

Cancer FLIM image classification

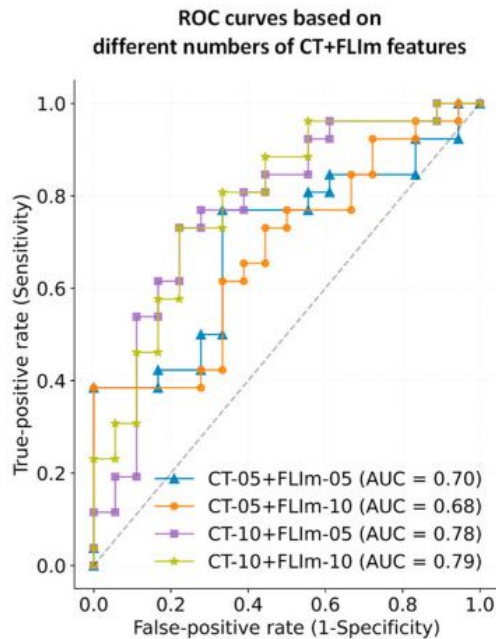
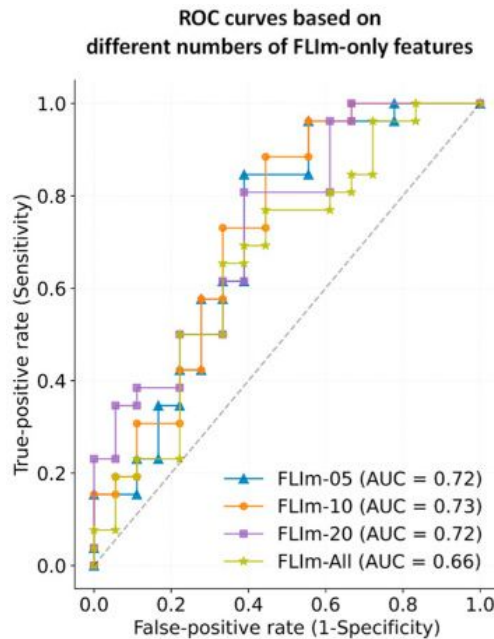
Petr Šícho

supervisor
Victoria Fay

Final Presentation

- Head and Neck Cancer (HNC)
 - ~1M of cases every year
 - Success of operations depends on removal of cancer margin
 - Margin testing at histopathology
 - Need for point-of-care method

- Classification of FLIM and CT data using support vector machine

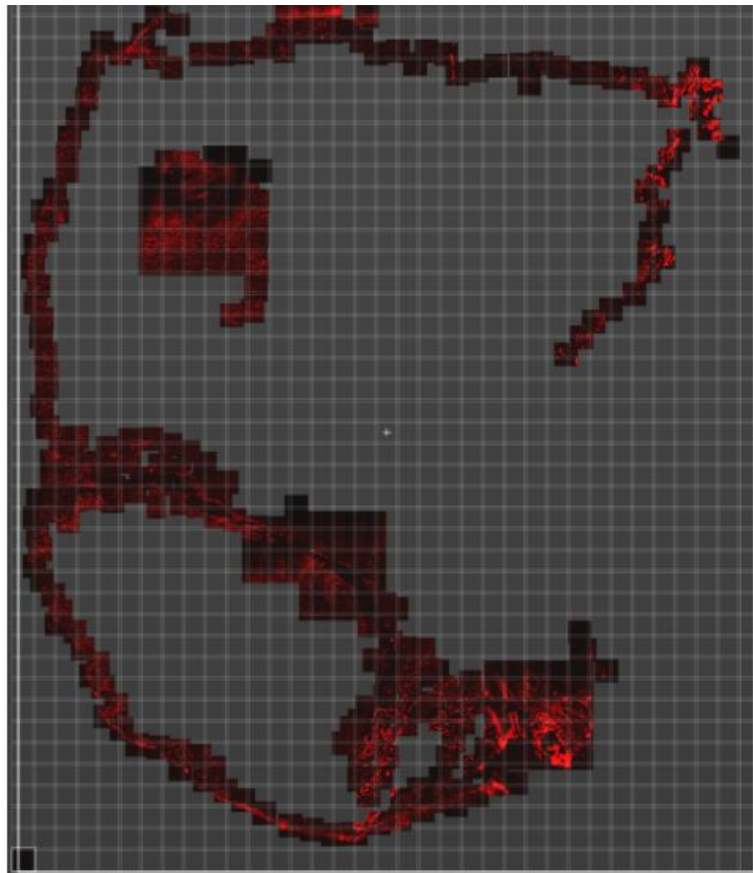
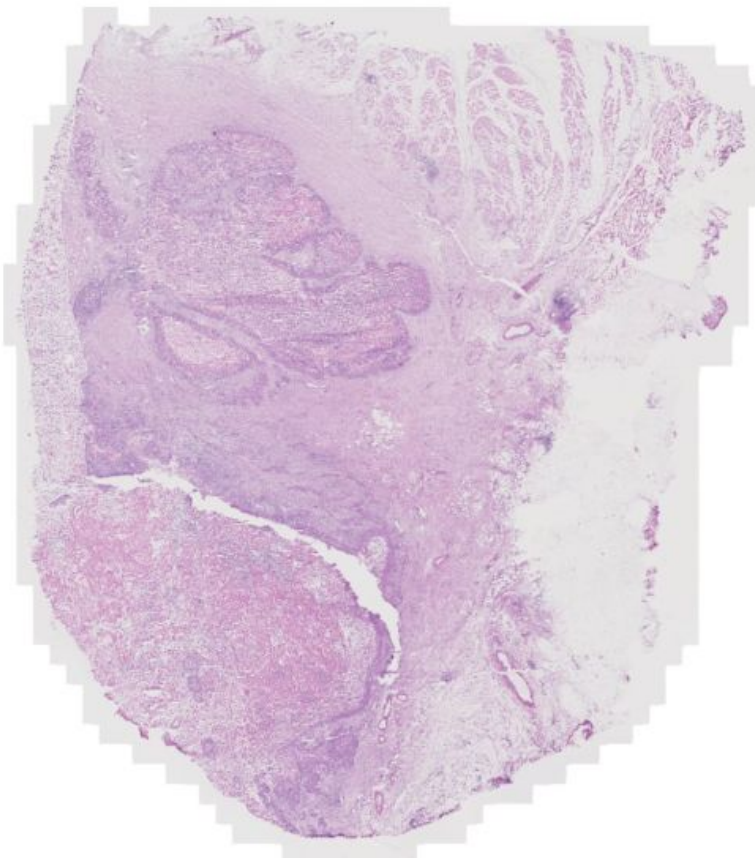


Yuan N et al. Early Detection of Lymph Node Metastasis Using Primary Head and Neck Cancer Computed Tomography and Fluorescence Lifetime Imaging, Diagnostics 18 (2024)

