# 7a.019.DU - Image Informatics for the Characterization of Molecular Subtypes in Breast Carcinoma Tissue

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Project Start: 1/1/18	End Date: 6/30/19	Project Budget: $45,000	Spent: $30,500

Project Summary: Histological examination of tumor and biopsy specimens remains the key diagnostic tool for pathology diagnosis and staging. The availability of large-scale architectural information and fine-scale features can serve as important cues from which to judge the aggressiveness of the tumor and the patient's prognosis. The predictive capabilities of histological image analysis, enhanced by informatics techniques, may be harnessed to objectively and reproducibly distinguish tumor subtypes. The key advantage of this approach tackles the two major criticisms of molecular subtyping: 1) the lack of spatial information, that makes gene expression analysis susceptible to artifacts in the presence of tumor heterogeneity, can be overcome with image analysis; 2) by defining tumor molecular subtype morphologically with a reduced number of variables (on the order of tens, rather than thousands), the "curse of dimensionality" no longer places a constraint on our ability to define groups based on pattern analysis.
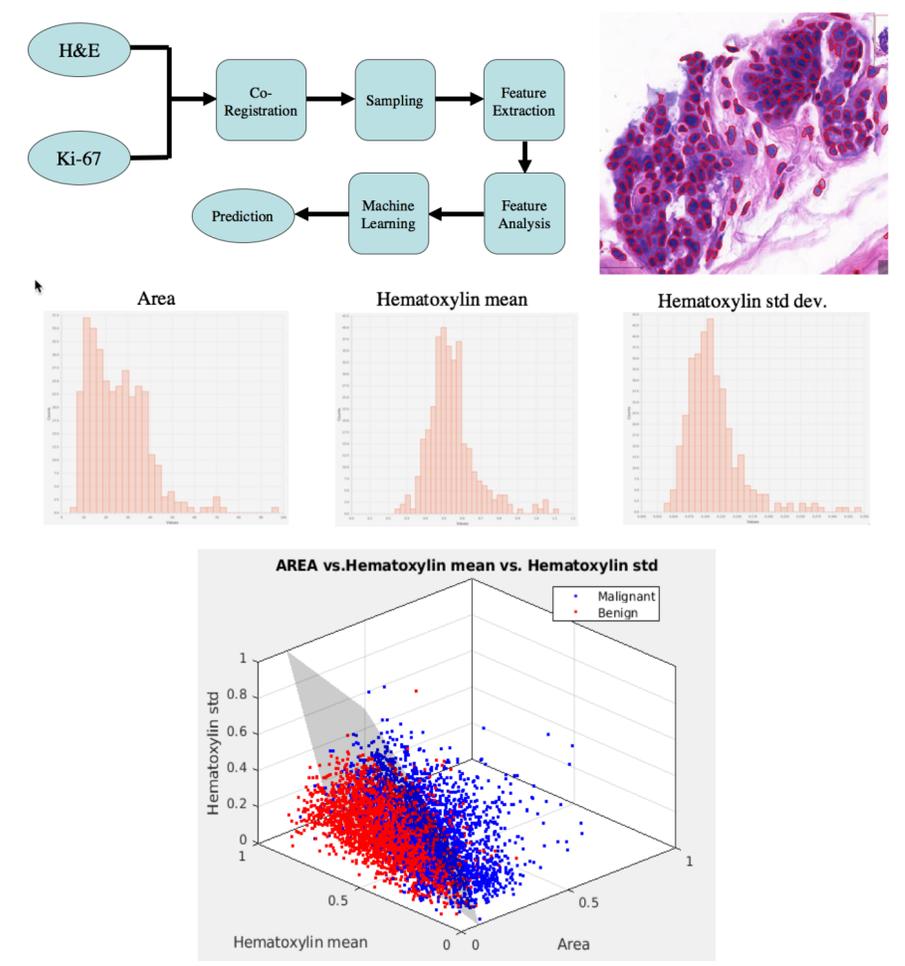
Details of Progress/Achievements:

1. We have developed a computational pipeline to rapidly extract nuclear features from tumor regions in a completely automated fashion. We demonstrate that the selected features have prognostic significance by showing that they segregate malignant and benign tumors.
2. The benefits of this approach over conventional methods in computational pathology is that it is fast (does not require extensive training) and operates on combinations of features.
3. The application of this computational pipeline has potential to provide objective and reproducible scoring in a number of cancers.

PROJECT DELIVERABLES

Deliverable	Achievements	Remaining To Do
Novel algorithms for molecular subtype identification and prediction of genetic traits from visual tissue analysis	The fundamental algorithmic components of the pipeline have been developed	Process the input data and apply algorithms to predicting molecular subtype
Implement prototype software	The algorithms have been implemented in a computational pipeline	Further test the software with additional images
Research publications	Nothing to report	Write up and publish our research results