

Multimodality Image Registration Between Acoustic and Optical Microscopy

Ian Jacobsen

Background

- M.S. candidate in Electrical Engineering at NYU.
- B.E. in Electrical Engineering from Stony Brook University.
- Summer intern at Riverside Research in the Biomed group.
- Working under Jonathan Mamou.

Introduction

- We aim to develop a method for multimodality image registration.
- The two modalities are optical and acoustic microscopy (SAM).
- Riverside has designed a SAM system, therefore SAM data is available.
 - Corresponding H&E histology data can be obtained.
 - Working with malignant human lymph node dataset, but the method is not dataset specific.

Motivation

- Histology studies the microscopic anatomy of cells and tissue.
- Acoustic microscopy is used to obtain mechanical properties of tissue.
- Combining information from the two modalities may provide greater insight for the identification of abnormalities within soft tissue.
 - Pathologist shows cancer on H&E, then we can see the mechanical properties via SAM.

SAM Basics

- Image is obtained via high frequency ultrasound (250 MHz).
- Nondestructive testing of soft tissue.
- Forms 2D images of mechanical properties.
- Resolution is 7 μm .
- Scanning time is ~20 minutes for 1mm x 1mm sample.
- Simple to operate.

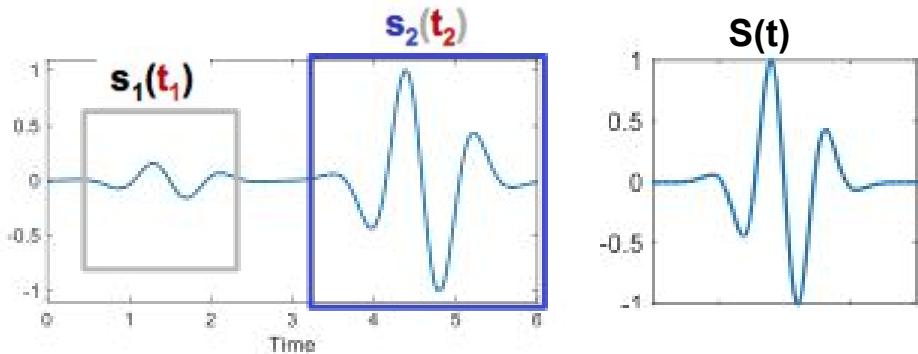
SAM Basics, ctnd

- A reference signal is emitted, and the reflected signals are measured.
 - Reflections occur at interfaces between materials.
- Time difference is used to calculate the speed of sound.
- Reflected amplitudes are used to find the acoustic impedance, and the attenuation coefficient.

SAM Basics, ctnd

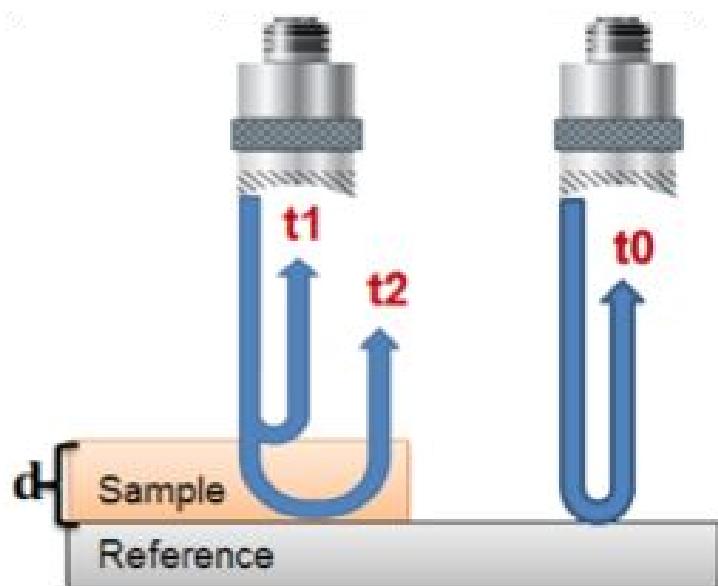
- These three parameters are independent.
- Each of these parameters warrant their own separate images.
- We use amplitude maps in the registration process.
 - Quick to obtain.
 - Closest to histology.

SAM Basics, ctnd

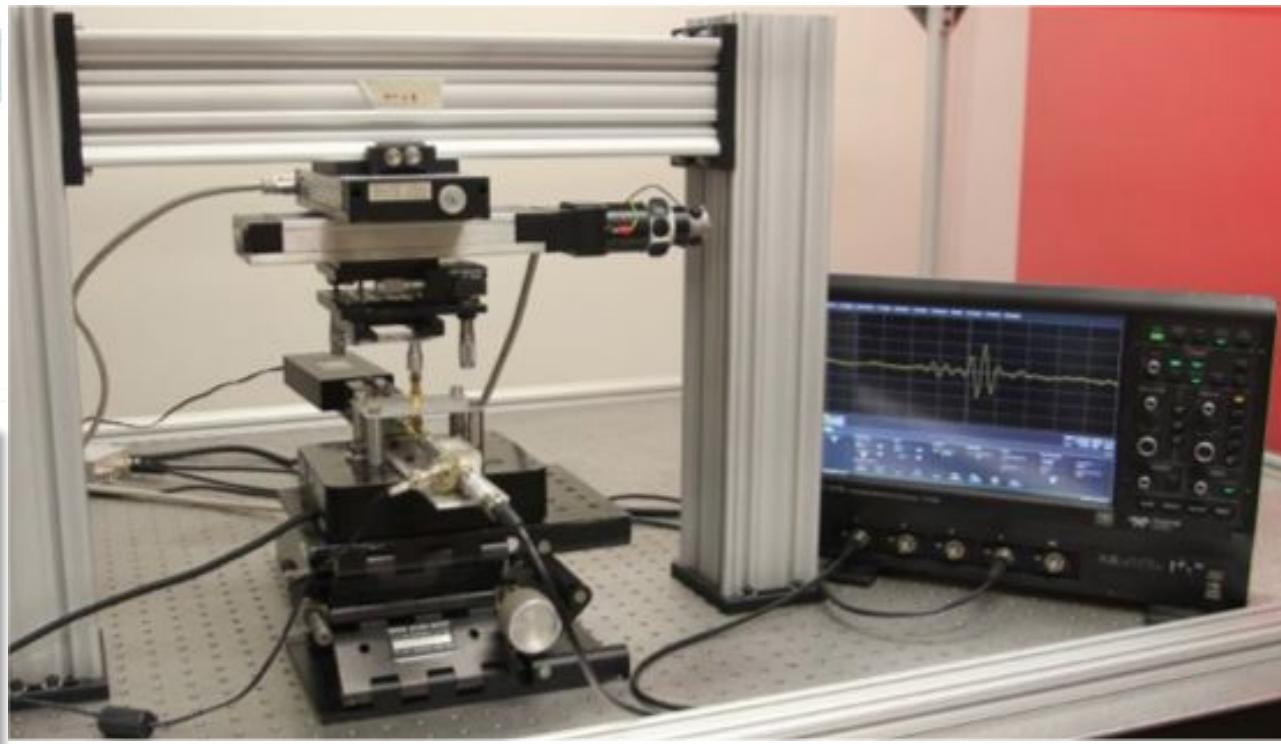
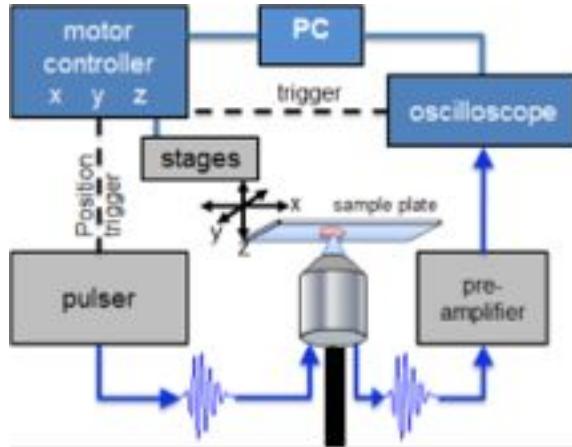


$$s(t) = s_1(t) + s_2(t),$$

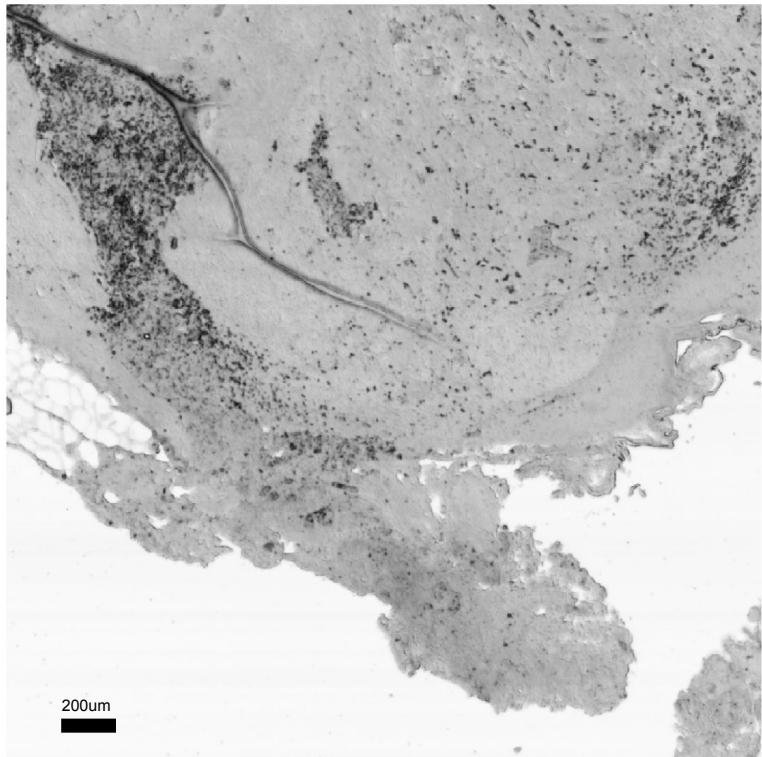
$$s_1(t) = ks_0(t - t_1),$$
$$s_2(t) = ms_0(t - t_2) * att.$$

