

Learning The Optimal Threshold : A Novel Method to Segment Histopathology Images

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Abstract. In the last decade, a lot of segmentation techniques had been proposed. Most of them include using an encoder-decoder network, such as the UNet model, to predict the mask for a certain image. The issue with UNet models and fully convolutional networks, in general, is that they require a substantial amount of data. In this study, we propose a novel technique to segment nuclei from breast histology patches. Instead of learning to generate a mask from an input image, we simplify the problem by using a regression network that learns to predict the optimal threshold value. To find the best threshold value for a certain histology image, we introduce a similarity guided search algorithm that compares the embeddings of the ground truth mask with the embedding of all masks generated from different possible threshold values. The proposed network manages to segment the nuclei from a small histology dataset with high accuracy i.e. 90%.

Keywords. Breast cancer, Thresholding, Segmentation, Nuclei, Autoencoder, Cosine Similarity, ResNet18

1. Introduction

In order to make accurate diagnosis of breast cancer [1], a biopsy followed by a microscopic analysis is essential. Sections are cut from biopsy material, stained using hematoxylin and eosin (H&E) which is considered as a gold standard in histopathology, and a pathologist evaluate the stained biopsy under different magnification levels.

This study introduces a novel technique to segment histology images. Instead of learning to generate a segmentation mask, we train a regression network to predict the optimal threshold value for each histology image. First, we train a convolutional autoencoder [2] on a large set of histology masks, then, we use the encoder to generate latent embeddings. The Similarity Guided Search (SGS) network takes as input the embeddings generated from the ground truth mask and the original images. The SGS manages to find the optimal threshold by iterating over all possible thresholding values and generating a mask and its associated embeddings. We use the cosine similarity [3] to compare between the thresholded image embeddings and the ground truth mask embeddings. Using this method, we manage to find the optimal threshold for a certain histology image. We train a ResNet18 [4] model with one output neuron to predict a threshold value for a given input image and using the mean square error loss (MSE) [5] function, that takes as input the predicted threshold and the optimal threshold, the regression network learns to predict the optimal threshold value.

Rezaei et al. [6] introduced a deep learning algorithm that uses the LinkNet model along with hand-crafted feature extraction models such as the local binary pattern. Their proposed algorithm exceeded the performance of state-of-the-art models on segmenting histology images from the Warwick-QU

dataset. Li et al. [7] compared the histology segmentation results of handcrafted feature extraction models with fine-tuned convolutional neural networks. They concluded that the use of pre-trained convolutional neural networks yields better accuracy and the combination of the two methods resulted in the best performance. Tang et al. [8] introduced a histology segmentation encoder-decoder model i.e. SegNet. Khatun et al. [9] used handcrafted features to train a histology segmentation algorithm that uses a random forest classifier. RGB histograms along with Haralick features are computed from histology patches and fed into a machine learning classifier to label each patch as either containing a gland or not. According to the labeled patches a gland segmentation is performed and a binary mask is constructed.

2. Terms Definition

2.1. Binary thresholding

For a certain pixel i in an image matrix M , binary thresholding using a threshold t is defined using equation 1. All pixels that are less than the threshold t are set to 0 and the other pixels are set to 255. The value 255 represents a white pixel in a grayscale image and the value 0 represents a black pixel.

$$f(x,t) = \begin{cases} 0 & \text{if } x < t \\ 255 & \text{if } x \geq t \end{cases} \quad (1)$$

2.2. Cosine similarity

Cosine similarity is the most used metric to compare two input embeddings. It is expressed using equation 2. If two input vectors are identical, their cosine similarity is equal to 1.

$$s(a,b) = \frac{\sum_{i=0}^n a_i b_i}{\sqrt{\sum_{i=0}^n a_i^2} \sqrt{\sum_{i=0}^n b_i^2}} \quad (2)$$

2.3. Mean square error

The MSE is the most used loss function in autoencoders and regression models. In our case, we used it to train the ResNet18 model to predict the optimal threshold. In equation 3, p is the predicted value and a is the actual value

$$mse(a,p) = \frac{1}{n} \sum_{i=0}^n (p_i - a_i)^2 \quad (3)$$

3. Dataset

We use the dataset proposed by Jack et al. [10] and it contains H&E stained breast histology patches of size 512 x 512 pixels. Each patient has at least 3 annotated images with their binary segmentation masks. The dataset includes 50 histology images from 11 patients.

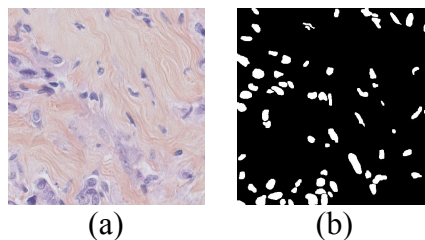


Fig 1 : (a) is H&E stained breast histology image and (b) is its ground truth mask

