

Automated Non-Tumor Segmentation to Improve Tumor Detection and Analysis using Modified U-NET Networks



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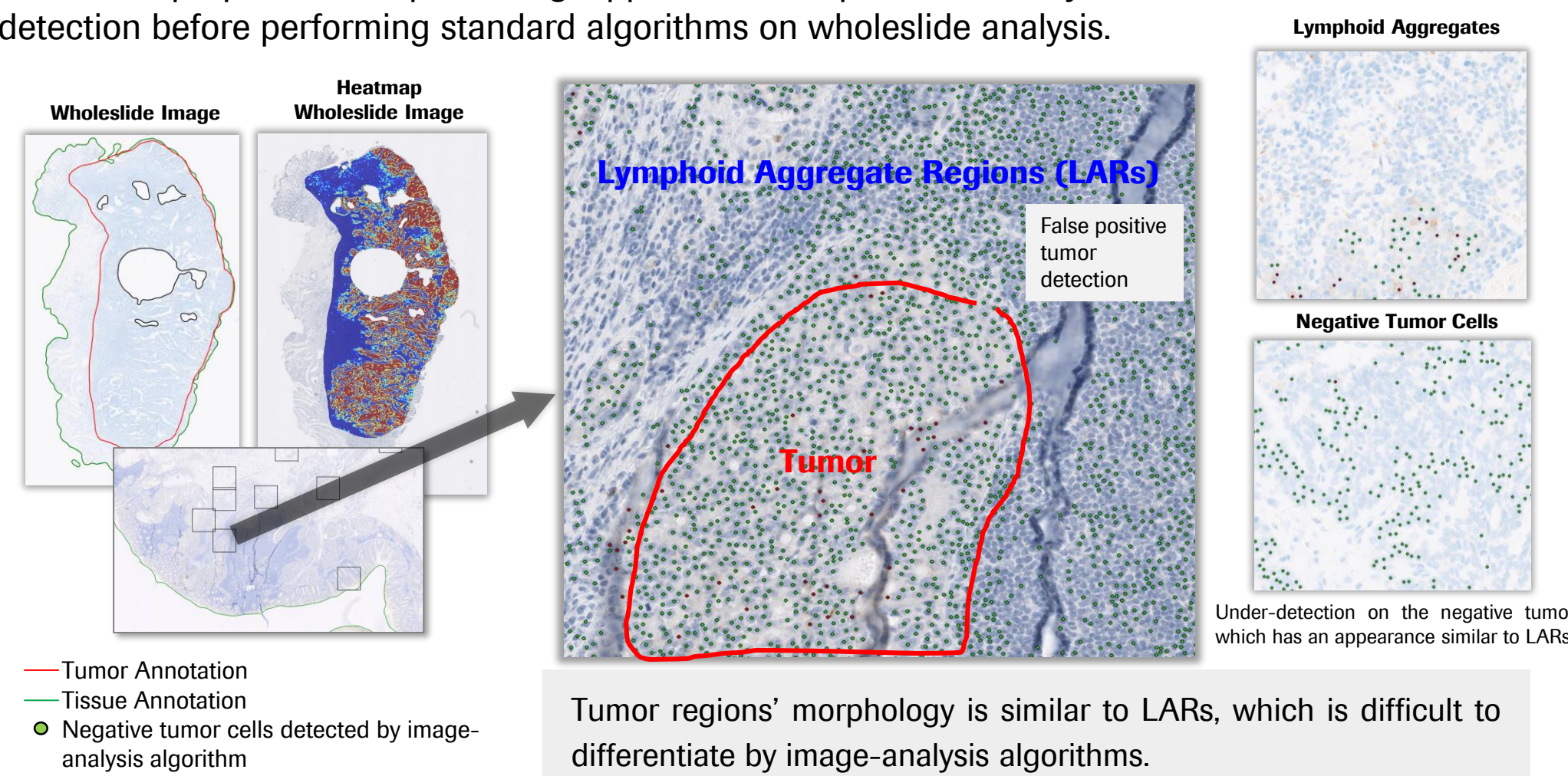
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1 – Background

