



Semantic Segmentation of Histopathological Images with Fully and Dilated Convolutional Networks

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Introduction

- The segmentation of different components in medical images is a major subject of study
 - numerous image segmentation methods are still being developed.
- Thanks to its comprehensive and wide usage area, computer vision has led many academicians to integrate with various scientific disciplines
- Almost every one of the levels has a defined problem in computer vision, such as image classification, object detection, semantic segmentation, and instance segmentation
- Advances in health technologies have also benefited from computer vision
- Computer vision algorithms can aid in the automation of tasks like
 - detecting malignant areas in images
 - identifying symptoms on x-ray and MRI scans

Introduction *(cont.)*

- Semantic segmentation may be thought of as a classification of the pixel problem using semantic tags
- Semantic segmentation labels all pixels in an image at the pixel level
 - can also be thought of as pixel-level image classification
- It's a trickier assumption to make than image classification, which mostly forecasts a single label for the whole image
- For example, segmentation will classify all items in an image containing multiple automobiles as 'car' objects
 - while instance segmentation, broadens the semantic segmentation scope by labeling specific instances of objects
- Instance segmentation is not included in the study

Introduction *(cont.)*

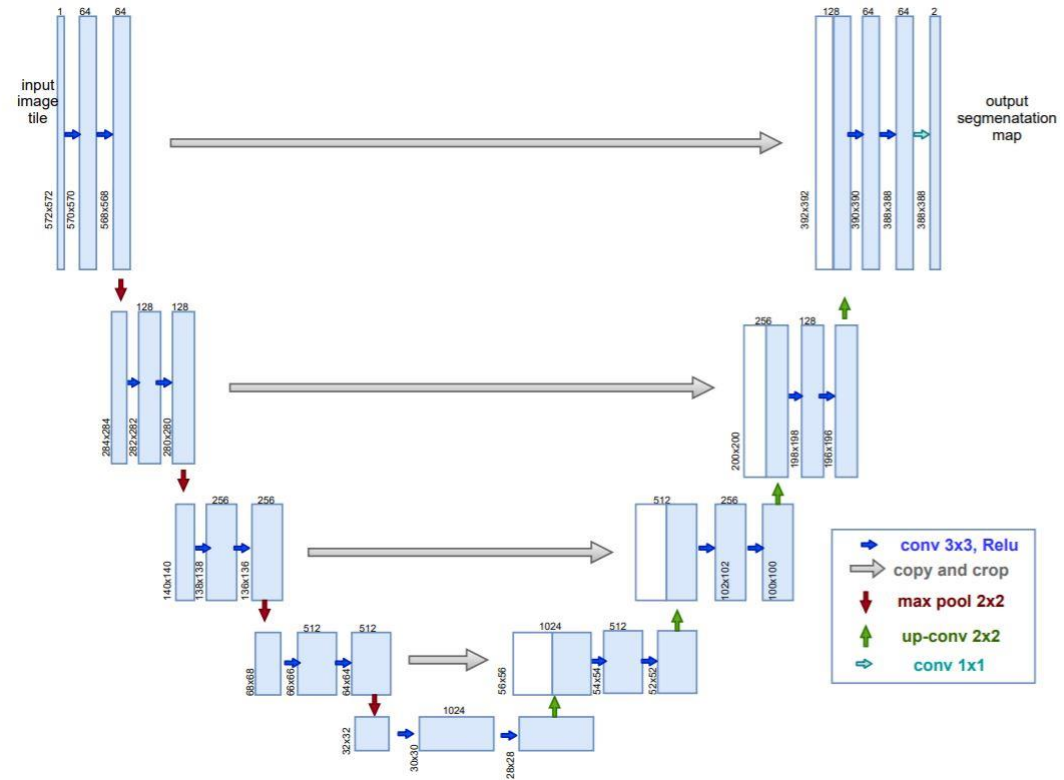
- While using Deep Convolutional Neural Networks for the semantic segmentation task, one of the two problems is the decreased feature resolution produced by
 - successive pooling operations
 - convolution striding
- Dense prediction tasks requiring specific spatial information may be hindered
- The use of dilated (atrous) convolution, which has been demonstrated to be successful for semantic image segmentation, is suggested as a solution
- Dilated convolution presents a new dilation rate parameter
- The dilated convolution of a signal $x(i)$ is specified as

