Lymph Node Landscapes

By Hendrik Schäfer, Martin-Leo Hansmann & Ina Koch

The research story

In routine pathology, immunohistological images are a standard tool for diagnostics. Tissue sections are stained highlighting specific parts or cells for visual inspection via light microscopy. Modern whole slide scanners can digitize such tissue samples in high resolution and allow the application of computer-aided methods. We examined classical Hodgkin lymphoma tissue sections. Hodgkin lymphoma is a malignancy of the lymph system and has some unusual characteristics. In contrast to other, solid tumors, only one percent of the tumor tissue is made of malignant cells, surrounded by a hetero-geneous environment of immune cells. The malignant cells are called Hodgkin and Reed-Sternberg (HRS) cells. The immuno staining binds to CD30, a protein expressed by HRS cells. Thus, malignant cells appear red in the histological image. A second stain, hematoxylin, binds to negatively charged molecules and color cell nuclei in blue.

The image

We applied an automated imaging pipeline to recognize and chart all HRS cells of the whole slide images [1]. A unit disk graph models the cell distribution in the image. Nodes represent the malignant cells, arcs define the local neighbor-hood of an HRS cell dependent on the spatial distances. The colored bubbles mark commu-nities computed by clique percolation. Graph theoretically, they are groups of nodes that are highly connected. The image was generated by merging the original histological image with two overlays generated by Impro, our in-house image processing software. The automated object detection yields additional objective data about the cell distribution and morphology and may support the diagnosis of pathologists in future.

Reference

[1] Schäfer H, Schäfer T, Ackermann J, Dichter N, Döring C, Hartmann S, Hansmann M-L, Koch I, CD30 cell graphs of Hodgkin lymphoma are not scale-free – an image analysis approach. Bioinformatics 32(1):122–129, 2016.