

Master project: Deep Learning for Histopathology

Project description

Histopathology is concerned with the study of diseased tissue by microscopy. Tissue sections are stained with specific dyes to highlight structures of interest at the cellular and tissular level. Today, slides can be scanned and then analyzed manually on the screen; this is usually referred to as Digital Pathology.

Digital pathology has paved the way for the development and application of algorithms to automatically or semi-automatically analyze histopathology images. The potential benefits of automatic analysis include comprehensive measurements on the whole slide and the development of quantitative profiles informative about disease status and prognosis.

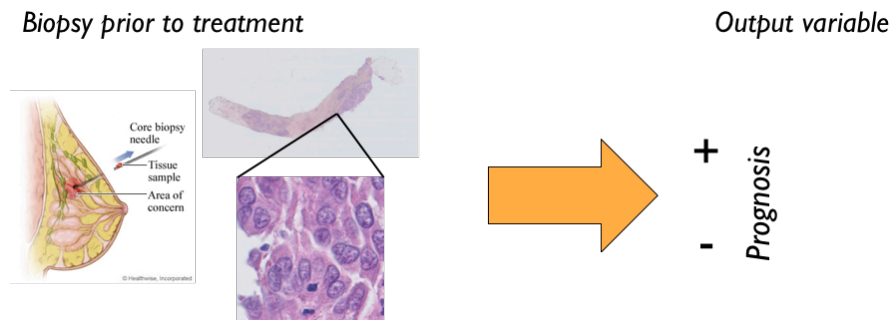


Figure 1 - Prediction of clinical variables from histopathology data.

Today, Deep Learning is the method of choice to solve tasks related to histopathology data, such as segmentation, classification of individual cells or classification of tissue types and prediction of clinical variables from the tissue slide (see Figure 1). However, due to the large size (typically in the range of $10^5 \times 10^5$) of tissue slides and their overwhelming complexity and variability, automatic analysis of such slides remains a very challenging and highly competitive subject today.

In this master project, we propose a project on a retrospective data set of 150 breast cancer cases with known outcome for all patients and also some additional annotation reflecting the pathologist's interpretation of the image data. The data set has been acquired by the pathology department of the Curie Institute, a hospital and research center dedicated to cancer. Based on our recently published work on nuclei segmentation [1, 2], we wish to design a network capable of cell type classification and to integrate the single cell classifications into our models for outcome prediction.

This master project could be the starting point of a PhD thesis.

References

- [1] Naylor, P., Lae, M., Reyal, F., & Walter, T. (2017). Nuclei Segmentation in Histopathology Images Using Deep Neural Networks. 2017 IEEE 14th International Symposium on Biomedical Imaging (ISBI 2017), <https://doi.org/10.1109/ISBI.2017.7950669>
- [2] Naylor, P., Lae, M., Reyal, F., & Walter, T. (2018). Segmentation of Nuclei in Histopathology Images by deep regression of the distance map. IEEE Transactions on Medical Imaging, 0062(c), 1–12. <https://doi.org/10.1109/TMI.2018.2865709>

Research group

The project will take place in the Centre for Computational Biology (CBIO — <http://cbio.ensmp.fr>), a joint laboratory between Mines ParisTech, a major engineering school, and Institut Curie, a major hospital and research institution dedicated to cancer. The CBIO is a group specialized in machine learning for biology. It benefits from an exceptional scientific environment with immediate access to experts and collaborators in biology and medicine, enabling a stimulating interdisciplinary exchange. The laboratory is located in the center of Paris.

Collaborating groups and supervision

This project is in the frame of a collaboration between the CBIO and the pathology department of the Curie Institute, headed by Anne-Vincent Salomon.

The main supervisor will be Thomas WALTER (Thomas.Walter@mines-paristech.fr). The project will be co-supervised by Anne-Vincent SALOMON and Guillaume BATAILLON at the Curie institute and Peter NAYLOR who is currently working on histopathology data at the CBIO.

Applications

The applicant should have a strong background in computer science and/or applied mathematics. Experience in machine learning, image analysis or computer vision, as well as good programming skills are required for this project. Basic knowledge in biology is an advantage, but not a requirement.

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