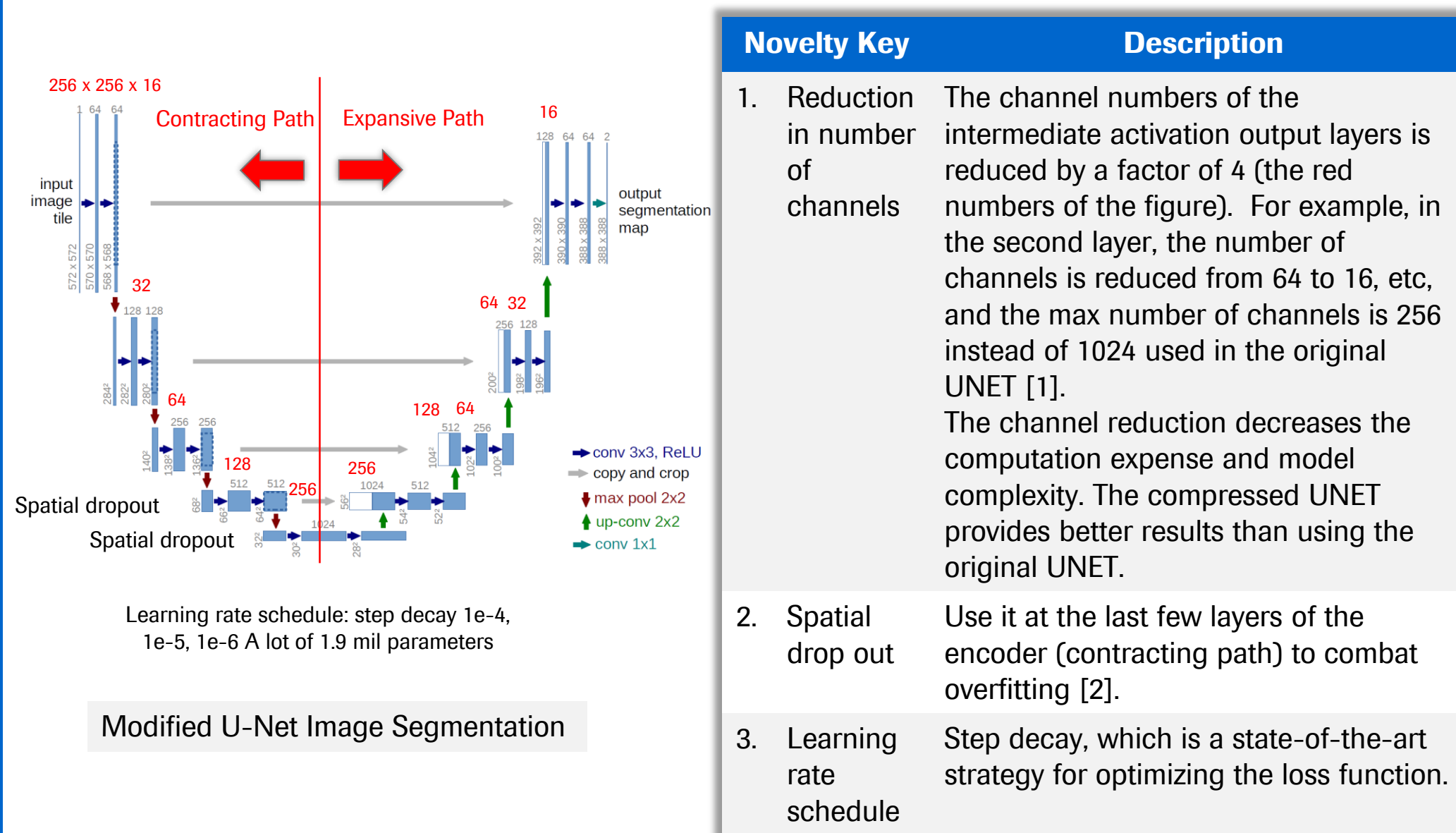
In digital pathology, whole-slide analysis with positive and negative tumor cells needs pathologists to initially provide tumor annotations that exclude non-target regions, such as normal tissue. It is difficult to exclude “Lymphoid Aggregate Regions (LARs),” which are clusters of immune cells and their morphology is frequently similar to group of negative tumor cells. As a result, image-analysis algorithms may provide false detection results for these LARs.

Goal: We propose a deep-learning approach to improve accuracy and reduce false non-tumor detection before performing standard algorithms on wholeslide analysis.

