Visualization and detection of tissue folds in Whole Slide Images by Image Segmentation

Laura Purcaro

Master thesis in Bioinformatics and Computational Biology

In recent digital pathology studies involving whole-slide images (WSI), researchers avoid tissue artifacts by manually selecting images or regions-of-interest (ROI). Even though manual selection ensures the quality of selected tissue regions, it limits the speed and objectivity of analysis by introducing a subjective user-interactive step. Moreover, manual selection is a tedious process for large datasets, and thus, their automatic identification is essential in order to save time and proceed with further analysis. Tissue folding is a common artifact in histological images that appear when the tissue folds over twice or more by a non-precise cutting due to defect in the blade edge or when placing it on the microscope slide. The aim of this study is to improve the visualization and detection of tissue folds from low-pixel resolution images. This information can be used to determine bad quality tissue slides from good quality tissue slides and therefore, being rejected or accepted by the algorithm. Here, three automated image analysis methods for identifying tissue folds in section images are presented and evaluated. The outputs were compared with manually annotated WSI and evaluated with three different metrics: the widely used Dice score and IoU metrics, and a localization metric specifically created for this study. Our results showed that the algorithm is able to detect a high percentage of folds making it possible to standardize a threshold to automate the classification of "Good" and "Folds" images. Likewise, the huge diversity of tissue types present in this dataset gives a great relevance to this study, confirming that, although difficult, it is possible to establish a generalized algorithm that works optimally for the whole dataset.

Supervisor : PD Dr. Inti Zlobec