Deep Leaning based Breast Cancer Tumor Detection and pN-Stage Prediction

Ravi Kiran, Xinghua Li

ABSTRACT

This paper presents an automatic method of tumor segmentation and slides classification. It also predicts the pN-stage at the patient level based on the slide's classification. The pN-stage for every patient is determined by the number of positive lymph nodes that consists of 5 categories. We used convolutional neural networks for slide level segmentation of tumor cells. The pN-stage evaluation has been done as post processing stage for detected positive regions by using blob analysis and trained XGboost.

This method is trained and validated on Camelyon17 challenge datasets. The method consists of two parts: tumor region detection using CNN and cancer metastasis stage prediction using XGboost.

Index Terms— ResNet-50, XGboost, convolutional neural networks, Camelyon17, breast cancer detection

1. INTRODUCTION

The focus of the challenge is on designing an automatic way to detect and classify breast cancer metastases in lymph nodes. To achieve the goal, whole slide images (WSI) of the hematoxylin and eosin stained lymph nodes tissue were provided. This is one of the ends that the Camelyon17 challenge [1] aims to provide for by predicting pN-stages of 100 patients. The challenge dataset consists of 5 hematoxylin and eosin stained slide images of different lymph nodes from each subject. Five patient-level classes of pN stage, namely pN0, pN0(i+), pN1mi, pN1, and pN2, are automatically determined by 5 slide-level metastases, which are negative, micro-metastases, macro-metastases, isolated tumor cells (ITCs). Therefore, it is critical to classify each slide correctly.

2. METHOD

We have trained a ResNet-50 network with Camalyon'16 and Camleyon'17 datasets. We used 50 annotated tumor slides and 70% of negative slides of Camleyon'17 for training and remaining negative slides for validation.

2.1 Patch Extraction

We have extracted valid tissue regions from whole slide imaging using Otsu methods [3,4]. Task was to get label for every patch extracted from valid tissue region. We have used ground truth given in training dataset to get appropriate label. We have taken a special care for the patches at the boundary. Used a threshold to decide a patch is tumor or normal.

2.2 Data Augmentation

We have use very diverse set of data augmentation to incorporate all possibilities. This includes- Random Image Rotation,

Random Image left right flip, Random Image Up and Down Flip, Random Hue, Random Saturation and Random Brightness. Sample of augmented images with rotation and HSV color variations Figure-1.
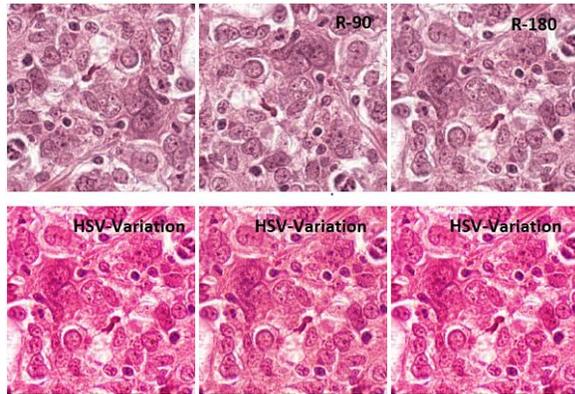

Figure -1 Data Augmented Samples

2.3 Convolutional Neural Network

The extracted patches after going through data augmentations are fed into Convolutional Neural Network, we have used a popular variant called ResNet-50. We initialized this with pretrained weights from ImageNet Challenge data. Our algorithm pipeline is shown in Figure-2.

2.4 Heatmap Generation

For each whole slide image, after extracting the tissue region from a lower magnification, we take the corresponding patch at highest magnification and run through our trained model, using the obtained probability we generate a probability heatmap for the whole slide image.