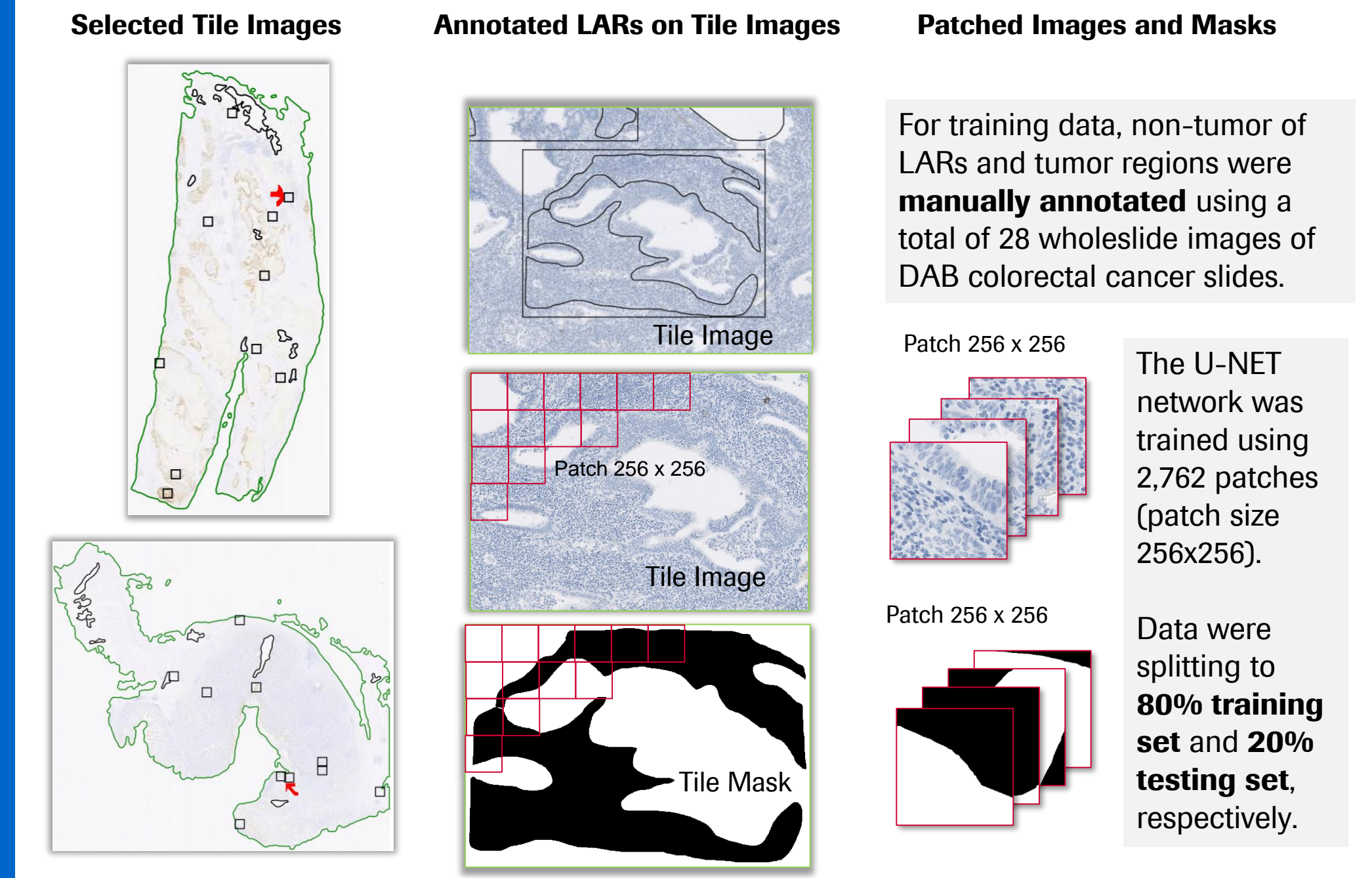


2.1 – Method: Modified U-NET, Tile-based Encoder Decoder

We proposed a modified U-NET that automatically detected and masked out LARs.

