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A few shot learning approach to classify breast histology images

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Abstract
Breast cancer screening starts with clinical evaluation and if an abnormality is detected the patient might undergo a tissue biopsy. Then, a pathologist take stained tissue samples from suspected breast areas. The tissue gets analysed under a microscope and a diagnosis gets established. This study introduces a few shot learning approach to classify breast histology images. We use a pre-trained convolutional neural network model to extract features from histology images and a prototypical network to classify the query embeddings into eight classes that represent the exact type of abnormality. To train the network, we have chosen to use the episodic training method. We experiment by changing the number of ways and the number of shot and we conclude that the model that uses 2-shots 2-ways yields the best classification accuracy, i.e. 92%, on a subset of the Break His dataset.

Keywords: Breast cancer, histology, few shot learning, prototypical networks, episodic training

Introduction

According to [1], breast cancer is one of leading causes of death in the world and it is estimate that there are 55,000 new cases each year in the United Kingdom.

We introduce a few shot learning approach to train a histology classifier with the aid of pre-trained convolutional neural networks (CNNs) [2] and prototypical networks [3]. A prototypical network takes as input the query embeddings and the support embeddings generated by the pre-trained CNN model and assigns a label to each query by determining the class centroid that has the closest euclidean distance [4]. We adopt the episodic training method to train the prototypical network.

Jakkaladiki *et al.* [5] introduced a hybrid deep learning algorithm that fuses the features from a DenseNet and a CNN while adding an attention mechanism. The resulting latent space vector is fed into another CNN that distinguish between benign and malignant histopathology images. Singh *et al.* [6] proposes a histology segmentation and classification framework that uses transfer learning. To segment histopathology images, the chanvese method is used and the result is fed to CNN classifiers. Pujari *et al.* [7] introduced a multi scale multi-stream network to classify histology images. The proposed deep learning model uses a feature sharing strategy that consists of sharing the learned features at each stream accross the network and the attention mechanism. Kaczmarzyk *et al.* [8] introduced a python package to classify histology patches. The proposed model is compared with pretrained models such as ResNet 18 and ResNet50. Saini *et al.* [9] introduced an improved VGG model that deals with the data imbalance issue. The method consists of freezing and concatenating all the layers till block 4 pool layer of the VGG16 pre-trained model with the layers of a randomly initialized Inception module.

Dataset

The breast histopathological image classification (BreakHis) [10] dataset has histology patches from 82 patients belonging to two classes, i.e. benign and malignant, and for each class there 4 subclasses that represents the exact type of abnormality. We select 10 images from each subclass for training and 5 images per subclass for testing.

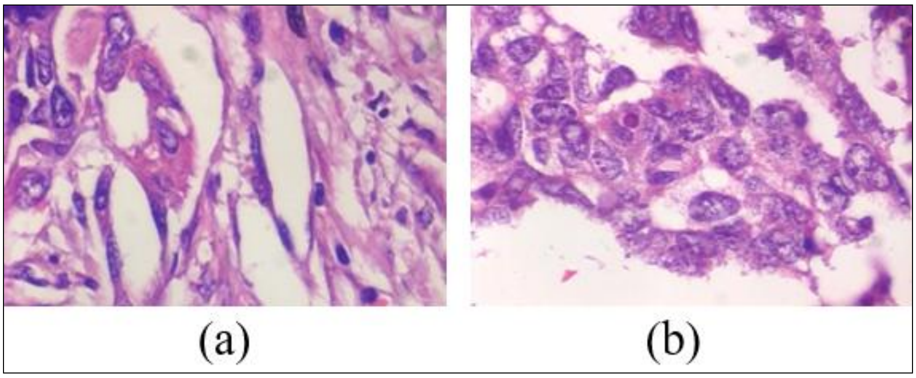

Fig 1: (a) is a histology patch from a patient suffering from ductal carcinoma and (b) is a histology patch from patient having papillary carcinoma