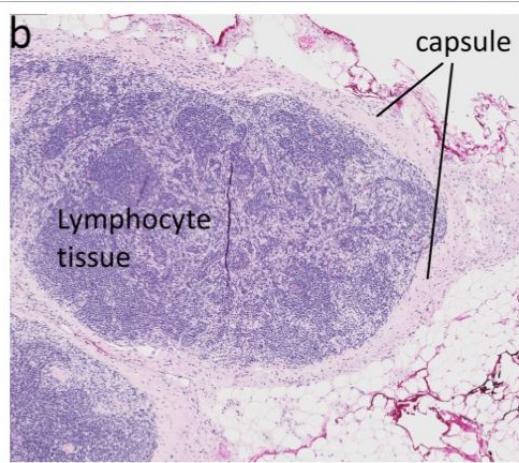
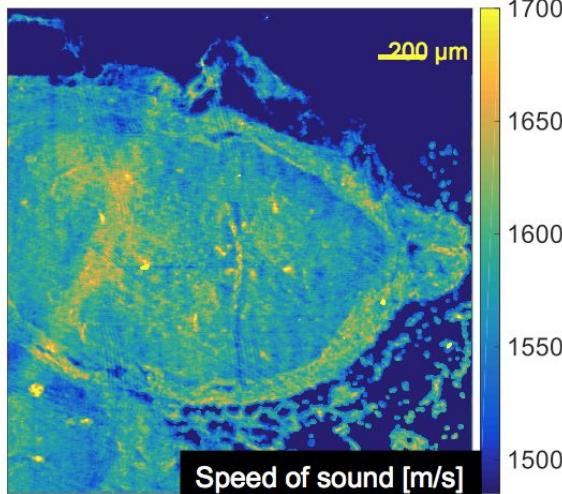
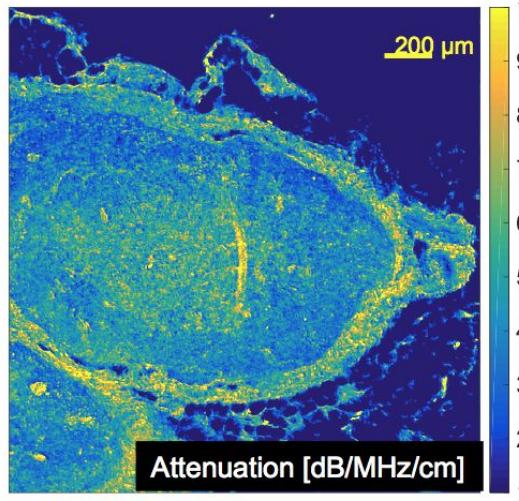
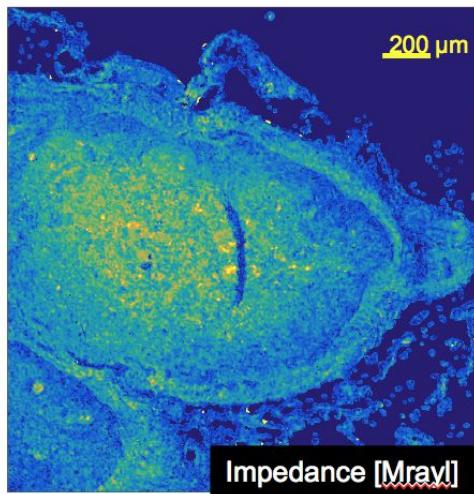


SAM Basics, ctnd



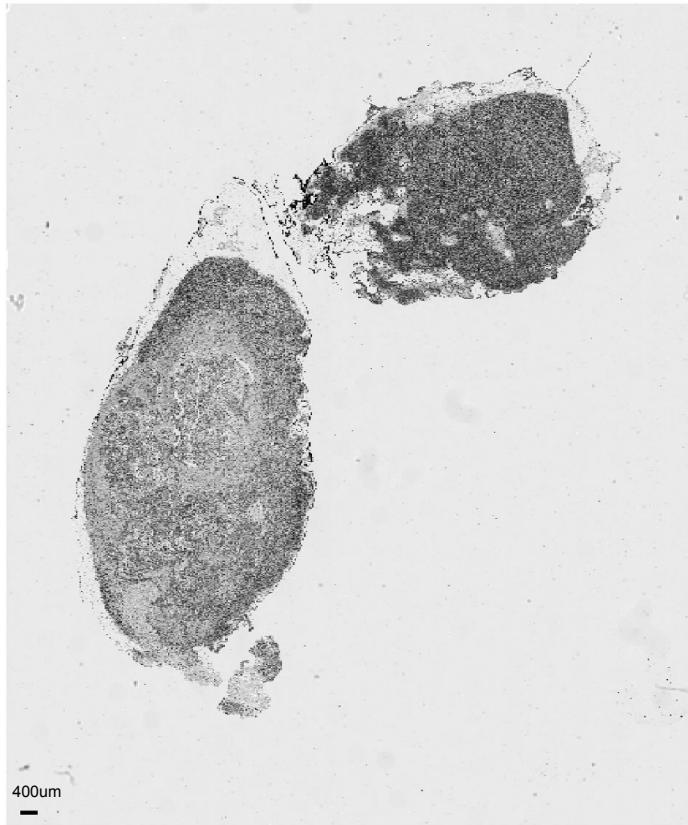
SAM Amplitude Image



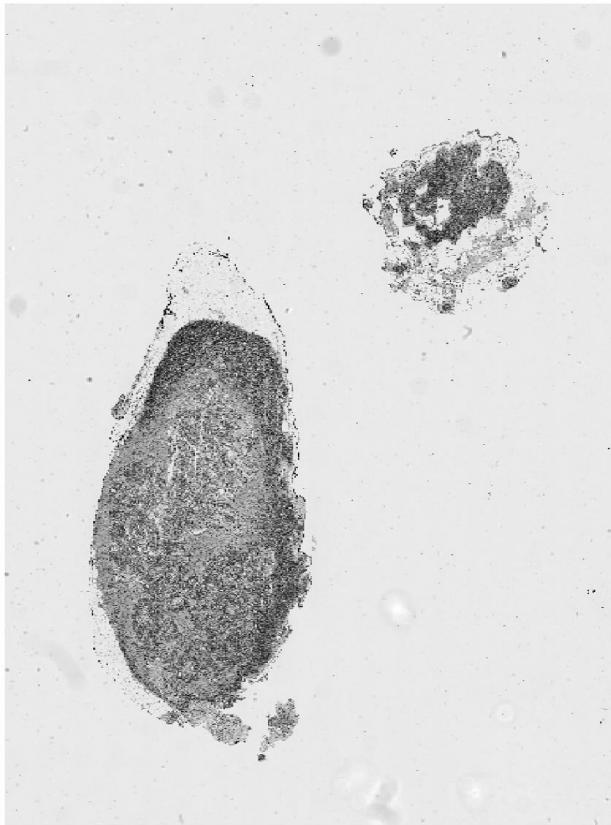


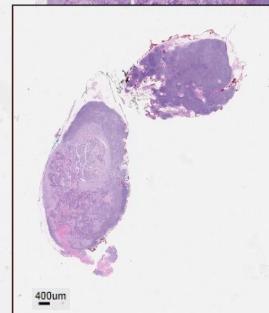
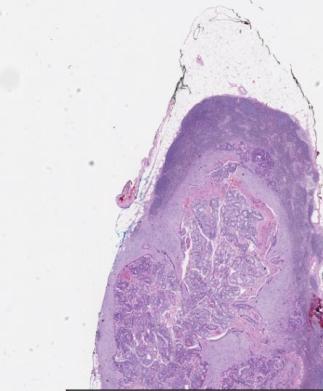
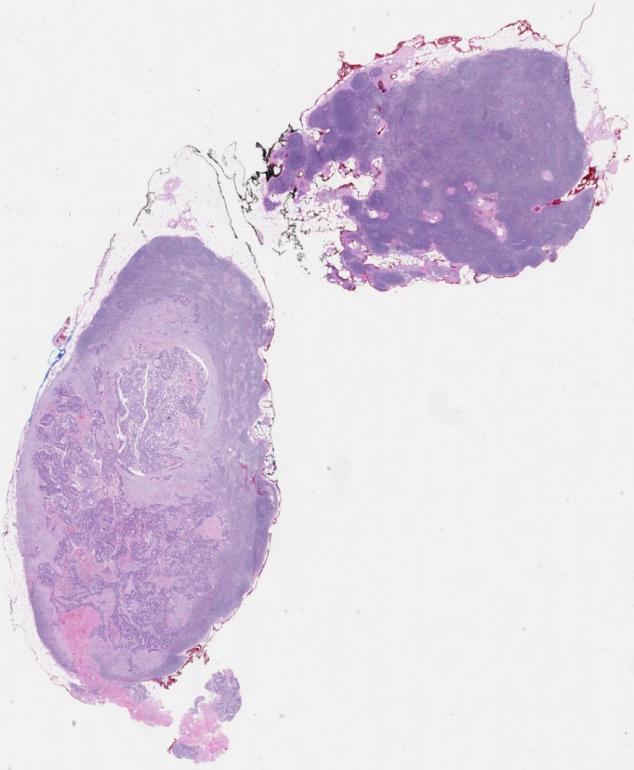
Histology Basics

- Image is obtained via light microscope.
- The tissue is stained in order to enhance the ability to view microscopic structures.
- H&E stain is used.

