



Segmentation of Breast Cancer Tissue Using Deep Learning

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Introduction

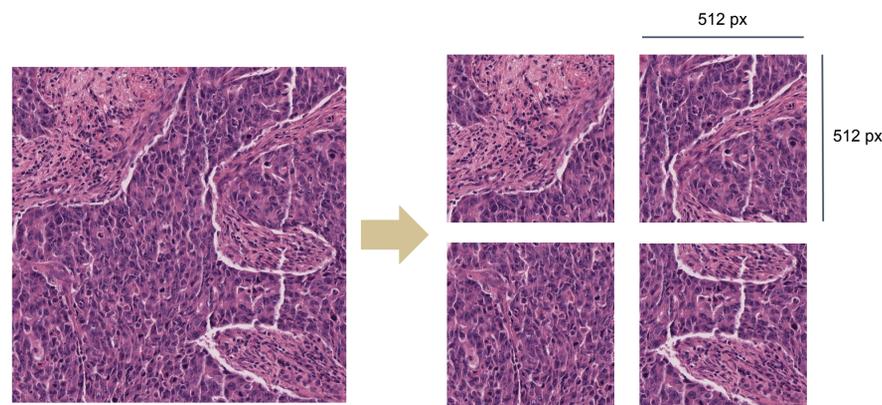
- Breast cancer is one of the most common cancers in the United States
- Automatic segmentation also can help speed up pathologists' workflows.
- Generating a segmentation is also an important prerequisite to automatically calculating the Tumor Infiltrating Lymphocytes (TILs) score.

Problem

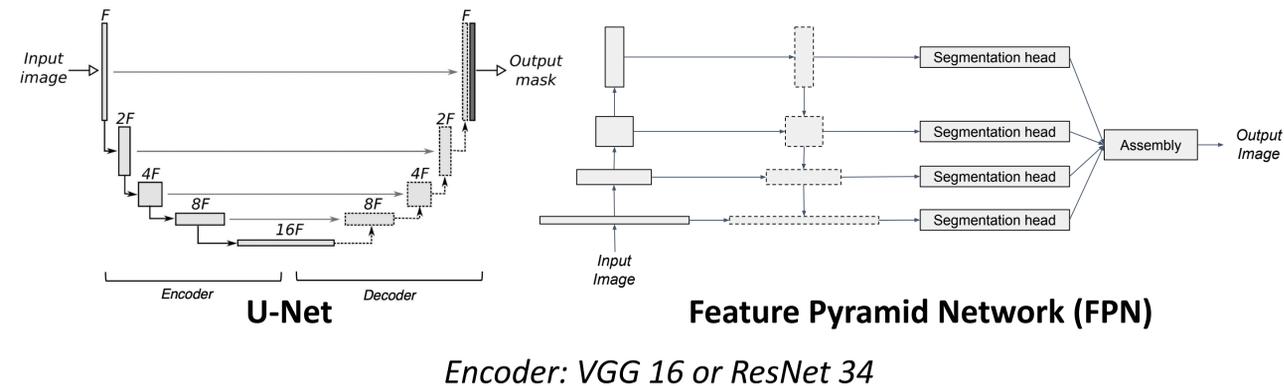
- We are given a Whole Slide Image (WSI) and the task is to segment this into different tissue types.
- As categorizing inflamed/tumor-associated stroma against all other classes is an important problem for the TIGER challenge to estimate a TILs score, we reduce our problem to a binary classification problem between these two classes.

