

# BMIF203/BMI702

## Week 6: Medical Imaging II

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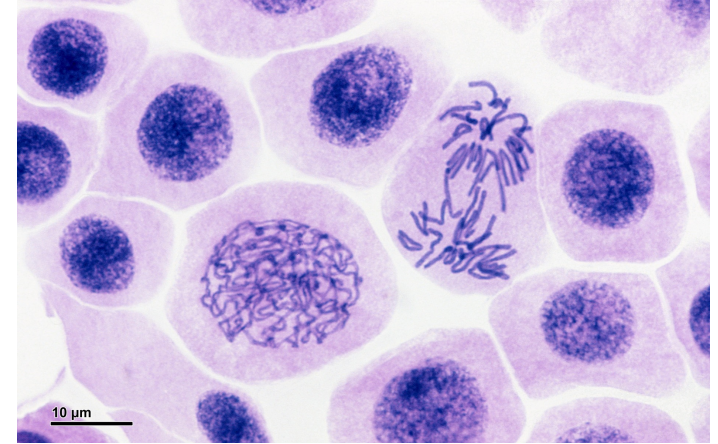
**March 4<sup>th</sup>, 2025**

# Outline

- Human-interpretable features + machine learning
- Deep learning methods
  - Multi-modal foundation models
  - Model interpretation
- Clinical applications in cancer pathology diagnoses

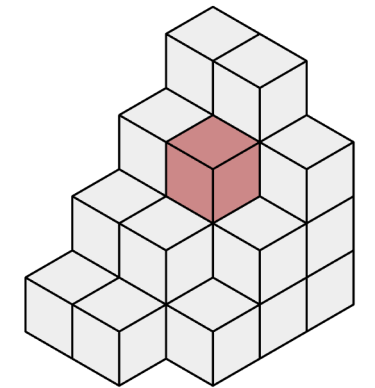
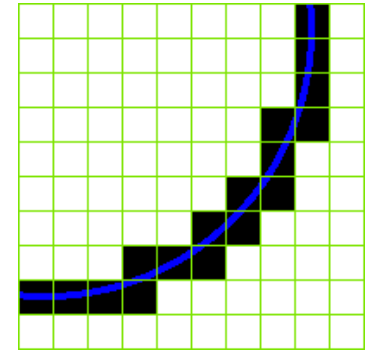
# Method 1: Image Analyses by Human-Interpretable Features

- Define human-interpretable features
  - e.g., size and shape of an object
- Extract these features computationally
- Connect these features with outcomes of interest



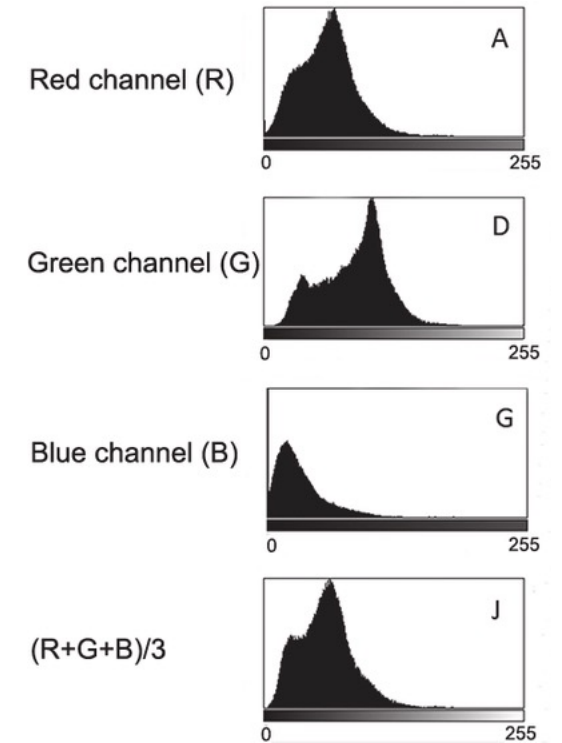
# Basic Features

- Size and shape (two-dimensional)
  - Area
    - Number of pixels in the region of interest
  - Perimeter
    - The total number of pixels around the boundary of each region
- Size and shape (three-dimensional)
  - Volume
    - Number of voxels in the region of interest
  - Surface area
    - The total number of voxels around the boundary of each region in the image



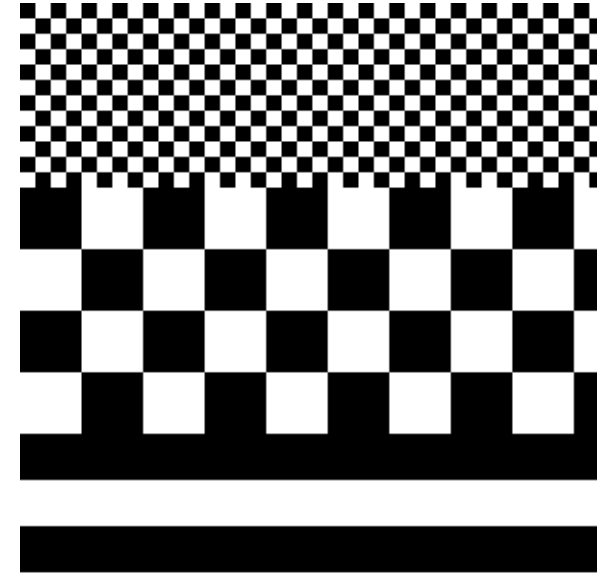
# Basic Features

- Form factor
  - $4 * \pi * Area / Perimeter^2$
  - Form factor of a perfect circle = 1
- Intensity metrics
  - Mean intensity
    - Mean of pixel intensity values in the region/image
  - Median intensity, standard deviation of intensity values, median absolute deviation of pixel intensity values
- Saturation metrics
  - Percent of pixels at the maximum/minimum intensity value of the image



# Texture Features

- Quantify the spatial arrangement of pixel intensities
- Example: Haralick texture features
  - Goal: to distinguish between rough and smooth patterns
  - Method: compute summary statistics of the gray-level co-occurrence matrices (GLCM; next slide)

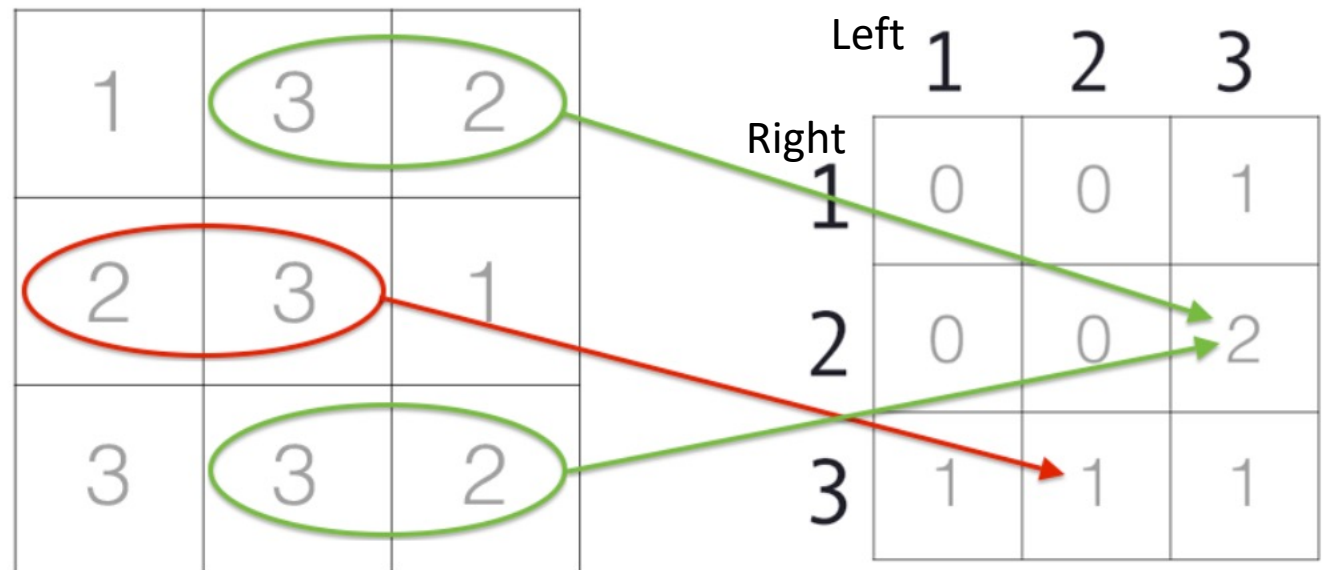


# Gray-Level Co-occurrence Matrix (GLCM)

- Example:

1	3	2
2	3	1
3	3	2

Left-right pairs of adjacent pixels:

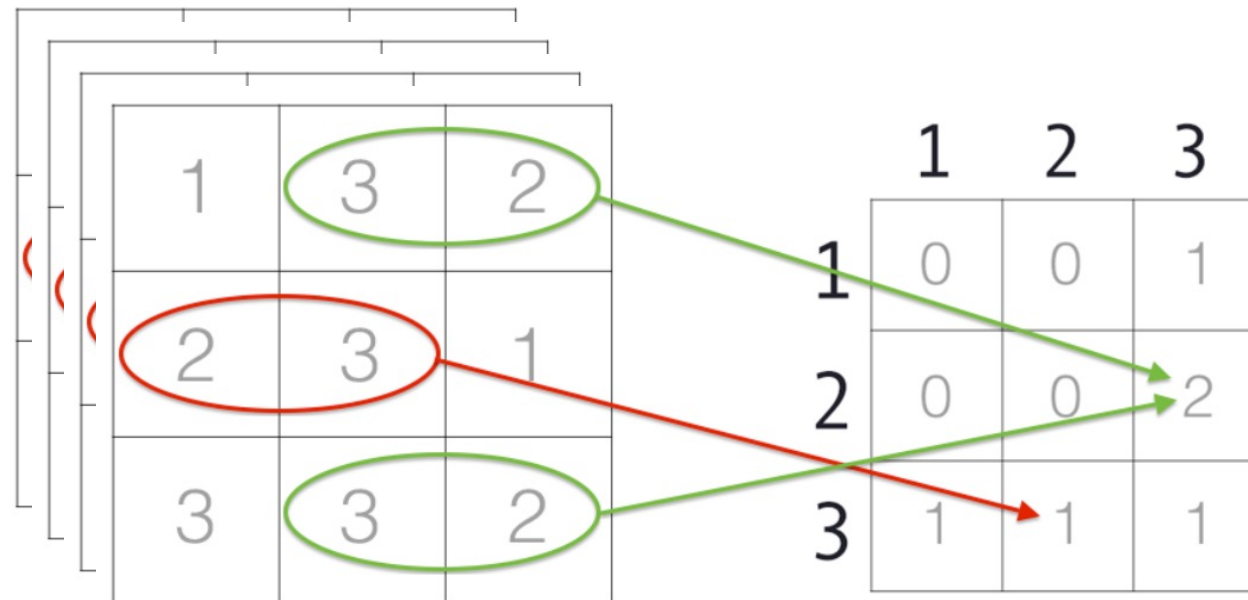


# Gray-Level Co-occurrence Matrix (GLCM)

- Four directions of adjacency:



- Construct GLCMs for each direction





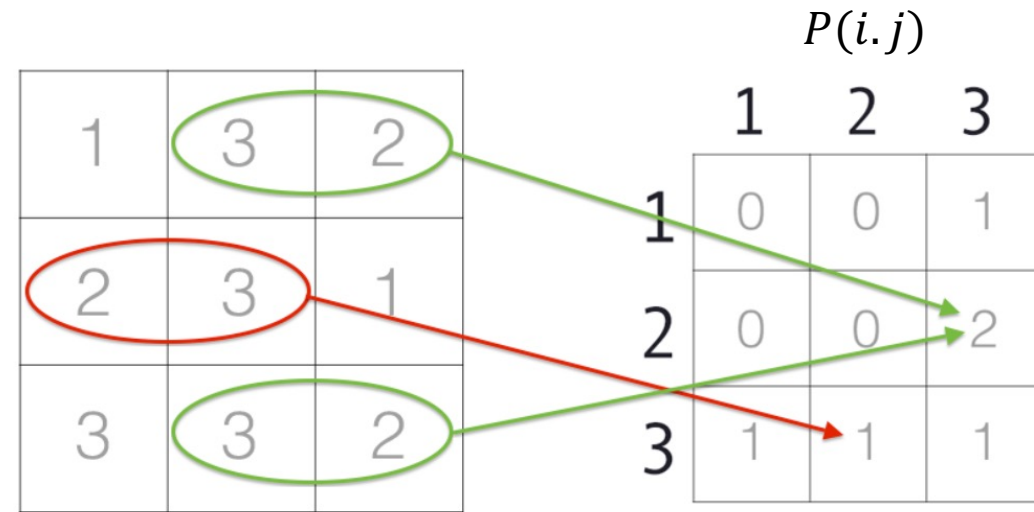
# Haralick Texture Features

- Notation

- $R$ : The sum of all entries in a GLCM
- $p(i, j)$ :  $(i, j)^{\text{th}}$  entry in a normalized GLCM
  - $p(i, j) = P(i, j)/R$

- Texture features for each GLCM

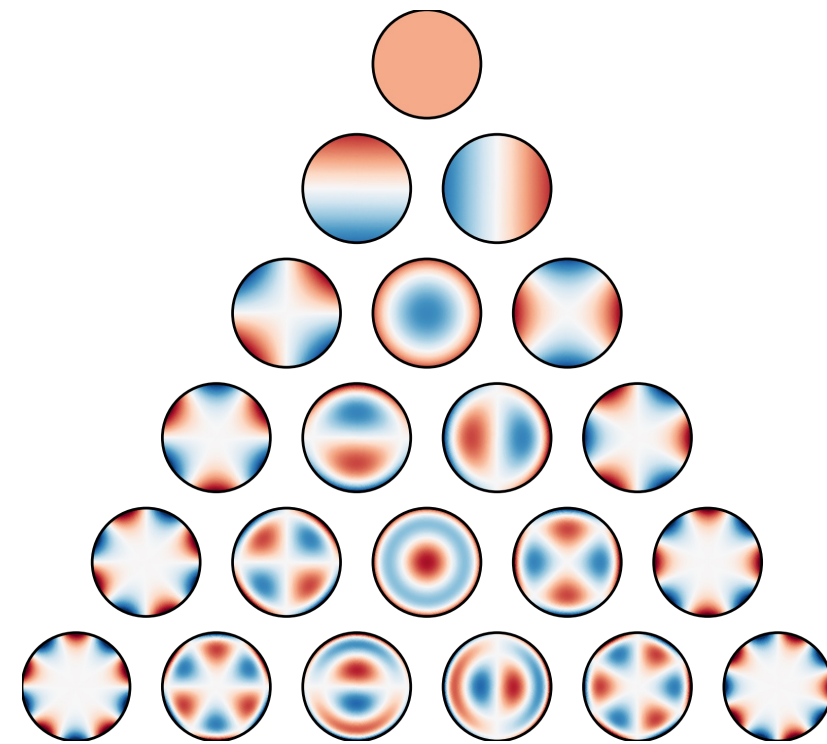
- Angular second moment
  - $\sum_i \sum_j (p(i, j))^2$
- Sum of squares
  - $\sum_i \sum_j (i - \mu)^2 p(i, j)$
- Inverse difference moment
  - $\sum_i \sum_j \frac{1}{1+(i-j)^2} p(i, j)$
- ... and 10 other features



- Finally, concatenate the features from each of the 4 GLCMs
  - Or simply take their average