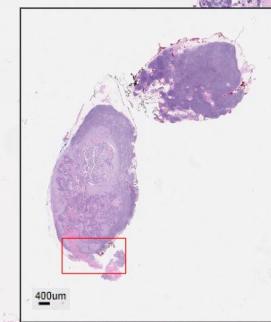
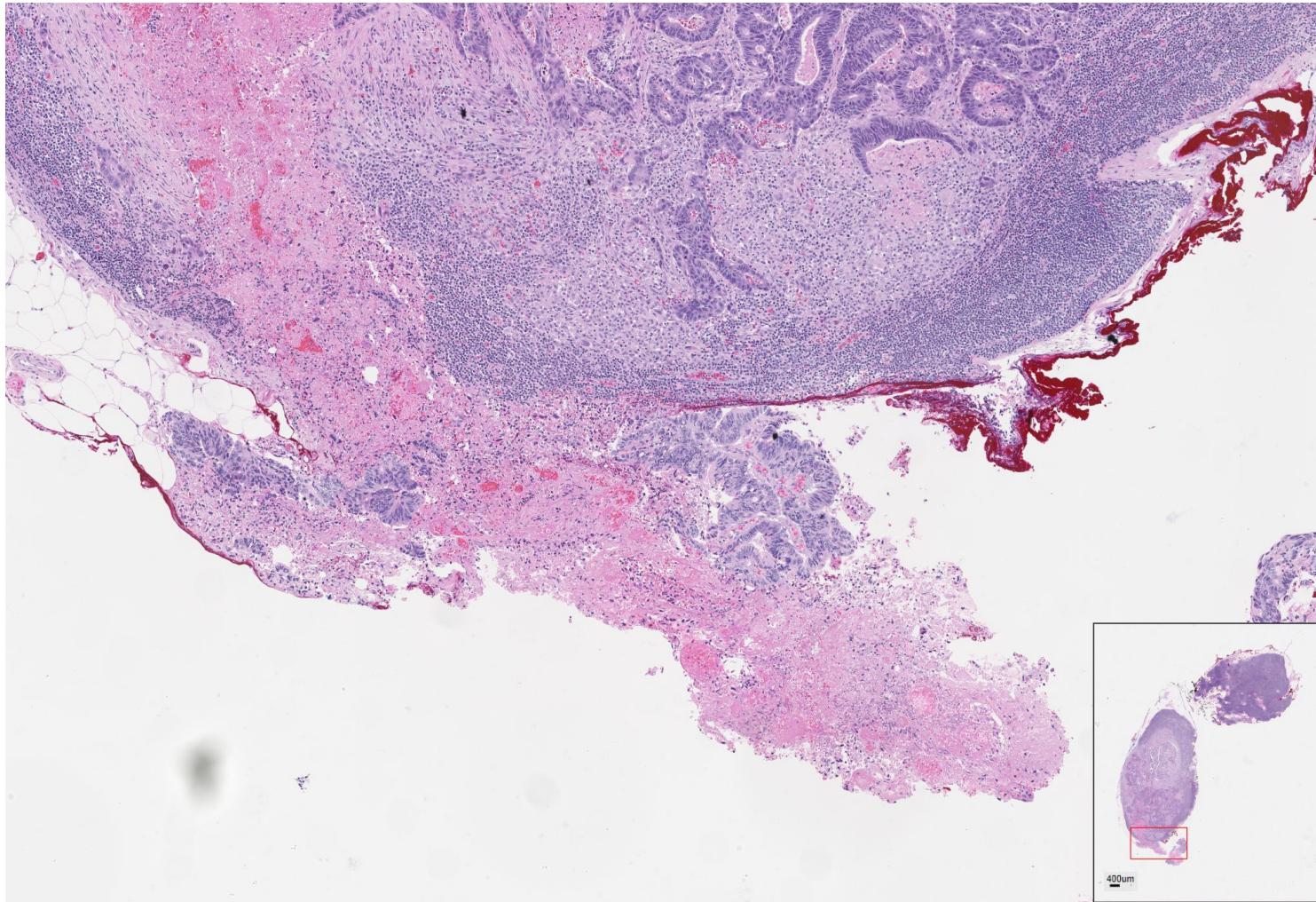


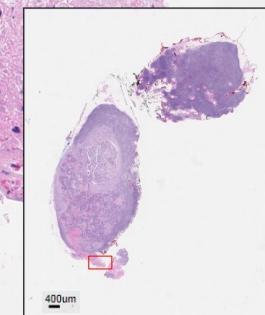
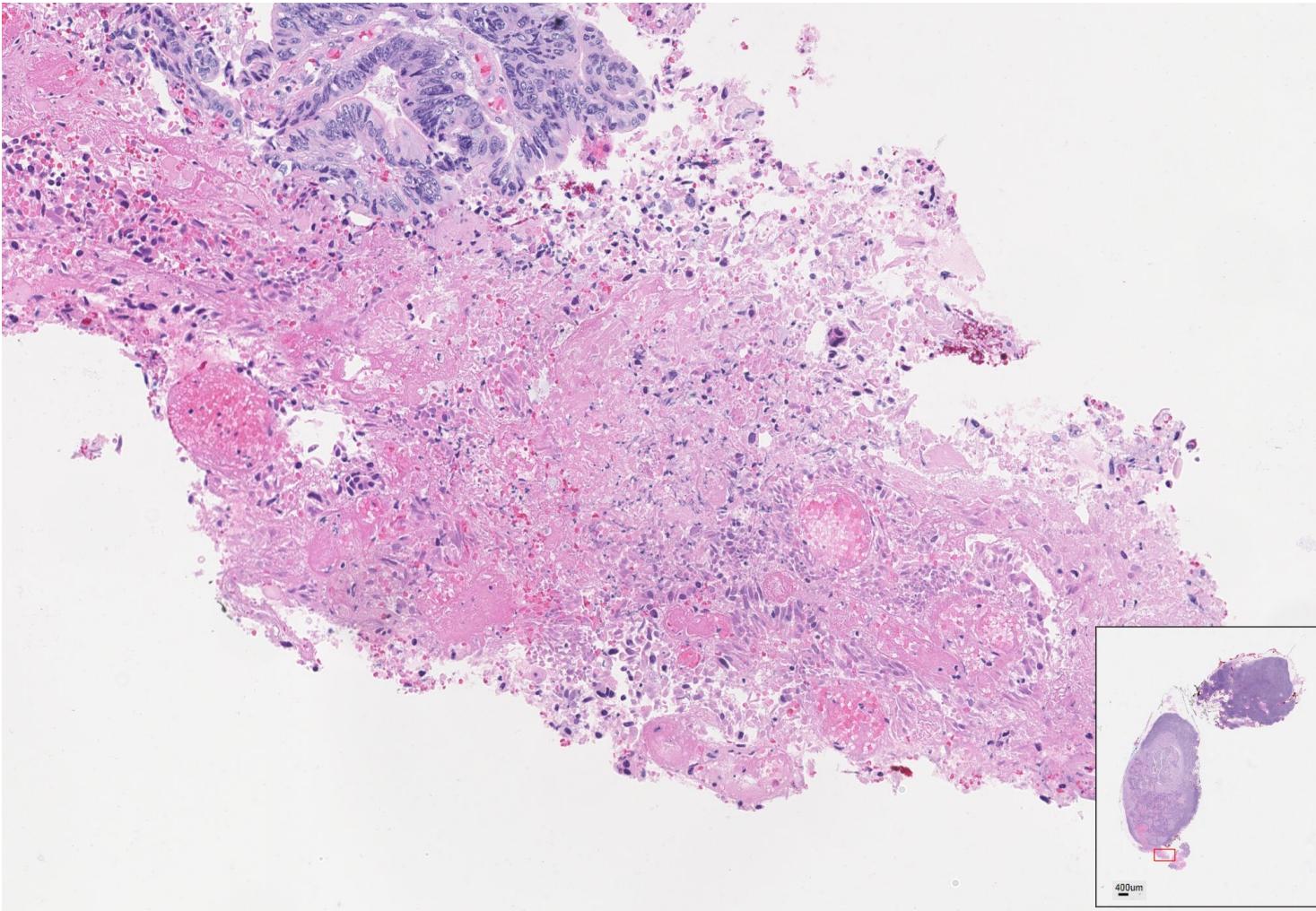
400um

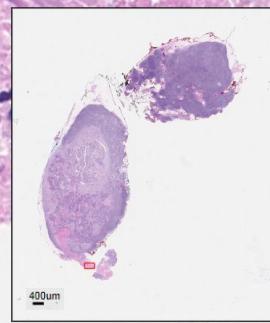
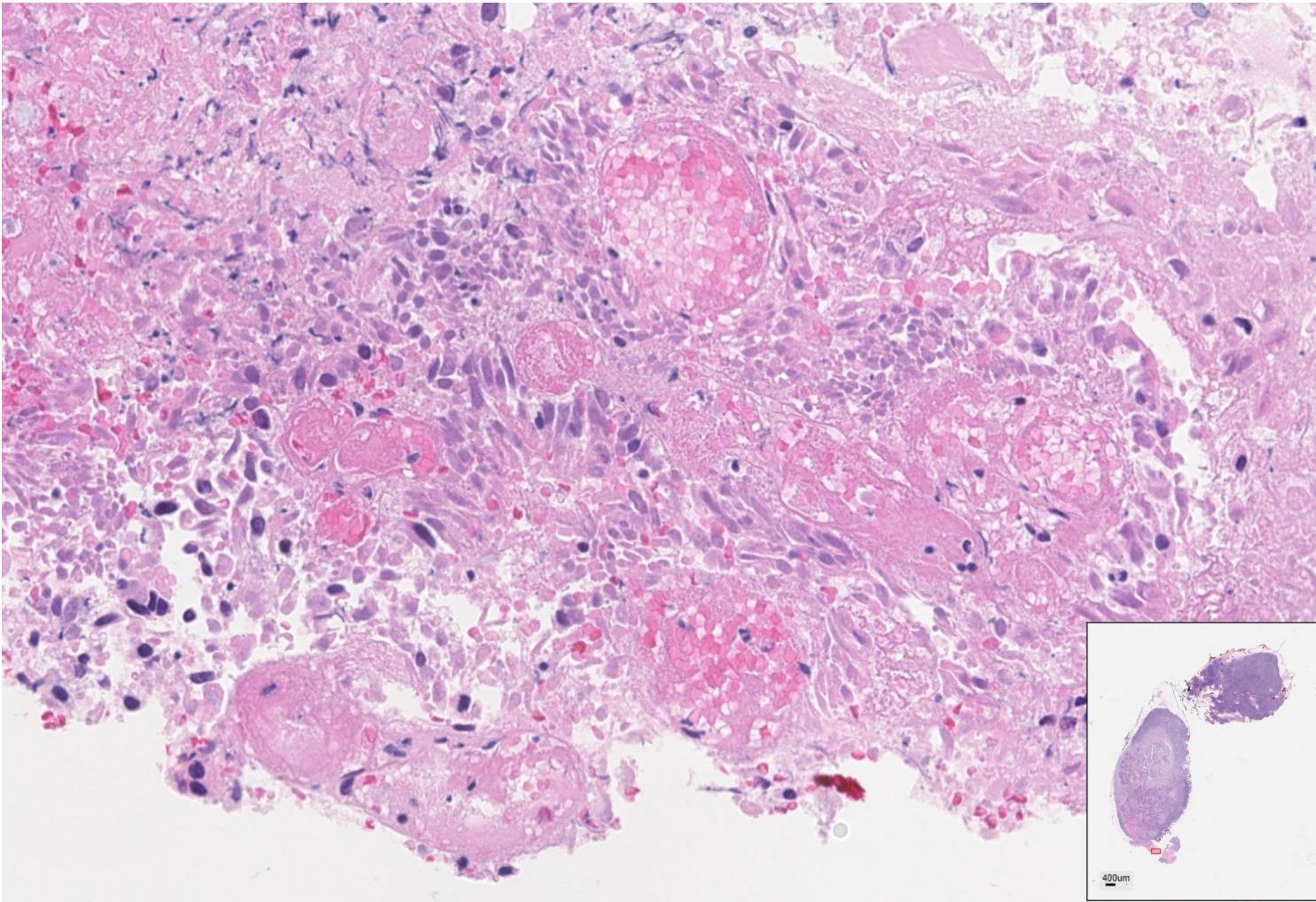




400 μ m







400 μ m

Image Properties

- SAM:
 - 2.00 μm x 2.00 μm pixel size.
- Histology:
 - 0.46 μm x 0.46 μm pixel size.