$$y_i = \sum_{k=1}^K x[i + rk] \omega[k]$$

- r is the dilation rate

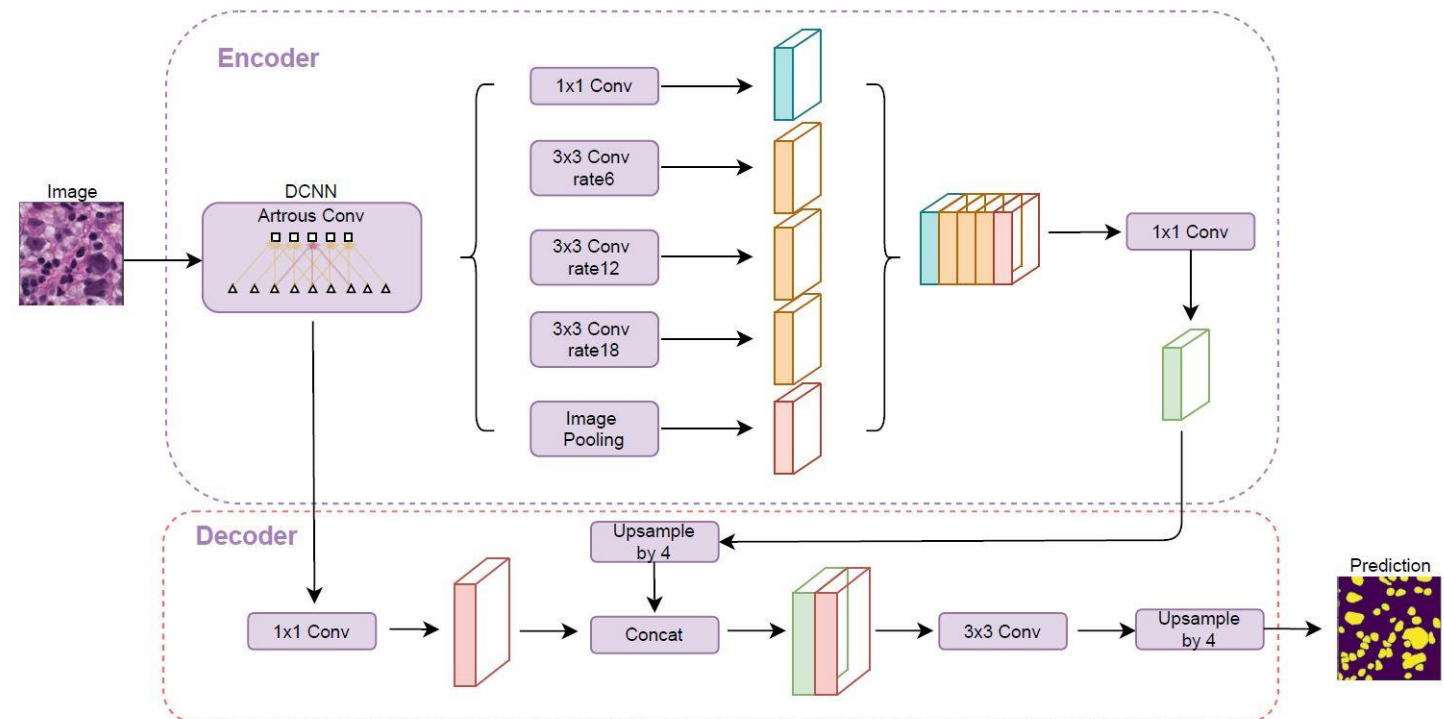
Methods – U-Net Model

- U-Net was developed by Olaf Ronneberger et al
 - for medical image segmentation
- U-Net architecture mainly includes two ways
 - the primary way is to use the encoder path (contraction) to get the image's context
 - the decoder path (symmetric expanding) is used to get accurate localization utilizing transposed convolutions
- U-Net is an end-to-end FCN that can handle any size image
- The defined U-Net model architecture at a basic level