# Zernike Shape Features

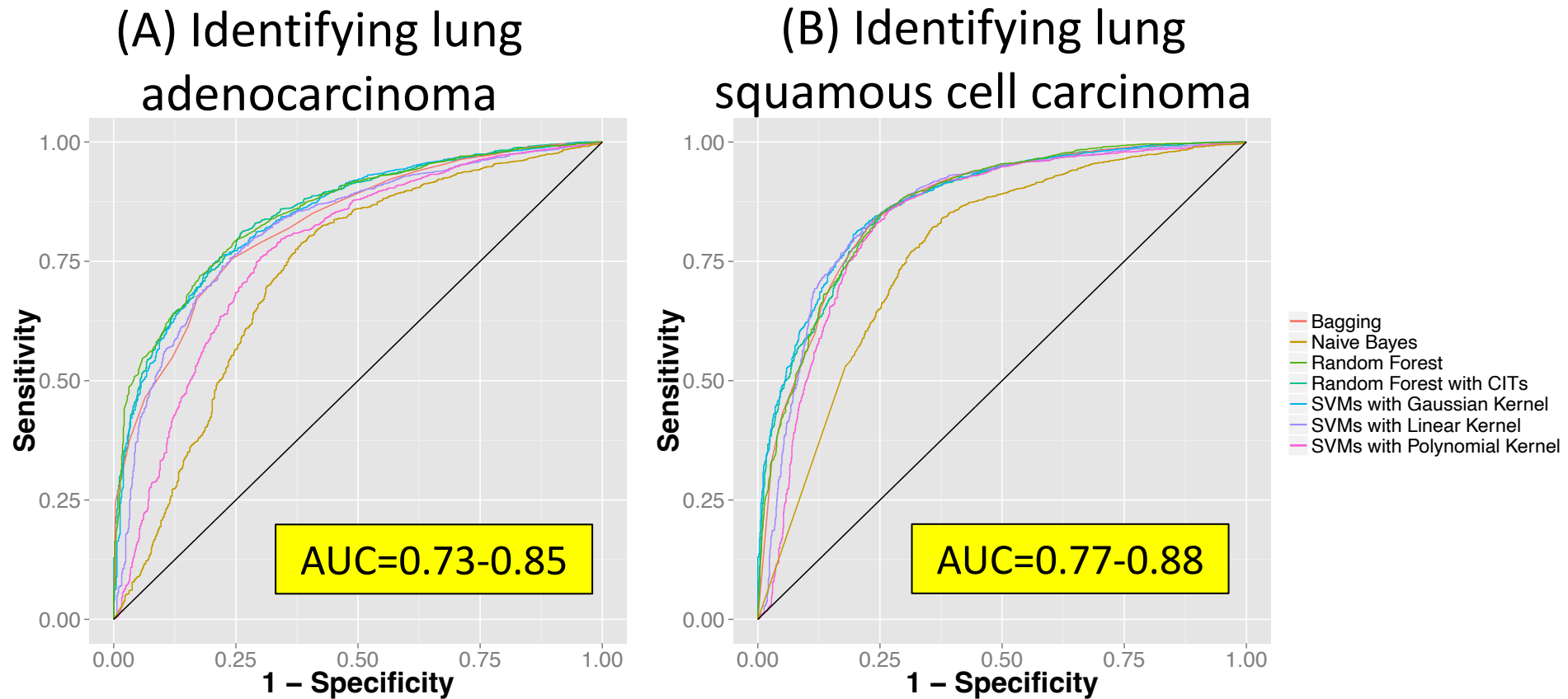
- Characterize the distribution of intensity across the object
  - Zernike polynomials: a sequence of polynomials that are orthogonal on the unit disk (a set of points whose distance from a given point  $P$  is less than 1)
  - We can decompose a region of interest into a weighted sum of a sequence of Zernike polynomials
- An example
  - Zernike (1,1): a prototype with a low intensity on one side and high on the other
- Note: these features are rotationally invariant



# Clinical Applications

- Dermatology
  - Melanoma screening
- Ophthalmology
  - Diabetic retinopathy assessment using fundus photographs
- Radiology
  - Automated region of interest identification
- Pathology
  - Cancer diagnosis and subtyping

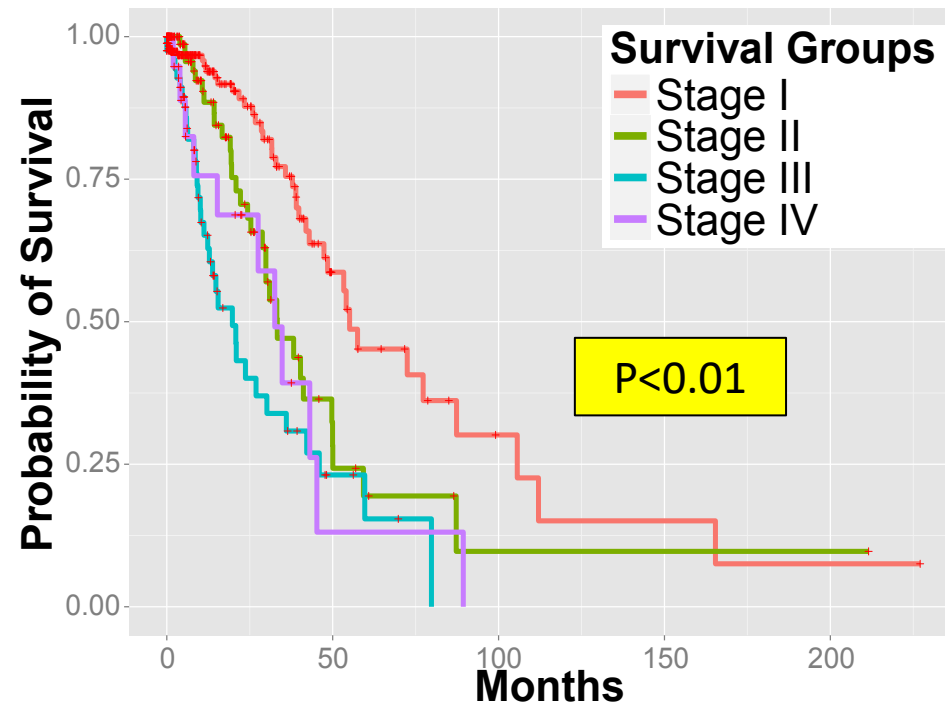
# Example: Human Interpretable Pathology Features Diagnose Cancers



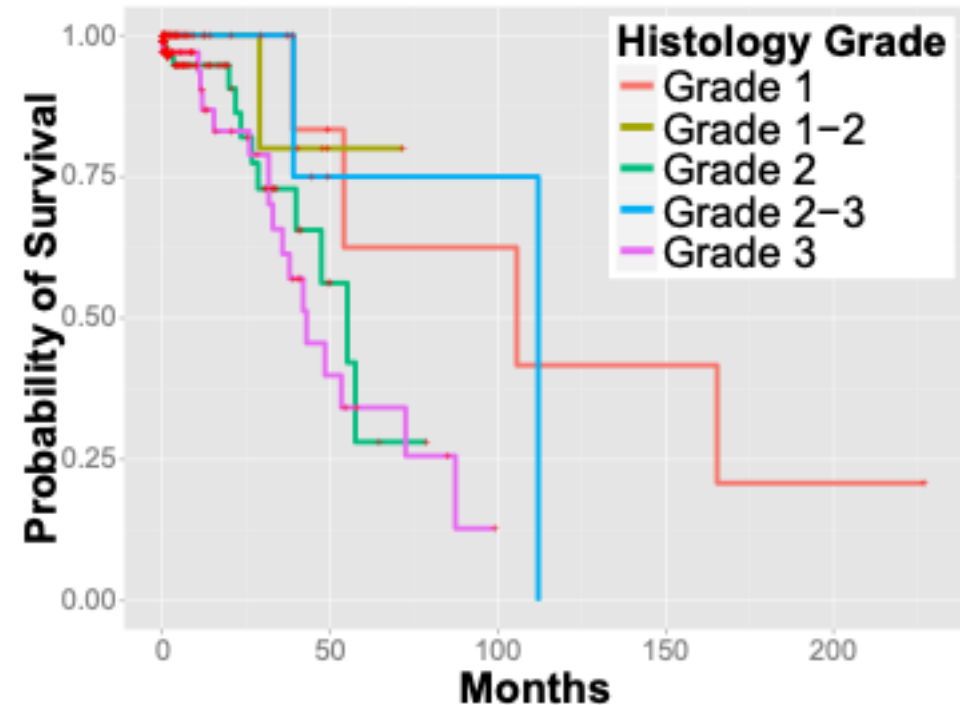
**Top features:** Textures (pixel correlations, intensity variance) of the nuclei

# Clinical Baseline: Stage and Grade are Often Insufficient to Predict Patient Survival

(A) Survival stratified by **stage**



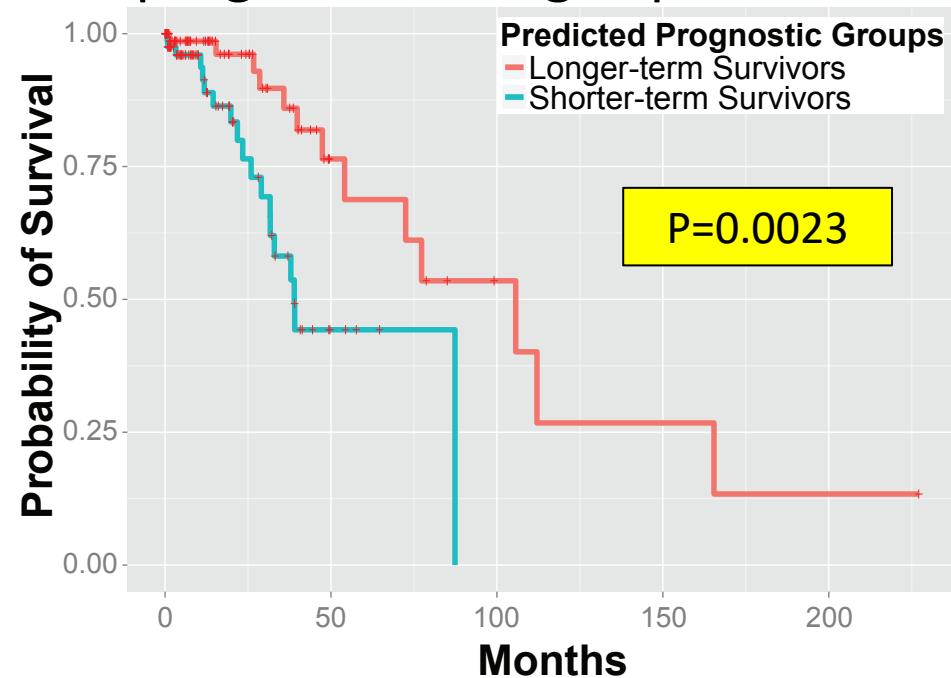
(B) Stage I patient survival stratified by **grade**



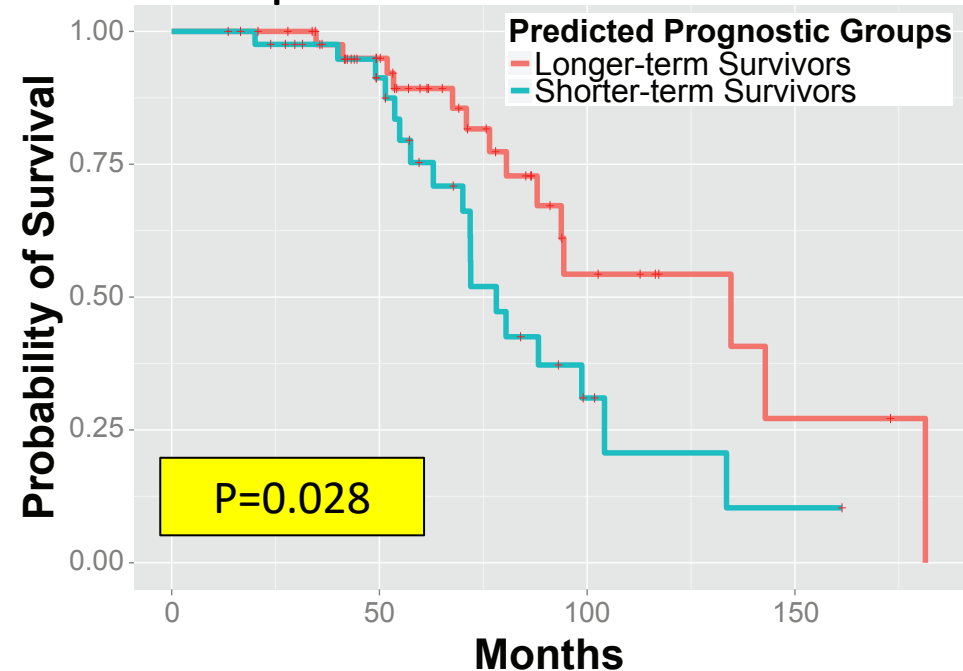
Dissimilar survival outcomes among stage I patients  
Pathology grade did NOT significantly correlate with survival

# Image Features Predicted Prognosis in Stage I Lung Adenocarcinoma Patients

(A) Image features predicted the prognosis of stage I patients



(B) Validated in an independent validation set



Quantitative features predicted survival, validated in TMA

**Top features:** Zernike shape features of the nuclei

# Method 2: Deep Learning Approaches for Medical Image Analyses

- Reusing the neural network architectures for nature image analyses + fine-tuning
  - Convolutional neural networks
    - AlexNet, VGGNet, ResNet, DenseNet, EfficientNet
  - Vision transformers
- Designing specific models for the tasks/image types of interest
  - Automated hyperparameter search for model optimization
  - Pathology/radiology foundation models

# Foundation Models

- Machine learning models trained on vast datasets and can be applied across a wide range of use cases
- Examples of foundation models:
  - GPT series
  - BERT
  - DALL-E (image generation)

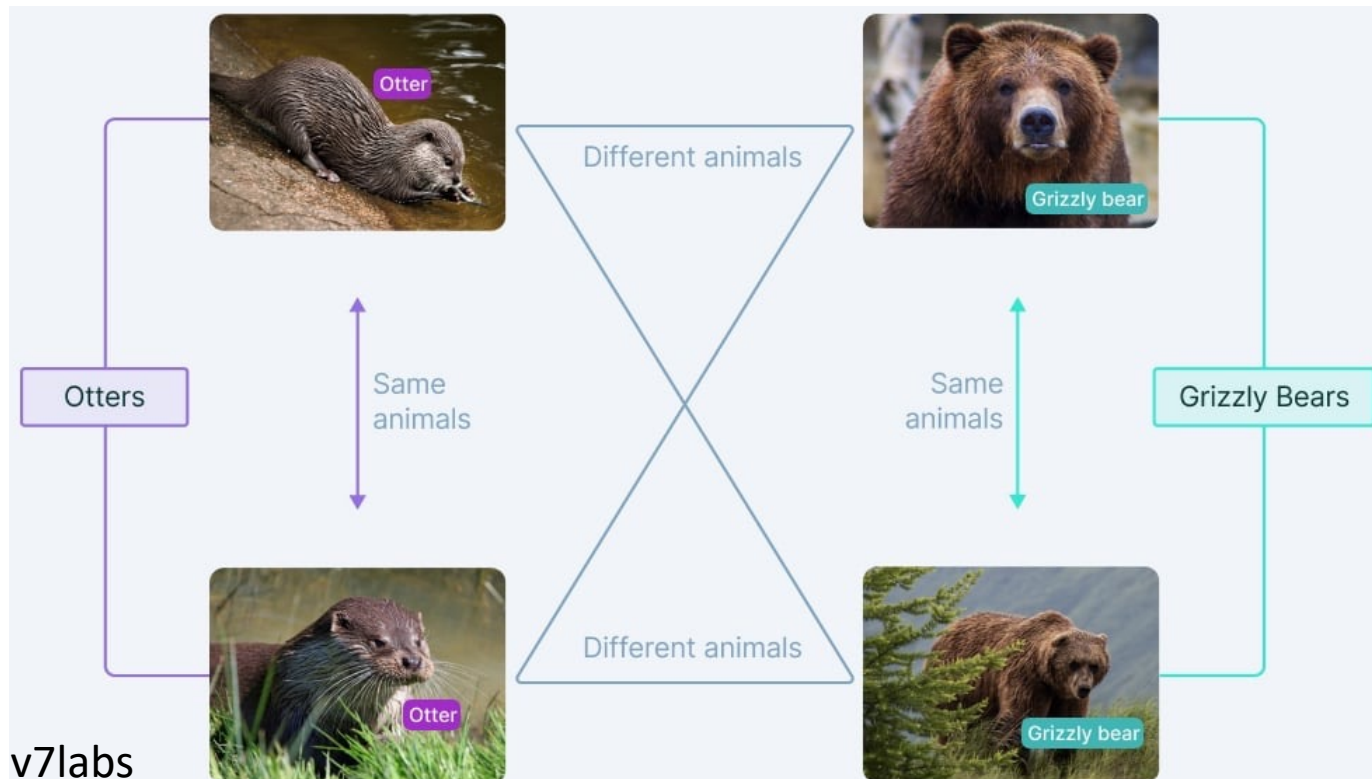


# Early Foundation Models for Pathology Imaging

- Vision-focused: CTransPath
  - A transformer-based feature extractor for pathology images
- Vision-language: Pathology language-image pretraining (PLIP)
  - A multimodal model trained with pathology images and natural language descriptions
- Other tile-level pathology foundation models
  - Lunit, Phikon, UNI, Virchow, etc.