Challenges of This Multimodality Registration

- Adjacent slides are used to form the images of different modalities.
 - Edges and corners don't perfectly align.
 - Difficult for feature based registration.
- 3 degrees of freedom.
 - 2D translation.
 - Rotation.
- The modalities contain different information.

Normalized Mutual Information

- Has a well defined range.
 - $1 \leq \text{nmi} \leq 2$
- Efficient computation.
- $\text{NMI}(A, B) = (H(A) + H(B)) / (H(A, B)).$

High Level Overview

- Rate change s.t. Pixel size is consistent between images.
- Downsample SAM and histology images.
- Generate random samples over coarse histology and filter.
- Run simplex optimization over random samples to find local optima.
- Select starting point as the optima with largest NMI.
- Trim histology to area surrounding starting point.
- Perform final optimization on full-scale histology.
- Fetch final resolution histology and SAM parameter image.

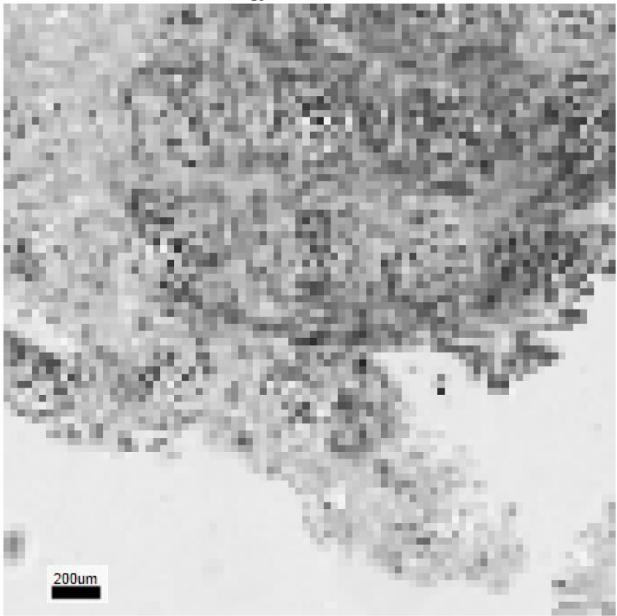
Rate Changing

- The SAM images are captured with a $2.00 \mu\text{m} \times 2.00 \mu\text{m}$ step size, and the histology images have a $1.83 \mu\text{m} \times 1.83 \mu\text{m}$ step size.
- MATLAB function *interp2* was used to perform the rate changing.
 - No visible difference between nearest neighbor, linear, cubic, and spline interpolation methods.

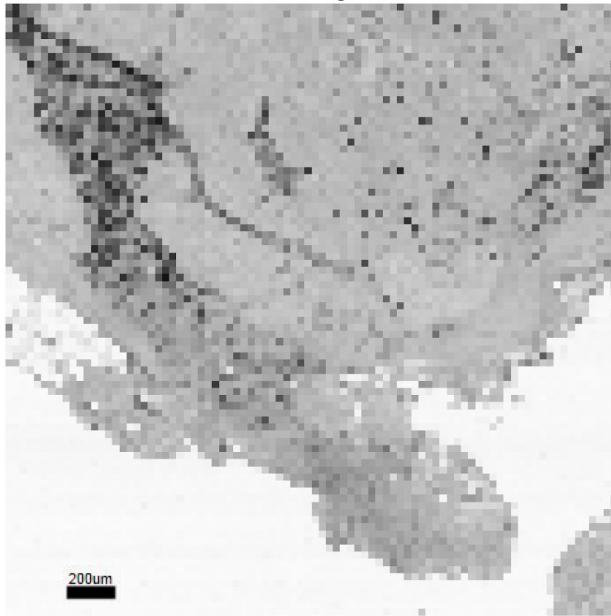
Downsampling

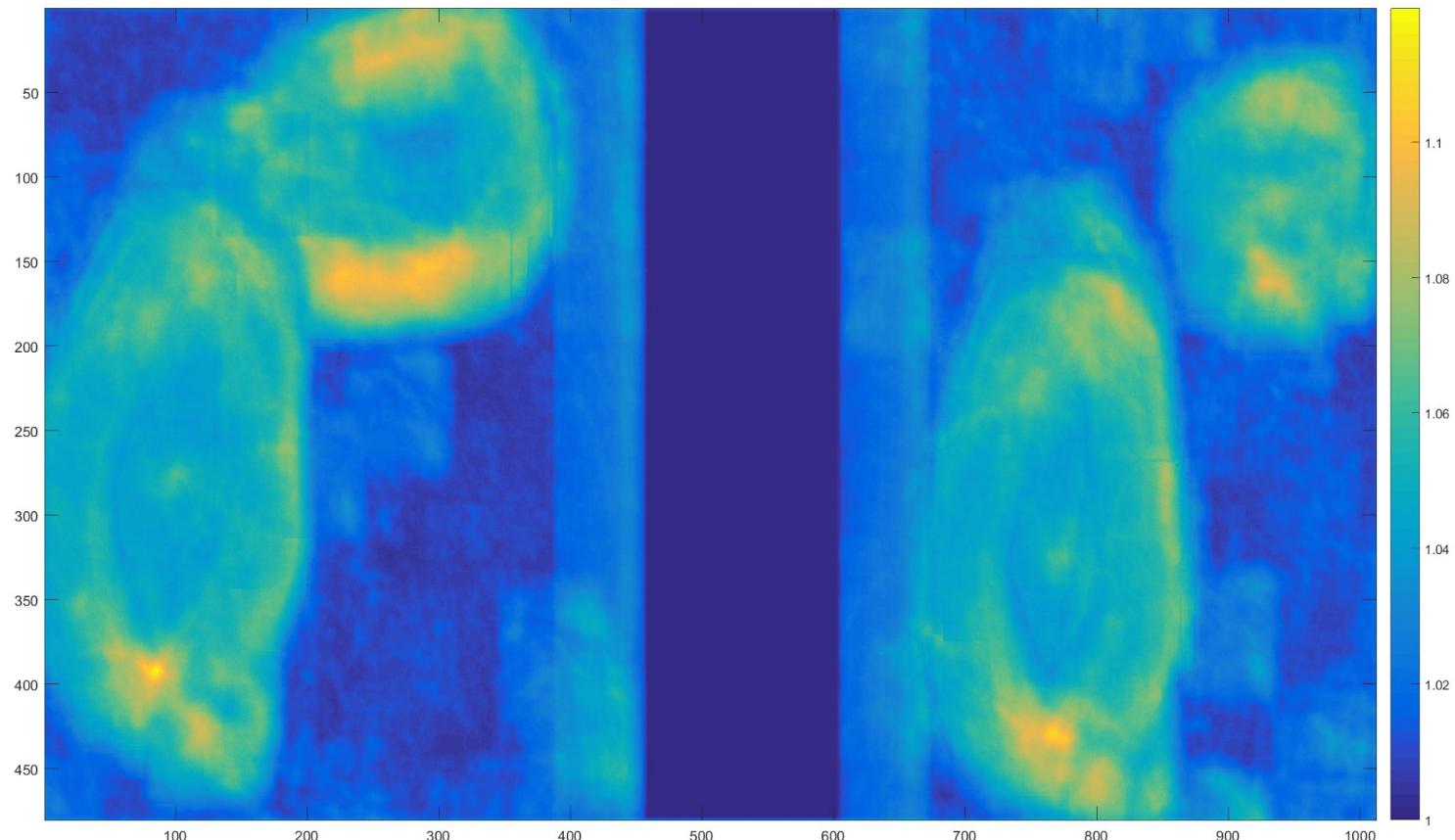
- Due to the large size of the histology images (on the order of 10,000 x 20,000 pixels), downsampling was performed to get a coarse starting point estimate.
- Downsampling by a factor of 16 in the x and y directions left sufficient information in the image, while remaining manageable.

Histology Match, NMI = 1.1754



SAM Image

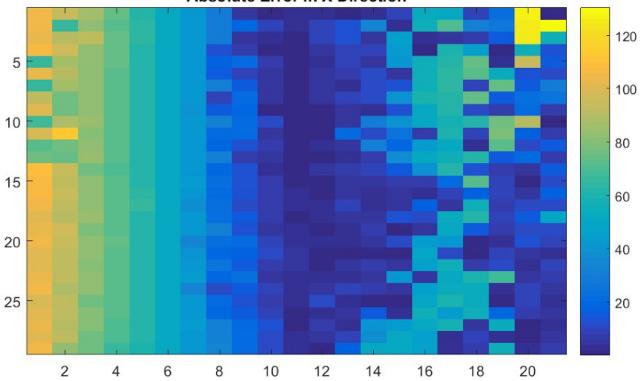




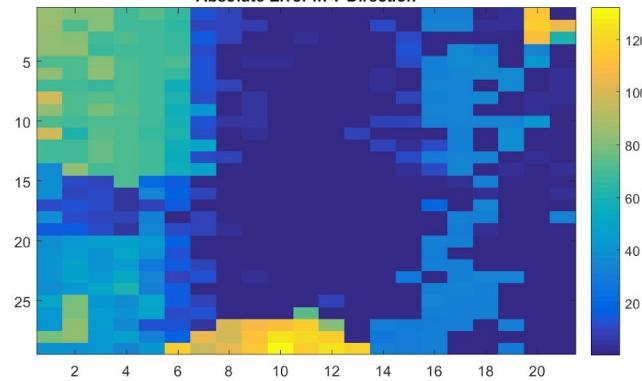
Initialization

- Optimization will find the correct registration if the initial starting point is within a 50 pixel radius of the best registration.
- This gives rise to initialization via random sampling.
 - How many samples required to generate a point within the basin of attraction with probability 0.95?
 - Binomial random process.

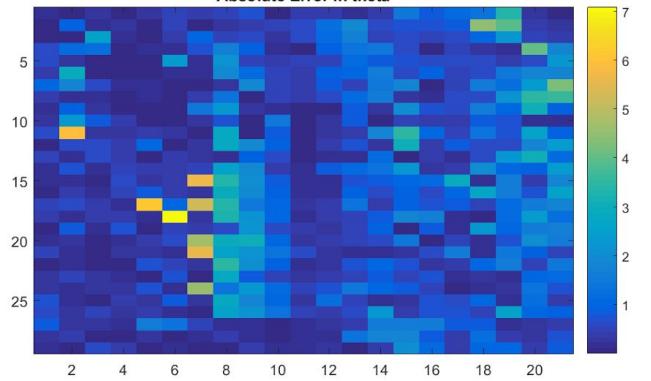
Absolute Error in X Direction



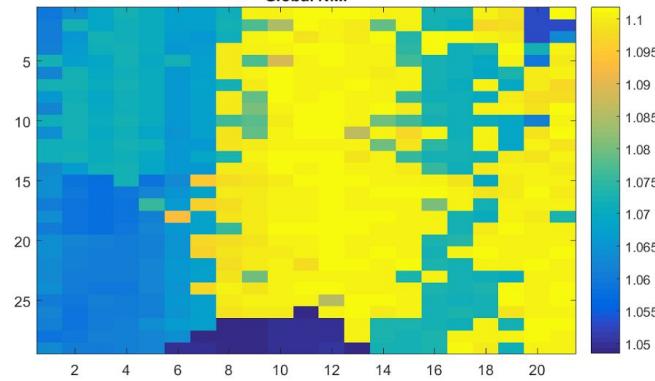
Absolute Error in Y Direction



Absolute Error in theta

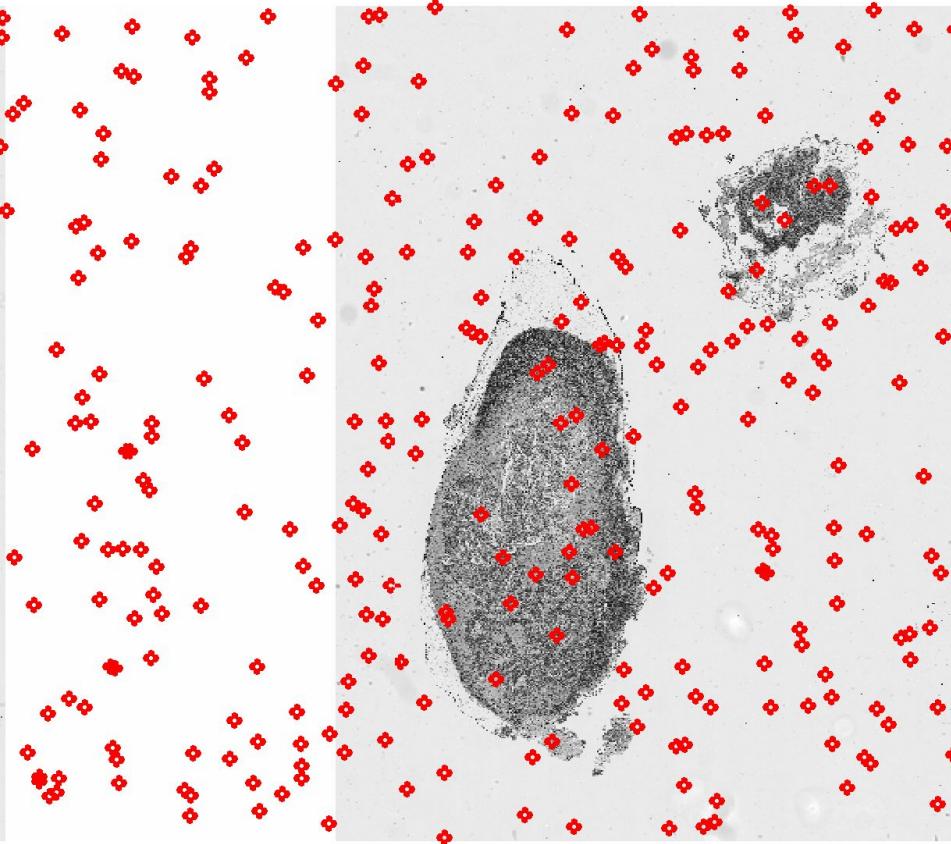
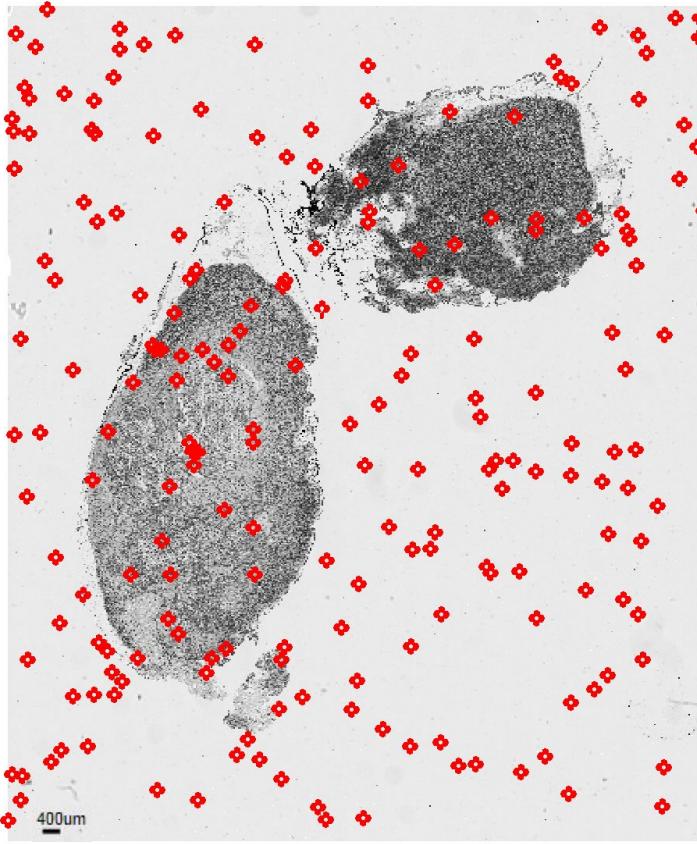


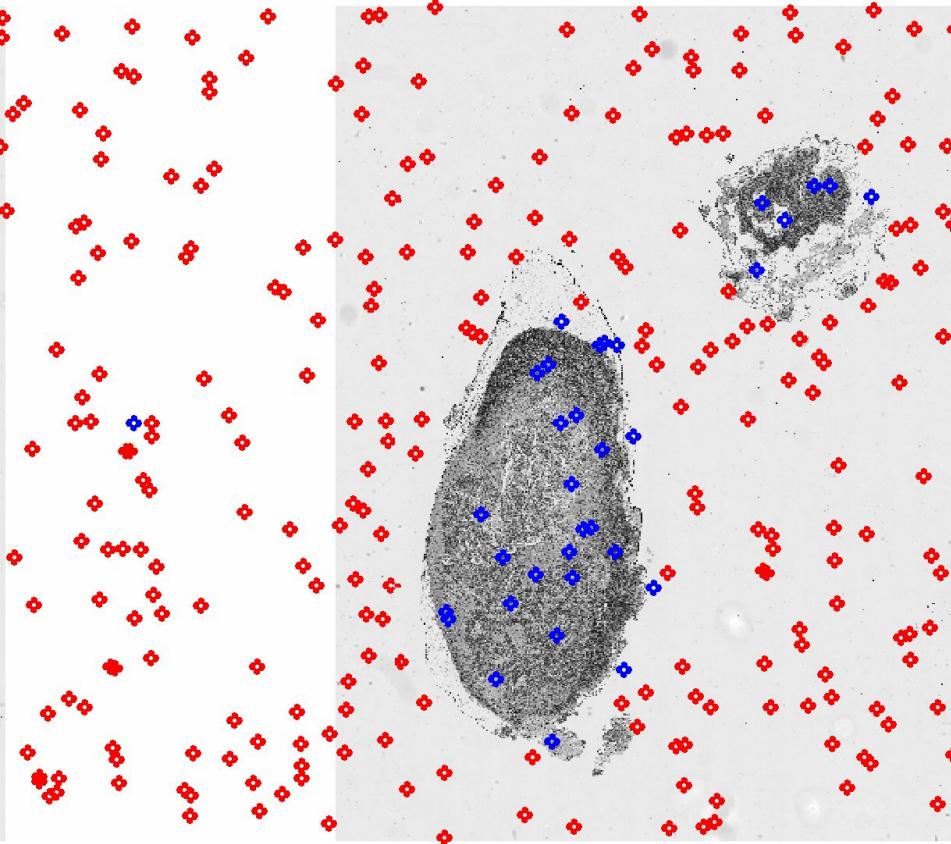
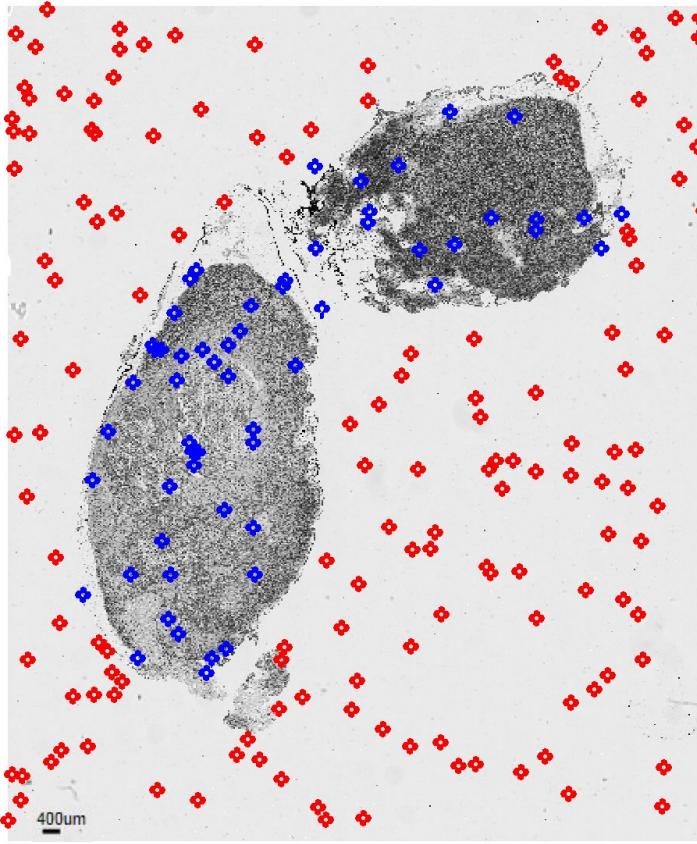
Global NMI



Filtering the Random Samples

- Many of the random samples can be filtered out immediately, based on the content of the surrounding image.
- If the entropy of the surrounding image is below a threshold, then the sample is discarded.
- This significantly speeds up the initialization process.

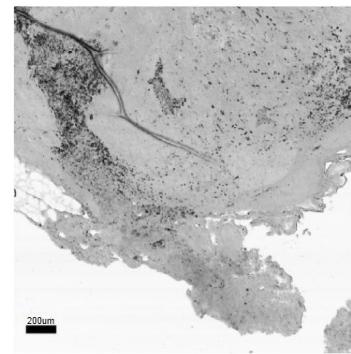
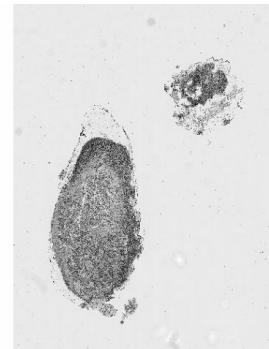
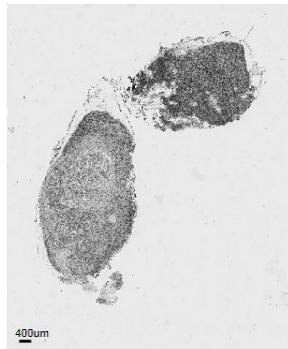


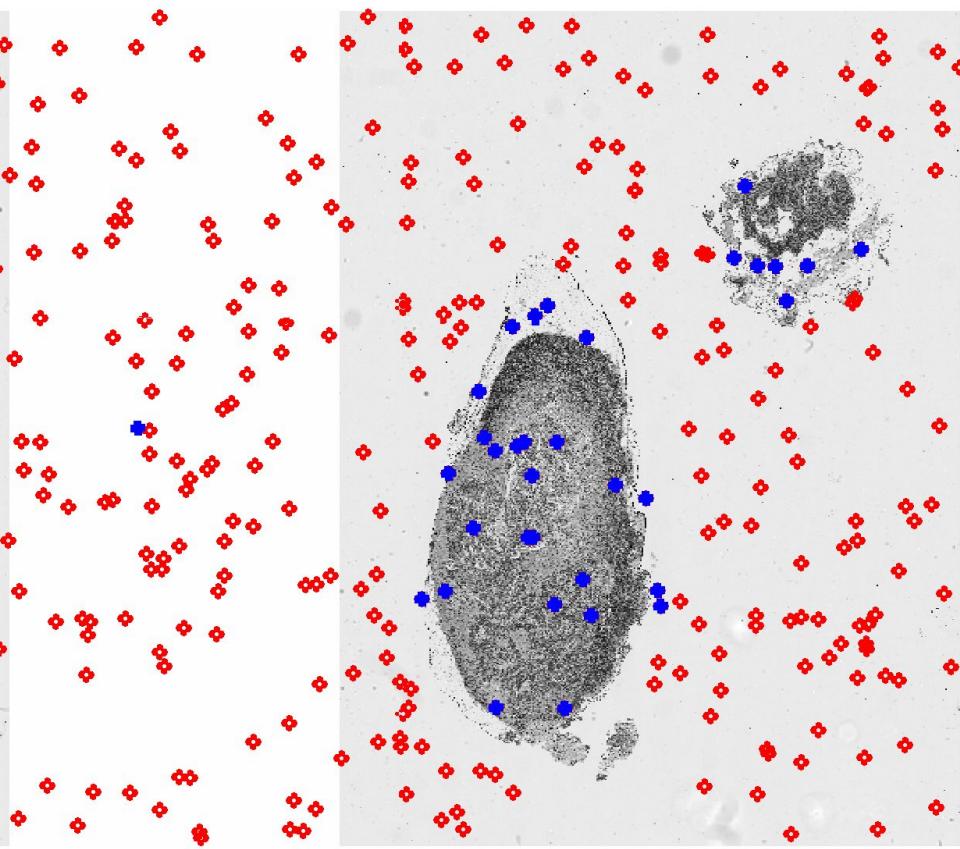
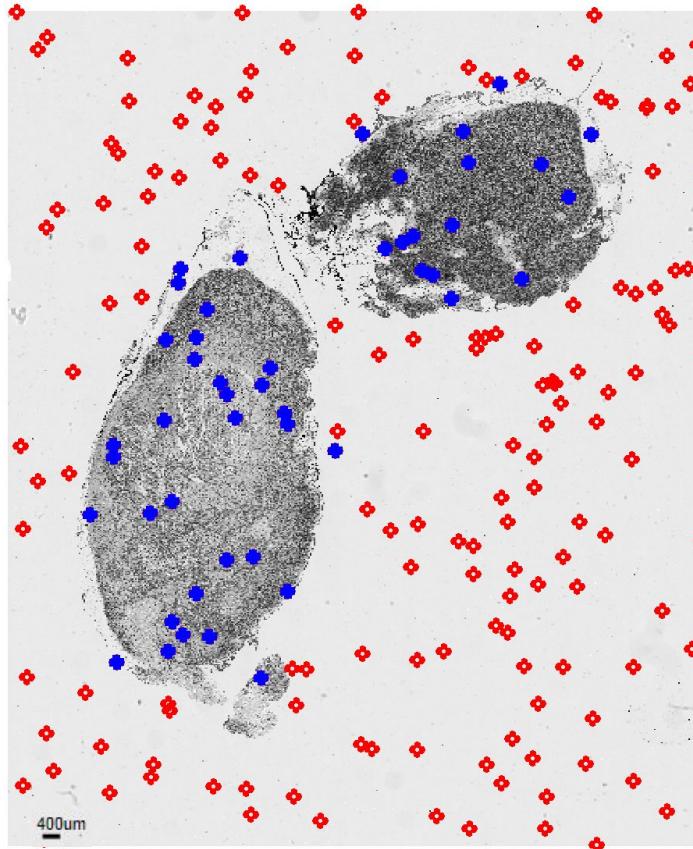


Optimization

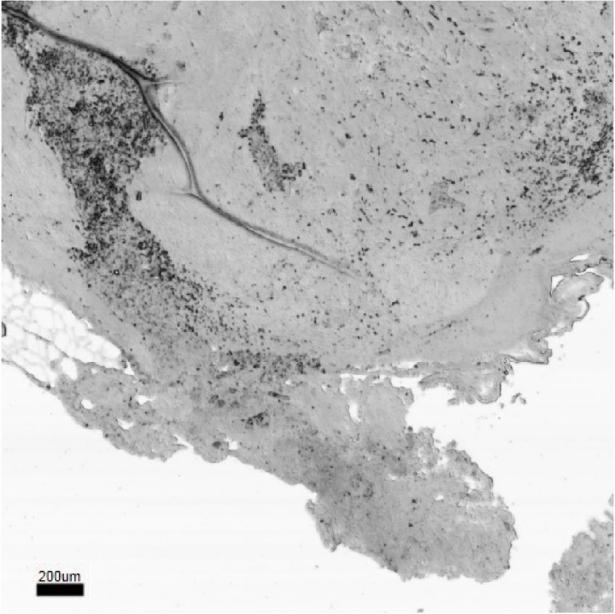
- MATLAB's *fminsearch* function was used for the optimization step.
- There are three parameters which define the registration, so *fminsearch* returns the optimal tuple which is obtained via a simplex optimization routine.

