Pixel-wise segmentation of cell images using U-NET and Mask-RCNN

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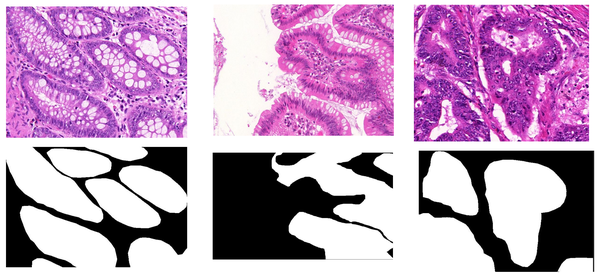
Motivation

Cell count is an important measure in pathological examinations of tissue biopsies since it is a highly relevant metric. It must be done precisely as over/underestimation can have significant influence on the chosen treatment.

This is a cumbersome and time-consuming task to do by hand and mistakes can easily occur. Therefore, it is desirable to automate this process. Since both the shape and size of the cells can influence this count the automated implementation can be complicated.

Data consists of 165 images from H&E stained histological sections arising from tumours in the glandular epithelium[1].

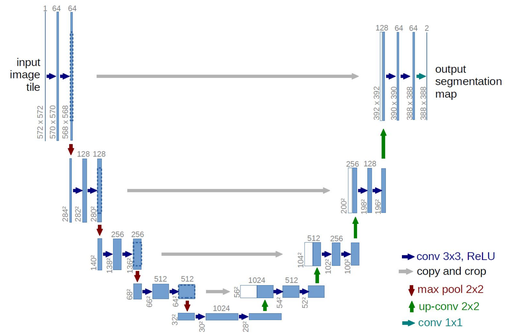


U-NET Model

The architecture of the U-net is symmetric and consists of two major parts [3]:

- Left part is the contracting path with convolutional layers and max-pooling.
- Right part is the expansive path, with transposed convolutional layers and concatenation with corresponding step in left part.

Zero-padding ensures original image dimensions for output in order to preserve data in border regions [4].

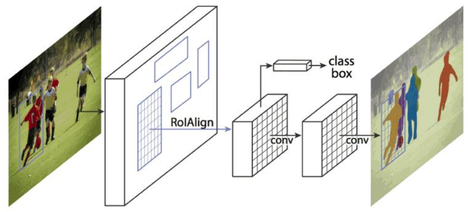


Mask-Faster RCNN Model

Instance segmentation algorithm that uses an image, to predict the object bounding boxes, classes and masks.
A regional proposed network

- Generates proposals about possible regions that might contain an object
- Predicts the class of the object, refines the bounding box and generates a mask in pixel level of the object based [8].

The architecture of the network is based on the same principle as for the U-net [3].

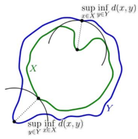


The Mask R-CNN framework for instance segmentation

Metrics

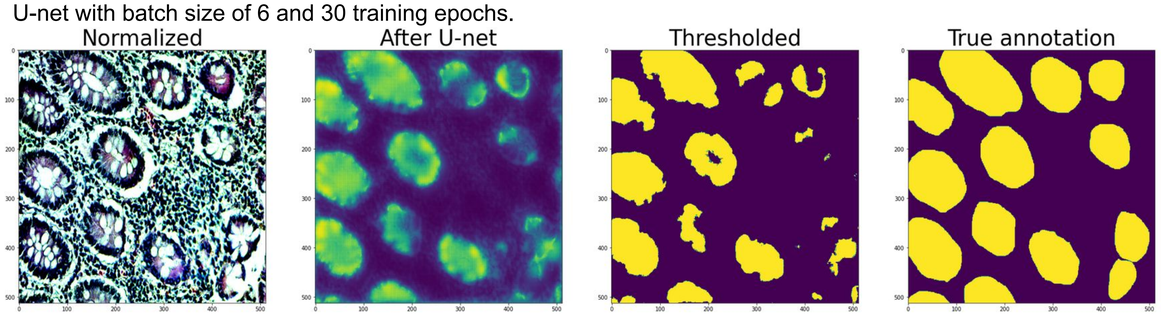
- F1 scores (Dice score)
  - Metric for overlap vs. union validation
  - Harmonic mean of the precision and recall

