Detection of lymph node metastasis in colorectal cancer with the help of deep neural network

Csaba Kindler¹, Giorgia Milli², Christel Ottosson¹, Kristian Euren², Lena Kajland-Wilén² , Maziar Nikberg³

¹Department of Pathology, Västmanland Hospital Västerås, Sweden, ²ContextVision AB, Stockholm, Sweden, ³Department of Surgery, Västmanland Hospital Västerås, Sweden

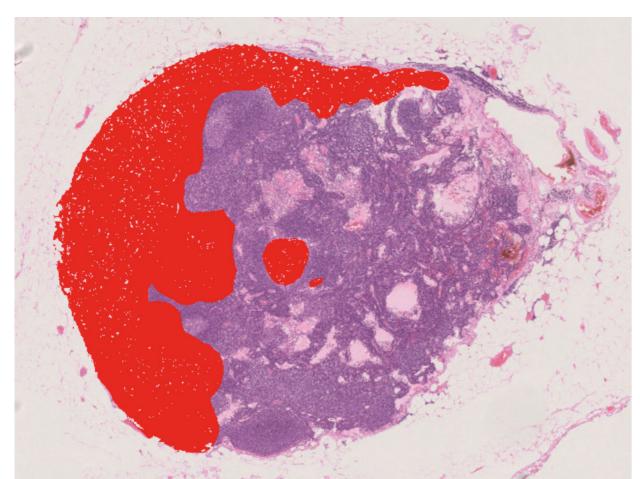
Introduction

About 40% of the patients undergoing resection of colorectal carcinoma have lymph node metastasis at the time of the operation. The histologic examination of lymph nodes is an important but tedious task. The primary aim is to develop a deep learning-based algorithm that can support the pathologists to detect metastatic cancer in digitalised histologic sections of colorectal lymph nodes. To be helpful the algorithm shall have at least the same pixel-level accuracy as annotations made by pathologists.

Methodology

In this study, we included lymph nodes from patients with stage I-III colorectal cancer operated at Västmanland's Hospital in Västerås. The histological sections were scanned on a Hamamatsu S60 scanner. Two pathologists, one reviewing the other, made pixel-level annotations of cancer areas, figure 1.

We used a U-Net neural network architecture [1], which was pre-trained on Camelyon data [2], to learn to segment cancer areas. The network was trained on 758 whole slide images (WSIs), 360 cancer slides and 398 benign slides. The performance was then evaluated on 43 cancer slides and 31 benign slides.



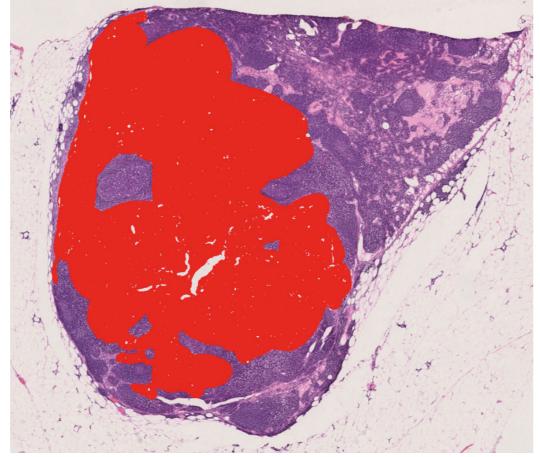
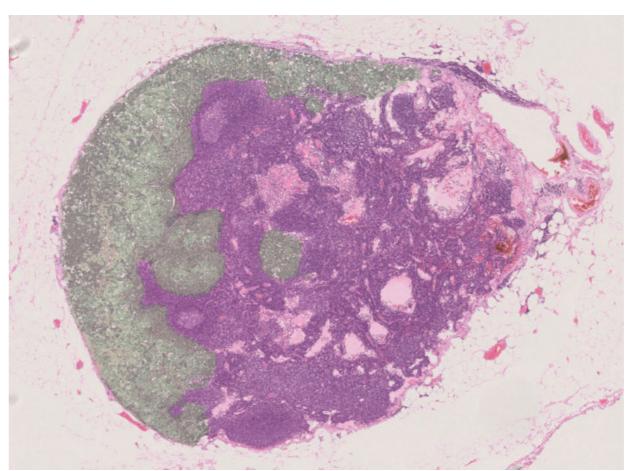


Fig 1. Examples of pathologists' pixel-level annotations of lymph node 1 and 2

Results

	Precision	Sensitivity	Specificity	Accuracy
Cancer slides	0.906	0.820	0.980	0.952
Benign slides	n/a	n/a	0.996	0.996

Median pixel-level performance on the evaluation images



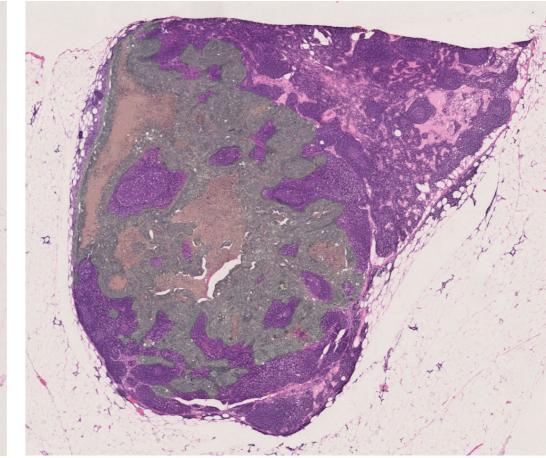


Fig 2. Pixel-level predictions of cancer overlaid (green) on evaluation H&E images of lymph node 1 and 2

Conclusion

We present a deep learning algorithm that can identify and outline lymph node metastasis in digitalized histological sections with encouraging accuracy, with potential to minimize the risk to miss any malignancy and at the same time save pathologists' time. This algorithm could be further developed and validated into a decision support tool for pathologists in their routine diagnostic process.

^[1] Ronneberger, O. et. al. (2015), arXiv:1505.04597 [2] Litjens, G. et. al. (2018). GigaScience