Methodology

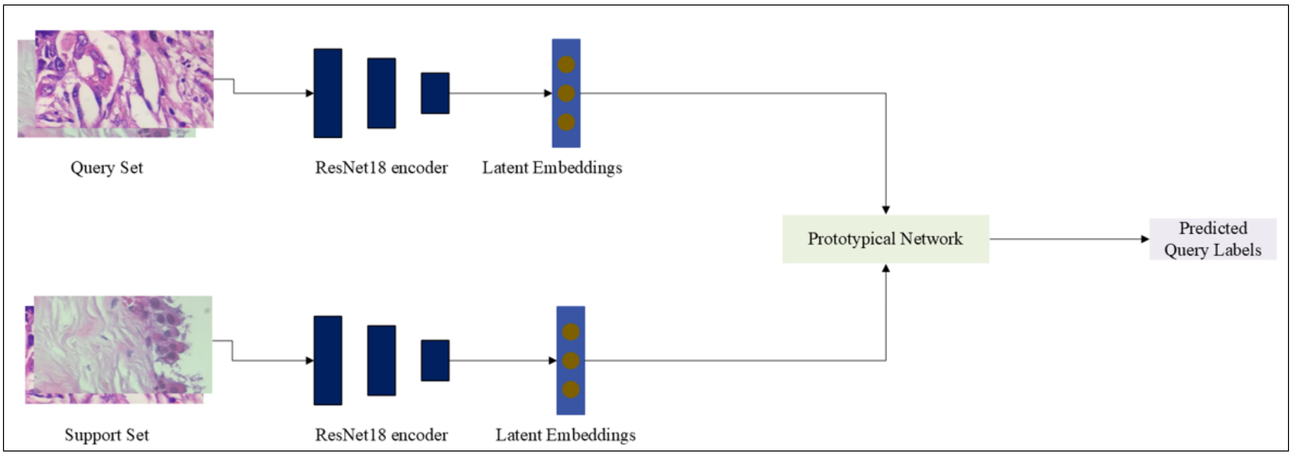

Fig 2: The proposed machine learning model

We train a ResNet18 [11] model on a large histology dataset to classify greyscale histology patches. The proposed network has 1 input channel and 8 output neurons. We substitute the fully connected network with a flattening layer to extract features from the last convolutional layer (see Figure 2). We use episodic training [12] to split the dataset progressively into support and query sets and a ResNet18 model to extract latent embeddings that are fed into a prototypical network. The prototypical network computes the embeddings' centroids for each class and measures the euclidean distance between the query embeddings and each centroid (see algorithm 1). The model assigns a label to each query according to the class that has the lowest distance from its embeddings. We set the number of tasks for training to 500 and the number of tasks for testing to 300. We use the stochastic gradient descent optimizer and the cross entropy loss to train the prototypical network. While training the model, we experiment by changing the number of shots and the number of ways.
As evaluation metrics, we use have chosen the accuracy and it is expressed using the formula belows;

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \qquad (1)$$

In equation 1, TP is the true positive value, TN is the true negative value, FP is the false positive value, and FN is the false negative value.

Algorithm 1: Prototypical network
Input: support embeddings, query embedding
Output: class label
Determine the number of class labels
Compute the centroid for each class using the support embeddings
Compare the query embedding with each class centroid
Return the label for the class that has the closest centroid

Results and Findings

To implement the prototypical network and the ResNet18 model, we used pytorch and numpy libraries.

Table 1: The recorded performance using different parameters

Parameters	Epochs	Accuracy
2-ways 2-shots	10 epochs	87%
	25 epochs	92%
2-ways 1-shot	10 epochs	74.7%
	25 epochs	85.5%

Table 1 shows that the prototypical network that uses 2-ways and 2-shots scores a 92% accuracy on the test set while being trained for 25 epochs.

Conclusion

This study introduced a machine learning algorithm that uses a pre-trained ResNet18 model as a feature extractor to generate embeddings that are used to episodically train a prototypical network to detect the exact type of abnormality. We conclude that the model that uses 2-ways and 2-shots results in the best classification accuracy and outperforms

other models.
In further studies, we propose using other few shot classification models such as the Siamese and Matching networks.

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