding. Even with its largest model size, the U-Net, which is now among the finest models for producing classification masks, particularly in the field of biology (histological imaging), still needed to improve significantly in order to meet the

baseline findings. This resulted in a crucial realization: by training the HoVer-Net for segmentation as well as classification.

Segmentation algorithm	Mean Squared Error Loss	Accuracy+	Dice Score
HoVer-Net	0.049	0.9606	0.9818
U-Net	0.115	0.9080	0.9188
V-Net	0.108	0.9025	0.9077

Table 2 - Comparing performance with different models.

Our strongest model, HoVer-Net model, obtained an IOU score of 0.9606 and a Dice score of 0.9824 when evaluated on unseen test data. The colon prediction made by the model based on the test data is shown below.



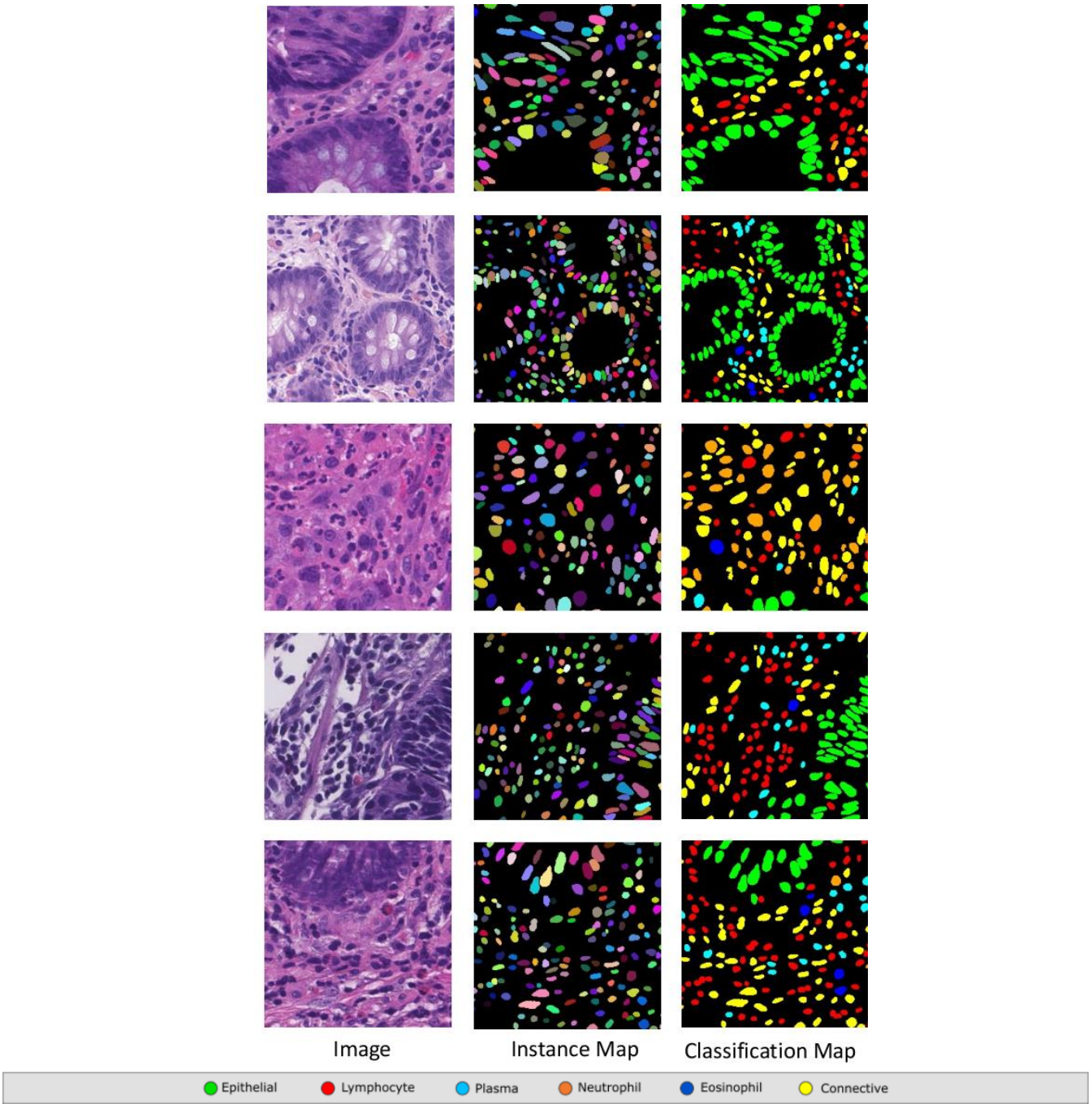


Figure 11 – Final Result of the HoVer-Net Model

Below is a comparison of the methods and metric scores used in various research papers with our best model (HoVer-Net).

Reference	Method	Dice Score
Our Strongest Model	HoVer-Net	0.9818
Böhland et al. [4]	Ciscnet	0.925
Weigert et al. [5]	Stardist	0.887
Liu et al. [3]	Mask R-CNN + U-Net	0.938

Table 3 - Comparing performance with existing models.

Chapter 5

Conclusion and Future Scope

5.1 Discussion

This project aims to develop a deep learning model for colon nuclei classification and segmentation from histology images. Enhancing pathological evaluations precision and effectiveness is the goal especially when it comes to the diagnosis of illnesses related to the colon. Data collection using the publicly available Lizard dataset which contains histology images with matching segmentation masks was the first step in the working method. The images undergo various processing techniques including resizing them applying Gaussian blurring to minimize noise and converting them into a standard format. Despite the different number of patches per image stratified sampling was used to guarantee that the dataset was divided into training and validation sets with a ratio that nearly matched the intended 80/20 split. The second step involved creating a deep learning model that would be used to segment and classify nuclei with high efficiency and reliability using HoVer-Net U-Net and V-Net. The IoU of the other models that were examined and contrasted with the strongest model HoVer-Net was nearly 0.9606 and a Dice score of 0.9584. Nonetheless, it was seen that the models like U-Net/and V-Net are also effective but not as efficient as the proposed. The results of this study imply that sophisticated deep learning models such as HoVer-Net can greatly improve the accuracy of colon nuclei classification and segmentation helping pathologists to make more precise diagnoses.

5.2 Conclusion

In the current study, a deep learning model was developed for the segmentation, classification, and counting of colon nuclei from histological images. The primary goal was to improve the effectiveness and precision of colon nuclei analysis, which is crucial for comprehending and identifying conditions related to the colon. The intention of the research was to enhance colon cancer detection and staging by utilizing HoVer-Net, U-Net or V-Net architecture for segmentation, along with data pre-processing techniques and training strategies to achieve optimal performance. It has been observed that during the course of developing deep learning models, scores of hyper parameters are selected owing to its crucial role in defining accuracy in classification systems. The CoNIC (Colon Nuclei Identification and Counting) Challenge provided a robust platform for this research, with its comprehensive dataset of around half a million labeled nuclei. This challenge facilitated a thorough evaluation of the developed models, ensuring that our results are both innovative and competitive. By leveraging a combination of data preprocessing, advanced deep learning architectures, and rigorous evaluation, this study contributes to enhancing the capabilities of computational pathology models. HoVer-Net demonstrated exceptional performance with a good dice score of 98.18% was obtained.

5.3 Future Scope

While this project establishes a foundation for colon segmentation and analysis, there's significant scope for further exploration:

- Model improvement: Experiment with different deep learning architectures, hyper parameter tuning, and data augmentation techniques to potentially enhance segmentation accuracy and generalizability.
- Clinical integration: Clinical trials conduct with pathologists & oncologists may also be utilized in assessing how the model influences diagnostic processes & the patients' outcomes. This may consist of evaluating the role of the tool in better diagnosis and staging of the colon cancer.
- Generalizability testing: Validate the model's performance on real-world clinical datasets from various hospitals to ensure generalizability beyond benchmark datasets.

By addressing these future directions, this project has the potential to evolve into a valuable tool for pathologists and oncologists in making accurate diagnosis of colon cancer hence enhancing the survival of the patients.

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Table B.1: Project Detail

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Project Duration	6 Months	Date of Reporting	29-08-2024

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