- Object F1-Scores
  - F1-based score
  - Evaluates individual objects (cells)
- Hausdorrf distance
  - Measure for shape similarity
  - Distance between corresponding points

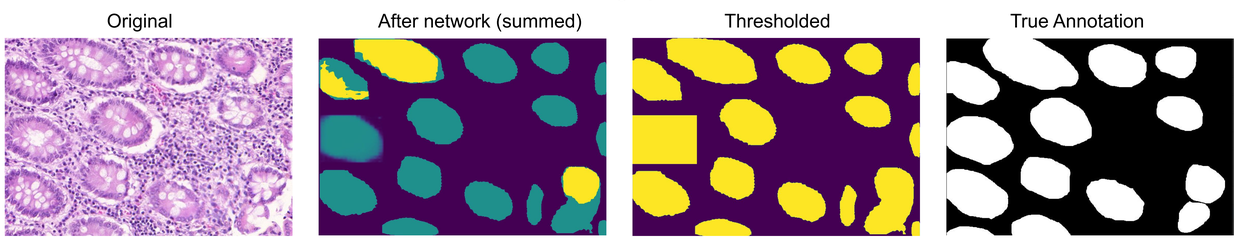


Results - Qualitative

U-net with batch size of 6 and 30 training epochs.

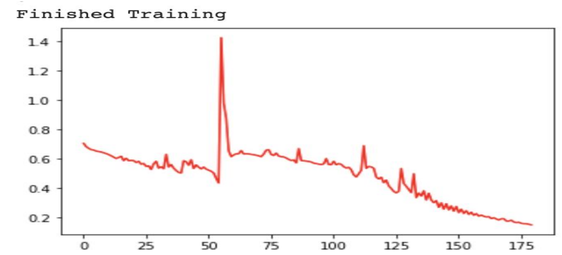


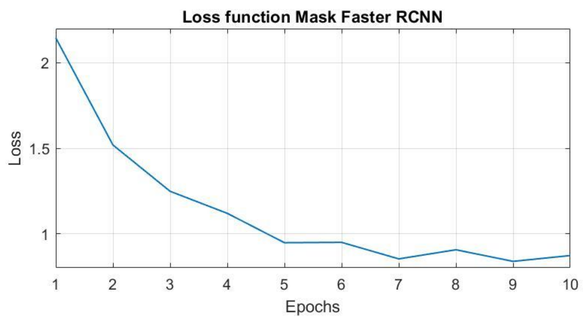
Mask Faster RCNN network with batch size 2 and 10 training epochs.

