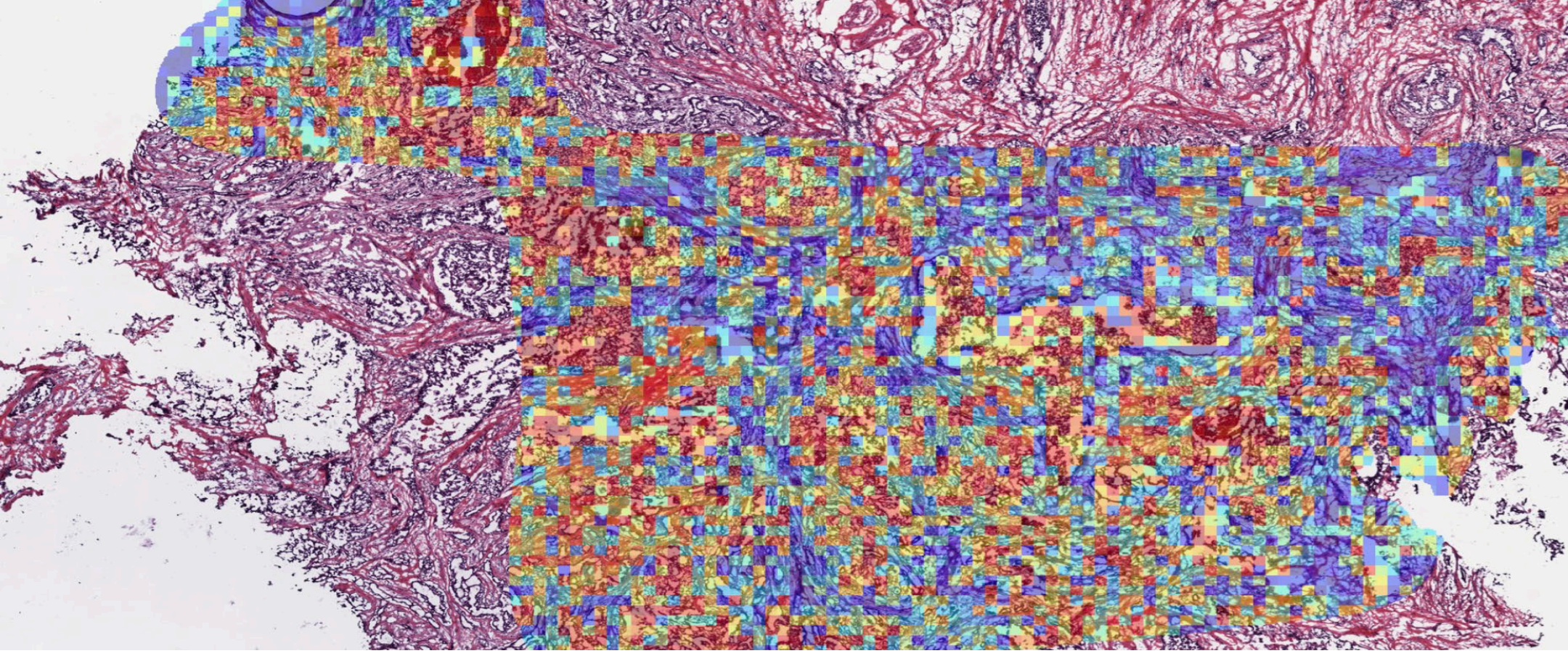
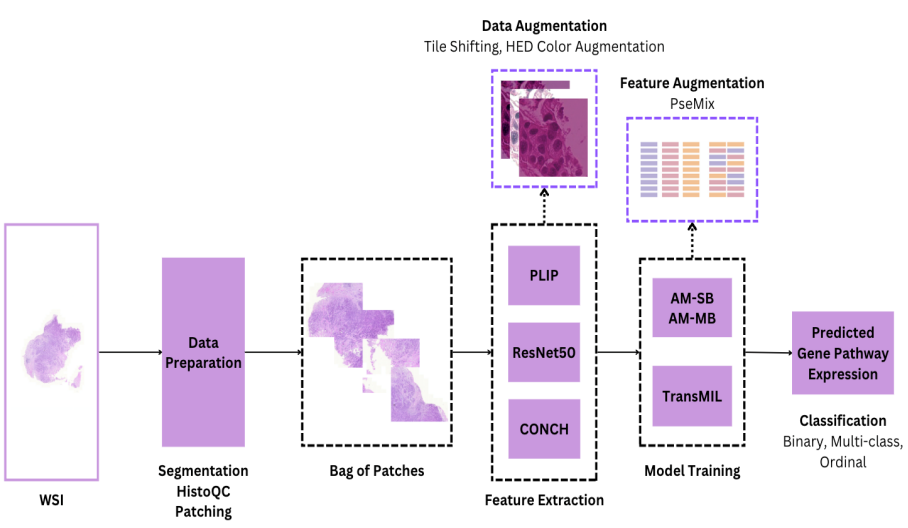


Reimagining Precision Oncology Through Deep Learning-Enabled Computational Pathology Tools



Clinical Need

Success in using precision-based approaches to inform treatment in modern oncology has been limited

Commercial biomarkers are based on a limited view of tumor biology and do not account for the role of tumor microenvironment (TME) in modulating therapeutic efficacy

Conventional approaches to evaluate the TME, such as RNA sequencing or proteomics, require tools that are not widely available in hospitals

Biomarkers that reflect a holistic view of interactions between tumor cells and TME could revolutionize precision oncology

Our Innovative Approach

We applied deep learning to extract and quantify diverse tumor and immune phenotypes from digitized hematoxylin and eosin (H&E) slides

We employed attention-based multiple instance learning on H&E whole slide images and bulk RNA sequencing data from core biopsies of breast cancer patients

Results

Our trained model yielded AUROC scores >0.80 for most transcriptional signatures, recognizing biologically relevant spatial patterns of cells in H&E whole slide images

Validation on a clinical trial dataset from triple-negative breast cancer patients is ongoing

Commercial Potential

Our computational H&E biomarkers facilitate widespread implementation of precision oncology as H&E slides are widely used

Potential application in nearly all solid tumors

We plan to optimize the model and train it on other metabolic/transcriptomic signatures

We are seeking $3-5M to form a NewCo

MGB Innovation Contact
Chris Guevara
cguevara1@mgb.org

Albert E. Kim, MD
Assistant Professor, Harvard Medical School
Assistant Physician, MGH Cancer Center
Investigator, Athinoula A. Martinos Center for Biomedical Imaging
akim46@mgh.harvard.edu