- Gather data on the FLIM microscope
- Process the data and create ground-truth masks
- Train Machine learning algorithm to classify tissue
- Test prediction results

Data acquisition

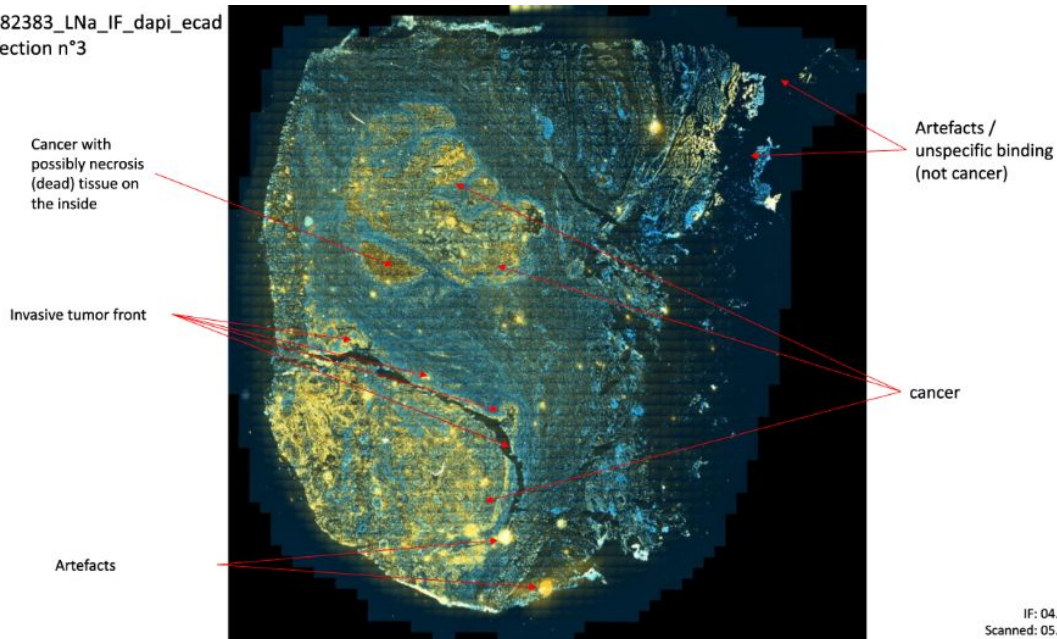
- Leica SP8-FLIM Microscope: 440nm pulsed laser, 25x Water objective
 - Image tissue in intensity, match with annotated section
 - Divide into grid of $465 \times 465 \mu\text{m}$



- Leica SP8-FLIM Microscope: 440nm pulsed laser, 25x Water objective
 - Image tissue in intensity, match with annotated section
 - Divide into grid of $465 \times 465 \mu\text{m}$
- 2 lifetime bands (460-487, 516-586), intensity ratio
- Automated measurements of 3x3 or 5x5 areas (18 or 50 mins, ~2 min/ tile)
- Issue - water, focus

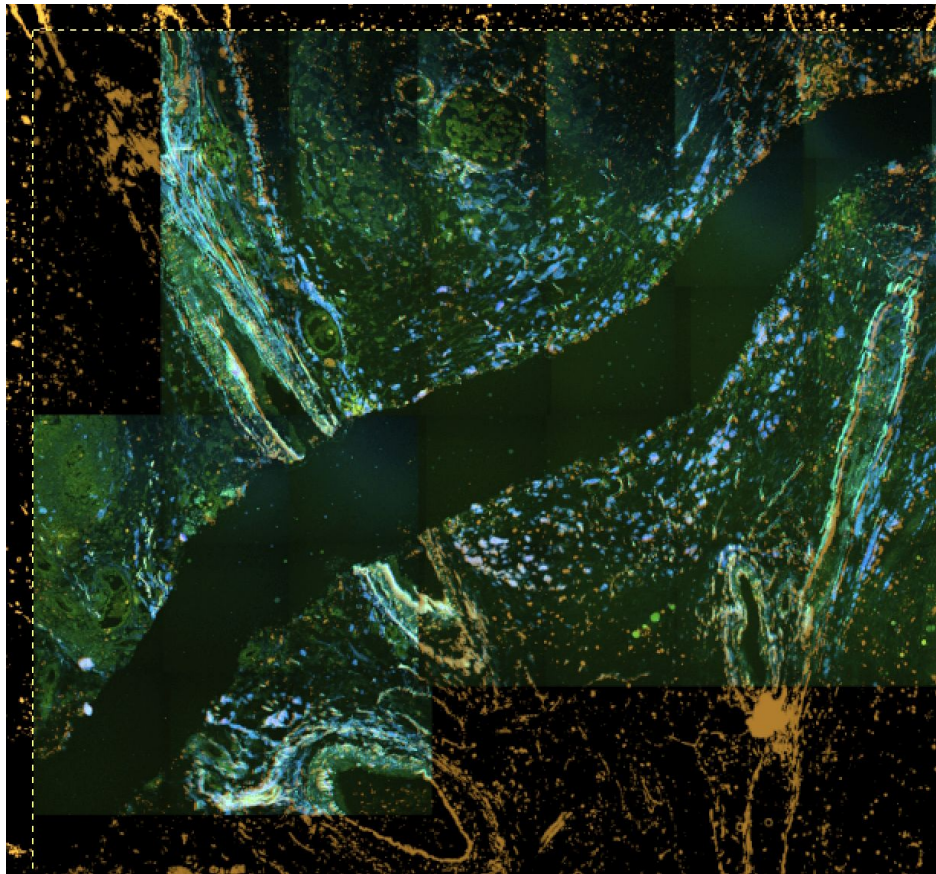
1. Export mask from E-cadherin staining (DAPI in blue)

