

Automatic colorectal cancer screening using deep-learning on spatial light interference microscopy data

Jingfang K. Zhang^{1,3,5}, Michael Fanous^{1,3,4}, Nahil Sobh⁶, Andre Balla, Gabriel Popescu^{1,2,3,4} 1) Quantitative Light Imaging Laboratory, University of Illinois at Urbana-Champaign, Urbana, IL 61801, USA 2) Department of Electrical and Computer Engineering, University of Illinois at Urbana-Champaign, Urbana, IL 61801, USA 3) Beckman Institute for Advanced Science and Technology, University of Illinois at Urbana-Champaign, Urbana, IL 61801, USA 4) Department of Bioengineering, University of Illinois at Urbana-Champaign, Urbana, IL 61801, USA 5)Informatics Programs, University of Illinois at Urbana-Champaign, Urbana, IL 61801, USA 6) Affiliate Professor NCSA Center for Artificial Intelligence Innovation, University of Illinois at Urbana-Champaign, Urbana, Illinois 61801, USA



ABSTRACT

Segmentation & Classification

Gland Capturing Performance By Training Epoch

The surgical pathology workflow currently adopted in the clinic uses staining to reveal tissue architecture within thin sections. A trained pathologist then conducts a visual examination of these slices and, as the investigation is based on an empirical assessment, a certain amount of subjectivity is unavoidable. Furthermore, the reliance on such external contrast agents like hematoxylin and eosin (H&E), albeit a well-established method, makes it difficult to standardize color balance, staining strength, and imaging conditions, hindering automated computational analysis. In response to these challenges, we applied spatial light interference microscopy (SLIM), a label-free method that generates contrast based on the intrinsic tissue refractive index signatures. Thus, we reduce human bias and make the image data comparable across instruments and clinics. We applied a Mask R-CNN deep learning algorithm to the SLIM data to achieve an automated colorectal cancer screening procedure, i.e., classifying normal vs. cancer specimens. Our results obtained on a tissue microarray consisting of specimens from 132 patients, resulted in 91% accuracy for gland detection, 99.71% accuracy in gland-level classification, and 97% accuracy in core-level classification. A SLIM tissue scanner accompanied by an applicationspecific deep learning algorithm may become a valuable clinical tool, enabling faster and more accurate assessment by the pathologist.





- a) Images of 32 testing cores.
- b) Cancer core.
- c) Prediction of gland detection and classification on the core in b).
- d) Zoom-in image of the cancer gland boxed in c).
- e) Normal core. f) Prediction of gland detection and classification.
- g) Zoom-in image of the normal gland boxed in
- f). Red color represents cancer and green color normal glands.



The network's gland classification performance is shown at three different training epochs, the 50th, 100th, and 390th, as indicated. The AUC (Area under the ROC Curve) is 0.87, 0.90, and 0.91, respectively.

System Setup



Gland Detection Errors



Normal: ground truth and detection



Summary & Discussions

In summary, we demonstrated promising results in colorectal tissue segmentation, classification, and whole core diagnosis, by combining Mask R-CNN deep learning network to SLIM images. The 91% of gland detection accuracy, the near perfect classification accuracy, and the 97% of whole core diagnosis accuracy show that this method can effectively assist pathologists to screen colorectal cancers. Histopathology combined with colonoscopy tissue resection remains the gold-standard for colorectal cancer diagnosis. However, we expect our method to complement valuable pathological information that can improve screening accuracy, reduce manual work, and multiply throughput at clinics. The SLIM module can be integrated with incumbent microscopes across clinics and then used a valuable tool to optimize colorectal screening workflows. Moreover, the SLIM module can also be used to quantify the aggressiveness of the cancer disease or detect other types of cancer.

With its common-path interferometric geometry, SLIM is highly reliable in providing nanoscale information about tissue architecture, enabling a high sensitivity and specificity for pathological examination. The AI inference method can be integrated with SLIM acquisition software. As the inference runs faster than the acquisition of a SLIM frame and it can also be operated parallelly, we anticipate performing image acquisition and diagnosis in a real-time way. In terms of overall throughput, the SLIM tissue scanner can match commercial whole slide scanners that only conduct bright field imaging on stained tissue sections. Theoretically, the diagnosis, with all critical areas of interest being highlighted for pathologists, can be given while the scanning is being done.

- SLIM system implemented as add-on to an existing phase contrast microscope. Pol, polarizer and SLM, spatial light modulator.
- The four independent frames corresponding to the 4 phase shifts imparted by the SLM are shown for a tissue sample.

. a) Ground truth (manual) segmentation of cancer glands. b) Network prediction, showing that the regions in the dash boxes were missed. c-d) Similar illustration as in a-b). e) Ground truth (manual) segmentation of normal glands. f) Network prediction, showing that the regions in the dash boxes were additional true positives. g-h) Similar illustration as in e-f). Note that all errors and additions occur at the boundaries of the cell cores.

Deep Learning Network



• Mask R-CNN (regional convolutional neural network) framework contains two stages: scan image and generate regional proposals for possible





Reference & Fundings

- 1. Popescu, G., Quantitative phase imaging of cells and tissues. 2011: McGraw Hill Professional.
- 2. Kandel, M.E., et al., *Label-free tissue scanner for colorectal cancer screening*. Journal of biomedical optics, 2017. **22**(6): p. 066016.
- 3. Zhang, J.K., et al., Label-free colorectal cancer screening using deep learning and spatial light interference microscopy (SLIM). APL Photonics, 2020. 5(4): p. 040805
- 4. Abdulla, W., Mask R-CNN for object detection and instance segmentation on Keras and TensorFlow <u>https://github</u>. com/matterport. Mask _ RCNN, 2017.
- 5. Park, Y., C. Depeursinge, and G. Popescu, *Quantitative phase imaging in biomedicine*. Nature Photonics, 2018. **12**(10): p. 578.
- 6. Majeed, H., et al., *Quantitative phase imaging for medical diagnosis*. Journal of biophotonics, 2017. 10(2): p. 177-205.
- 7. Majeed, H., et al., Quantitative histopathology of stained tissues using color spatial light interference microscopy (cSLIM). Scientific reports, 2019. 9.

Fundings: National Science Foundation (Grant Nos. 0939511, R01 GM129709, R01 CA238191, and R43GM133280-01).

objects; classify the proposals and generate bounding boxes and pixel-wise masks.

- This specific network adopts a backbone of ResNet101 plus FPN for feature extraction. RPN (Region Proposal Network) scans over backbone feature maps, which allows reuse of the extracted features and remove duplicate calculations.
- The final masks for objects will be scaled up to match the ROI bounding box. The other branch, of fully connected layers, takes the outputs of the ROI Pooling and outputs two values: a class label and a bounding box prediction per object.

a) Confusion matrix, which shows that 95 instances of the detected cancer glands are correctly classified, while 1 is wrongly classified as normal. All the 248 instances of the detected normal glands are perfectly classified. b) Confusion matrix, which shows that 96 cancer glands are detected, with 95 correctly classified and 1 wrongly classified; 20 cancer glands are missed. 248 normal glands are detected and correctly classified, while 3 normal glands are missed. c) Confusion matrix, which shows that all the 14 cancer cores are correctly diagnosed as cancer; 17 out of the 18 normal images are correctly diagnosed, while 1 normal core is wrongly diagnosed as cancer. d) Gland detection performance at three different detection confidence scores: 90%, 80%, and 70%, as indicated.

Acknowledgements