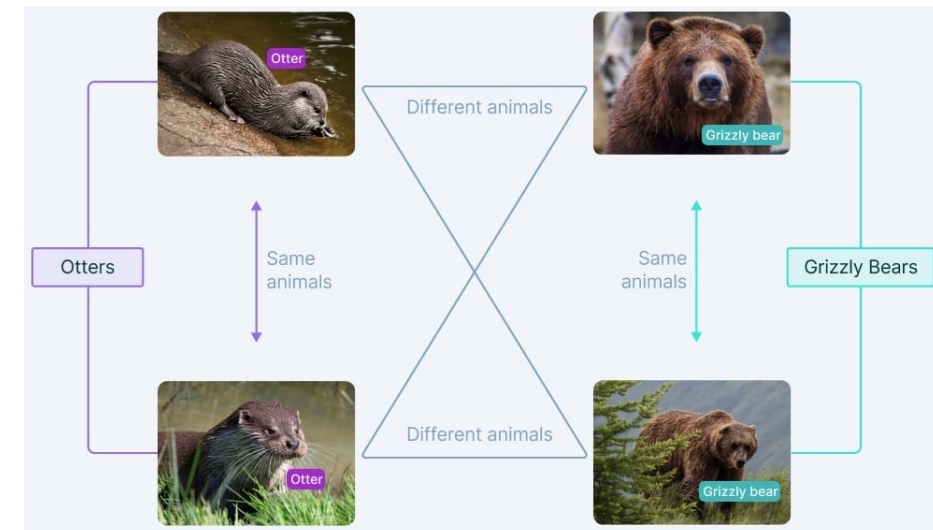
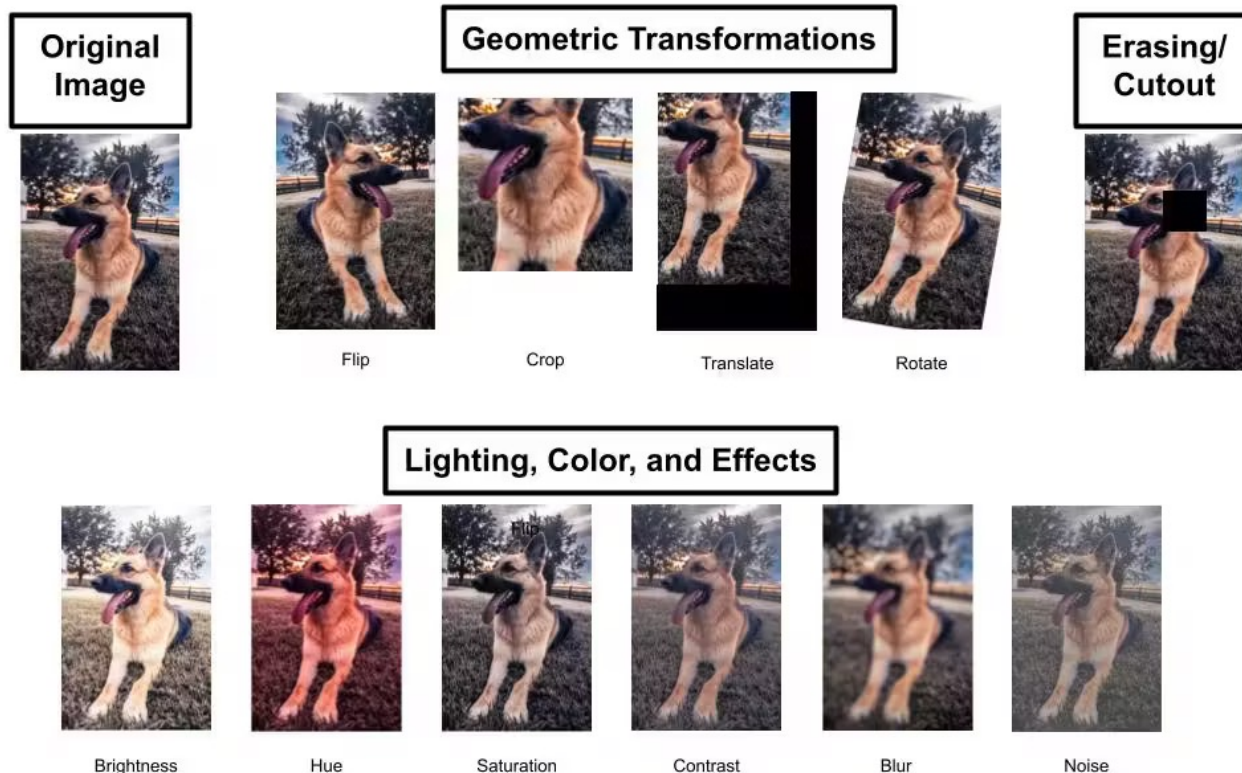
# A Frequently-Employed Module in Image Foundation Models: **Contrastive Learning**

- Goal: Enhances the model performance by
  - Maximizing the differences between samples of different categories
  - Minimizing the differences between samples of the same category



# Self-Supervised Contrastive Learning

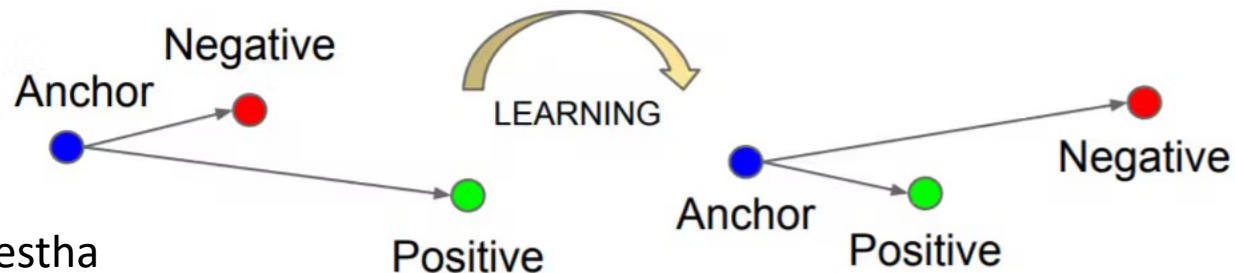
- What can we do if we don't have a lot of labeled data?
  - Use augmented data as the positive instances!



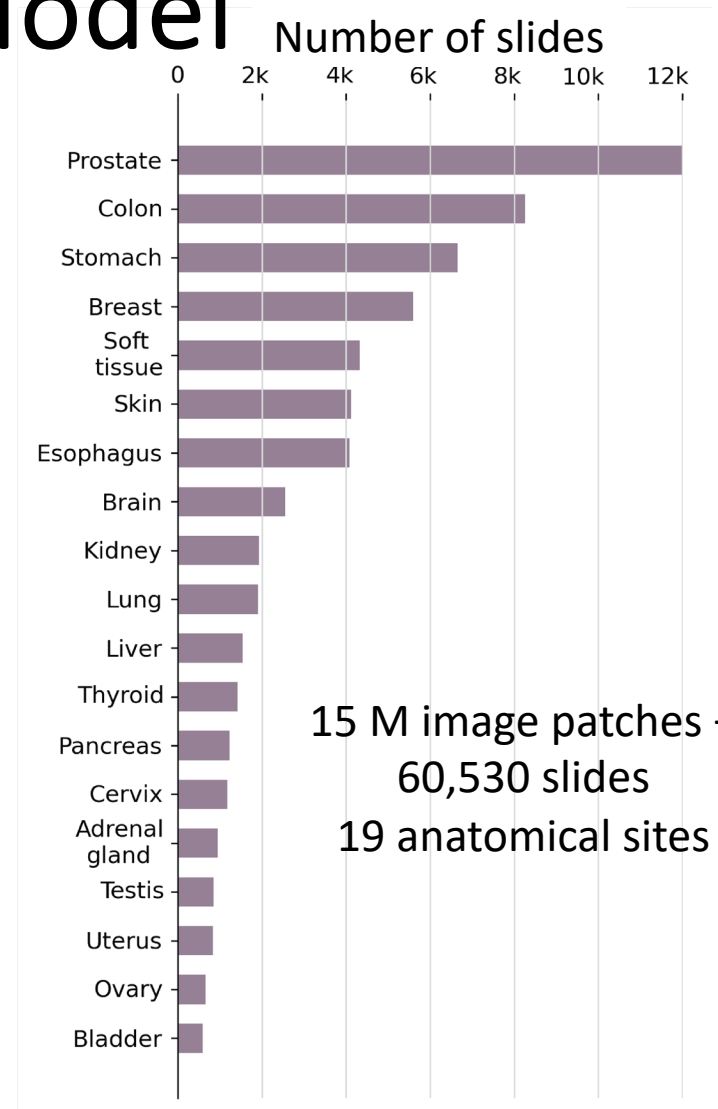
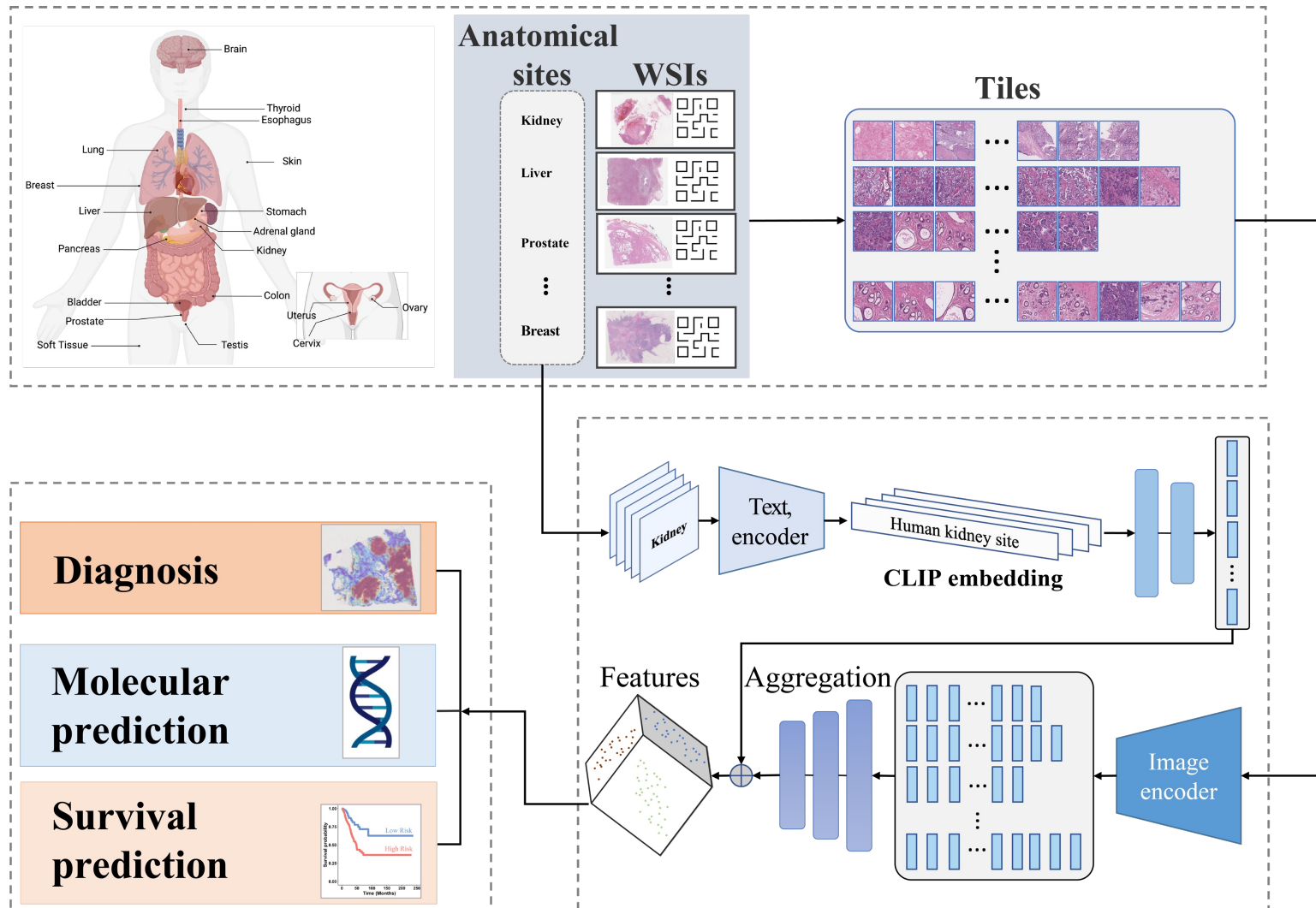
# Loss Functions for Contrastive Learning

- Contrastive loss
  - Maximize the agreement between positive pairs (instances from the same category) in the embedding space
  - Minimize the agreement between negative pairs (instances from different categories) in the embedding space
- Triplet loss
  - Triplets of instances: an anchor instance, a positive sample (similar to the anchor), and a negative sample (dissimilar to the anchor)
  - Goal:  $\text{Distance}(\text{anchor}, \text{positive sample}) < \text{Distance}(\text{anchor}, \text{negative sample}) + \varepsilon$

• ...

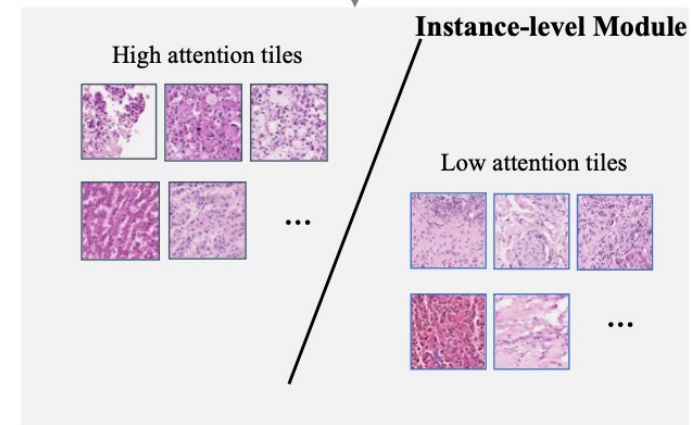
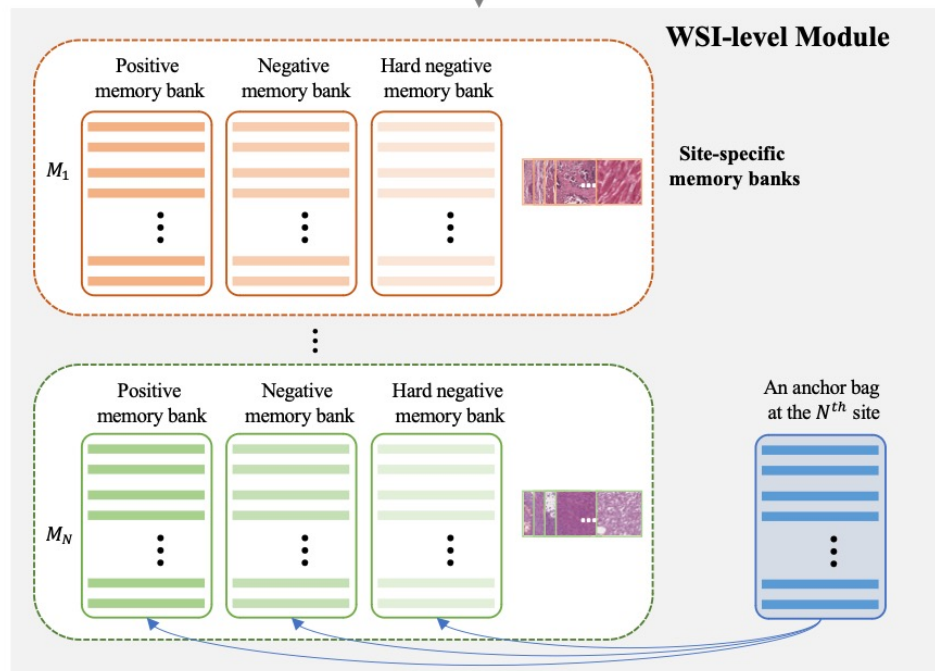
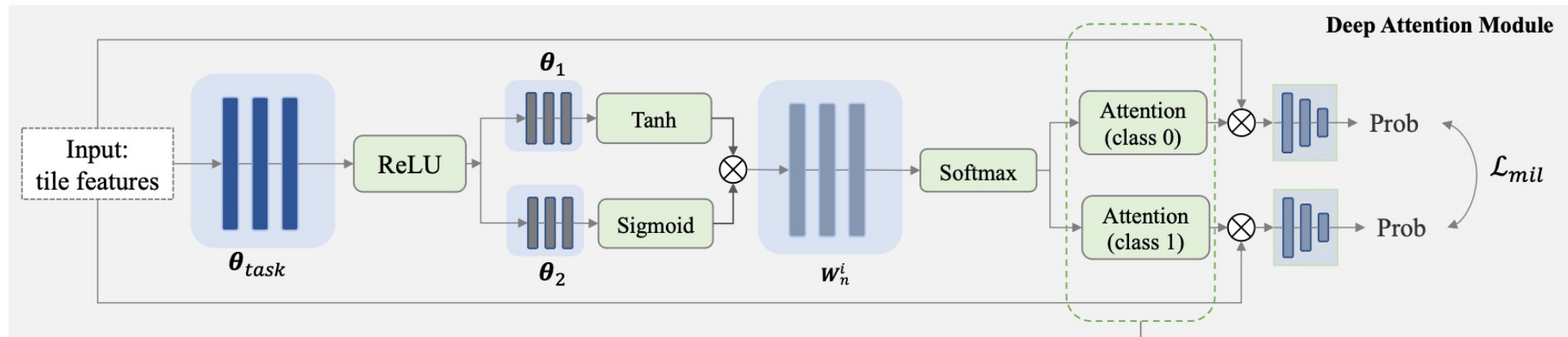