4. Methodology

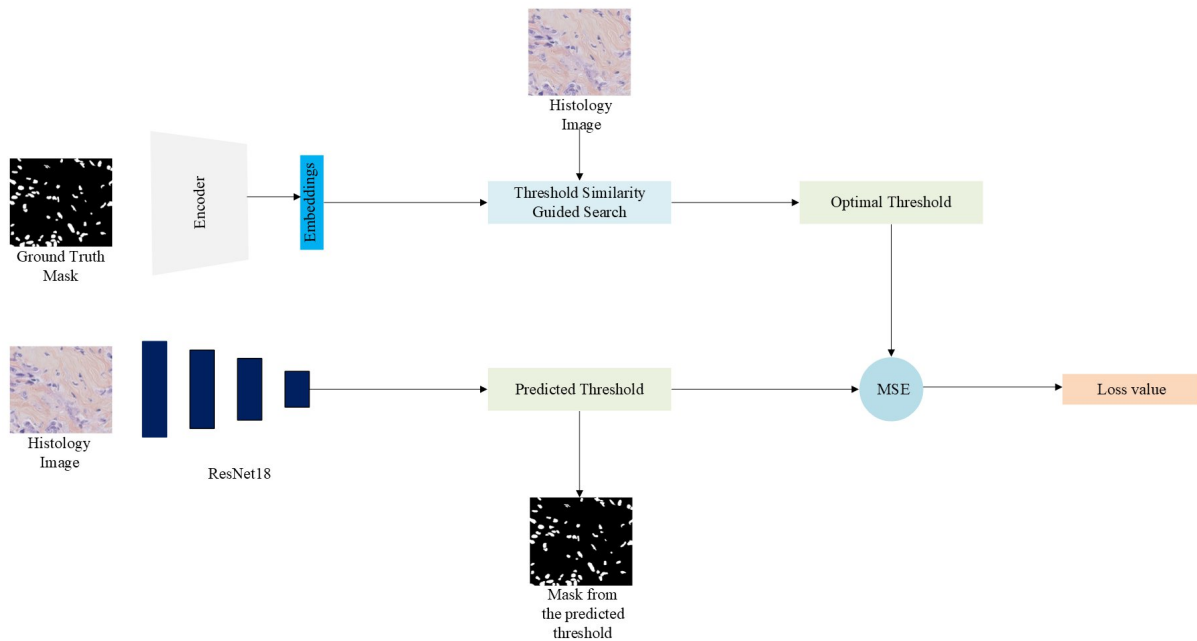


Fig 2: The proposed segmentation framework in the training phase

Figure 2 shows our proposed framework during the training phase. To find the optimal threshold, we use an encoder to generate embeddings from the ground truth mask and we feed the result along with the original image to an SGS algorithm that uses the cosine similarity to compare the original mask embeddings with the embeddings of the masks generated using all possible threshold values. We train a ResNet18 model to predict the optimal threshold for an unseen histology image. The loss function, i.e. The MSE, takes as input the predicted threshold and the optimal threshold and tries to minimize the difference between those to values. Our proposed model manages to learn this mapping in 300 epochs and, thus, converge to an optimal solution. We modify the original architecture of the ReNet18 by substituting the input channels for the first layer in order to take grayscale images and we change the number of output neurons for the last layer to match our regression problem.

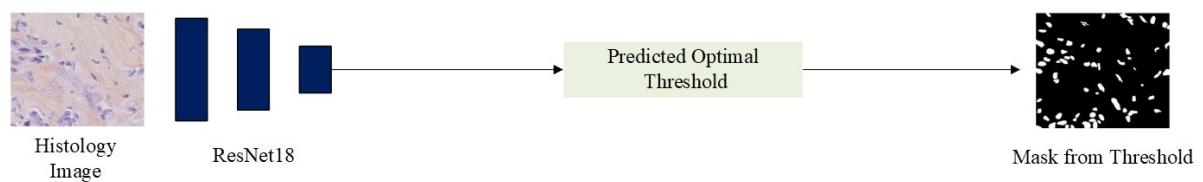


Fig 3 : Our proposed model during the inference phase

Figure 3 shows our proposed model during the inference/application phase. The ResNet18 takes as input a histology patch and the trained network predicts the optimal threshold value. We use the predicted value to generate a nuclei segmentation mask.

Algorithm 1: Similarity Guided Search (SGS)

Input : ground truth mask embeddings, original image in grayscale color

Output : optimal threshold

for i=0 **to** 255 **do**

 Threshold the original image using i

 Encode the thresholded image

 Compare the embeddings of the encoded image and the ground truth embeddings

 Update the optimal threshold value

Algorithm 1 shows our proposed SGS method. Another approach for comparing between the ground truth and the generated mask is to use the frechet inception distance (FID) [11] or the structural similarity (SSM) [12] and return the threshold value associated with the lowest FID or the highest SSM. Using this method, we eliminate the need to train an autoencoder to extract embeddings from the ground truth mask.

5. Results and Findings

During this section, we compare the results of our model with a standard Otsu [13] thresholding technique and we show that our method outperforms classical thresholding techniques on small size datasets.

Table 1 shows a the recorded metrics of our model and Otsu thresholding method. Our proposed model reaches 90% accuracy and 80% SSM and clearly outperforms other methods.

Method	Accuracy	Precision	Structural Similarity
Otsu thresholding	65%	22%	24%
Our method	90%	87%	80%

Table 1: The recorded metrics using our proposed segmentation model and Otsu thresholding method

Figure 4 shows a segmented histology image using Otsu method and our proposed model. Unlike Otsu method, our model manages to predict an accurate threshold value to segment nuclei from the input image.

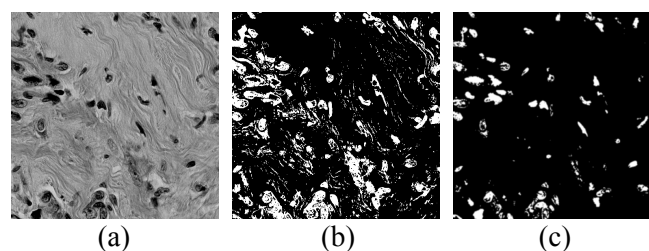


Fig 4: (a) is a grayscale histology image, (b) is the thresholded image using Otsu method, and (c) is the segmented image using our proposed model

6. Conclusion

To conclude, we proposed a machine learning model that learns the optimal threshold value in order to segment histology images and we showed that our proposed model outperforms classical thresholding methods, such as Otsu, on small size datasets.

In further studies, we propose using other types of metrics to compare between the original mask and the predicted mask.

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