Image analysis of cancerous cells

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Hodgkin's lymphoma is a malignant disease of the lymphatic system caused by abnormal transformations of lymphatic cells. The groundwork for understanding this type of lymphoma was set in 1832 by Thomas Hodgkin, who described the disease for the first time and is linked to the lymphoma, nowadays known as Hodgkin's lymphoma. The characteristics for Hodgkin's lymphoma are the presence of multinucleated Reed-Sternberg cells (RS-cells) and classical mononucleated Hodgkin's cells, together designated as HRS-cells. Figure 1 shows a typical RS-cell. The HRS-cells contribute only about one percent of the total cell mass in the lymphoid tissue, what complicates diagnosis and analysis of the disease. The origin of HRS-cells was unclear for a long time. Today it is mostly accepted that HRS-cells result from transformations of lymphatic B-cells which lack to undergo apoptosis. But, the reason for these malignant transformations is still unclear and will be a topic of further investigations.

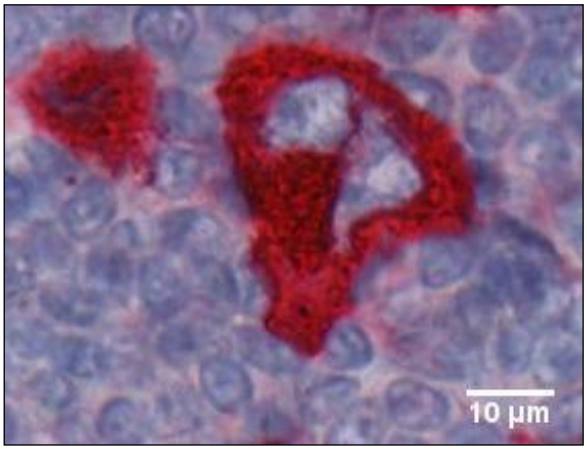

Figure 1: Reed-Sternberg cell in classical Hodgkin's Lymphoma. The image is extracted from the baseline image of a SVS file (Scanscope Virtual Slide), which has a 40x resolution. The SVS file was created by the Aperio scanning system for slides of tissue sections. One large Reed-Sternberg cell is shown at the center and one smaller at the upper left corner of the image. Several small lymphocytes are also visible. The cancerous cells are CD30-immunostained.

To study the development of Hodgkin's lymphoma, we combine medical knowledge with bioinformatics methods. Starting point are digital image data of tissue sections in which cells are immune-stained with various markers (such as CD30, CD20) to highlight cancerous cells as well as surrounding lymphatic cells. The samples originate from different types and different stages of Hodgkin's disease. The images are generated by scanning whole slides of

tissue sections using a scanning system provided by Aperio. The resolution allows gaining information of the disease on cellular level.

First, we use standard techniques of image preprocessing to optimize image quality and to accentuate the cancerous cells. We want to compare the usability of different approaches of preprocessing. Second, segmentation algorithms are applied to identify cancerous cells within slide images. Third, we characterize the identified tumor cells by various descriptors e.g. cell size, cell-shape, spatial distribution of cells, density in various tissue types, or intercellular correlation, to refine the applied methods. In our poster we will introduce the conceptual idea of the project, discuss the methods used, and present first results.

References

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