# Example: Clinical Histopathology Imaging Evaluation Foundation (CHIEF) Model



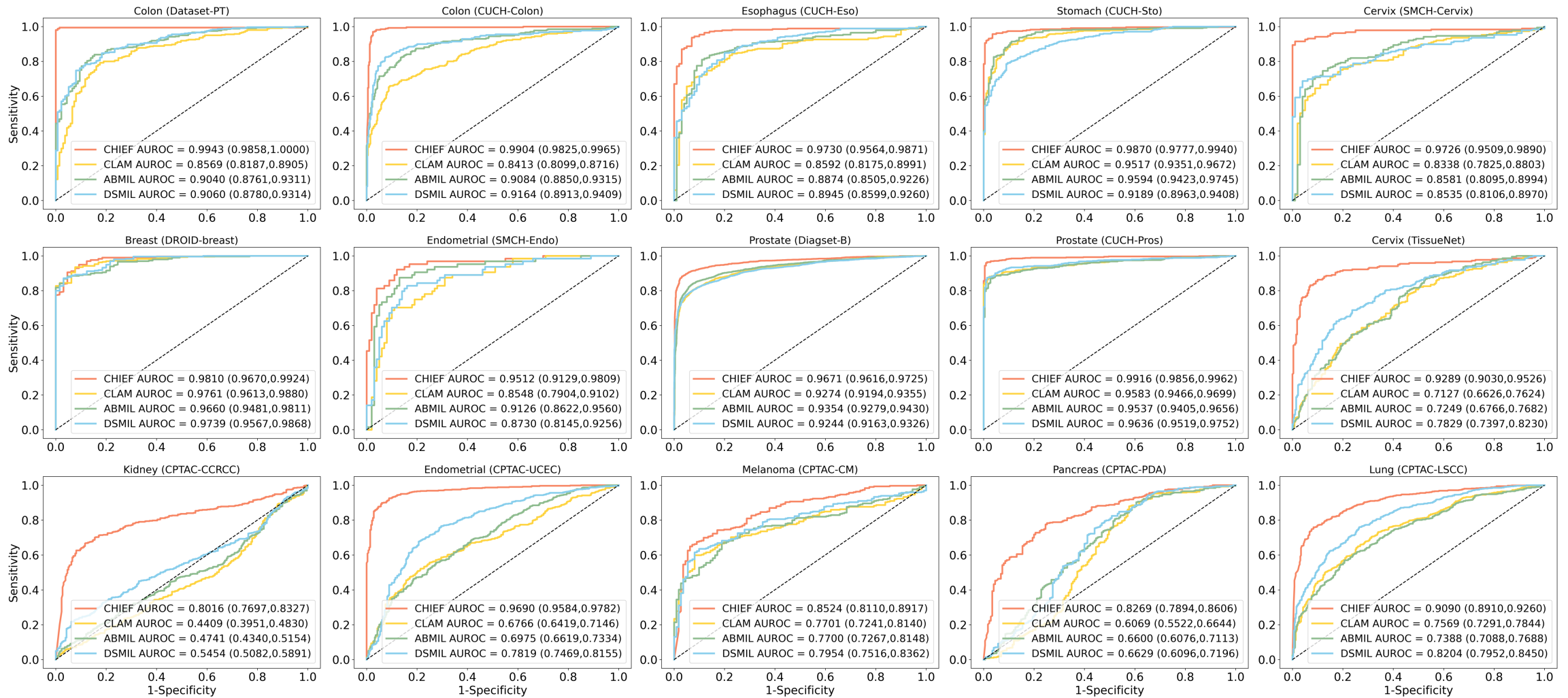
15 M image patches +  
60,530 slides  
19 anatomical sites

# CHIEF's Image Feature Aggregation Framework

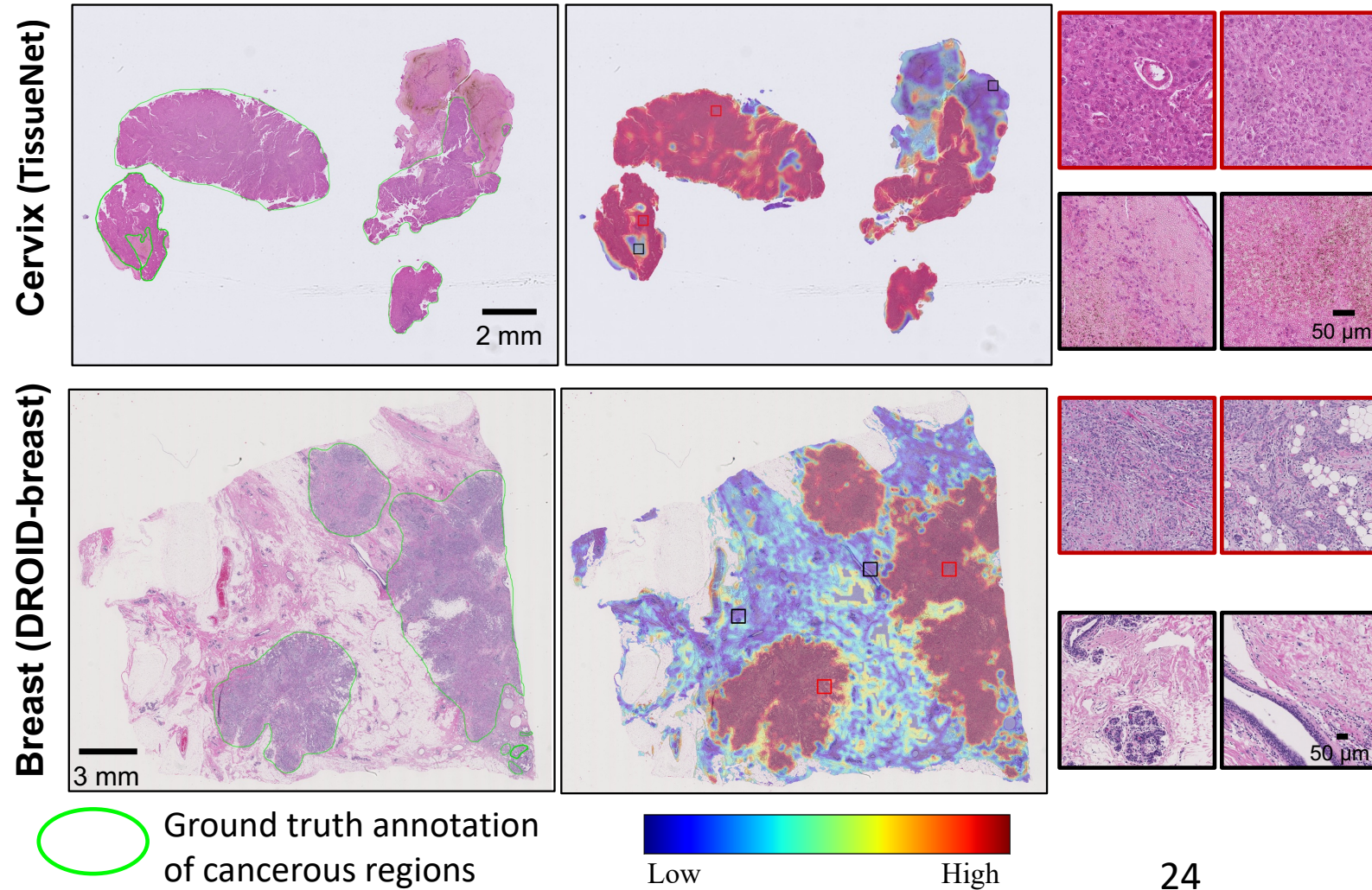


$$\mathcal{L}_{total} = \mathcal{L}_{mil} + \lambda_1 * \mathcal{L}_{instance-level} + \lambda_2 * \mathcal{L}_{WSI-level}$$

# Cancer Cell Detection

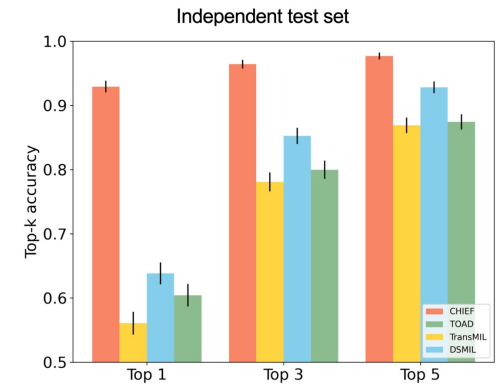
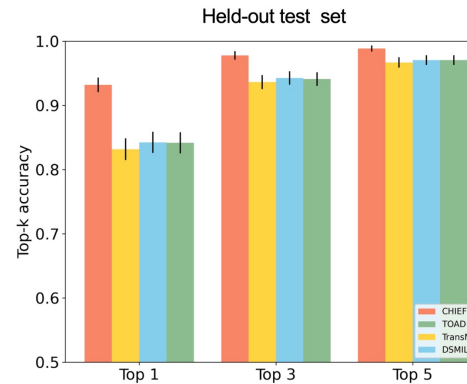
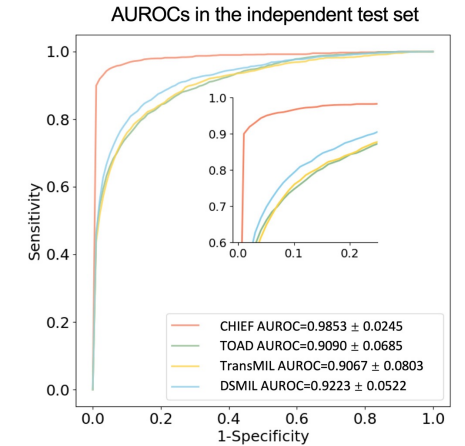
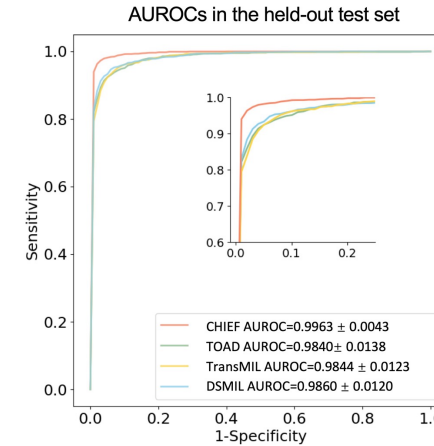
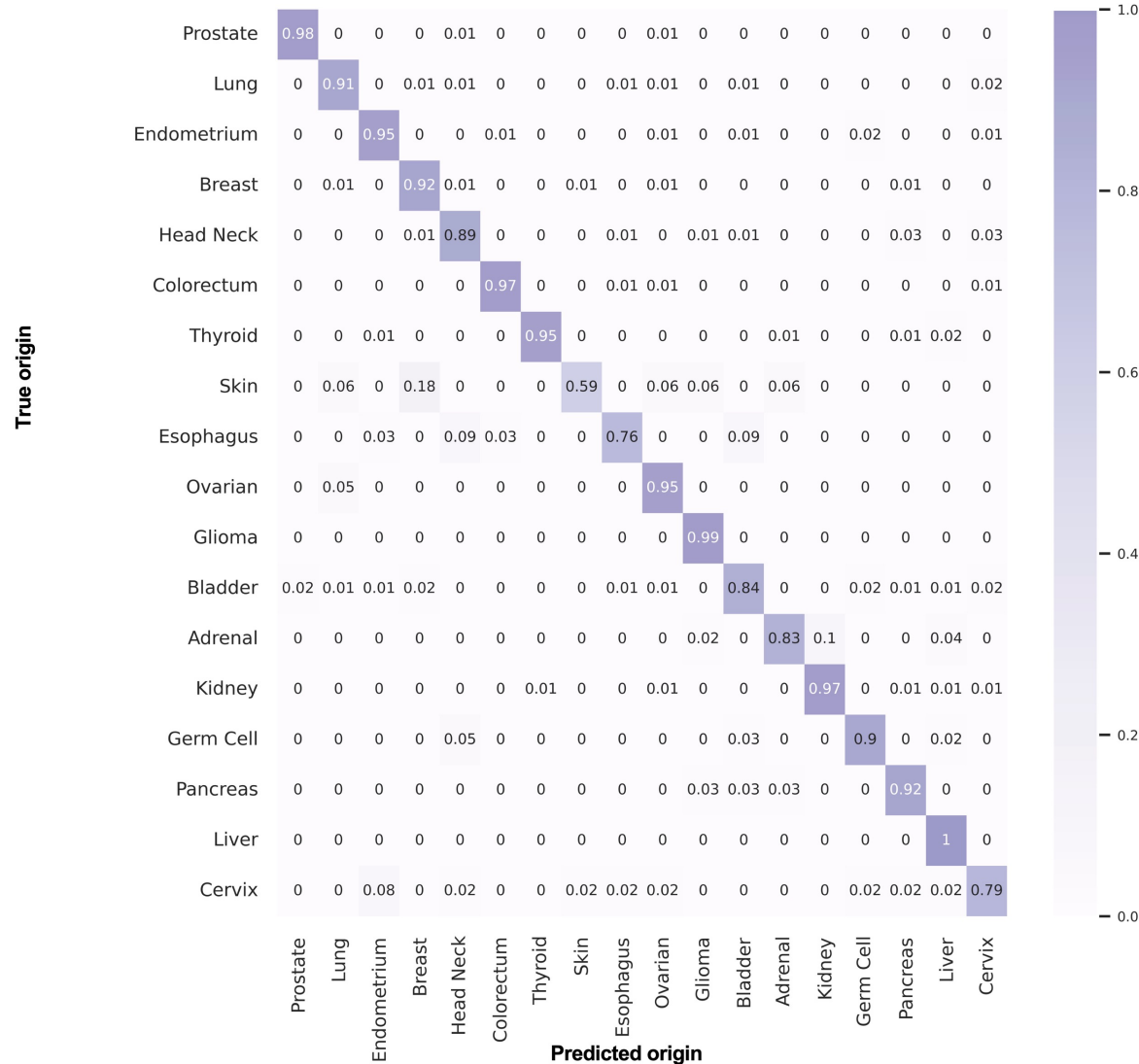


# Weakly-Supervised Foundation Models Identified Cancer Cells Without Pixel-Level Segmentation

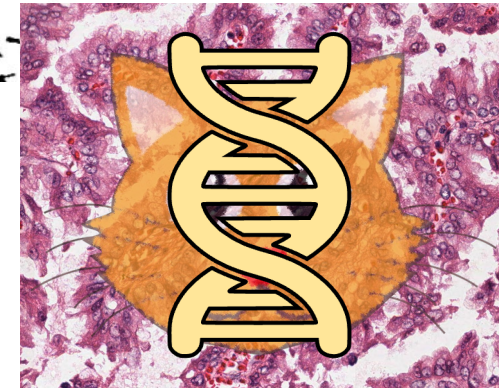
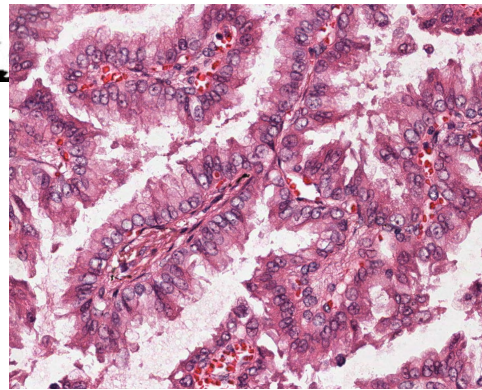




# Cancer Origin Identification

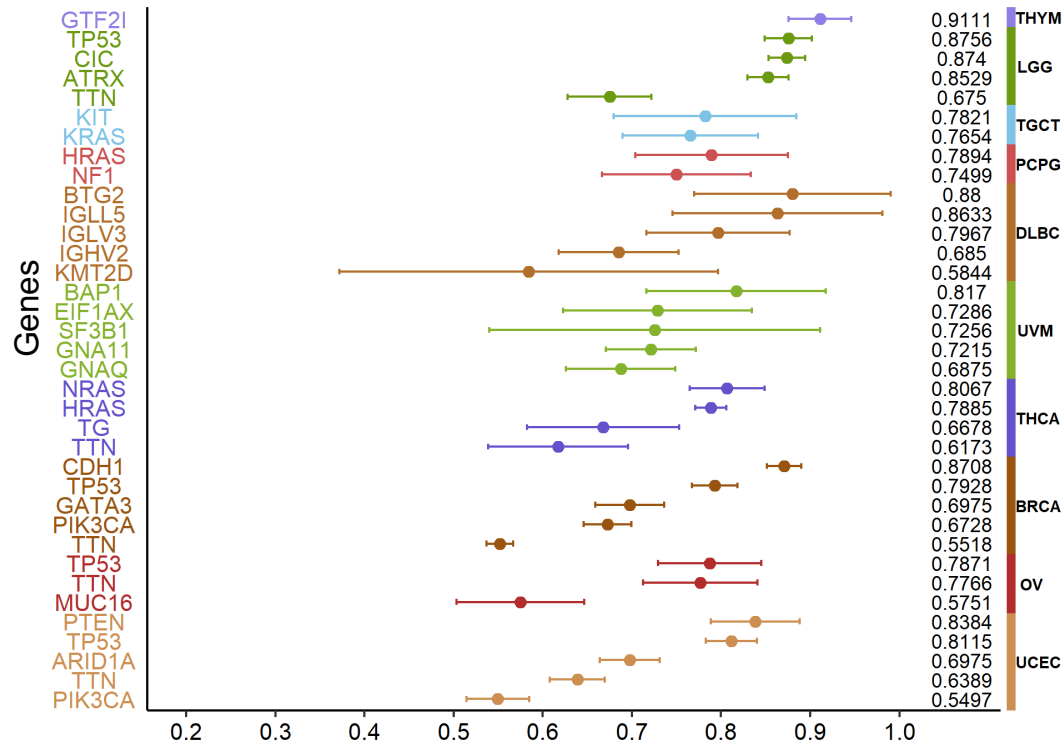


- Is there **hidden** information in histopathology images?
  - e.g., genomic variations?