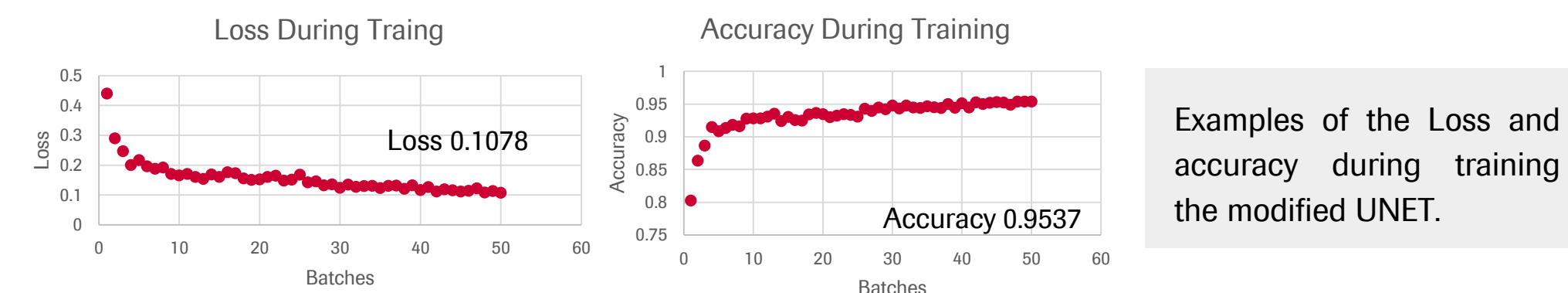


2.2 – Method: Ground Truth Collections for Training the Networks



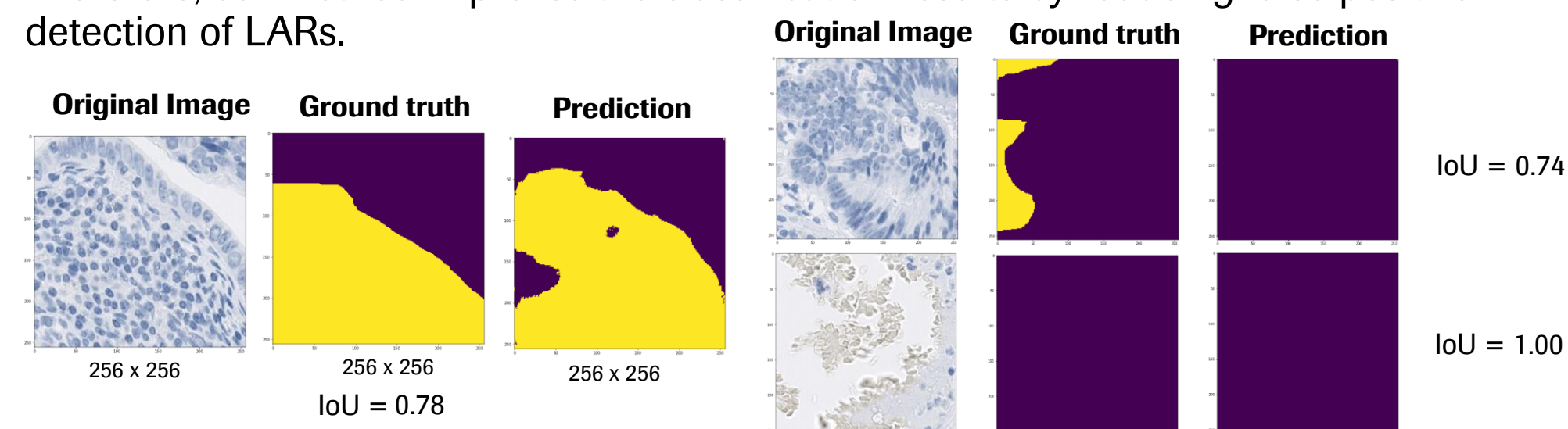
2.3 – Method: U-NET Model Training

To optimize the network parameters, we used a binary cross-entropy loss function, 100 epochs, batch size of 1, and learning rate of 1x10e-5 with Adam optimizer. Two levels of image resolution, 20X and 10X, were used to optimize the network parameters.