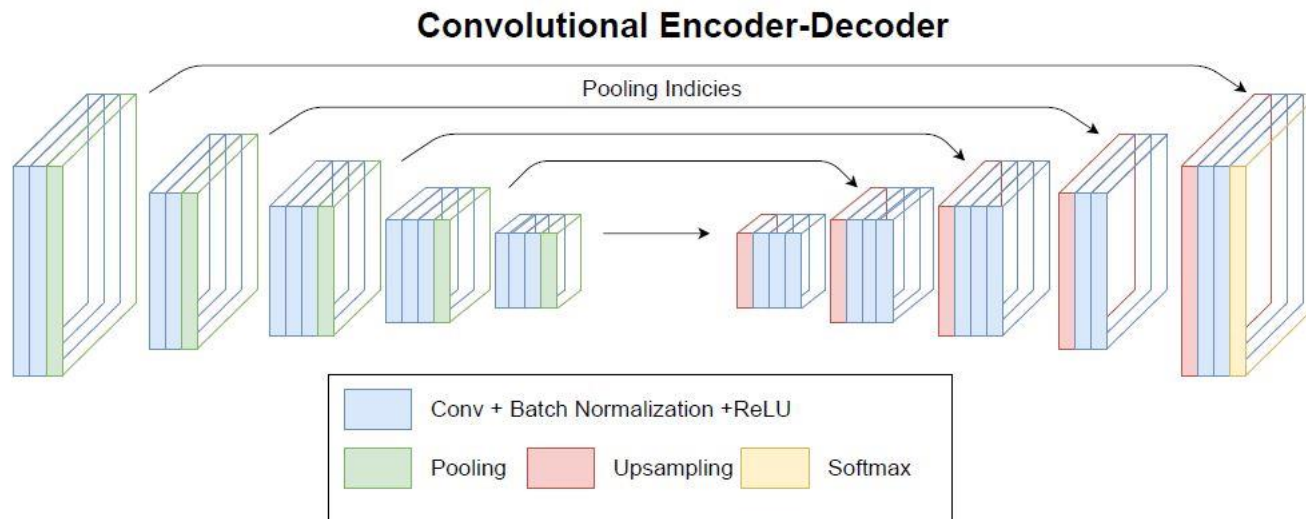
Methods – DeepLabV3+ Model

- DeepLabV3+ proposed by Chen et al
 - which extends DeepLabV3 to using an encoder-decoder structure
- DeepLabV3+ encodes multi-scale contextual information while optimizing segmentation results across object boundaries with the decoder module
- On the PASCAL VOC 2012 and Cityscapes datasets, DeepLabV3+ outperformed many high-end segmentation networks
- The defined DeepLabV3+ model architecture at a basic level



Methods – SegNet Model

- SegNet was developed by Badrinarayanan et al.
 - is a convolutional encoder-decoder architecture for image segmentation,
- SegNet is an FCN
- SegNet is made up of a pixel-based classification layer, an encoder network, and a matching decoder network
- In terms of the number of trainable parameters, SegNet is also much less than rival designs
- The defined SegNet model architecture at a basic level