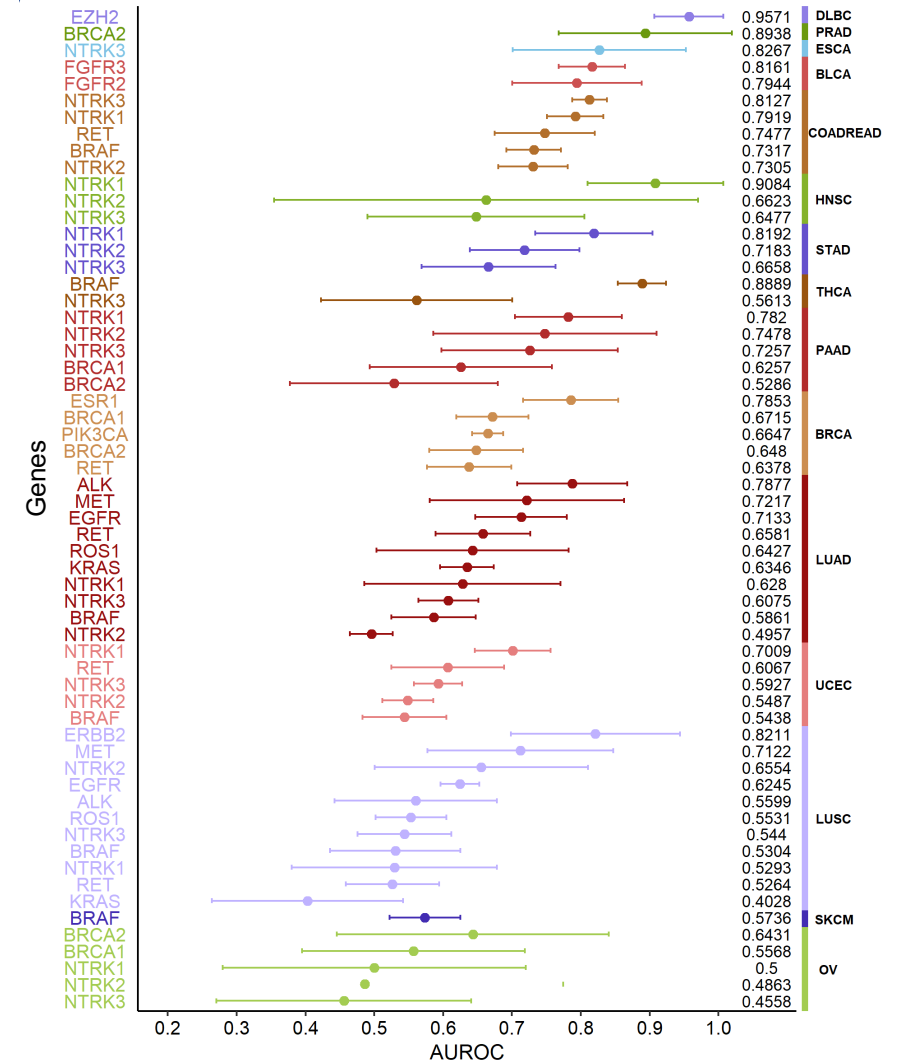


# Predicting the Mutation Statuses of Clinically Important Genes

Prevalent mutations

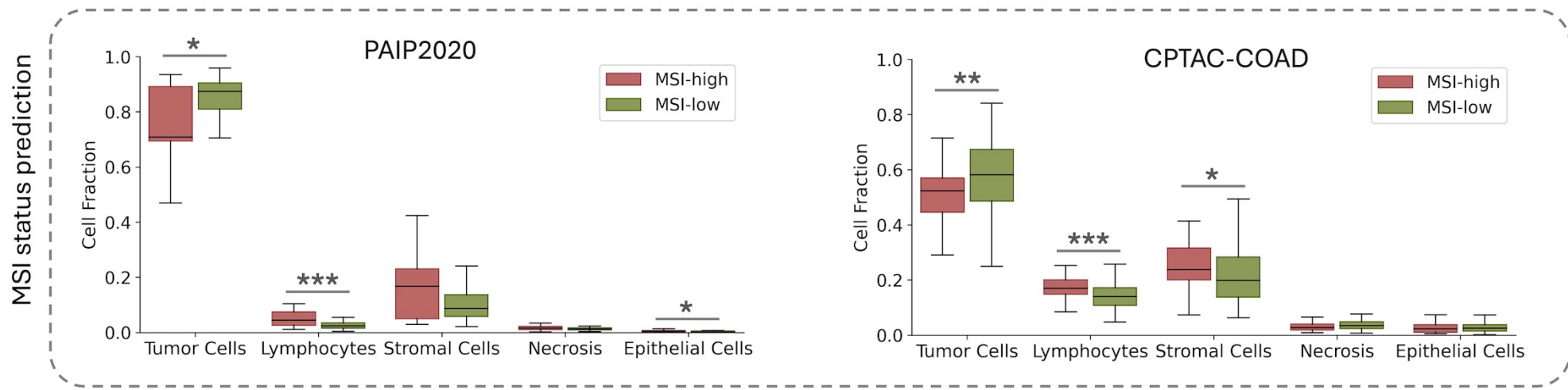
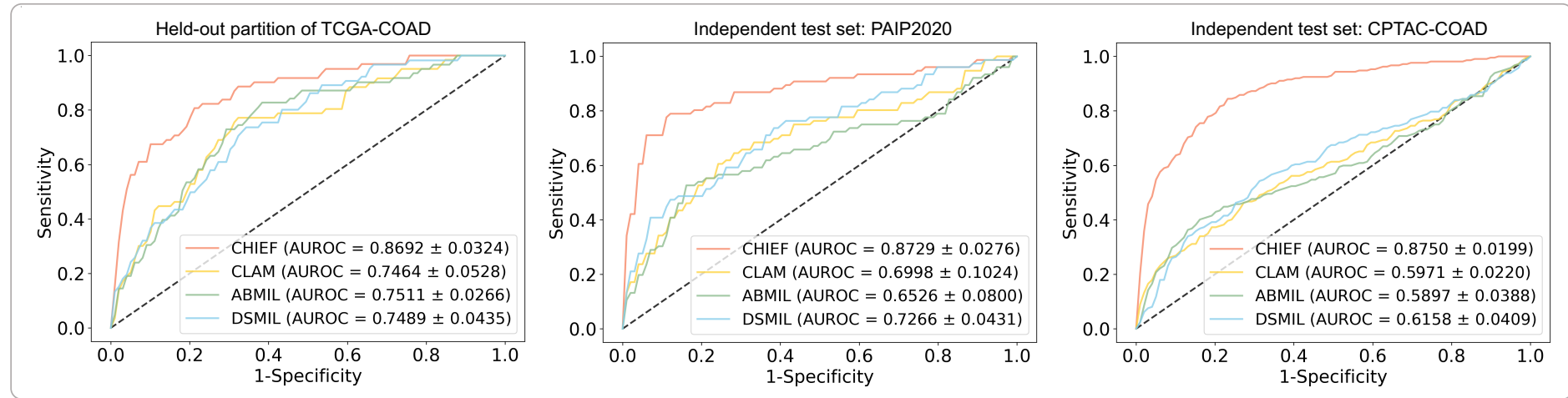


Mutations related to targeted therapies



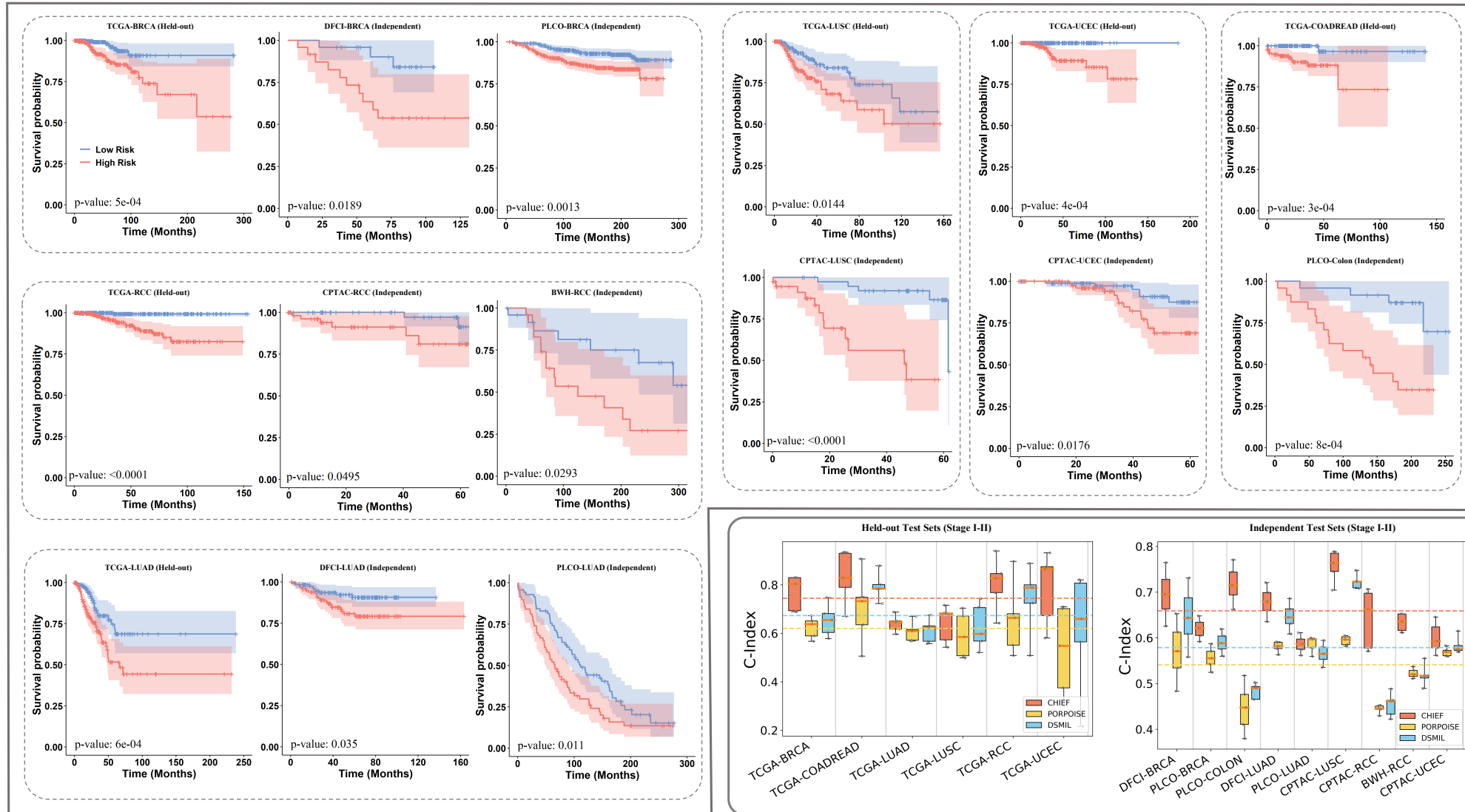
# Identifying Molecular Profiles Related to Responses to Immune Checkpoint Blockade

Microsatellite instability (MSI) prediction for colorectal cancers:

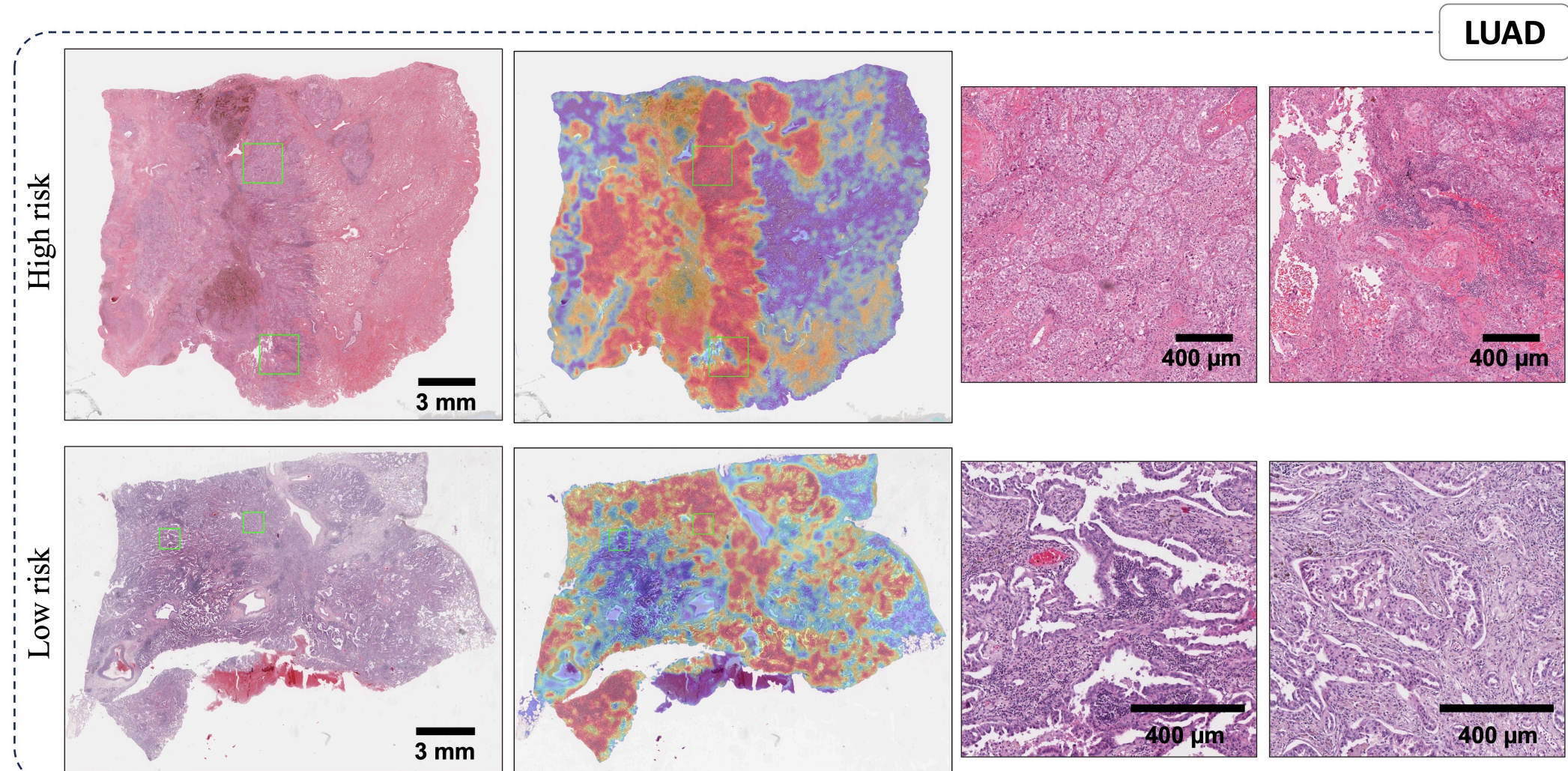


\* P-value < 0.05  
 \*\* P-value < 0.01  
 \*\*\* P-value < 0.001

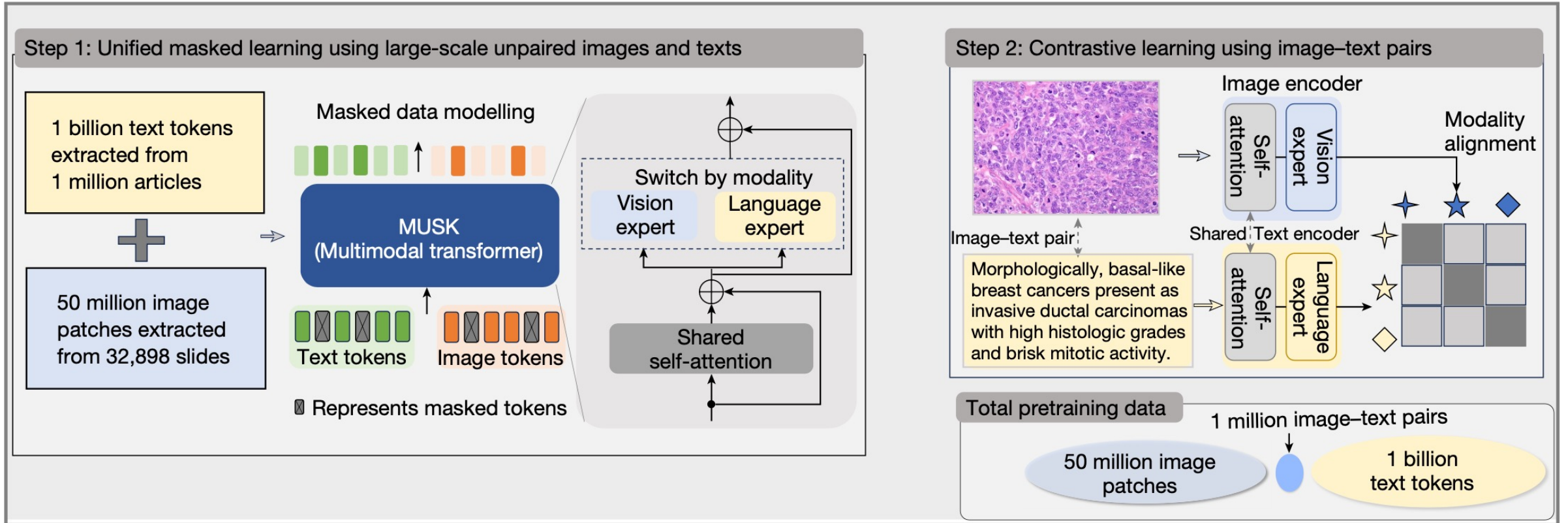
# CHIEF Predicts Cancer Patients' Survival Outcomes



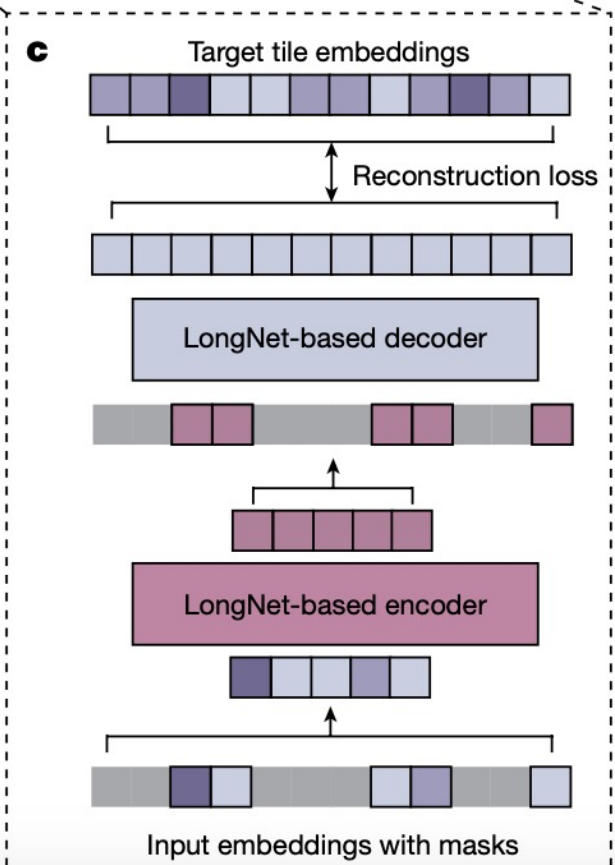
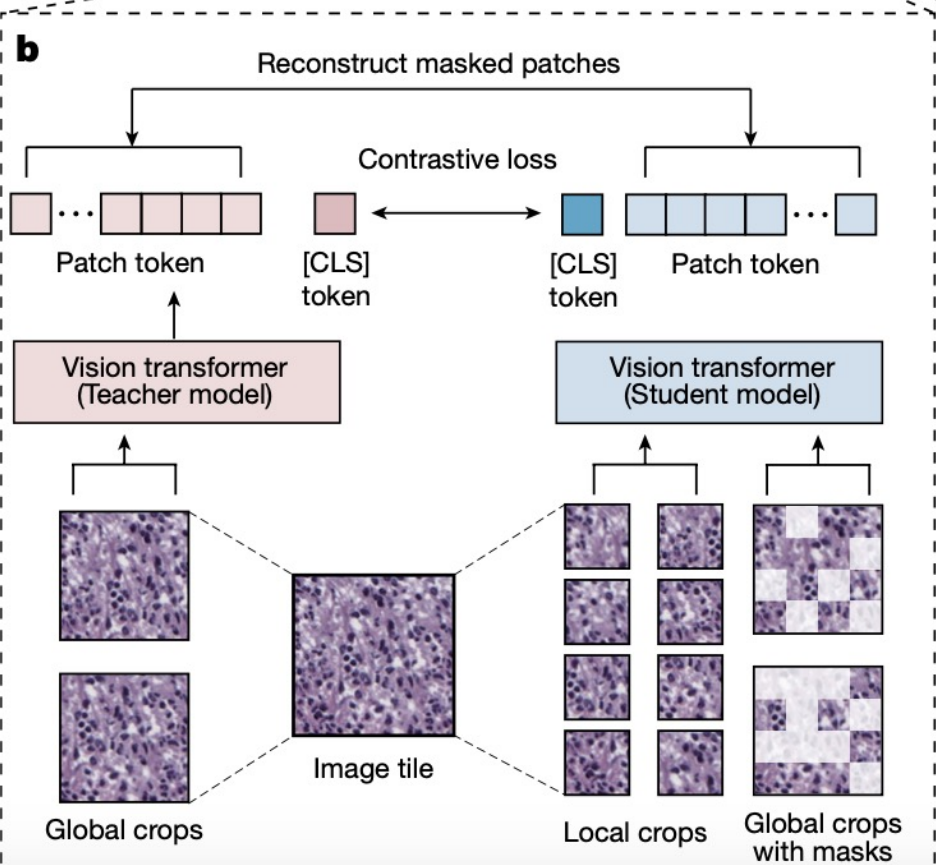
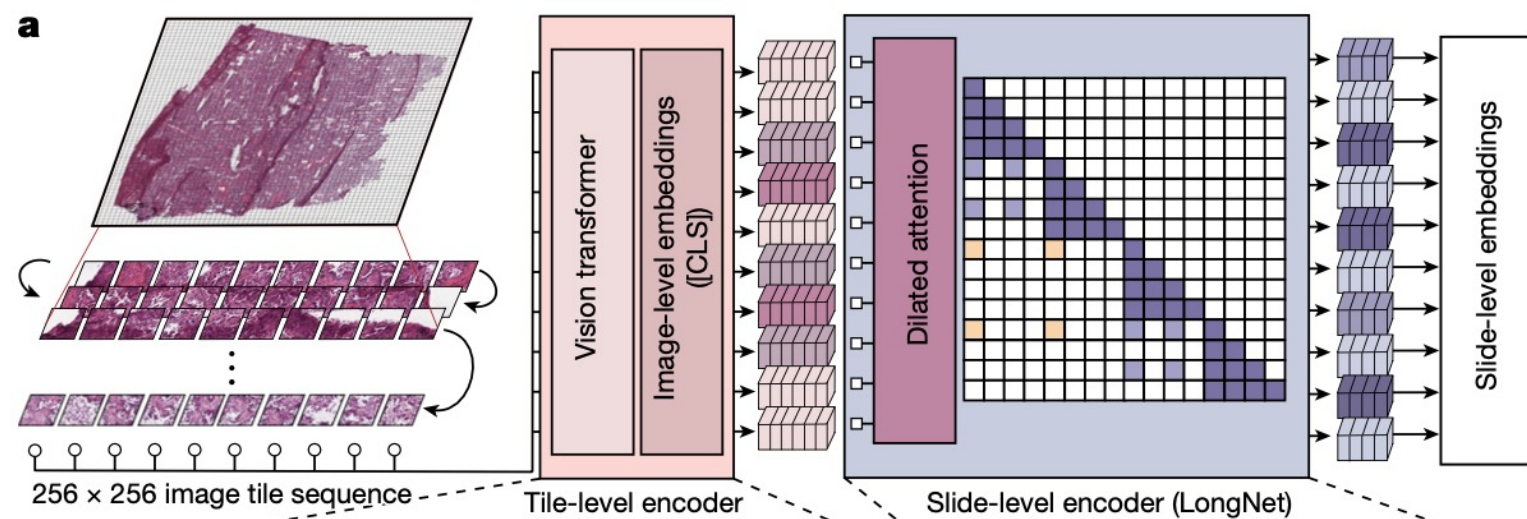
# Tumor Microenvironment Patterns Associated with Survival Outcomes



# Multimodal transformer with Unified maSKed modeling (MUSK)



# Prov-GigaPath



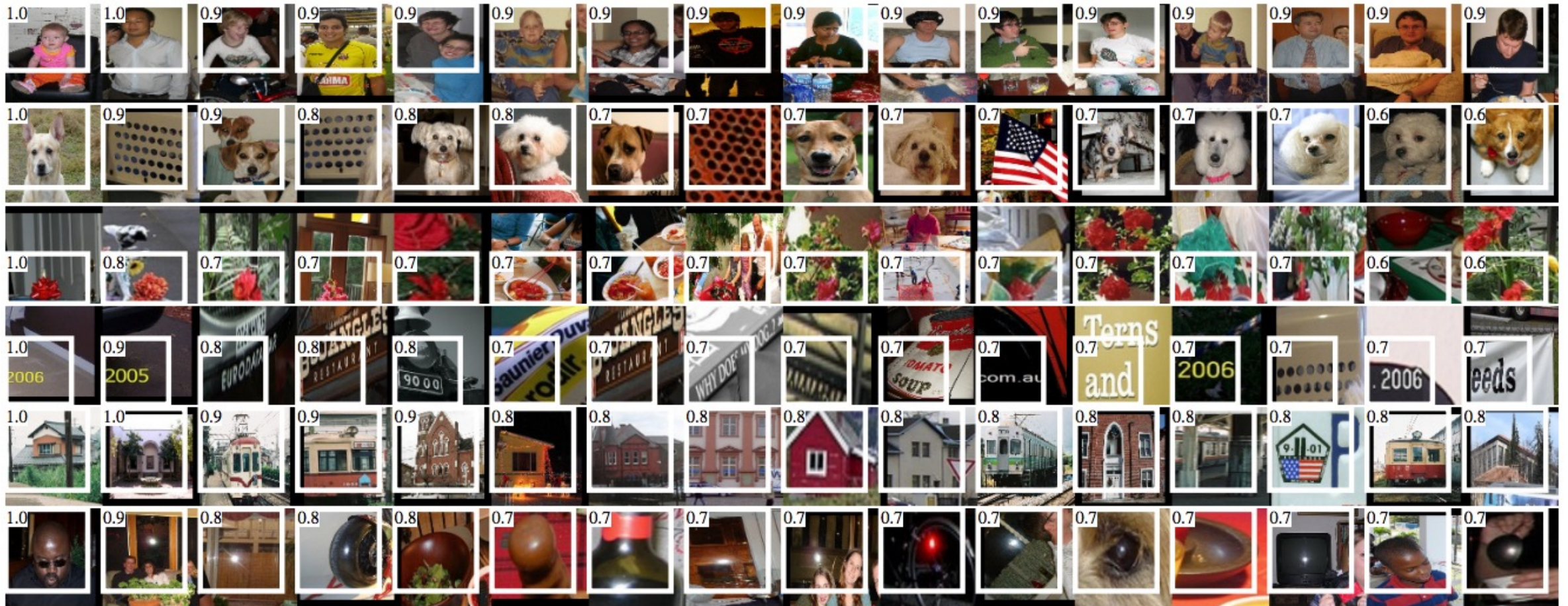


# Interpreting Deep Learning Models

# Approaches for Model Interpretation

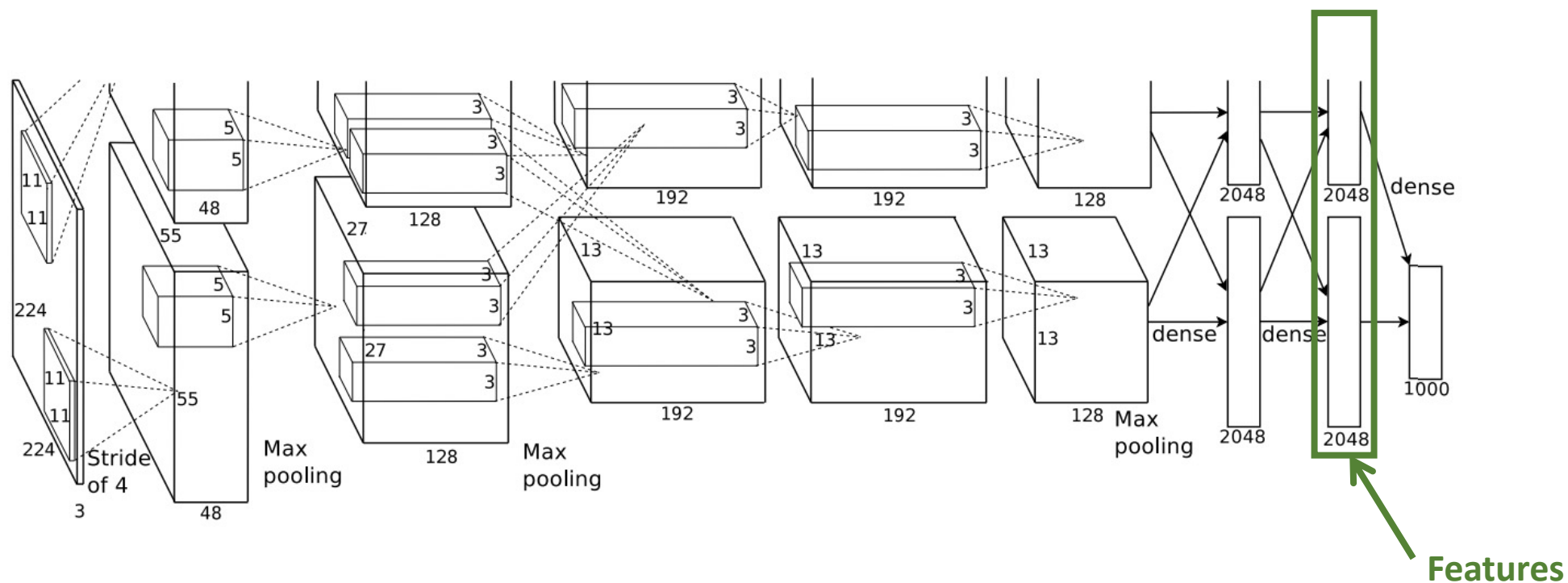
- Visualize image patches that maximally activated neurons
- Visualize the “feature” space
- Visualize the convolution filters
- Occlusion
- Attention maps
- “Deconv”
- Optimize to image
- ...

