Classification of Histologic Images Using a Single Staining: Experiments with Deep Learning on Deconvolved Images

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Abstract. The automated analysis of digitized immunohistochemistry microscope slides is usually a challenging task, because markers should be analysed on the tumor area only. Tumor areas could be recognized on a different slide, stained with Haematoxylin-Eosin. The basic idea of the present poster is to evaluate how well deep learning methods perform on the single haematoxylin component of staining, with the prospective possibility of developing a classifier able to recognize tumor areas on IHC slides on their haematoxylin component only. In a preliminary experiment, single stain images obtained by H-E color deconvolution showed an accuracy of 0.808 and 0.812 for Hematoxilyn and Eosin components, respectively.

Keywords. Deep Learning, Digital slides, cancer

1. Introduction

The automated analysis of digitized immunohistochemistry (IHC) microscope slides is an actual and challenging problem, because markers should be analysed on the tumor area only. The IHC samples are stained with diaminobenzidine (DAB) to reveal a specific biological marker, and counterstained with Haematoxylin (H) to identify the cellular context. Tumor areas could be recognized on a different slide, stained with Haematoxylin Eosin (H-E). This normally raises the complexity of an automated analysis, introducing new tasks such as the alignment of the differently counterstained samples. In the last years, however, notable results have been obtained in tumor and metastases detection on H-E stained digital slides using deep learning techniques [1,2].

The basic idea of the present poster is to evaluate how well deep learning methods perform on the single stainings, with the prospective possibility of developing a classifier able to recognize tumor areas on IHC slides on their H component only. A preliminary experiment has been made on H-E stained images coming from the Bach Challenge [2].

2. Methods

The dataset for the classification tasks comes from the BACH Challenge [2], Part A. It consists of training (n=400) histologic images from breast cancer, acquired at 0.42μm

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and labelled with 4 categories, imagewise (normal, benign, in-situ carcinoma, invasive carcinoma). As a baseline, a model has been trained on the original, full color images, split into 1024x1024 tiles with a 128 pixels stride, using Fastai as programming framework [3]. Images were then transformed into their H and E components, using the Color Deconvolution plugin of ImageJ [4] with its standard H-E vectors.

The same model has been trained separately on the two staining components, after RGB conversion to make them compatible with the model. Accuracy evaluation has been carried out with the Bach Challenge rules [2].

3. Results

The baseline model was based on ResNet152, pretrained on Imagenet on 3 epochs on the last layer, plus 3 epochs for fine tuning on the whole network. The model achieved almost state-of-the-art accuracy (average of 0.845 on 4 runs, with a maximum of 0.88). The Haematoxylin model reached an average accuracy of 0.8075 on 4 runs (maximum: 0.84), while the eosin model reached 0.812 (maximum: 0.83).

4. Discussion

The models trained on single staining images obtained an accuracy lower than the full image one, although, if compared with the challenge results, they could still rank among the best 10 [2]. This result has been obtained without any specific optimization for these images, as the model architecture and hyperparameters of the baseline model have been fully replicated. Furthermore, no custom deconvolution vectors could have been computed, and this could have lowered the classification performance.

Further work includes running the experiment on images acquired in a controlled environment, to compute the deconvolution vectors. Furthermore, classification of deconvolved H-DAB images in their Haematoxylin component will be also considered to prove a cancer recognition method for IHC in alternative to image registration

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