Dataset

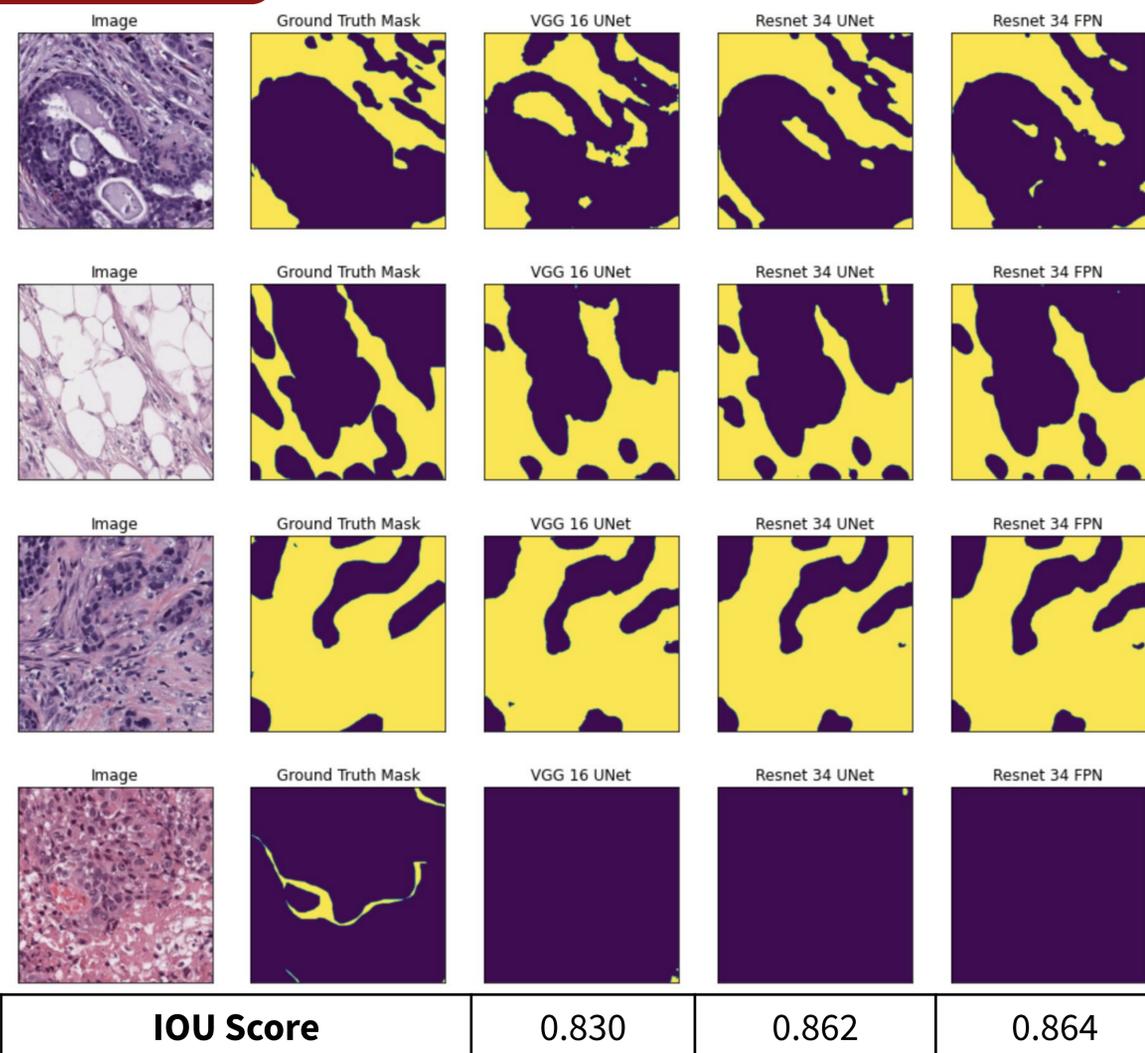
- Public training data released as part of the Tumor Infiltrating Lymphocytes in Breast Cancer (TIGER) Grand Challenge.
- Used WSIROIS section - after filtering and patch generation this had a size of 2064, which was split 80-10-10 in to training, validation, and testing sets.



Methods



Experiments



Analysis

- VGG16 seems to give more precise edge boundaries than the other methods.
- Regions between cell types sometimes not accurate in human annotations.
- Smaller regions of positive class such as in the last row the models do not predict correctly.
- Qualitatively, in most cases the ResNet based models gave outputs closer to the ground truth

Conclusion

- Investigated multiple segmentation network architectures to segment breast cancer tissue into inflamed/tumor associated stroma
- Results showed that FPN with ResNet 34 encoder gave highest performance

Future Work

- Explore transformer based methods.
- Complete more detailed comparison of current network architectures.
- Use object detection to detect TIL cells and compute TILs score and compare with other methods in the TIGER challenge.