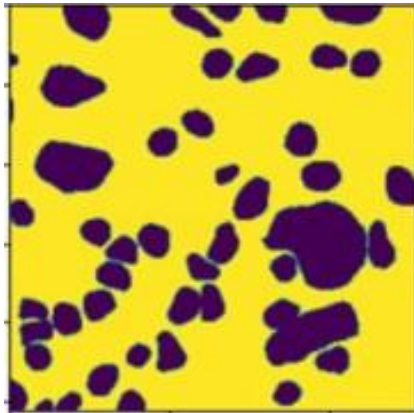
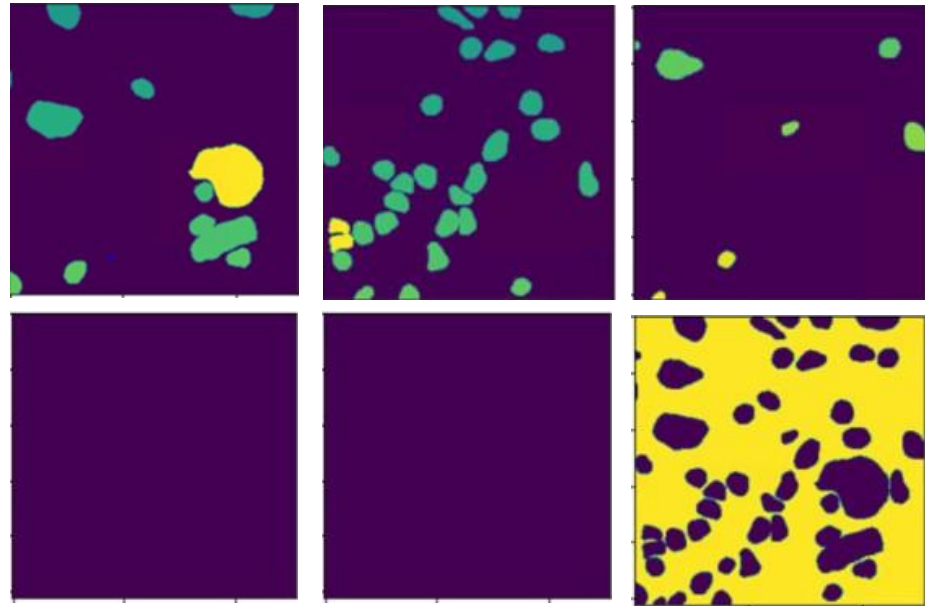
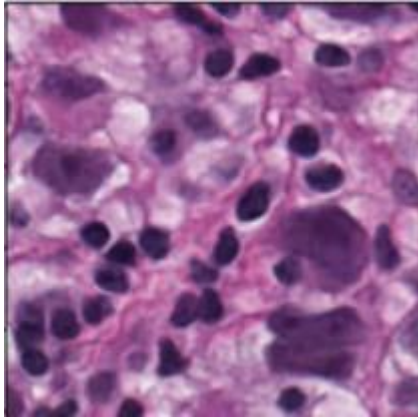
Methods – PanNuke Dataset

- Experimental dataset has been generated semi-automatically with 6 different exhaustive nuclei labels over 19 different tissue types
- The dataset contains 481 visual fields, most of which were selected at random from over 20K whole slide images
- Over 205 thousand labeled nuclei in the dataset, each with its own instance segmentation mask
 - Neoplastic, Inflammatory, Connective, Dead, Epithelial, and Non-Nuclei
- 256 x 256 x 3 RGB images were used as the model input, while 256 x 256 nuclei masks were used as control labels to evaluate
- The original masks folder contains 6 layers of depth as labeled nuclei classes
- The ‘non-nuclei’ layer were used as the mask layer, in other words, ‘all-nuclei’ layer

Methods – PanNuke Dataset *(cont.)*

image masks of 256 x 256 for all 6 layers

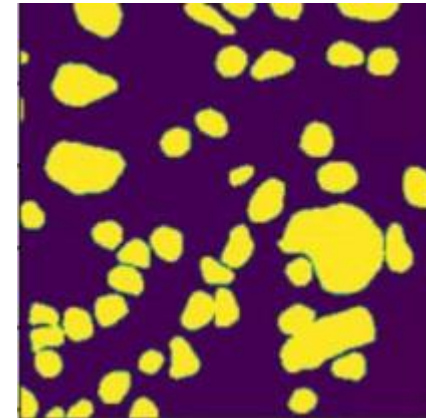
256 x 256 RGB image



raw image



pre-processing



all-nuclei

Numerical Results

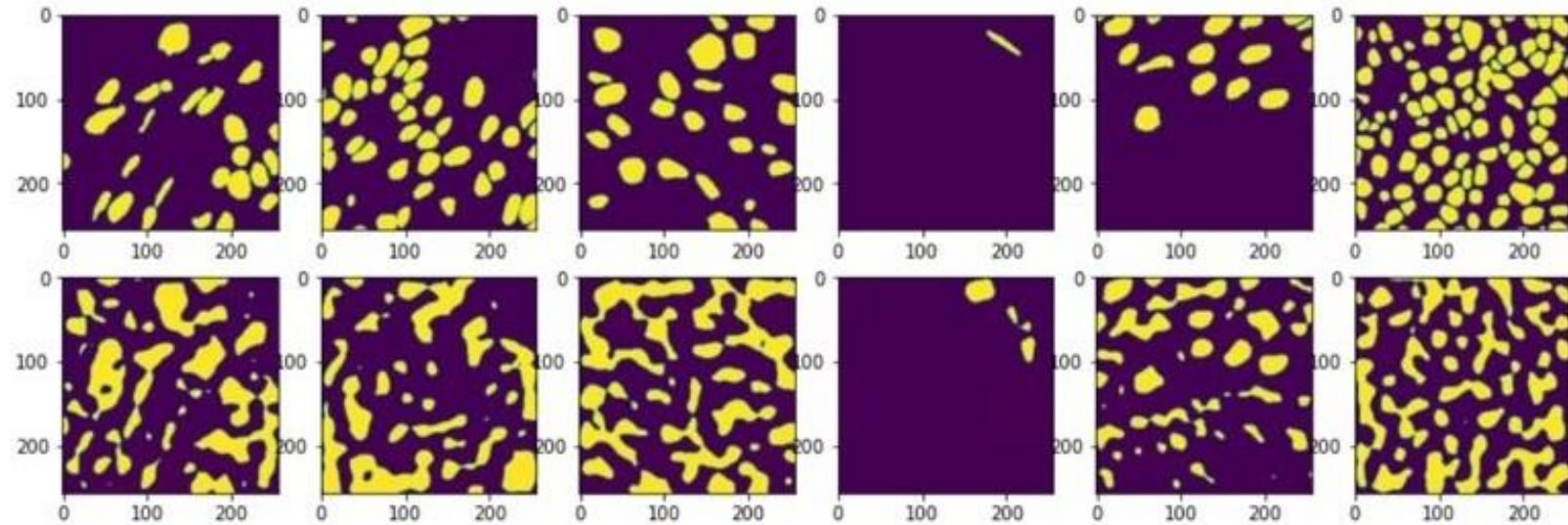
- Python Tensorflow Keras Library
- Models were run between 15 and 50 epochs if the loss was suitable for recovery
- The weights of the highest success were reloaded to the models and the test phase were completed

Model	Accuracy	F1/Dice-score	Kappa
DeepLabV3+	0,922	0,802	0,753
U-Net	0,916	0,786	0,667
SegNet	0,812	0,554	0,436

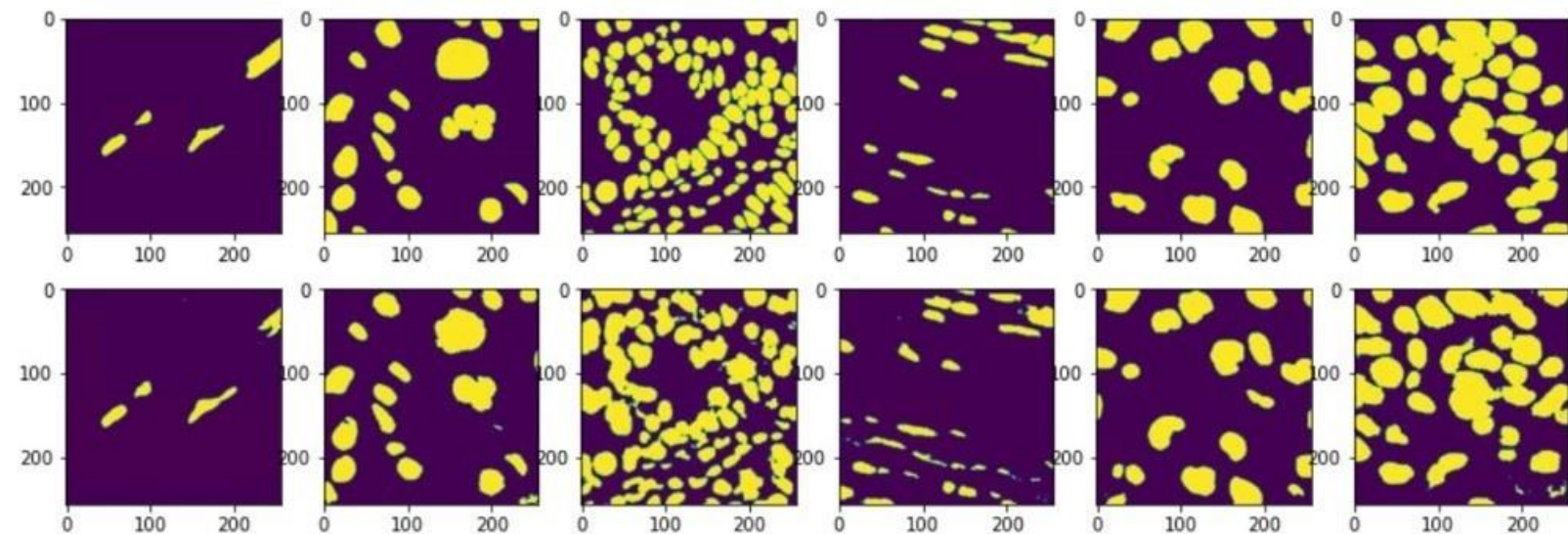
- As the data set was imbalanced, F1 / Dice-score is preferred as the main evaluation metric
- The DeepLabV3+ with an F1 / Dice-score was measured as the model with the highest success

Visualization of the Results

SegNet Model Predictions

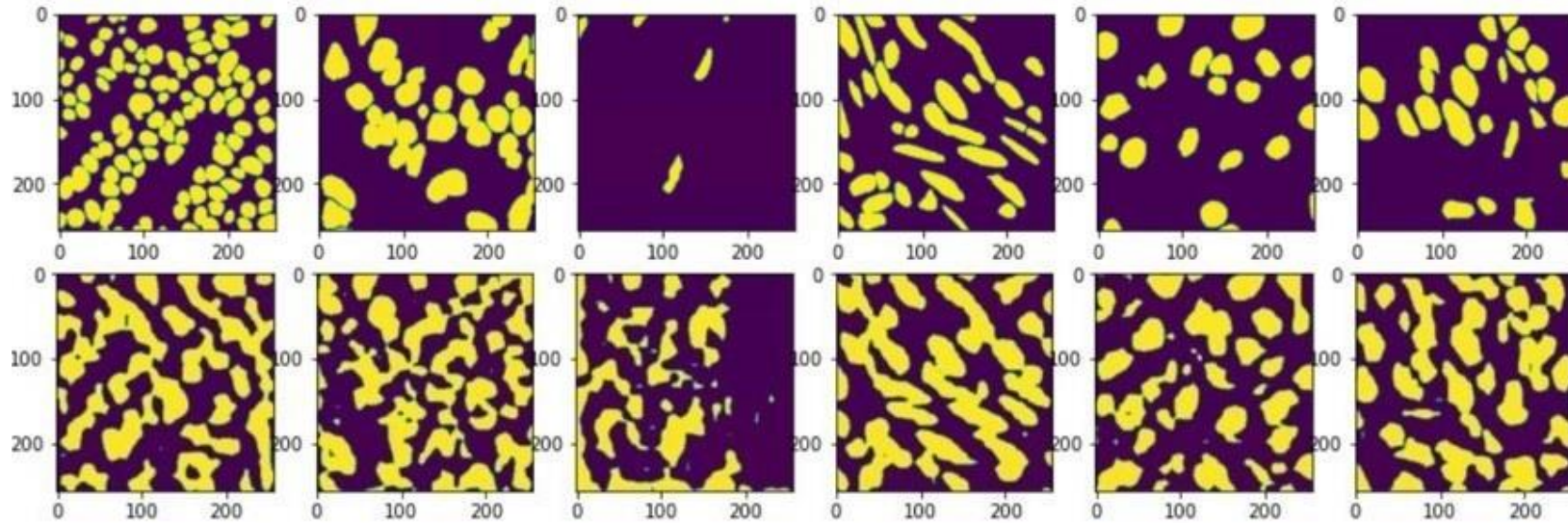


U-Net Model Predictions



Visualization of the Results *(cont.)*

DeepLabV3+ Model Predictions



Results and Discussion

- The Overall Accuracy achieved over 90 percent
- The F1 / Dice-score was the main preferred metric in the evaluation due to the imbalance of the data set
 - because the amount of nuclei pixels in the total of the dataset is about 1/5 relative to the non-nuclei pixels
 - F1 / Dice-score 80.2% was considered the best success
- When model in which we use the F1 / Dice-score in the evaluation phase, be trained with the Dice coefficient loss function
 - the results will be more reliable
 - the success will be higher

Thank You