Deep Learning for Biomedical Texture Image Analysis

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Abstract

This paper shows promising results in the application of Convolutional Neural Networks (CNN) to biomedical imaging. Texture is often dominant in biomedical imaging and its analysis is essential to automatically obtain meaningful information. Therefore, we introduce a method using a Texture CNN for the classification of biomedical images. We test our approach on three datasets of liver tissues images and significantly improve the state of the art.

Keywords: Texture classification, biomedical imaging, Convolutional Neural Network

1 Introduction

In this paper we show that deep learning, which has established new states of the art in many domains including image classification and segmentation, can be very beneficial to biomedical imaging. Deep learning has recently shown impressive results in texture analysis as a feature extraction tool [1] or in an end-to-end training scheme [2, 3]. The analysis of texture is crucial in medical imaging for applications such as the detection, segmentation and classification of tissues, proteins and lesions. Therefore, we develop a method specifically designed for texture images based on Convolutional Neural Network (CNN) to classify liver tissues. Our neural network approach is of low complexity (memory and computation), which is particularly important in biomedical imaging to allow laboratories or research groups to train the network on a generally limited number of training images (avoiding overfitting) for possibly real-time applications, without requiring extremely powerful Graphical Processing Units (GPUs).

2 Work in progress

The architecture of the Texture-CNN with three convolution layers (T-CNN-3) is described in [2][1]. It uses an energy layer which densely pools (average pooling) the output features from an intermediate convolution layer. This approach discards the overall shape analysis needed for an object recognition task and of negligible importance in texture analysis. The complexity of this network is greatly reduced as compared to classic networks such as AlexNet (nearly three times fewer parameters) while obtaining better results on texture datasets.

Biomedical images are generally large (more than 1000×1000 pixels) and the number of training samples is often limited due to data privacy as opposed to the large training sets for object detection. Since we analyse texture images with repeated patterns, we can split the input images and use a voting score for classification. Thus, we do not need downscaling, which causes a loss of information, and we can increase the size of our training set, which is important for training neural networks.

Our approach is summarized in Figure 1. In this paper we use the IICBU database [4] with images of size 1388×1040. We split these images into 24 sub-images as shown in Figure 1(6 on the horizontal axis and 4 on the vertical axis) and resize them to 227×227. In the training phase, we use all the sub-images as independent samples to finetune the network, while in the testing phase we use a sum voting score among the 24 sub-images to classify the original full-size images. To this end, we sum the classification probabilities given as the softmax

[1] An implementation of the T-CNN-3 is available here:
https://github.com/v-andrearczyk/caffe-TCNN

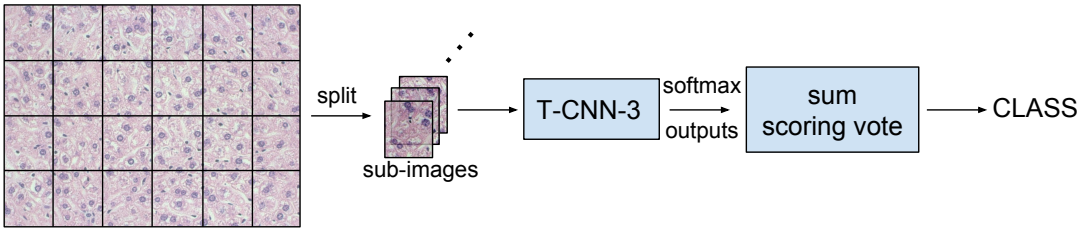

Figure 1: Proposed method including images split, neural network classification and collective classification by sum scoring vote.

outputs of the network of all the 24 sub-images and assign the class with the highest sum to the full-size image. The algorithm behaves as an ensemble method which takes a collective decision by summing the classification probabilities of different parts (sub-images) of the image.

3 Experiments

We test the proposed method on three datasets derived from the IICBU database [4]. An example of a tissue image is shown in Figure 1.

In the first experiment, we reproduce the Across-Subject Liver Aging (*AS-LA*) setup from [5] and report the accuracy averaged over 30 runs. The *AS-LA* dataset contains 1027 images obtained from 21 mice grouped into 4 classes. For each mouse, all the images are randomly divided into training (5/6) and test images (1/6).

The second and third experiments, respectively Liver Gender 6 Male (*LG6MAL*) and *Lymphoma*, are reproduced from [6]. We report the Mean Average Precision (MAP) measure averaged over 5000 runs as suggested in [6]. The *LG6MAL* experiment contains 265 images grouped into 2 classes (male/female). We report the results on the male class to compare to the state of the art. The *Lymphoma* dataset contains 374 images from 3 types of malignant lymphoma. For both *LG6MAL* and *Lymphoma*, 5% of the data is used for training and the rest for testing.

The results are reported and compared to the state of the art in Table 1. Our method significantly outperforms the state of the art on the three datasets. Even better results can be obtained with deeper networks and/or data augmentation. These results show that our approach could be very beneficial to the field of biomedical imaging. One could extend this approach to the detection and segmentation of tissues, tumors and lesions. However, the number of publicly available biomedical imaging datasets is small which is a significant barrier to the design of better suited and adapted computer vision methods including our approach.

Methods	AS-LA (accuracy)	LG6MAL (MAP)	Lymphoma (MAP)
Our method	**99.1%**	**98.2%**	**65.1%**
SoA	97.01% [5]	97.3% [6]	63.3% [6]

Table 1: Comparison between our method and the state of the art (SoA) in the classification results of tissue images.

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