482383_LNa_IF_dapi_ecad
Section n°3



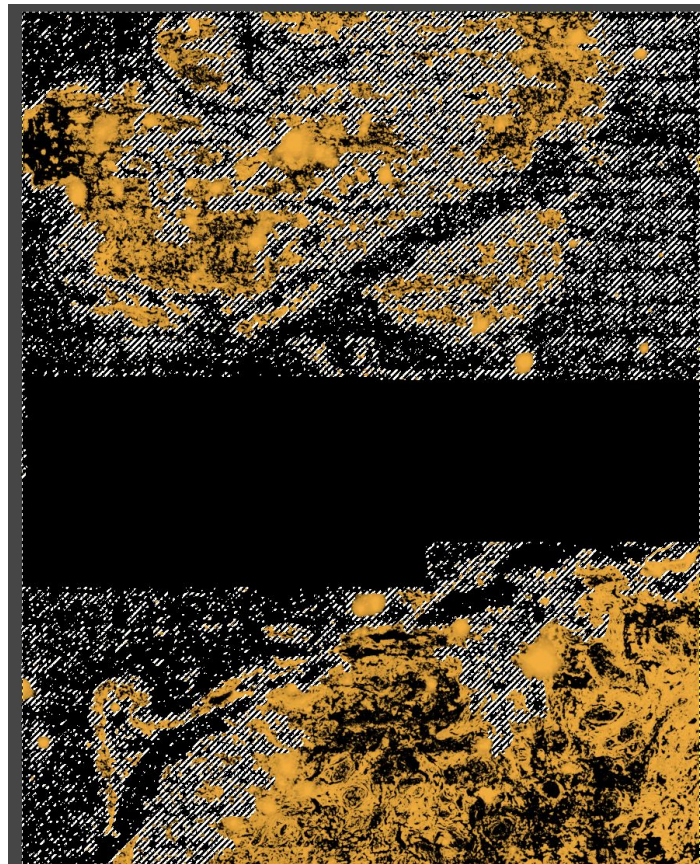
2. Match mask with visualization

- use veins/ducts
- cross
- move-rotate

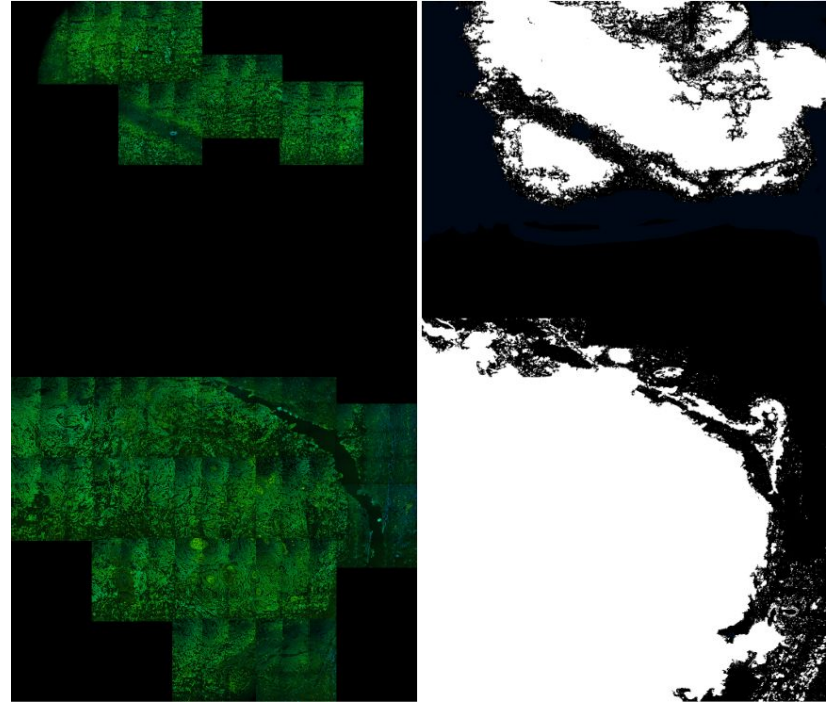


3. Post process

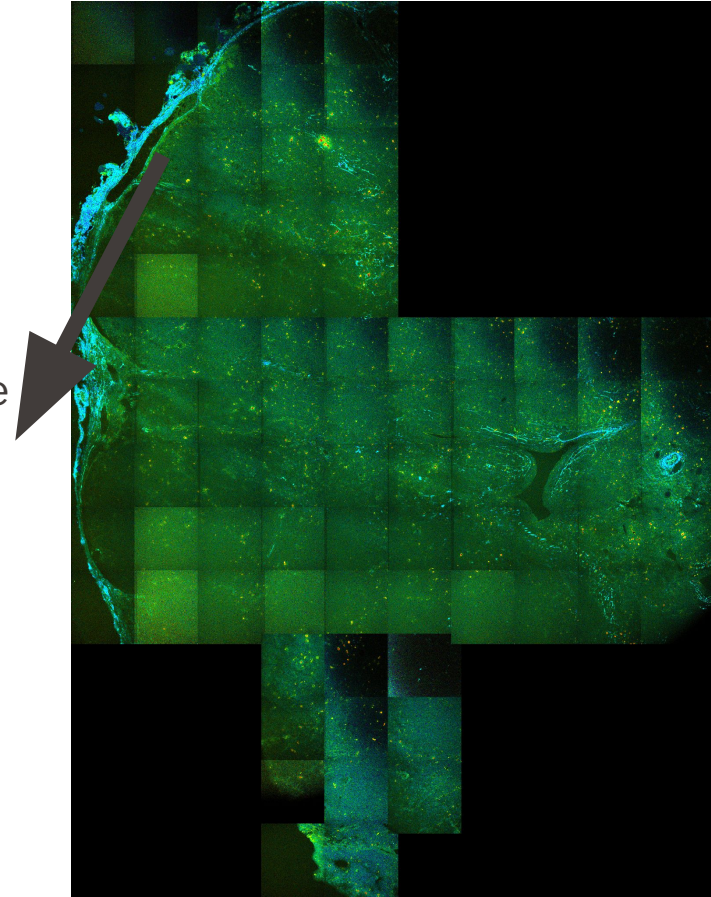
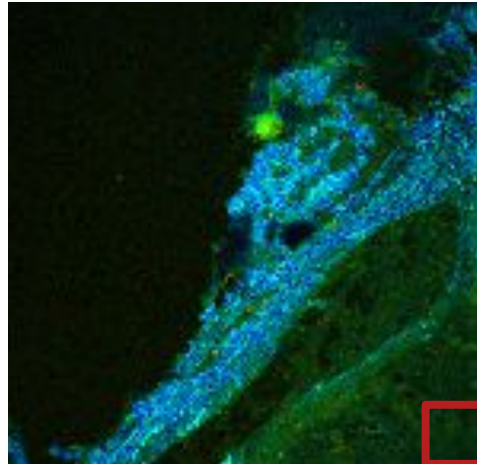
- remove false positives / artifacts
- fill and clean
- convert to black-white
- crop to same size



1. Export mask from E-cadherin staining
2. Match mask with visualization
3. Post process
4. Cut and match to tiles



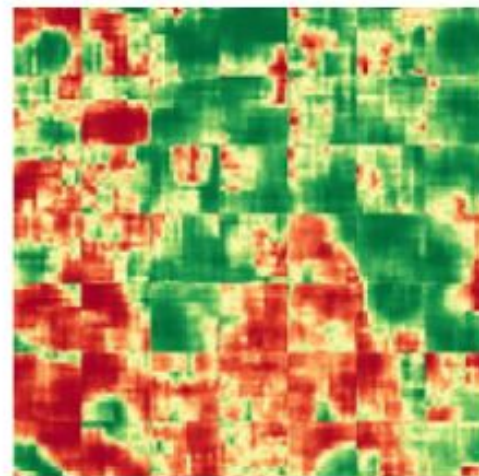
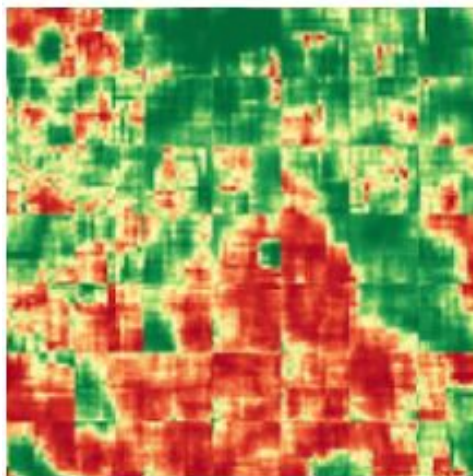
- Gathered 815 tiles on the FLIM (512x512 pixels)
 - 7 sections of lymph nodes (5 patients)
- Tiles split into 64x64 pixels to match endoscope
 - 52'160 tiles