# Method 1: Visualize Image Patches that Activate the Selected Neurons



# Method 2: Visualize the “Feature” Space

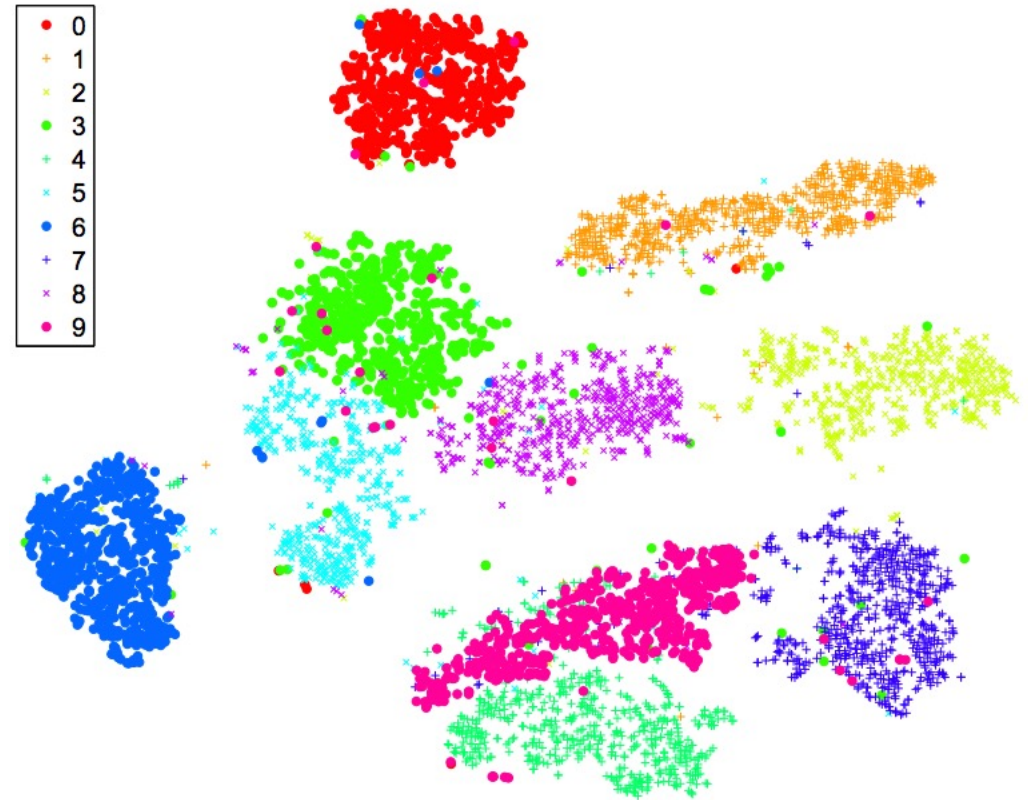
- Treat the values in the fully-connected layer as “features”



# Method 2: Visualize the “Feature” Space

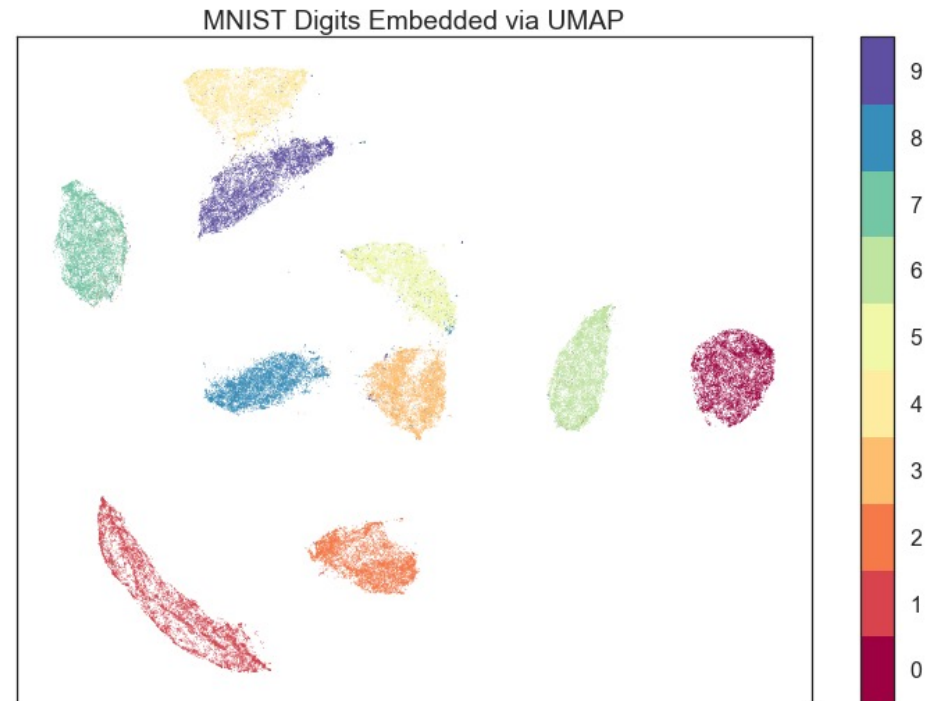
- Principal component analysis
  - Convert a set of features into a set of linearly uncorrelated variables
- t-SNE (t-distributed stochastic neighbor embedding)
  - Similar objects have a high probability of being picked as neighbors

t-SNE

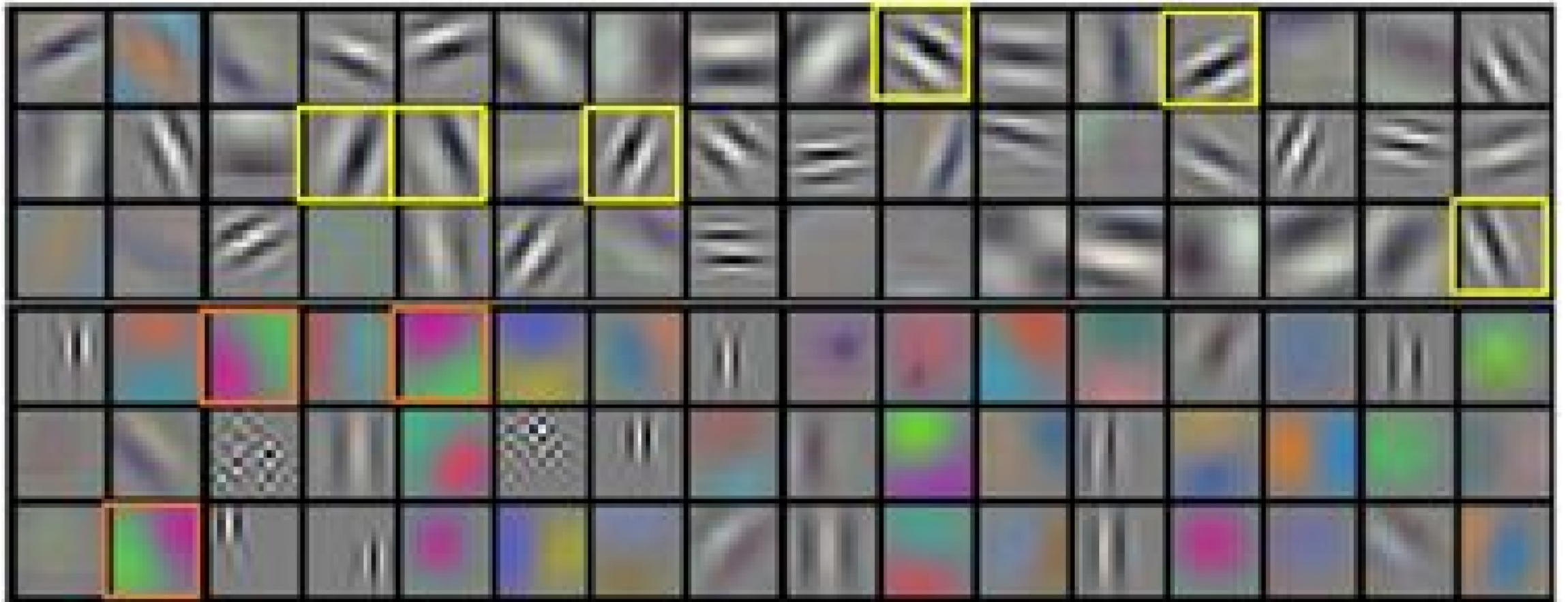


# Method 2: Visualize the “Feature” Space

- U-Map (Uniform Manifold Approximation and Projection)
  - Assumptions
    - The data is uniformly distributed on a Riemannian manifold
    - The Riemannian metric can be approximated as constant locally
    - The manifold is locally connected
  - Preserves more global structure
  - Faster than t-SNE

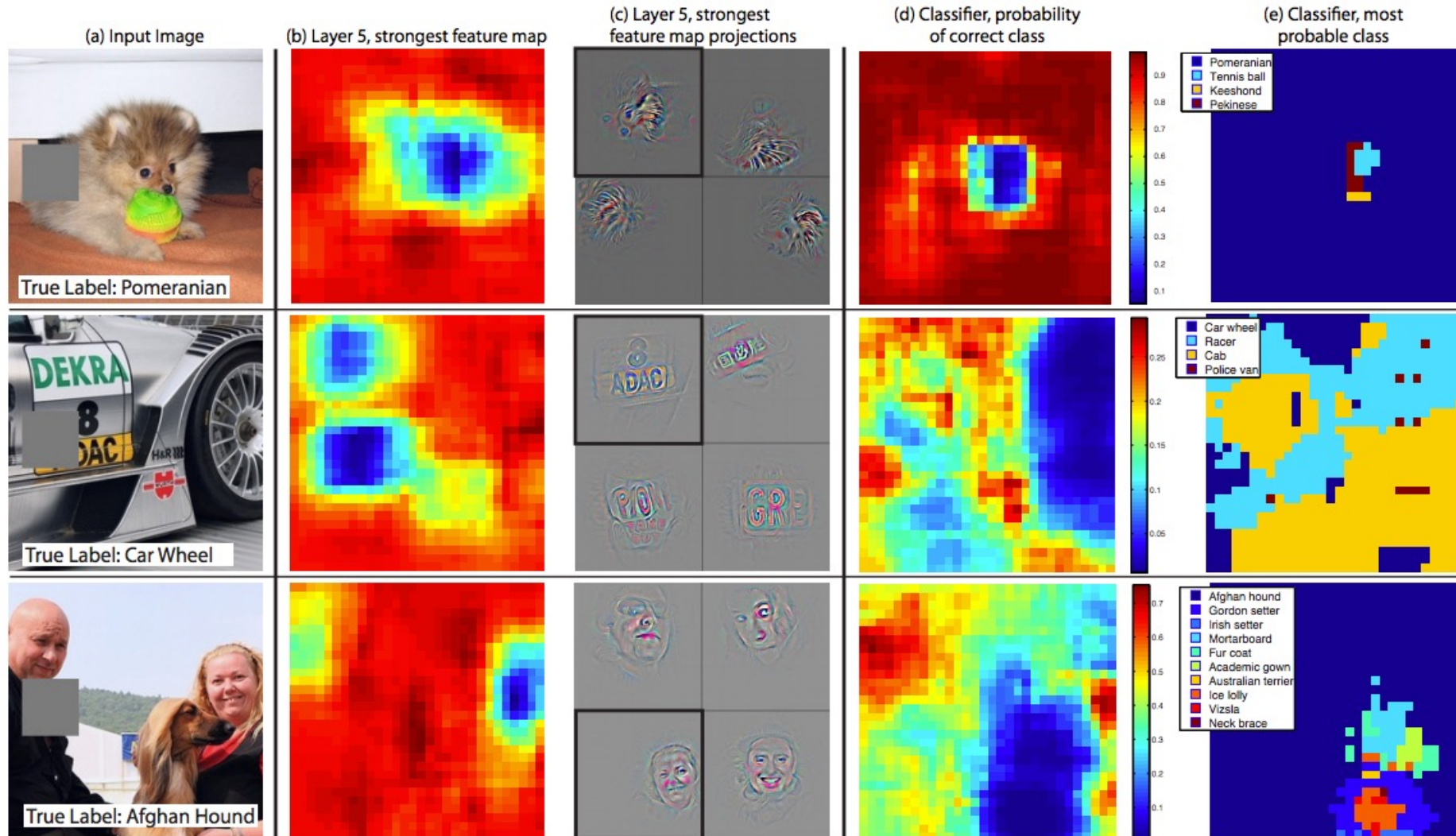


# Method 3: Visualize the Convolutional Filters



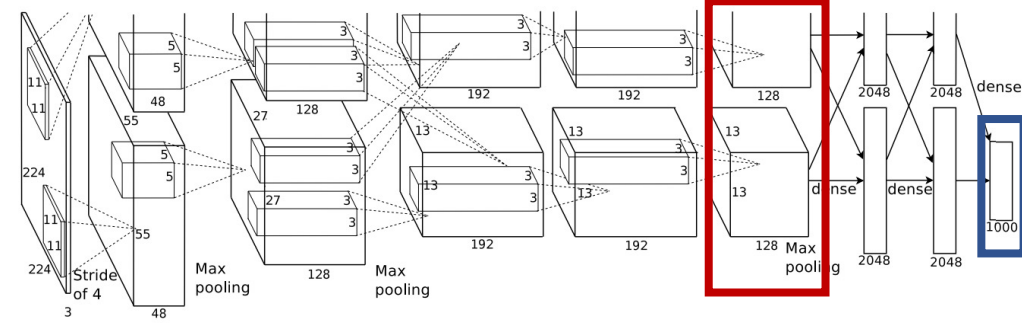
- Show the raw weights of the filters

# Method 4: Occlusion

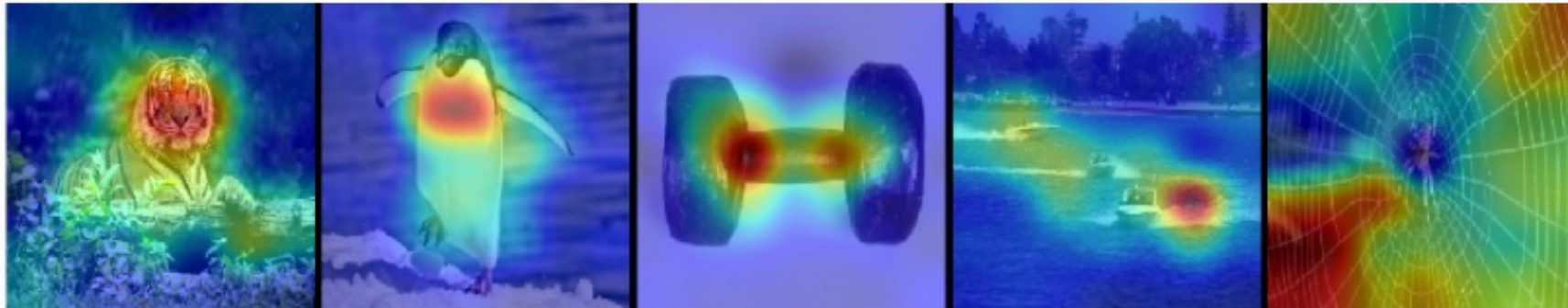




# Method 5: Attention Maps

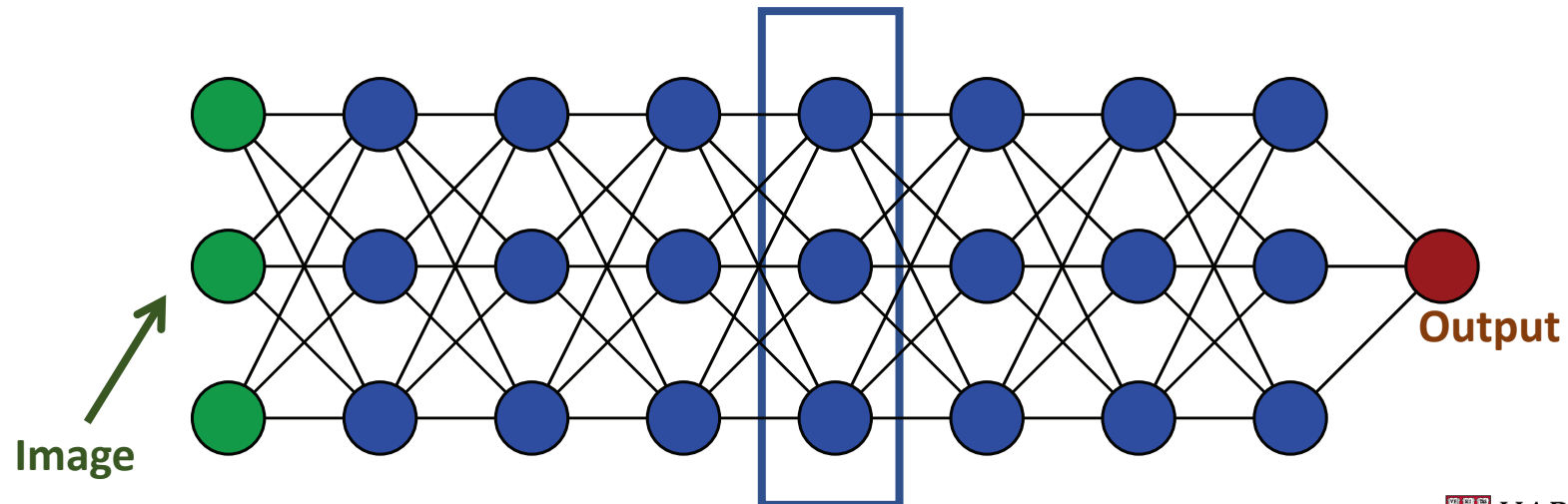


- Saliency map
  - Visualize how the output category would change if we tweak the input image pixels (i.e., visualize the gradient with respect to the **output category**)
- Class activation map
  - Visualize the gradient with respect to **the layer right before the fully connected layer**