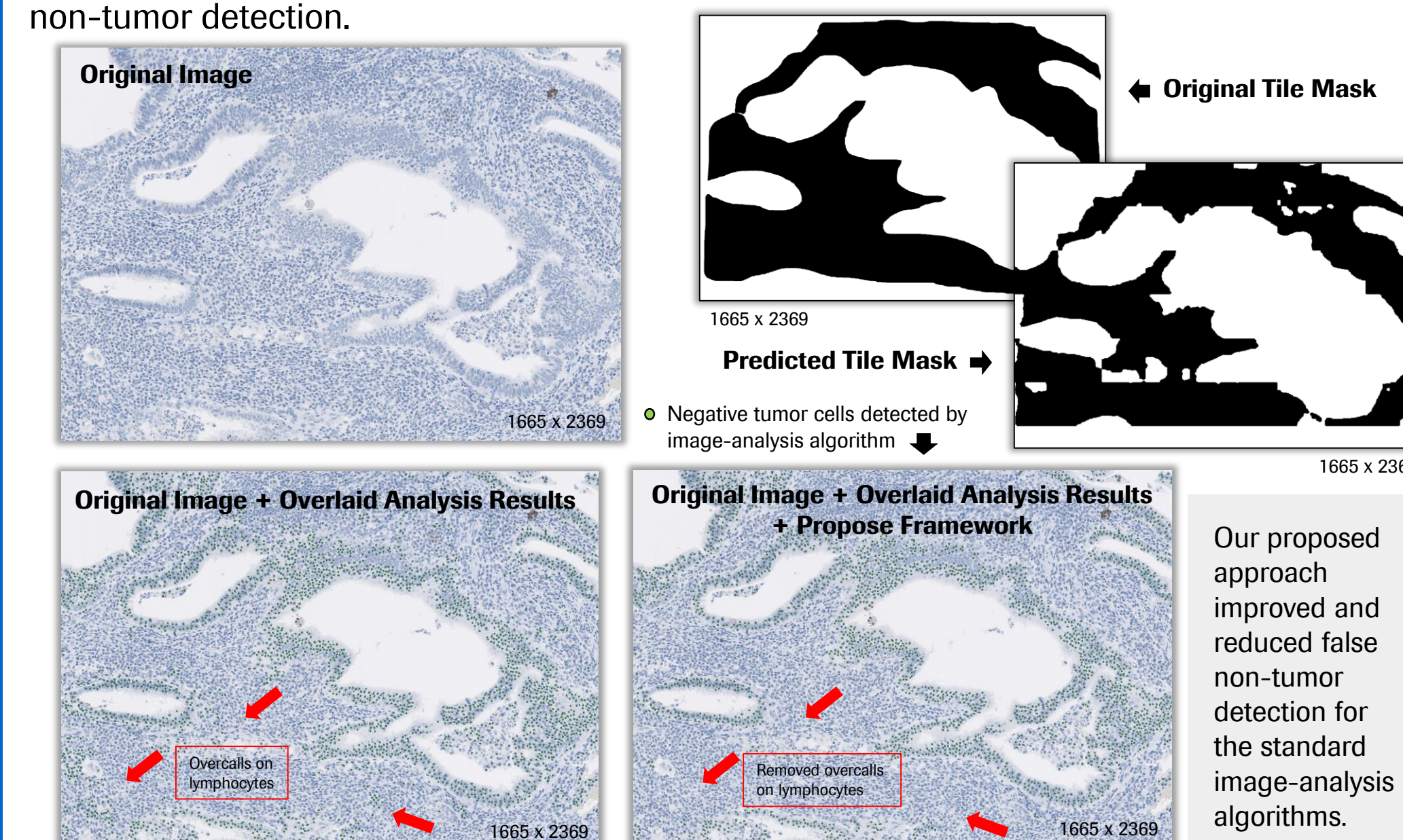
3.1 – Results

The testing results achieved average intersection-over-union (IoU) scores of 0.97 across the tested resolution levels, where the 20X image resolution provided better results. Therefore, our method improves the classification results by reducing false positive detection of LARs.



3.2 – Results

The 256 x 256 patch images were stitched to become a tile mask image. This mask was used to correct the analysis results that were over-detected in LARs, which reduced false non-tumor detection.



4 – Conclusions

Our proposed method locates and identifies LARs to improve tumor classification tasks. This approach is not limited to segmenting LARs in tissue, but it easily be adapted to other non-tumor areas such as necrosis, scanner artifacts, and tissue folds. For the future work, we can integrate this proposed framework to wholeslide image analysis.

5 – References

[1] Ronneberger O., Fischer P., Brox T. (2015) U-Net: Convolutional Networks for Biomedical Image Segmentation. In: Navab N., Hornegger J., Wells W., Frangi A. (eds) Medical Image Computing and Computer-Assisted Intervention – MICCAI 2015. Lecture Notes in Computer Science, vol 9351. Springer, Cham. https://doi.org/10.1007/978-3-319-24574-4_28

[2] <https://github.com/keras-team/keras/blob/master/keras/layers/core.py#L178>

6 – Acknowledgements

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