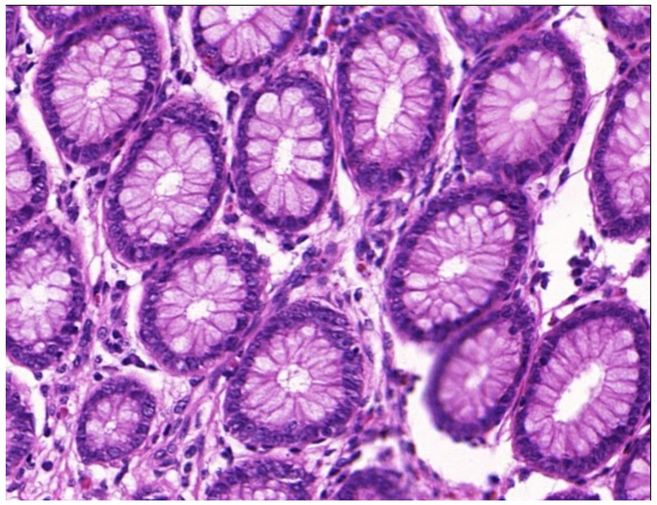
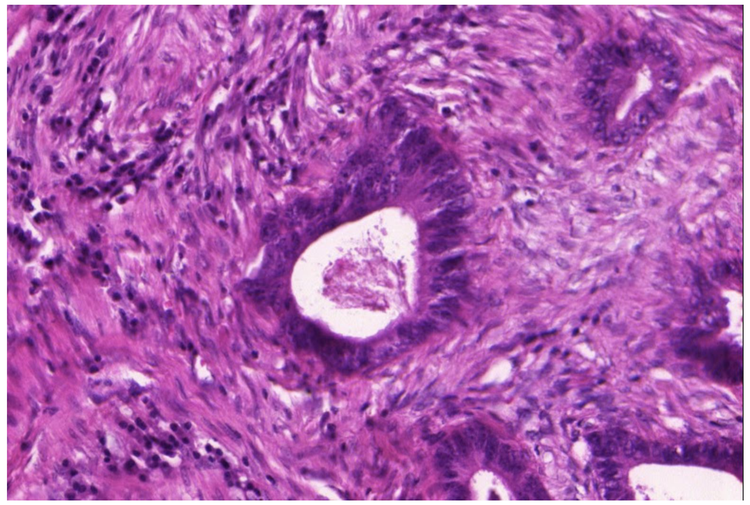
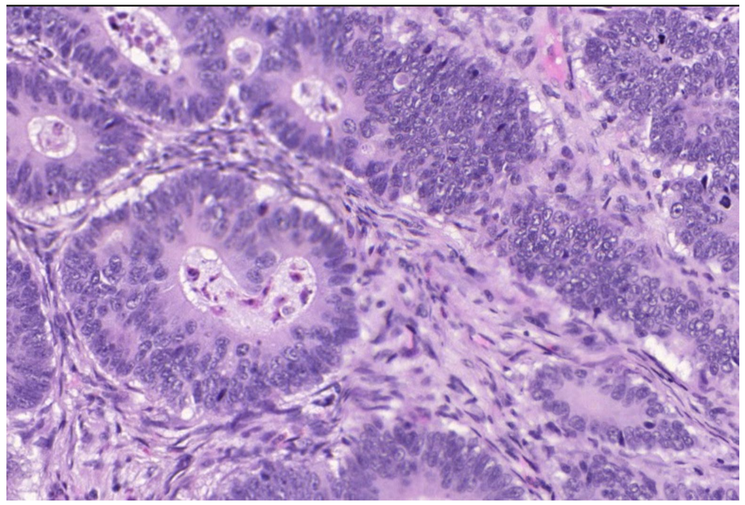
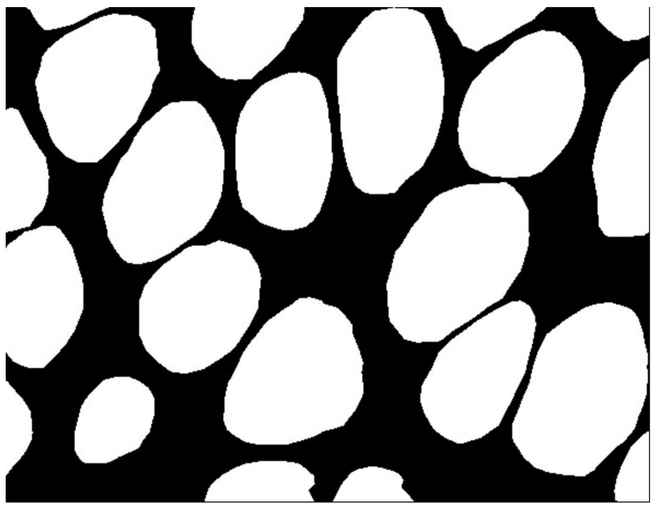


Results - Quantitative

Model:	F-score	Dice Index	Hausdorff Distance
Bioimage-Informatics [2]	0.78	0.71 ± 0.16	152.48 ± 84.78
U-net	0.3244	0.3294	179.45
Mask-Faster	0.825	0.8491	25.69





References

[1] https://warwick.ac.uk/fac/sci/dcs/research/tia/glascontest/download/
[2] Presentation by BioImage Informatics Team (https://warwick.ac.uk/fac/sci/dcs/research/tia/glascontest/presentations/bioimage_informatics_team_glas_final_no_animation.pdf)
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[5] TorchVision Object Detection Finetuning Tutorial (https://pytorch.org/tutorials/intermediate/torchvision_tutorial.html)
[6] https://en.wikipedia.org/wiki/F-score
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