Recognizing Microscopic Structures using Deep Learning

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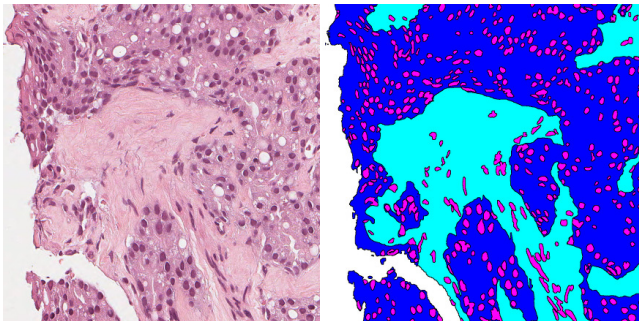
To make a significant dent in the issues the healthcare sector faces today in terms of costs and overextended employees, a great increase of viable automated tools will sooner or later be needed. For pathologists this is no different. However, the complexity and size of microscopy images makes automated analysis of them difficult. This thesis achieved promising and first-of-its-kind results in tackling the very under-explored challenge of recognizing several structures in microscopy images at once. By using a deep learning approach heavily inspired from a pair of popular artificial neural networks a score of 80 % mean IU was reached. The resulting networks are prospects for use in several different pre-processing steps in medical image analysis applications – possibly enabling or improving automated tools in the pathological field in the future.

The healthcare sector is under constant pressure to reduce its expenditures and the workload of its employees. Meanwhile, pathologists have to manually analyze large amounts of images as quickly as possible. An automated tool that considerably assists in or performs some of those analyses is therefore highly desirable. Yet, due to the complexity of both the images and the analyses, no such tool exists today. In an effort to change this, *Vinnova*, the Swedish state's innovation authority, has granted financing to a collaboration between *Lund University* and *Sectra* named Digital Pathology for Optimized Gleason Score in Prostate Cancer, or *DOGS*. The goal of the project is to reach an image analysis solution that will increase the precision and decrease the cost of Gleason grading: a system to categorize the severity of prostate cancer in a patient. With the vast increase of performance that deep learning – or artificial and convolutional neural networks – in machine learning and image analysis has yielded over traditional approaches, it is very probable that such networks will be included in the project's end product.

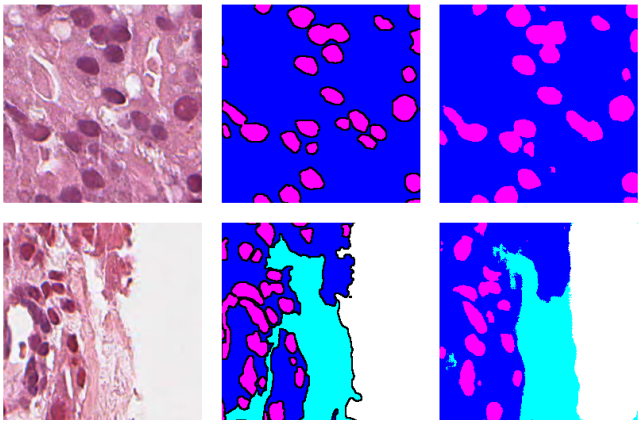
The goal of this thesis was to investigate if deep learning could be used to recognize microscopic structures, or more specifically, perform semantic segmentation of histo-



Semantic segmentation in histopathology

pathologically relevant classes. As segmentation maps makes it trivial to perform analysis on a single class or object in an image, well-performed semantic segmentation allows for further analyses ranging from relatively simple: find color variation in specific classes; to more complex: count and look at the shapes of objects. From the DOGS project's perspective, this would have potential as a pre-processing step that could aid the following analyses, which ultimately might make automated Gleason grading or other helpful tasks possible.

By originating from well-known artificial neural networks already used in other semantic segmentation tasks, and training on manually segmented ground truth, three relatively high-performing networks were produced. These networks achieved scores of between 75-80 % IU in nuclei segmentation and between 78-80 % mean IU in overall segmentation. After visual investigation it was concluded that all networks show promise, but depending on what they are to be used for less to extensive improvements are needed. A few implementation errors aside, the networks themselves might prove adequate in their current forms, but both a reconsideration about the ground truth segmentation as well as a vast expansion of it is needed.



Input, ground truth and network segmentation