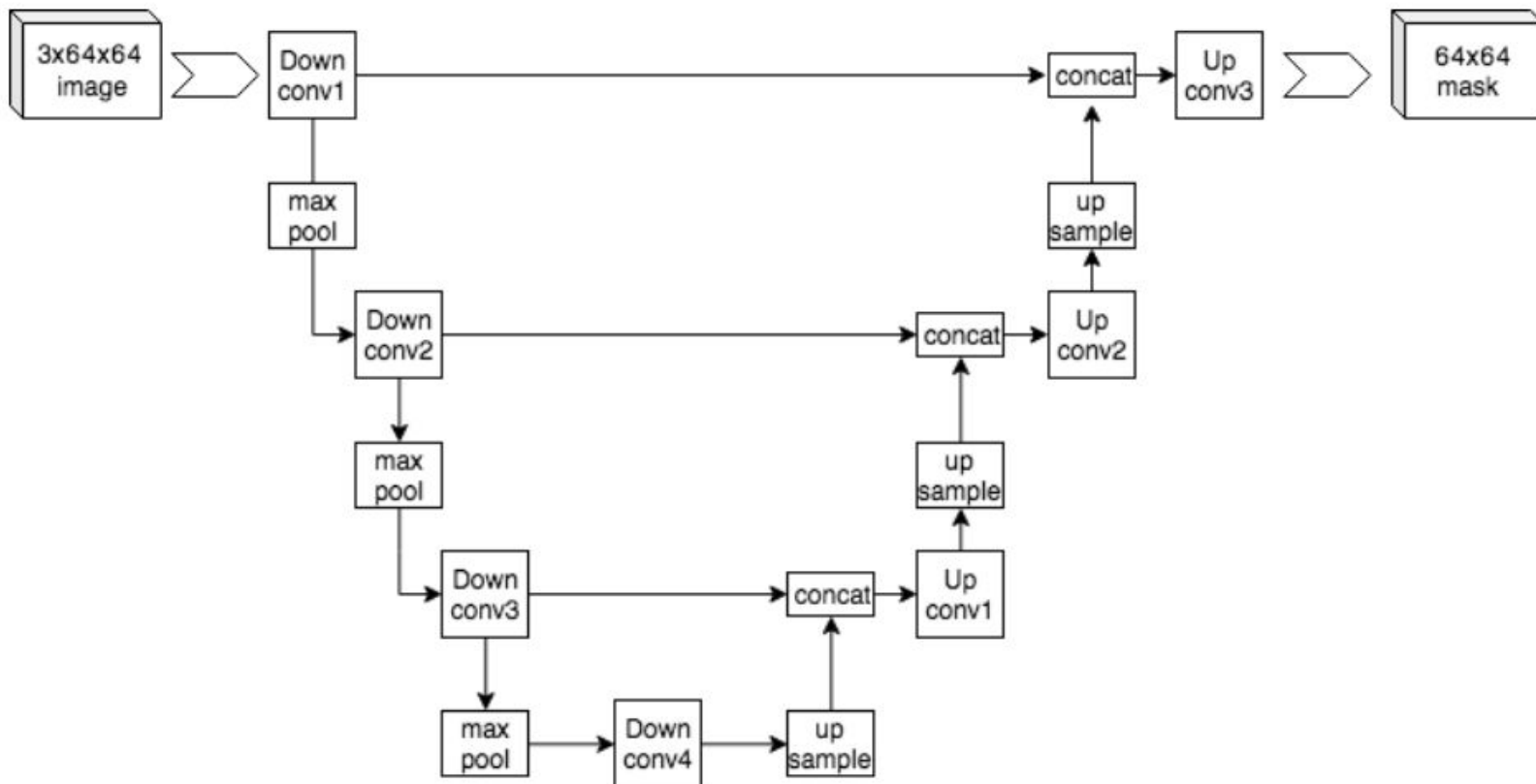


Machine learning

- Cancer and normal tissue not balanced (less than 25% of cancer pixels)
 - rotate and/or flip cancer images
 - Size of dataset doubled
 - Cancer majority in about 70% of tiles

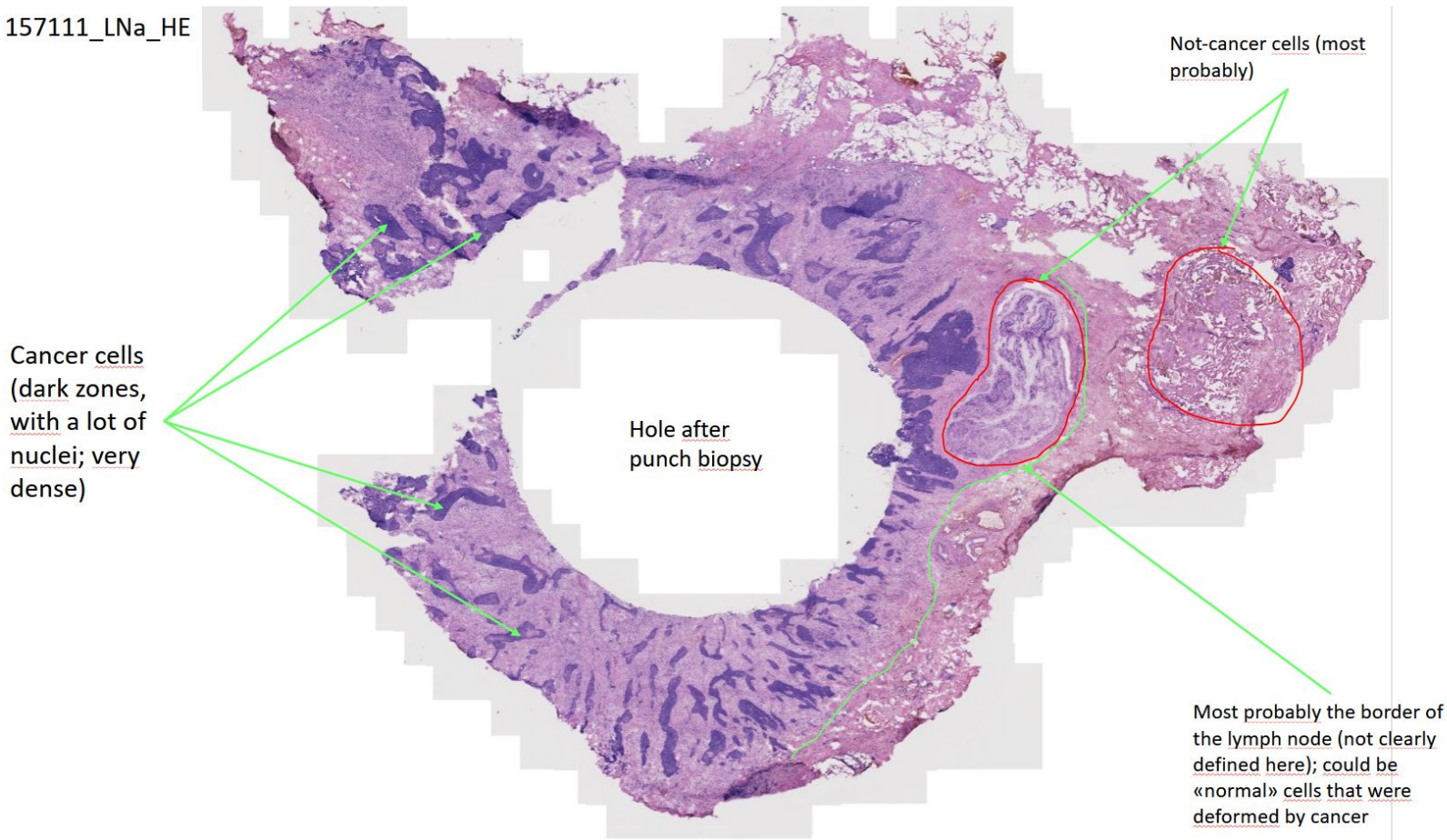
- Borders of tiles visible in classification
 - added another cropping variant shifted by 32 pixel from origin
 - data augmentation