3. Whole Slide Classification

We have develop a XGboost based model which takes features out of heatmaps and predict the class of the slides. These classes are – Negative , ITC, Micro & Macro. We have designed the features to be extracted from
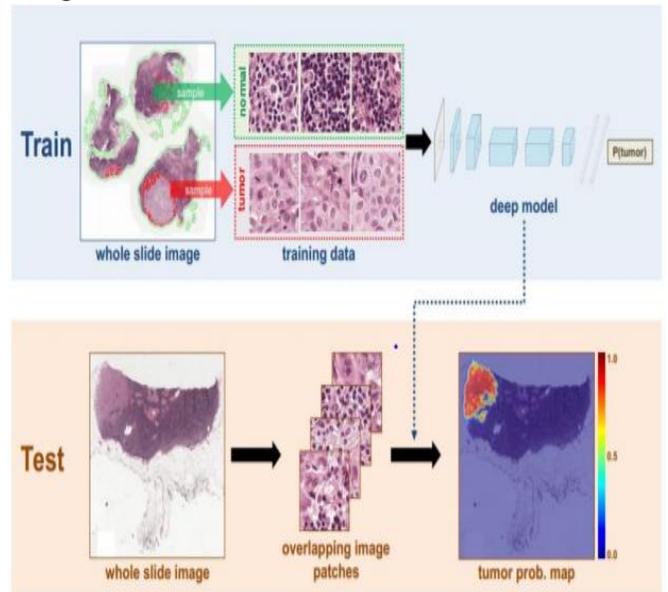

Figure -2 Algorithm Pipeline

heatmaps. Some of those features are listed below in the table-

Max probability in biggest tumor blob	Maximum probability in whole slide tumor
Avg probability in biggest tumor blob	Area of ellipse fit on biggest tumor blob
Major axis of ellipse fit of biggest tumor blob	Solidity of ellipse fit on biggest tumor blob
Minor axis of ellipse fit on biggest tumor blob	
Equivalent Diameter of biggest tumor blob	

We have extract 15 features for each threshold of heatmaps. We have used two threshold values.

XGboost model is trained with 5-fold cross validation.

4. RESULTS

We have trained our model first only on CAMELYON16 Training dataset, to evaluate how good is it. We achieved a FROC score of 0.65.

Using the same model, we trained it on the remaining datasets (Camelyon16 Test as well as Camelyon17 Training). Our whole slide classifier was trained using the features extracted from the heatmaps generated by above model. Our results are as follows-, our five-fold cross validation average scores are as follows.

Model	Score	Metric
ResNet-50	0.65	FROC
XGboost (overall)	0.85(Train) 0.52(Avg 5-folds Cross Validation)	Quadratic Kappa

We have achieved competitive performance on our tumor classification model and whole slide image classification model.

4. References

[1] Meier, Frederick A. "The Landscape of Error in Surgical Pathology." Error Reduction and Prevention in Surgical Pathology. Springer New York, 2015. 3-26.

[2]https://camelyon16.grand-challenge.org/site/CAMELYON16/serve/public_html/Results/Presentations/Camelyon16_BIDMC_CSAIL.pdf/

[3] Nobuyuki Otsu, "A threshold selection method from gray-level histograms," IEEE transactions on systems, man, and cybernetics, vol. 9, no. 1, pp. 62–66, 1979

[4] Yun Liu, Krishna Gadepalli, Mohammad Norouzi, George E Dahl, Timo Kohlberger, Aleksey Boyko, Subhashini Venugopalan, Aleksei Timofeev, Philip Q Nelson, Greg S Corrado, et al., "Detecting cancer metastases on gigapixel pathology images, arXiv preprint arXiv:1703.02442, 2017.

[5] Andrew Janowczyk and Anant Madabhushi, "Deep learning for digital pathology image analysis: A comprehensive tutorial with selected use cases," Journal of pathology informatics, vol. 7, 2016.

[6] David Rolnick, Andreas Veit, Serge Belongie, and Nir Shavit, "Deep learning is robust to massive label noise," arXiv preprint arXiv:1705.10694, 2017.

[7] "Camelyon 2017," https://camelyon17.grand-challenge.org/, Accessed: 2017-07-24.

[8] Mart´ın Abadi, Ashish Agarwal, Paul Barham, Eugene Brevdo, Zhifeng Chen, Craig Citro, Greg S Corrado, Andy Davis, Jeffrey Dean, Matthieu

Devin, et al., "Tensorflow: Large-scale machine learning on heterogeneous distributed systems," arXiv preprint arXiv:1603.04467, 2016.