INTRODUCTION

The context
- Endoscopic specimens of the gastrointestinal tract generate a large amount of slides
- Identifying tissue abnormalities by pathologists is a hard and time consuming task
- 90% of the pathologist activities concern the analysis of benign slides
- We design a completely automatic algorithm to identify unhealthy slides and localize potentially tumorous areas

The difficulties
- Automatic slide analysis encounters different challenges such as tissue variation
- This variation is due to inherent tissue heterogeneity, inconsistent conditions during slide preparation, staining and acquisition
- Color normalization to reduce stain variation
- Supervised deep learning algorithm to discriminate two tissue classes: healthy vs unhealthy tissues

METHODS

Stain Normalisation
To uniformize the slide stains along the dataset we use Reinhard’s normalization method. The principle of this method is to use one slide as a reference image whose colours will be reproduced on all other slides.

Image Segmentation
- We are provided with images from the digestPath MICCAI challenge in which biopsy slides were associated with binary masks representing the abnormal areas. Among the dataset the slides have different dimensions, up to 30 000 pixels per dimension. To have uniform data we split each slide into small patches of 1024x1024 pixels.
- The goal of the segmentation algorithm is to produce a binary mask representing abnormal areas for any unseen slide. For that, we use a U-net algorithm applied at a patch-wise level i.e. the slide is decomposed into small patches, that are resized to lower-resolution to fit our computing capacity.

Principle of U-net
U-net uses convolutional layers to encode the image into a feature vector. This feature vector is then transformed into a binary mask with upsampling layers. Those layers are built symmetrically to the encoding part.

For each convolutional layer in the encoding part, we have an up-sampling layer in the decoding part. The output of the convolution is added to the output of an up-sampling layer to take advantage of spatial information contained in convolution filters.

RESULTS

Mask Prediction
- The output of the network is a probability map, defining for each pixel the likelihood to belong to an abnormal area. A global heatmap covering the whole slide is reconstructed from the patch-wise results. Finally, to create the binary mask, a threshold is applied on that probability.

We choose the threshold such that the number of false negative predictions is as low as possible while maintaining an acceptable rate of true positive predictions.
- You can see below an original mask, a probability map generated with our model and a binary mask created from the probability map.

ROC curve and AUC score
To evaluate the model we plot a Receiver Operating Characteristic (ROC) curves which shows the true positive rate given a false positive rate. The true positive rate denotes the proportion of pixels predicted as abnormal among all pixels labelled as abnormal.

The false positive rate represent the proportion of pixels predicted as abnormal among all pixels labelled as healthy. From this curve the AUC score (Area Under the Curve) is 0.95 which is comparable to state of the art methods.

CONCLUSIONS

Our current model is quite effective to detect healthy tissues but has some weaknesses namely on gland areas. This is probably due to the sub-representation of this kind of tissue in our dataset and the low analysis resolution. Our future work will be focused on improving our model to reduce false positive predictions on glands.

This could be achieved by combining a multi-resolution analysis as well as gland augmentation.
- We achieve an AUC score of 0.95 and a Dice of 0.86 on the validation dataset which is comparable to state of the art scores.

REFERENCES & ACKNOWLEDGEMENTS