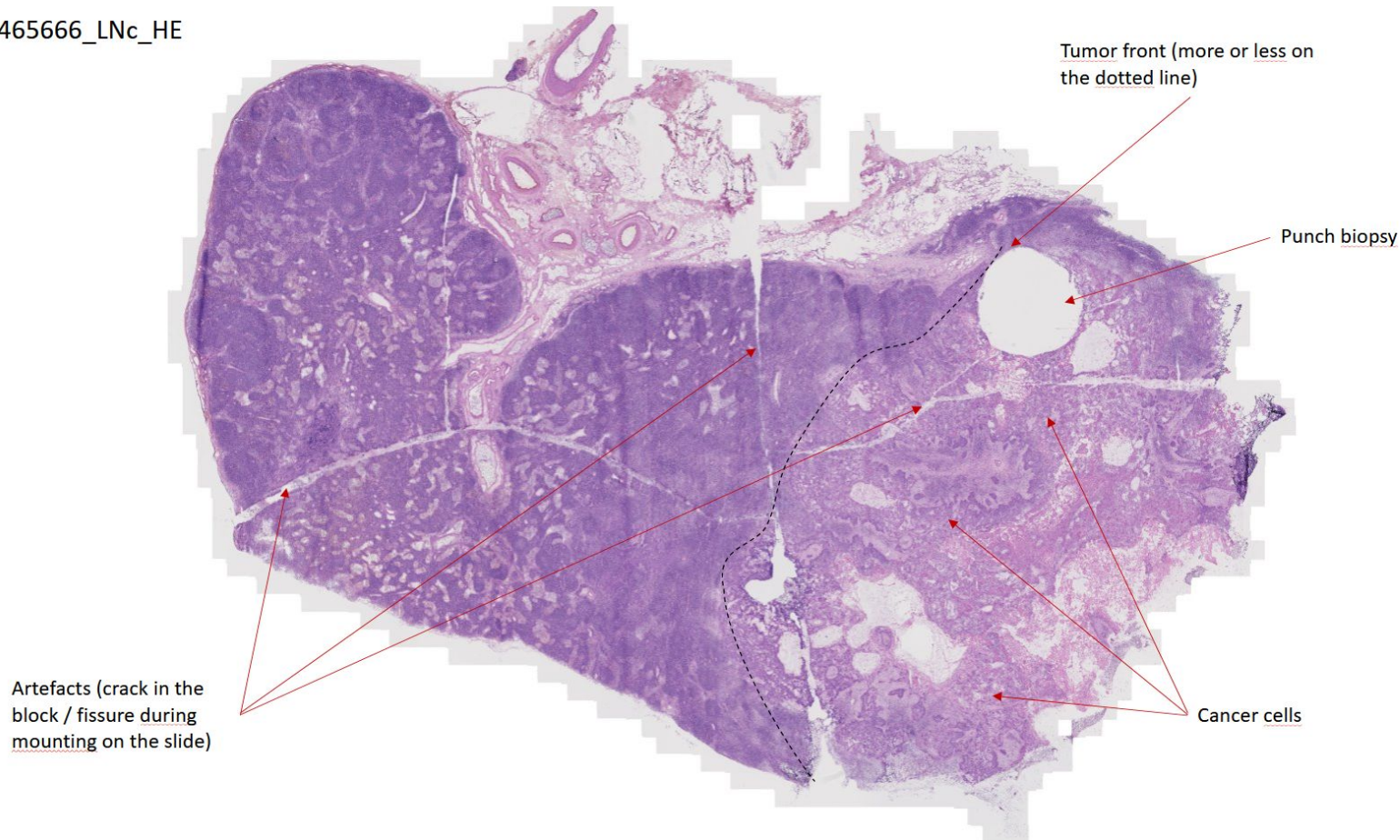


- Select one section for use only in testing

157111_LNa_HE



465666_LNc_HE



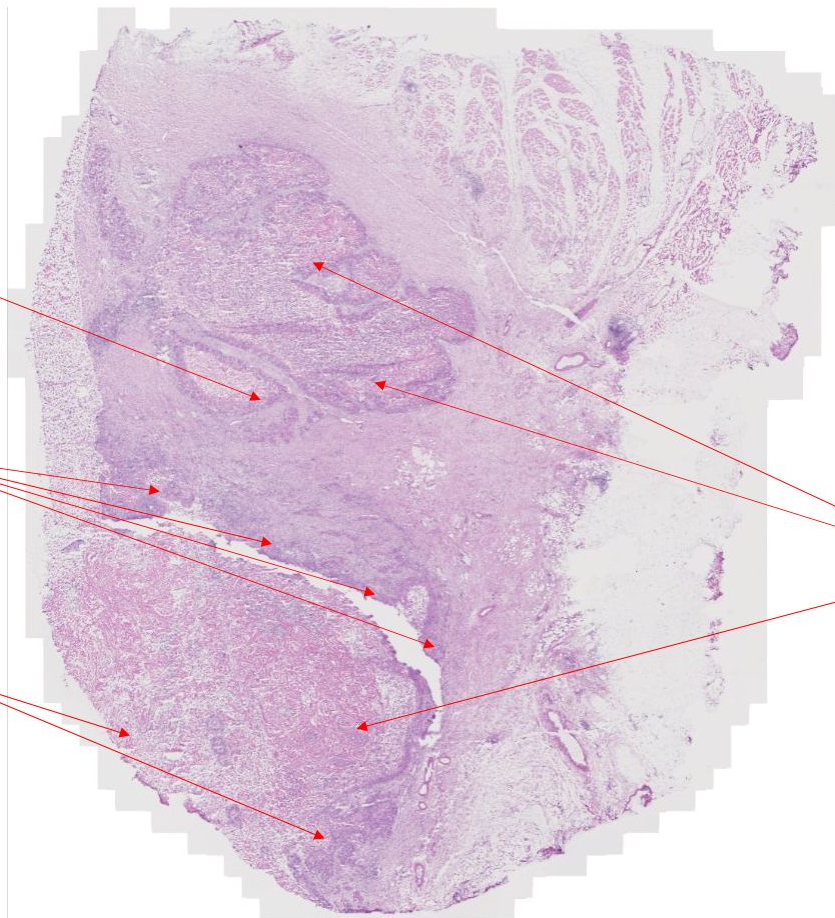
482383_LNa_HE

Cancer with
possibly necrosis
(dead) tissue on
the inside

Invasive tumor front

Artefacts of nail polish

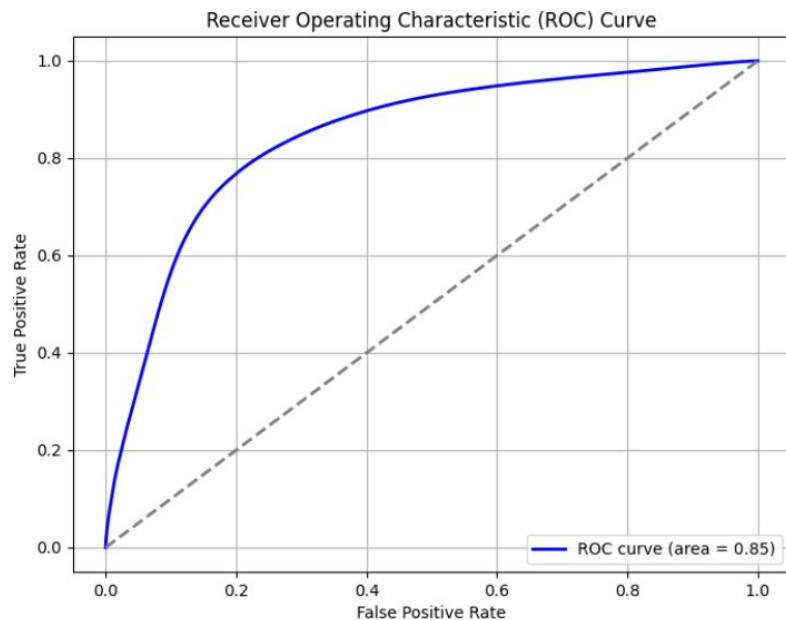
cancer



$$Dice = \frac{2 \times TP}{2 \times TP + FP + FN}$$

- Accuracy - percentage of correct tiles (cancer >0.5)
- Dice coefficient
 - disregards true negatives
- ROC curve and Area under curve (AUC)

Test of U-net



Testing model architectures

Batch Normalization & Dropout:

- *Simple_bn*: Adds Batch Normalization for stable training.
- *Simple_do*: Uses Dropout for overfitting reduction.
- *Dropout_augment*: Combines Dropout and Batch Normalization.

Depth Variants:

- *Deep_bn*: Increases depth with additional layers and Batch Normalization.
- *Shallow_net*: Reduces depth for faster, lightweight processing.

Testing model architectures

Filter Adjustments:

- *Wide_filters*: Doubles filters for better feature extraction.
- *Reduced_filters*: Halves filters for a simpler model.

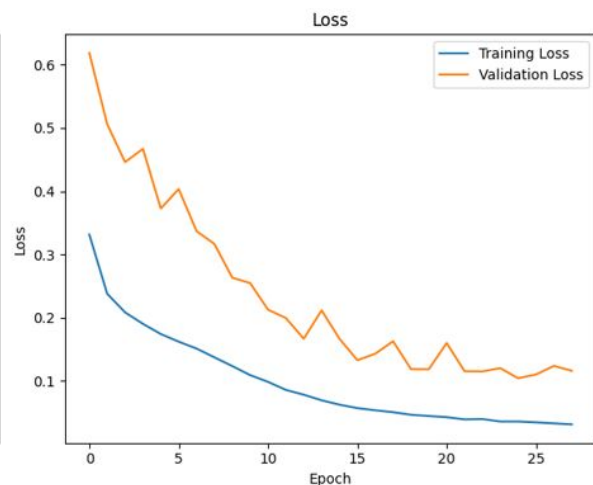
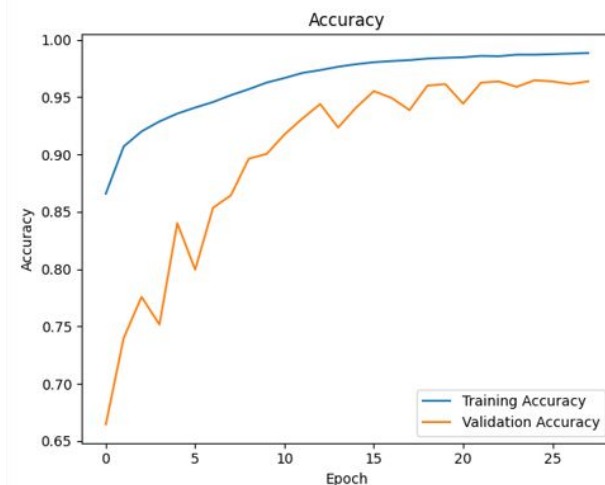
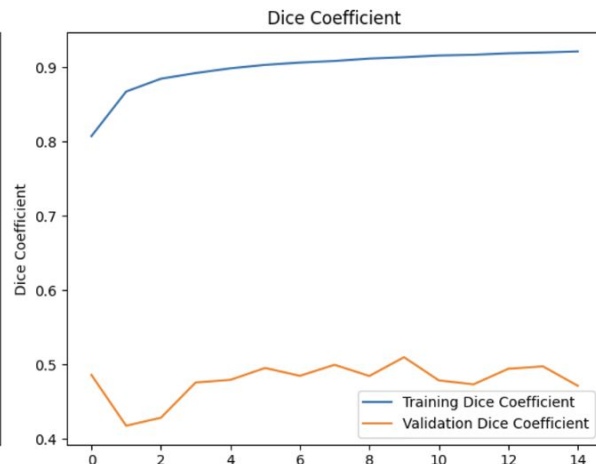
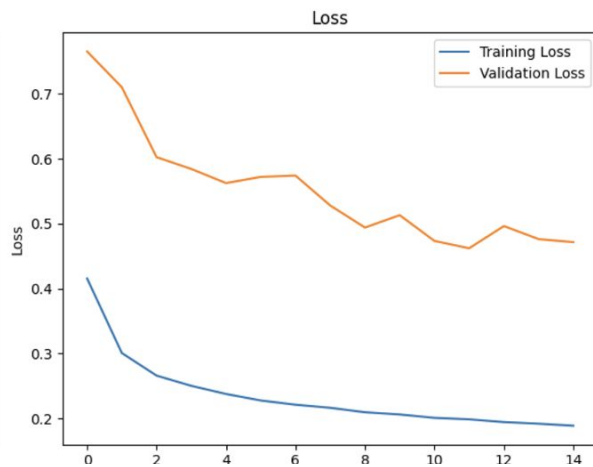
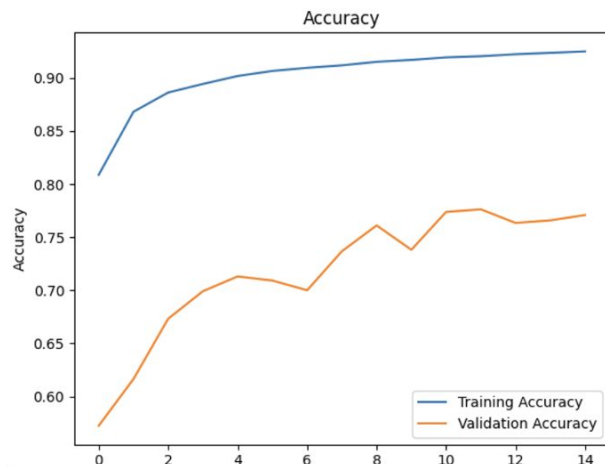
Architectural Enhancements:

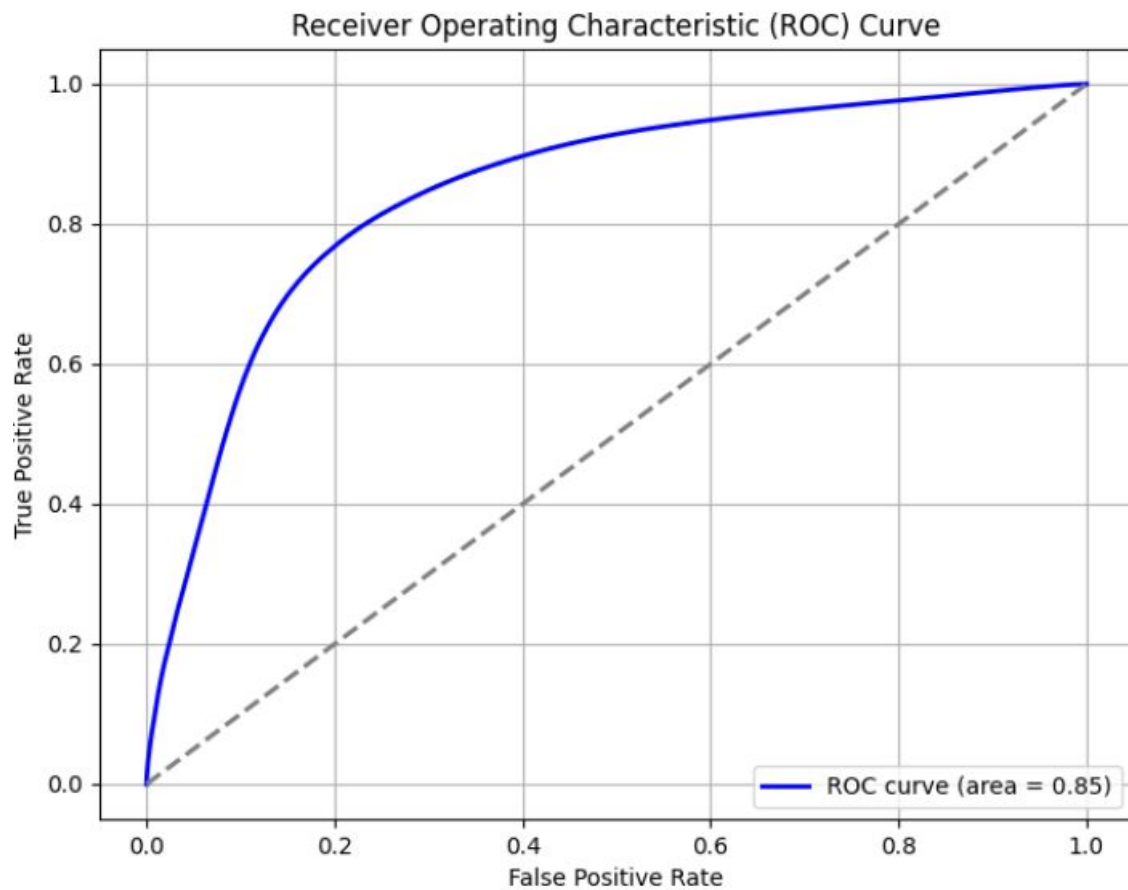
- *Simple_res*: Adds residual connections for improved gradient flow.
- *Increased_kernel*: Enlarges kernel size to capture broader features.
- *Dilated_conv*: Uses dilated convolutions for expanded receptive field.

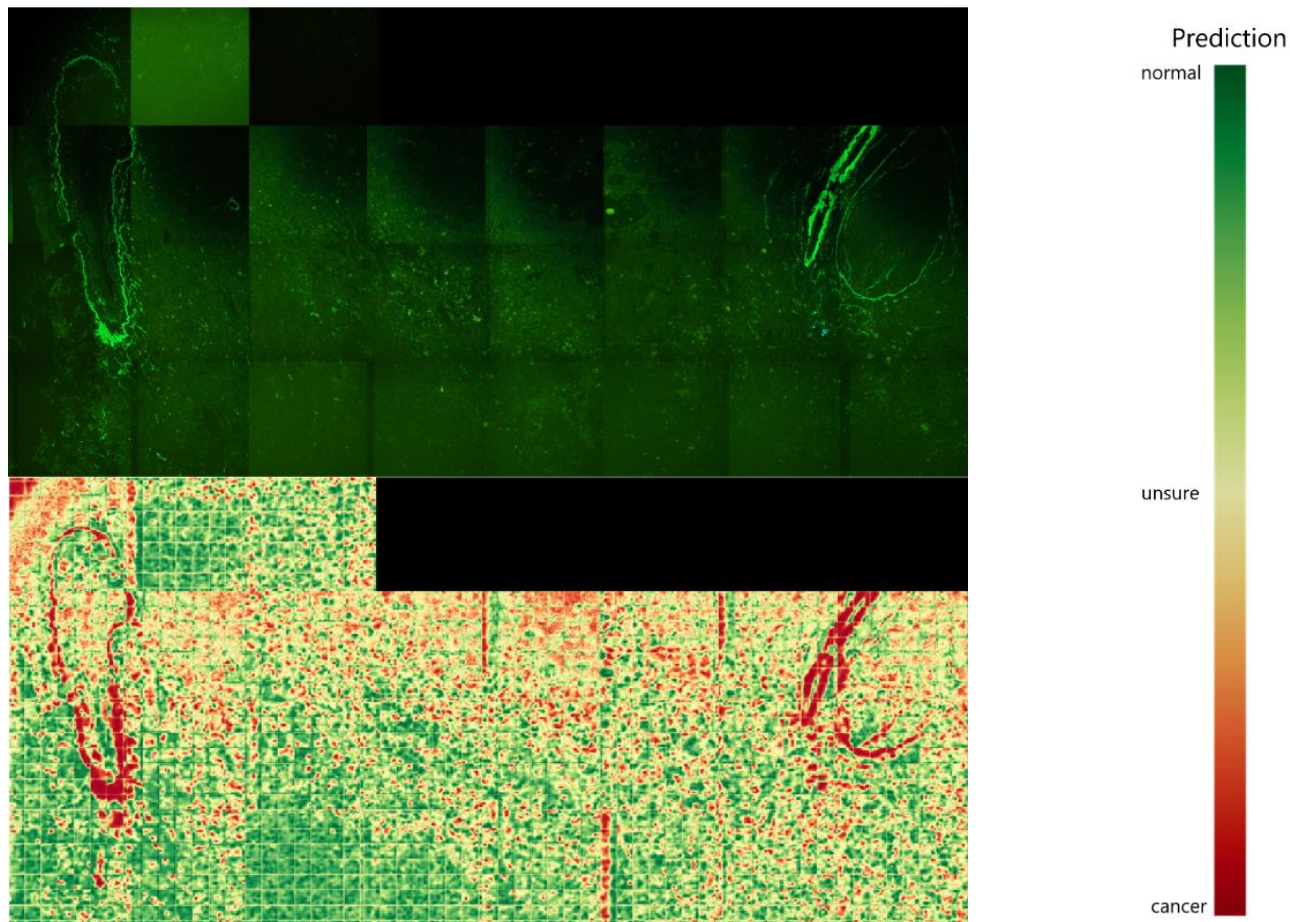
Results

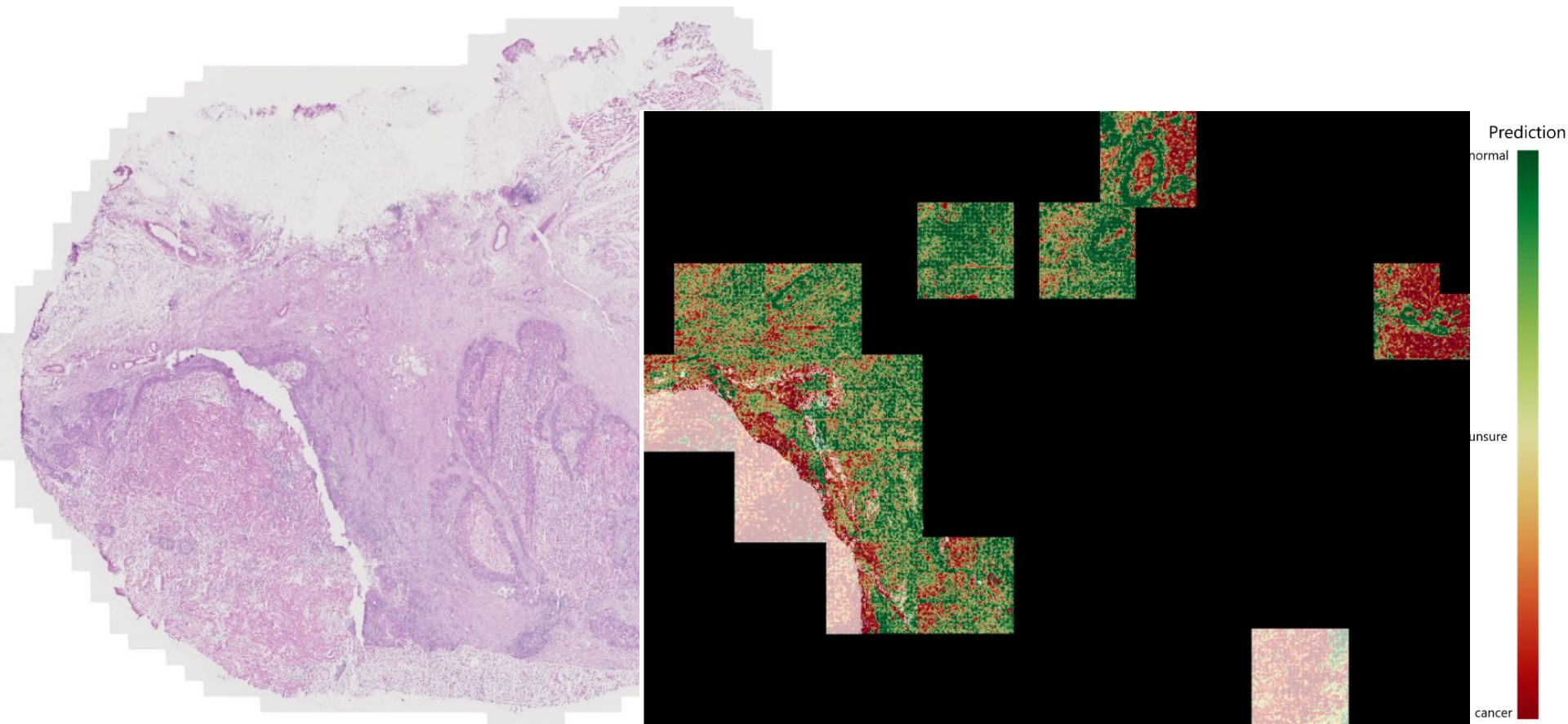
Table 5.1: Performance metrics for U-Net model variants.

Model Variant	Test Accuracy	Dice Coefficient	ROC AUC
Simple Model	0.73	0.73	0.85
Simple_bn	0.71	0.72	0.86
Simple_do	0.71	0.70	0.84
Deep_bn	0.72	0.71	0.88
Wide_filters	0.71	0.72	0.86
Reduced_filters	0.71	0.70	0.82
Simple_res	0.71	0.72	0.85
Shallow_net	0.64	0.67	0.80
Increased_kernel	0.71	0.69	0.88
Dropout_augment	0.69	0.71	0.87
Dilated_conv	0.70	0.68	0.87









Conclusion

- Classifies well on section of same cancer types
- Cancer diverse in HNC patients - did not generalize well
- Need more data
- ML promising for cancer classification

Questions?