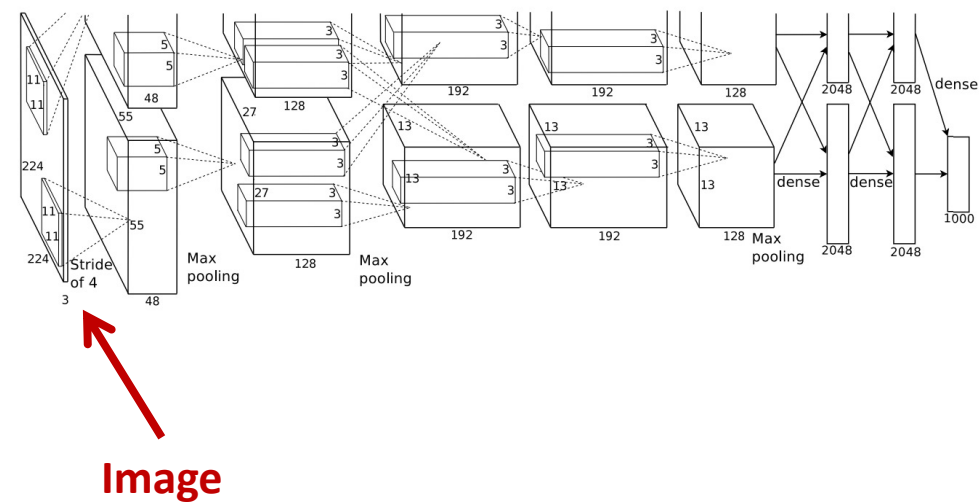
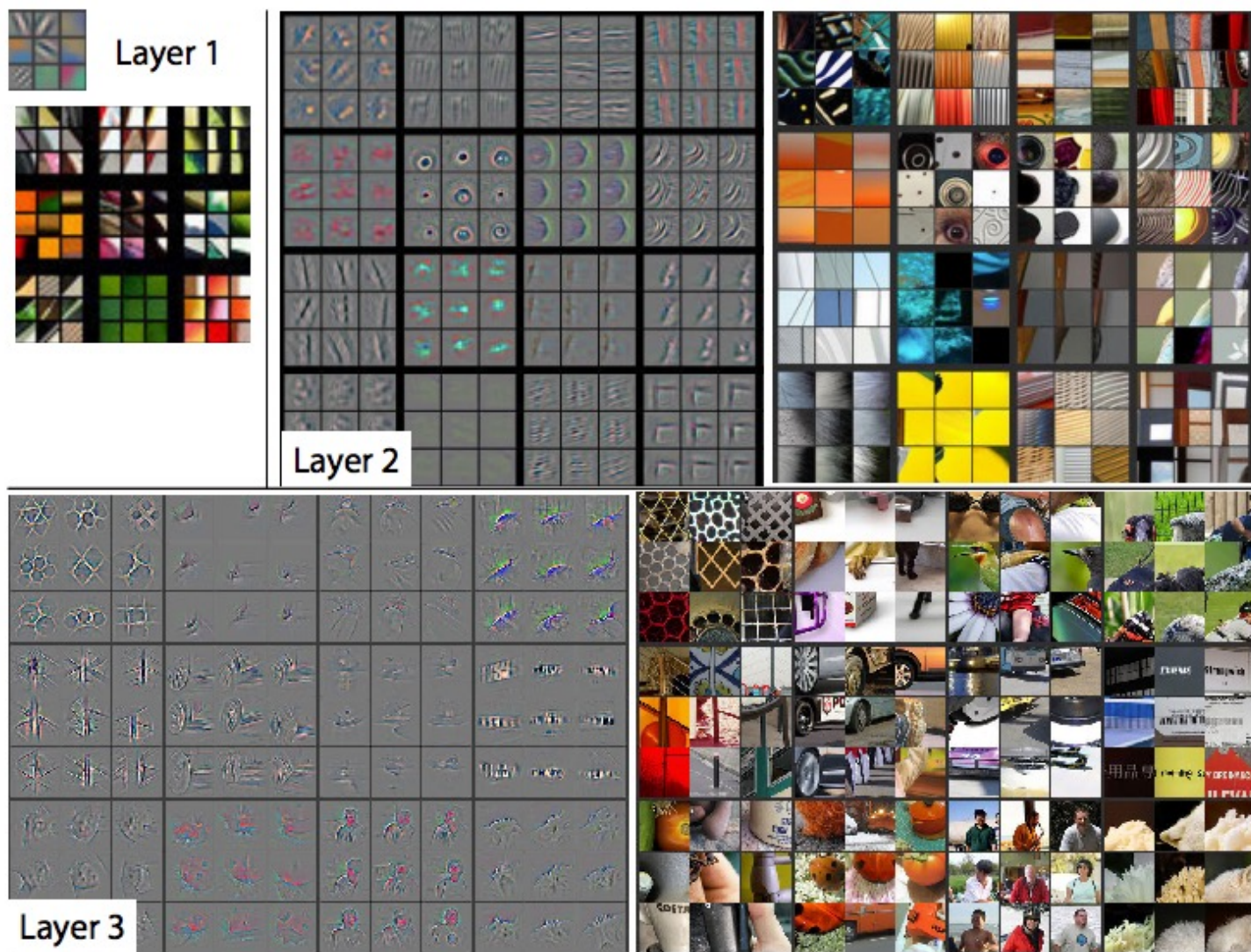


# Method 6: “Deconv”

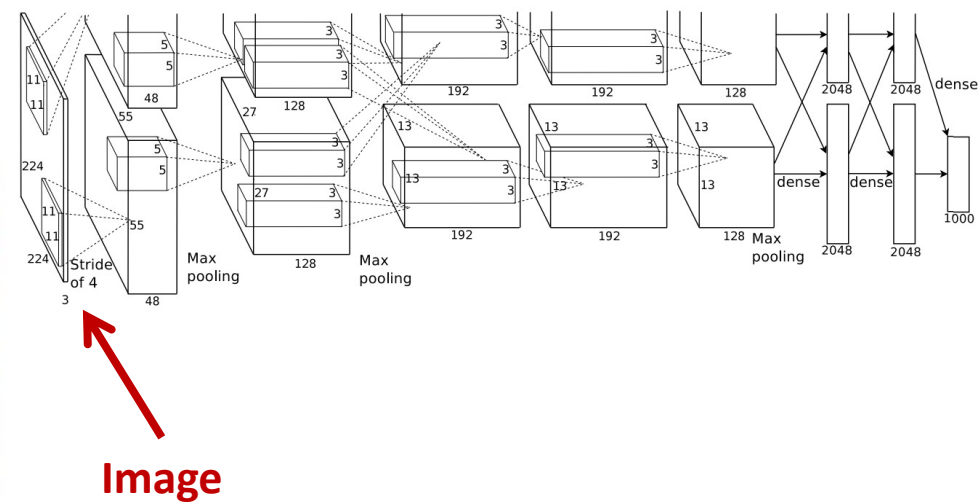
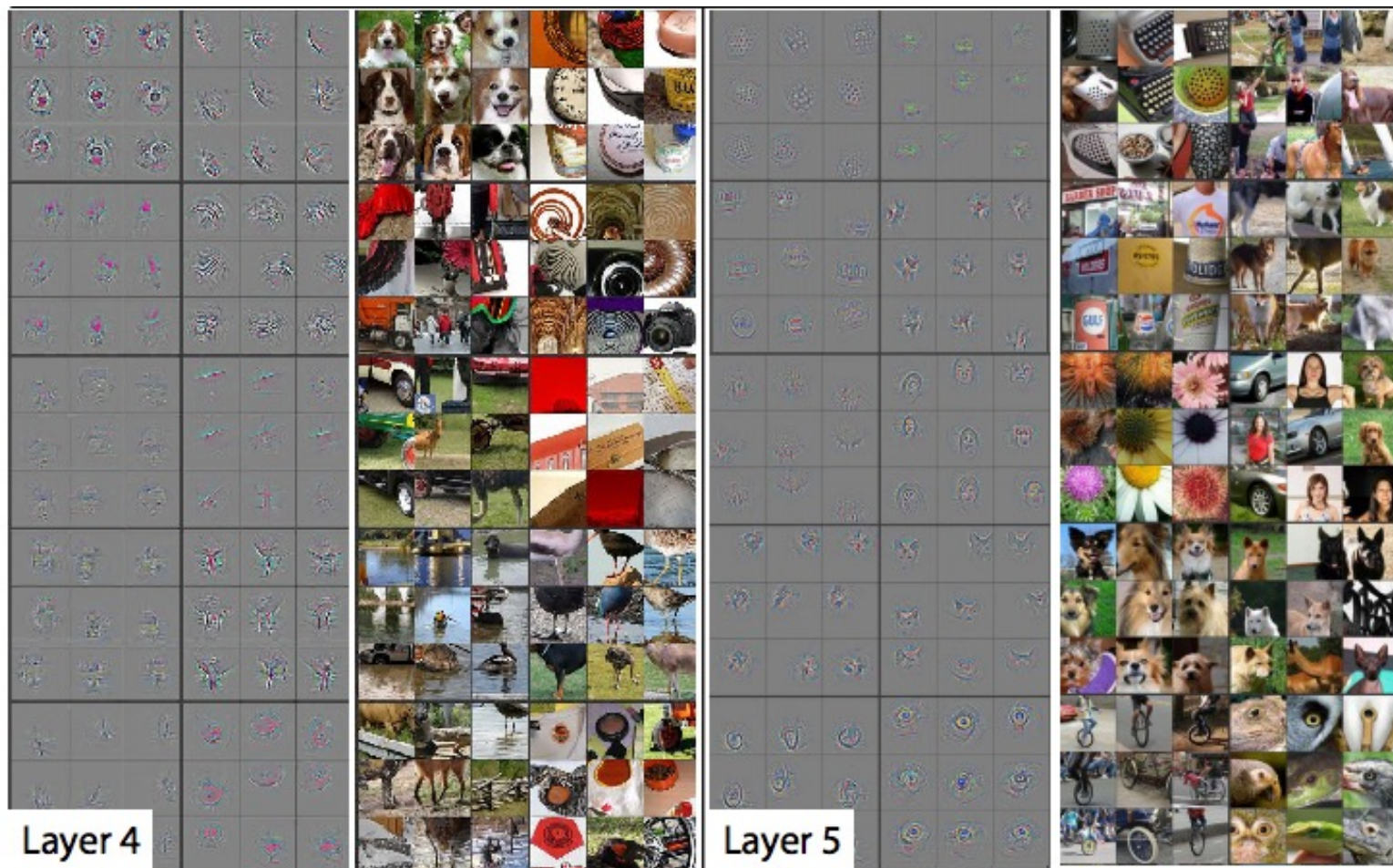
- Feed image into a CNN
- Pick a layer, set the gradient of that layer to be  $[0, 0, \dots, 1, \dots, 0]$
- Backprop to image



# Method 6: "Deconv"

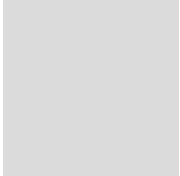


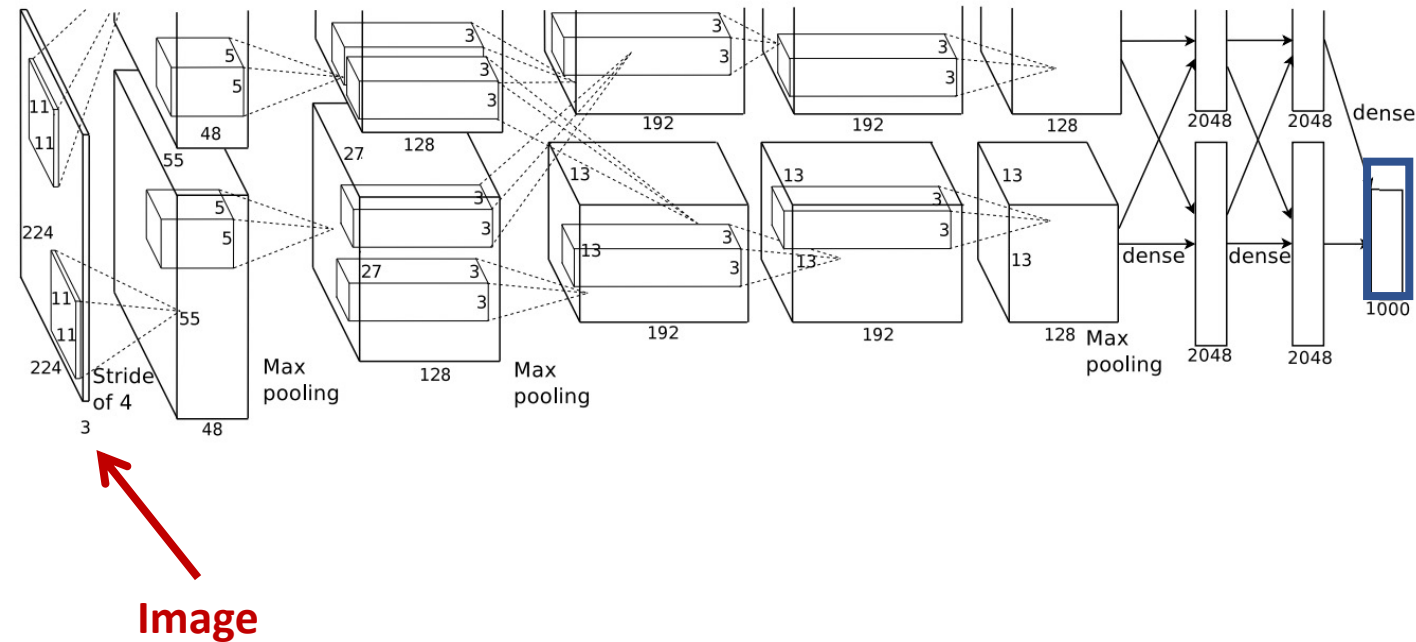
# Method 6: "Deconv"



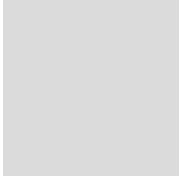
**Note:** "Deconv" consists of a single backward pass

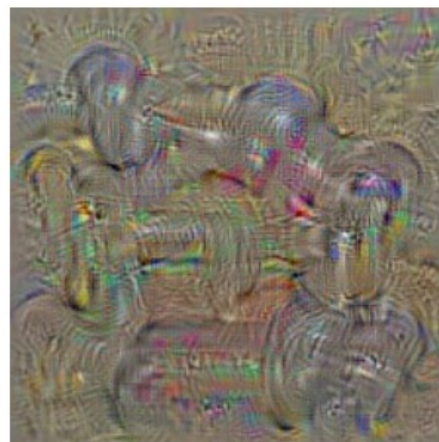
# Method 7: “Optimize” the Image

- Start with a neutral image 
- Do
  - Set the gradient of the score vector to be  $[0, 0, \dots, 1, \dots, 0]$
  - Backprop to the image
  - Forward the image through the network



# Method 7: “Optimize” the Image

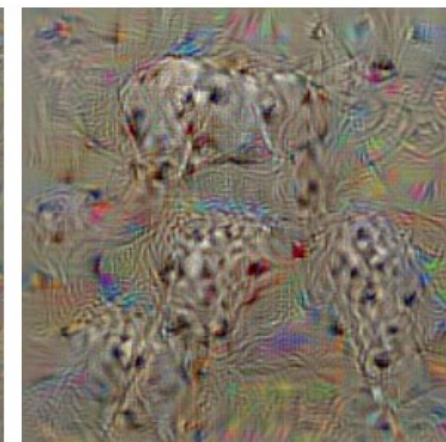
- Start with a neutral image 
- Do
  - Set the gradient of the score vector to be  $[0, 0, \dots, 1, \dots, 0]$
  - Backprop to the image
  - