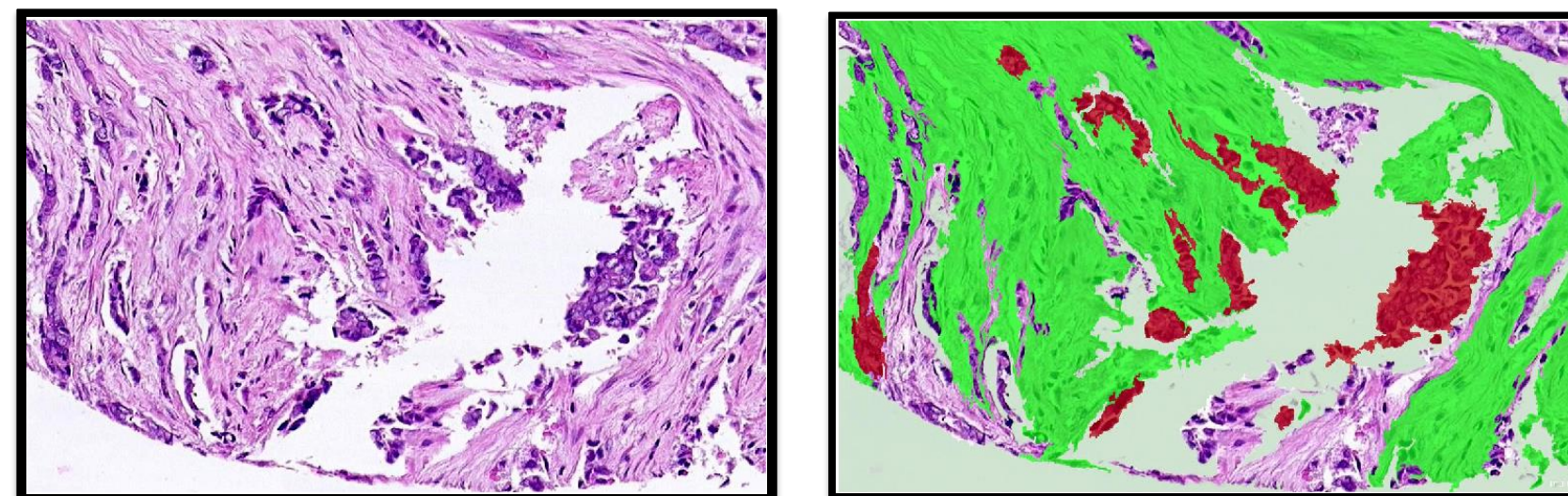


Deep Learning Image Classification for Histopathology

Sean Fischer

Methodology

Training Tissue Samples (x150)

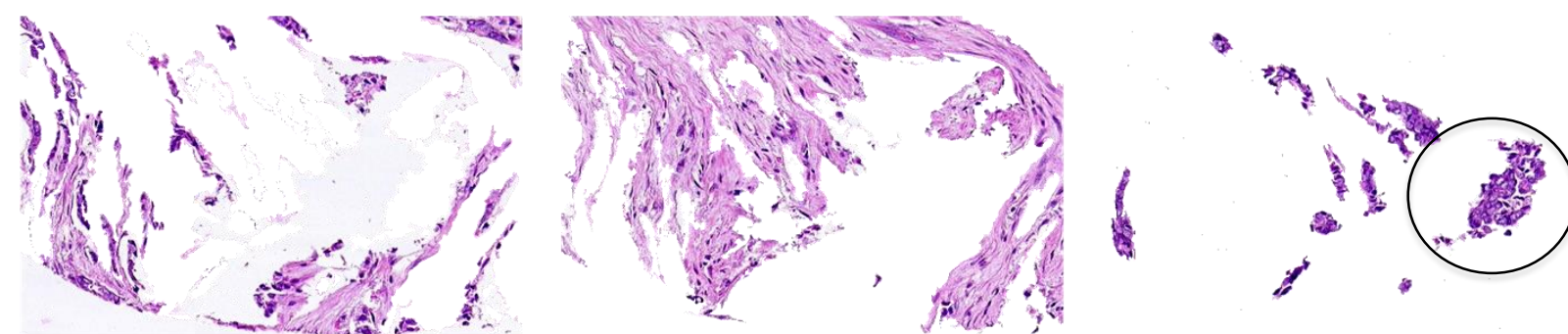


K-means
(for training)

Background

Stromal Tissue

Epithelial Tissue



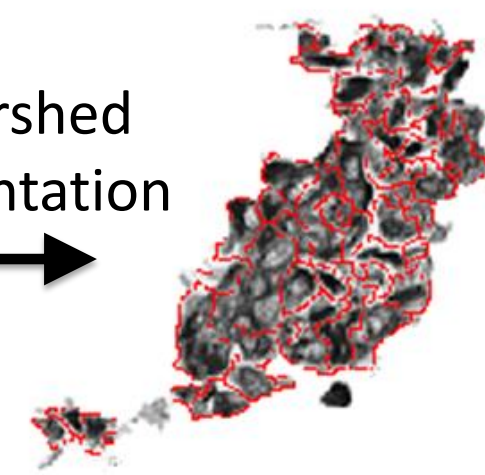
Data

- Digitized slides obtained from Stanford Tissue Microarray Database. Supplemental material from Beck et. al., *Science translational medicine* (2011)
- Slides labeled with **epithelial tissue** and **stromal tissue**
- 200 slides used in this work

Goal

Classify super-pixels
(watershed basins)

Watershed
Segmentation



Logistic
Regression

Prediction

Epithelial
vs.
Stroma

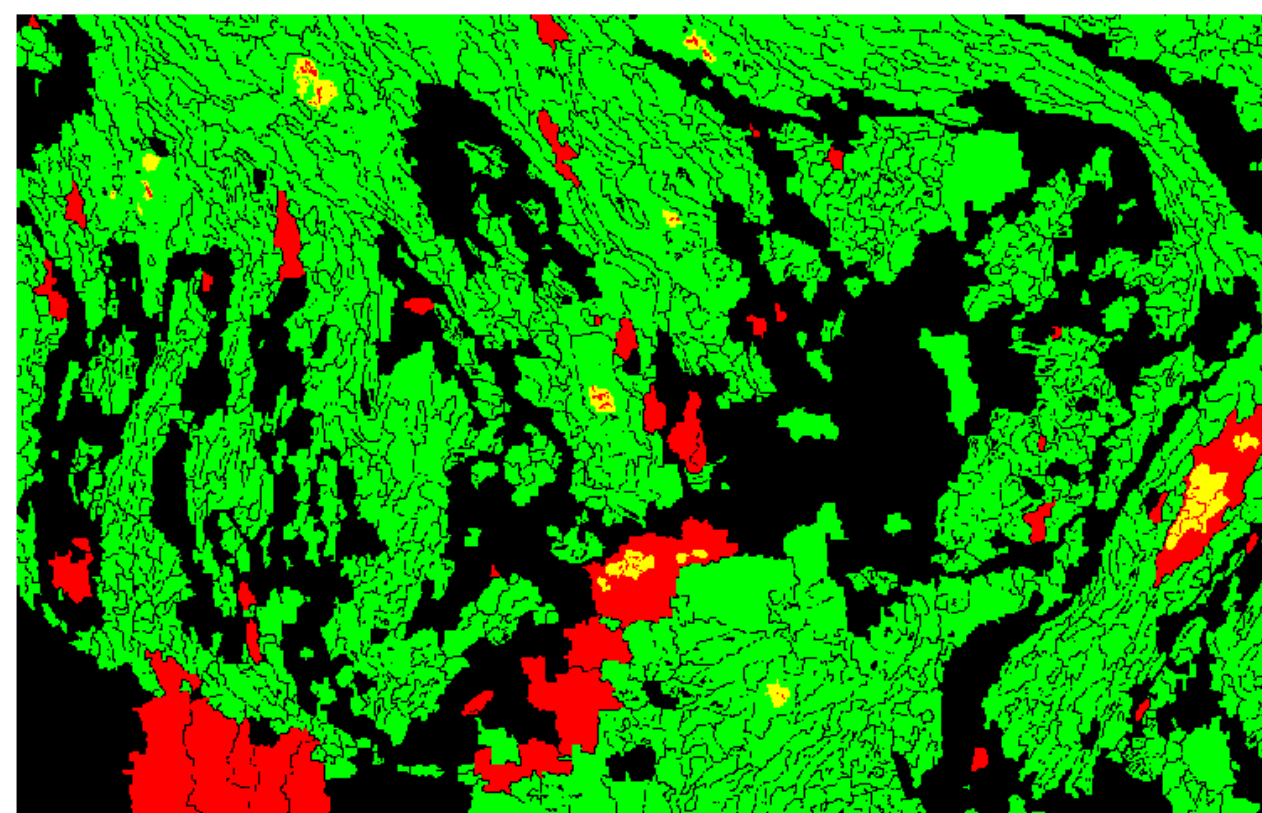
Background
vs.
Epi./Stroma

Validation Tissue Samples (x50)

S

E

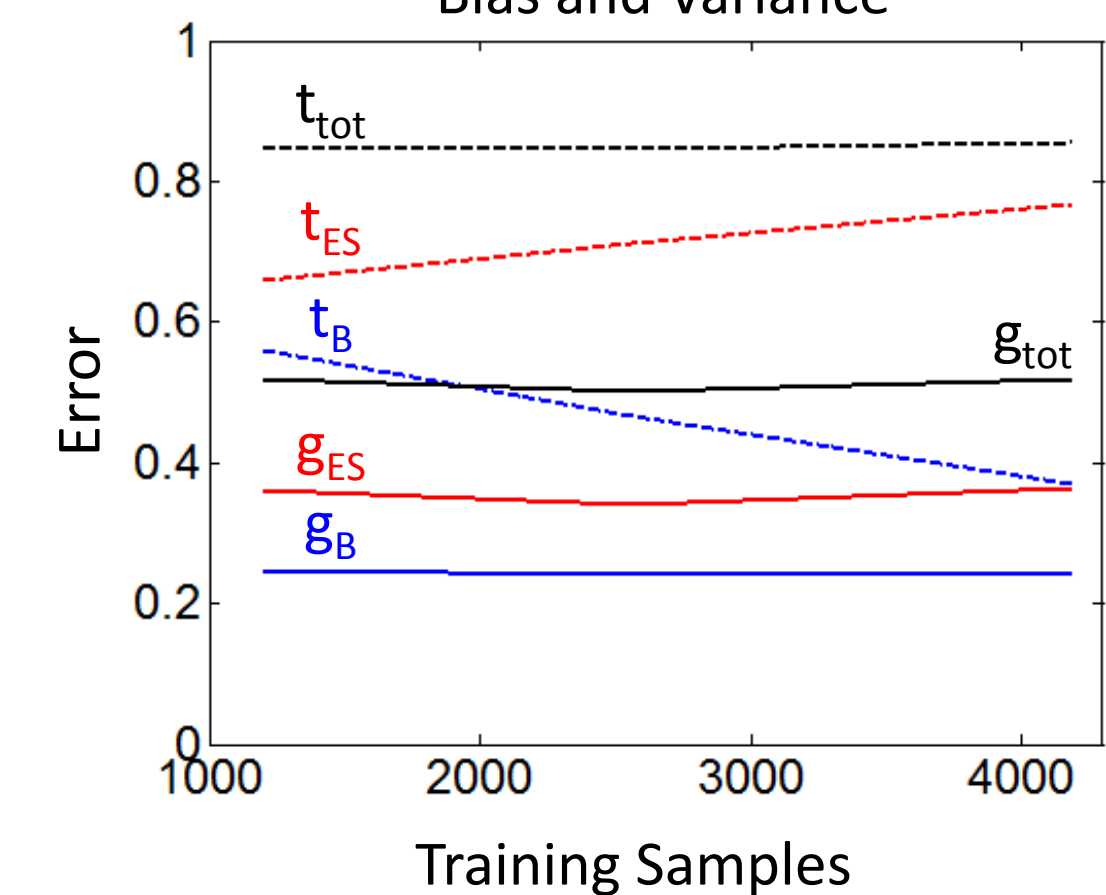
B



Error_B = 0.39 Error_{ES} = 0.11 Error_{TOT} = 0.45

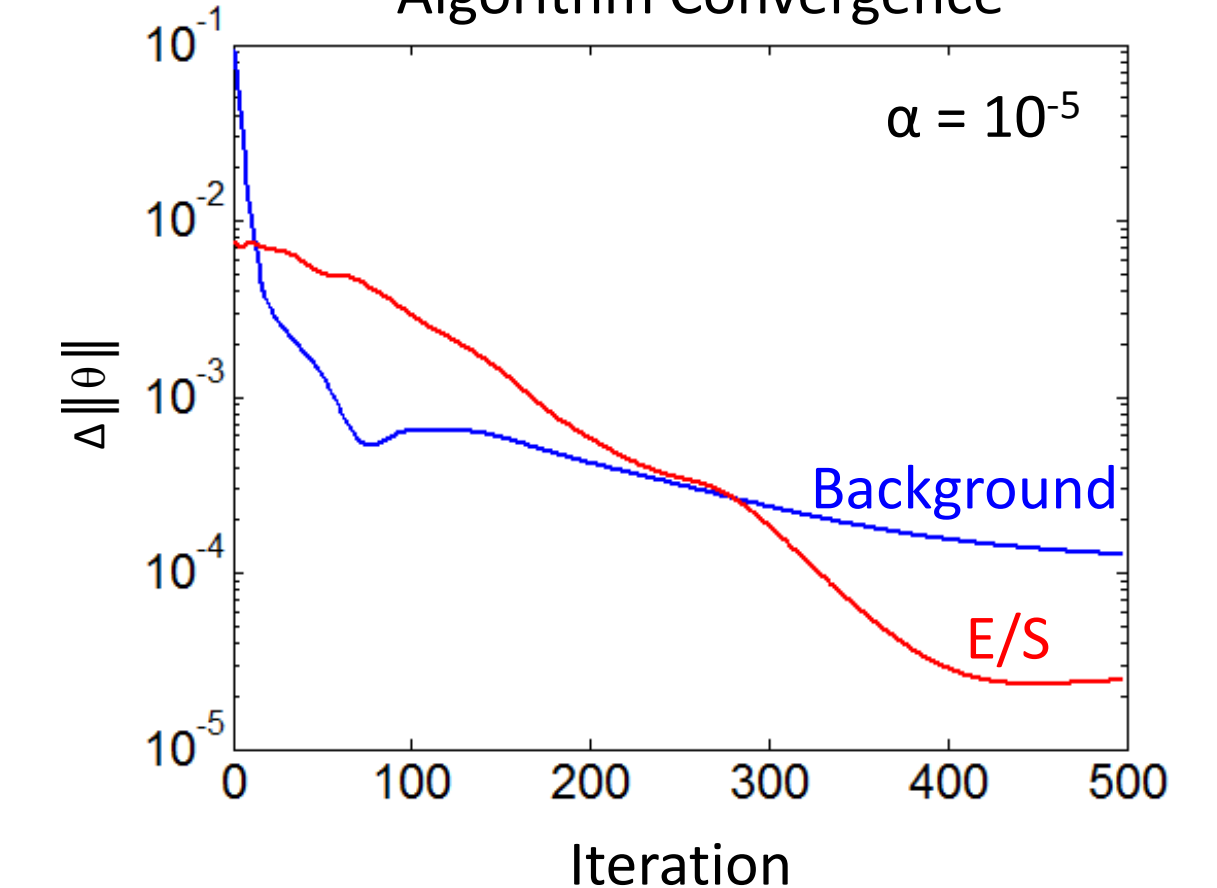
Results

Bias and Variance



- High bias \rightarrow need more features
- $g_{TOT} < t_{TOT} \rightarrow$ poor model selection, bug in code...

Algorithm Convergence



- Convergence when $\|\theta\|$ stops changing
- Learning rate is sufficiently slow when convergence curve is smooth.

Future Work

Add More Features

- Current features layer based (RGB, Int.)
- Add textural features
- Add geometrical features

Different Model

- Multinomial logistic regression
- k-means for tissue classification

More Image Pre-Processing

- New color model (HSI)
- Different segmentation schemes