Results

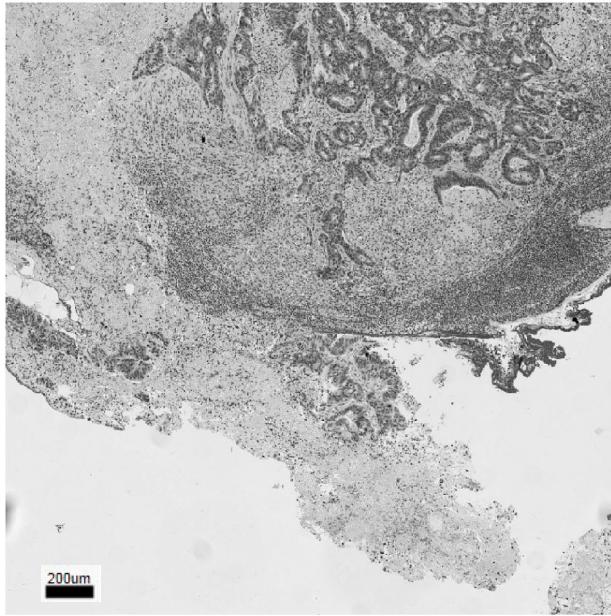


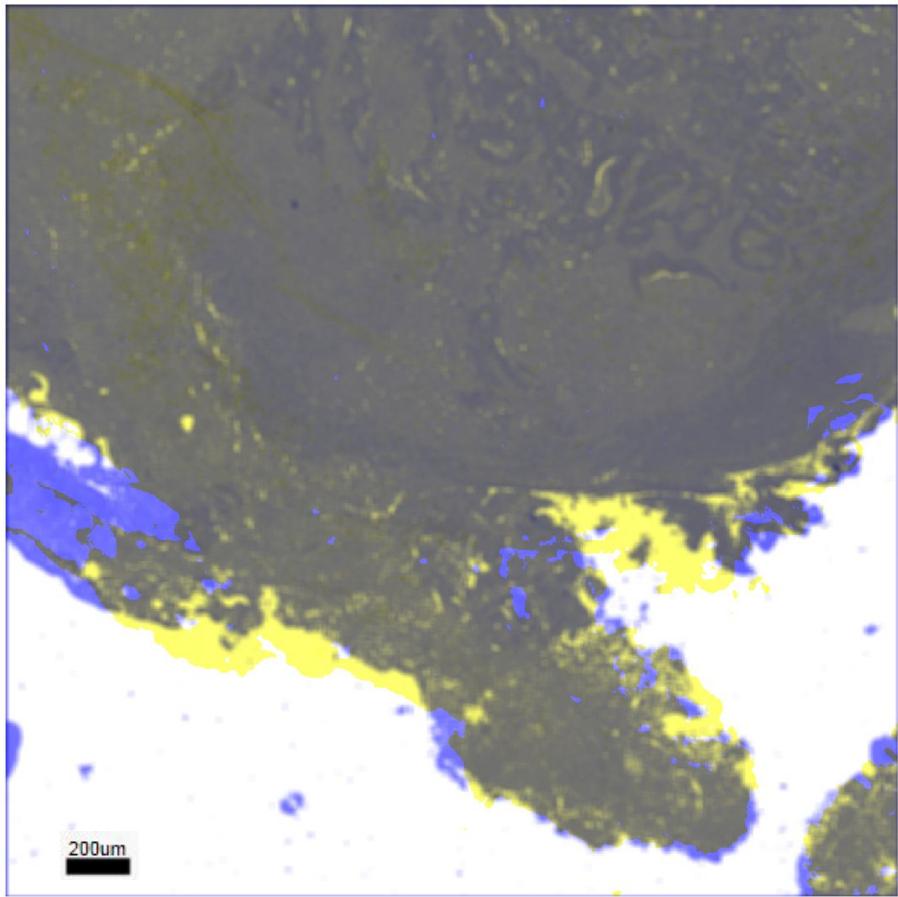


SAM Image

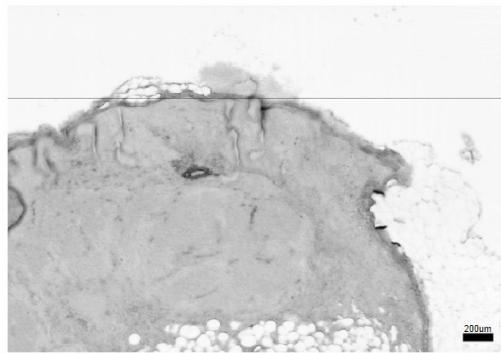
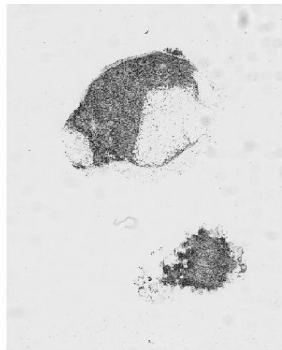
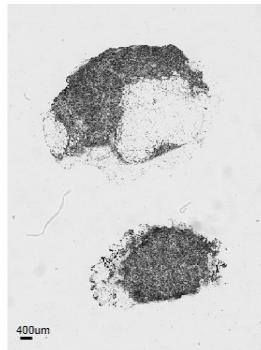


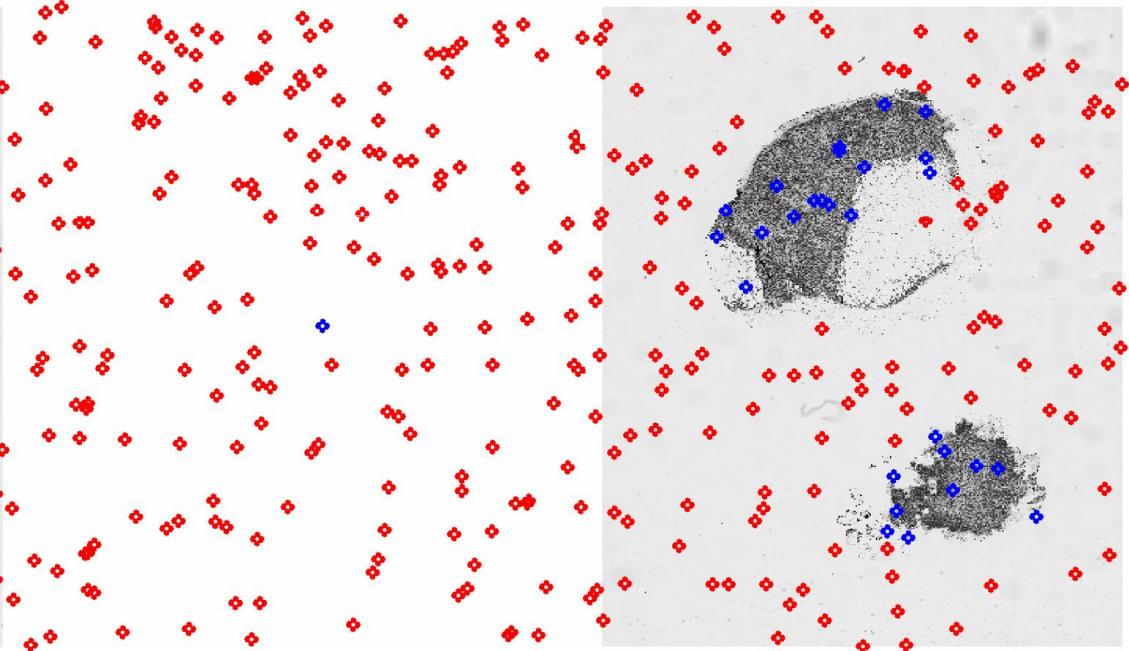
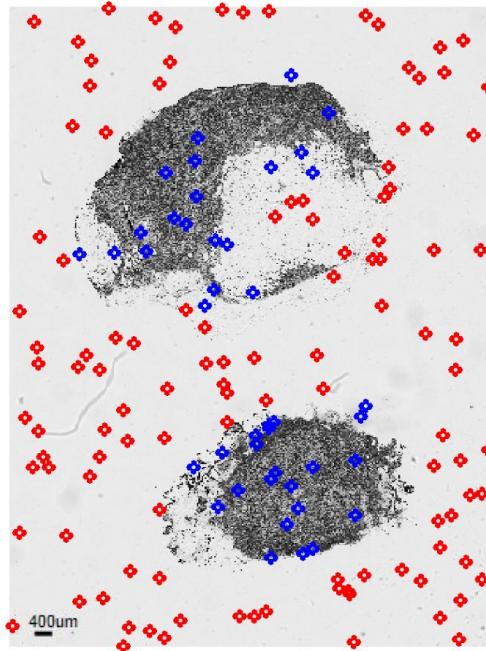
Histology Image



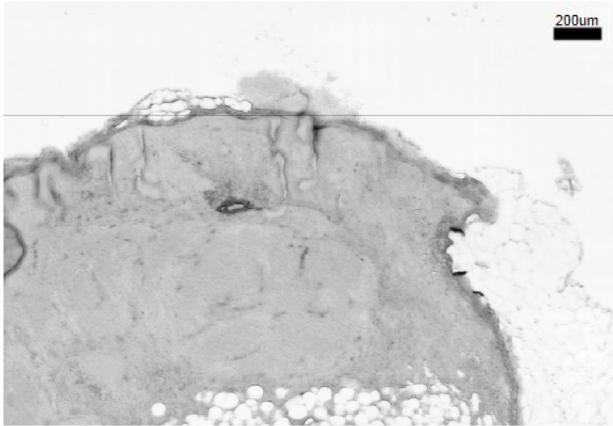


200 μ m

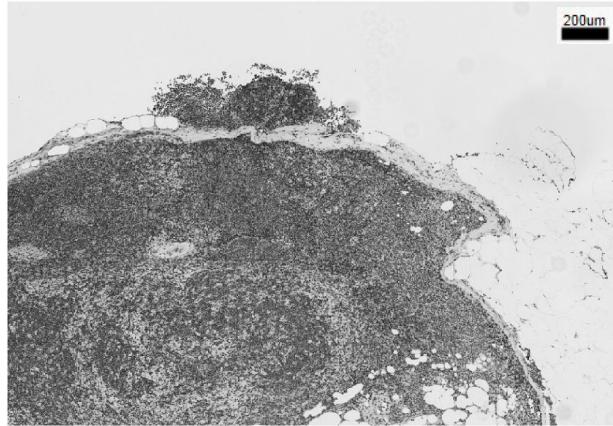


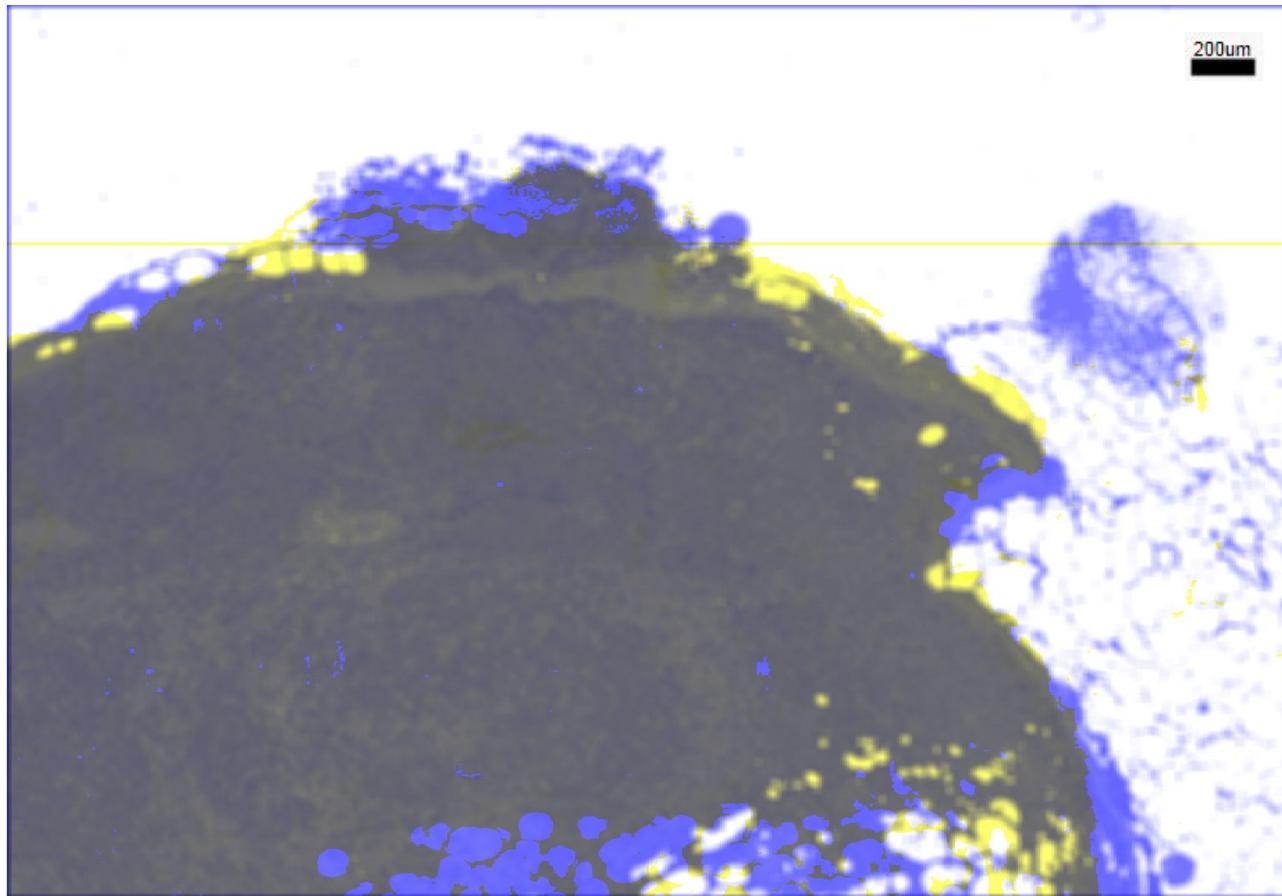


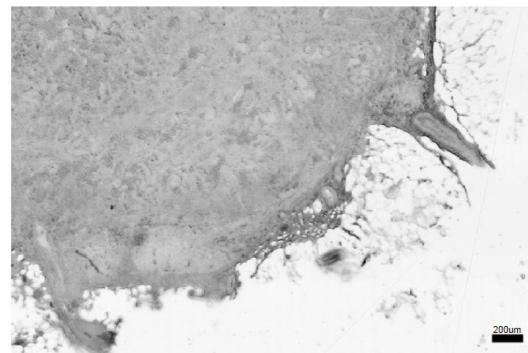
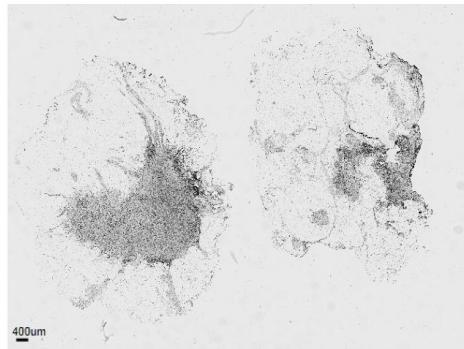
SAM Image

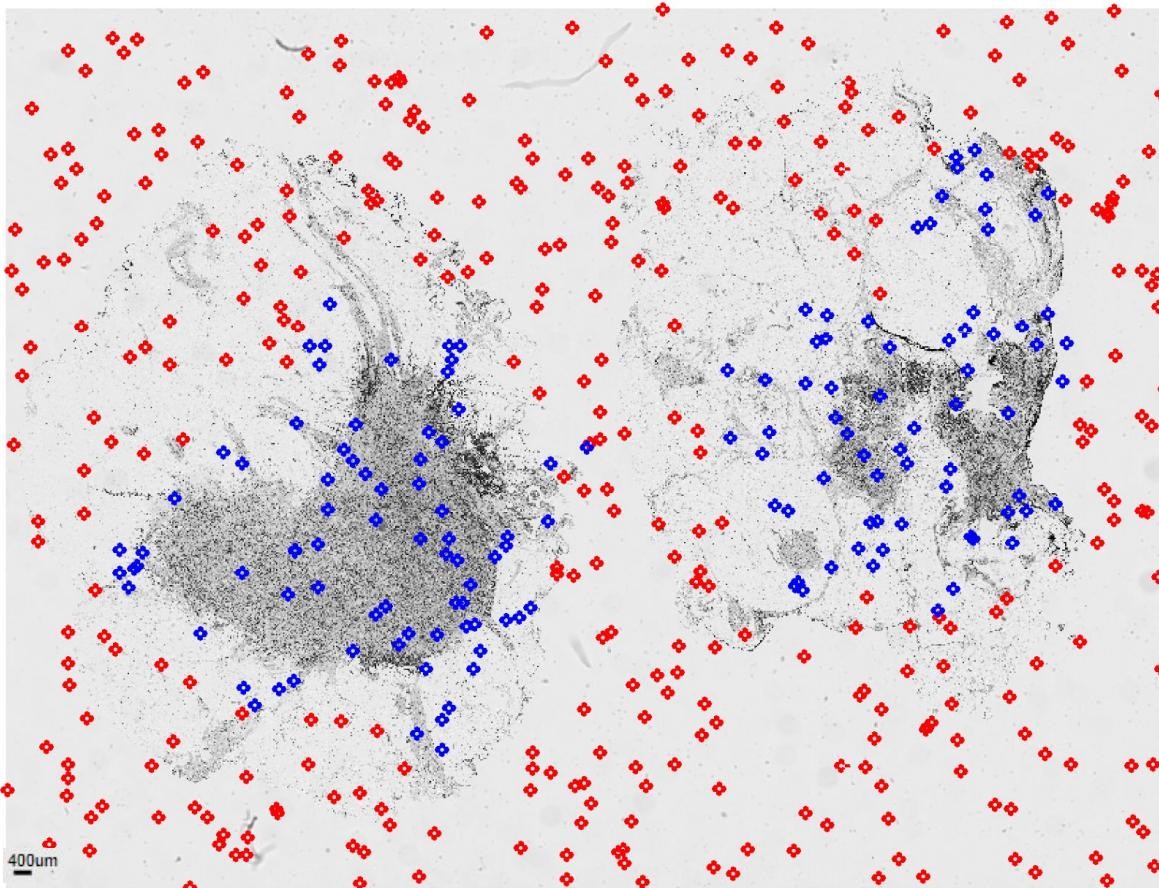


Histology Image

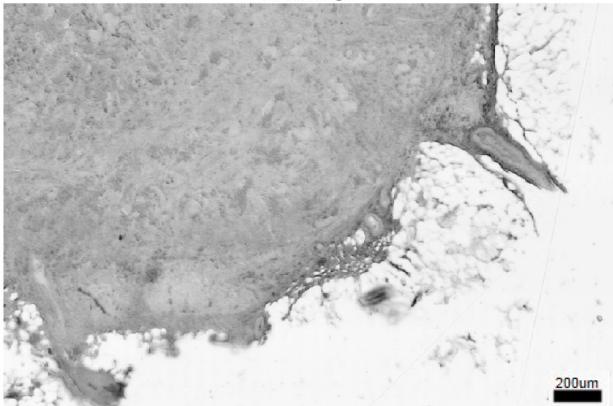




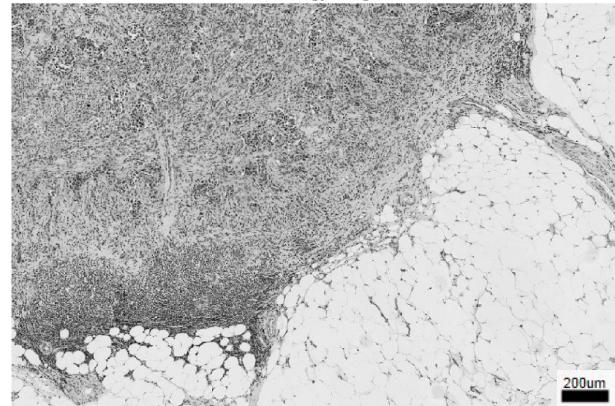


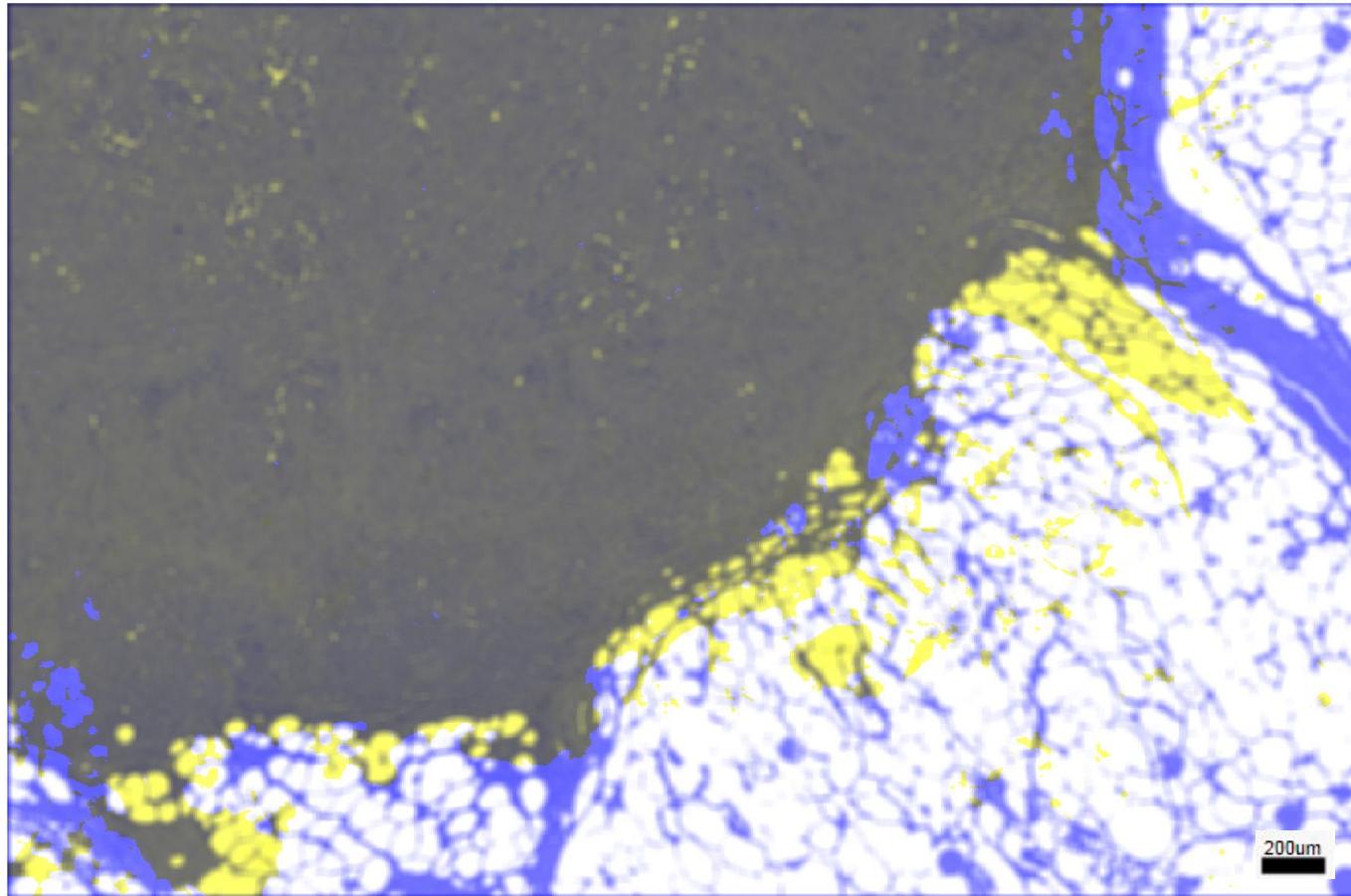


SAM Image



Histology Image





Conclusion

- This method works well for the available dataset.
- Further testing will be done on different datasets, but we believe that the method is general enough to hold.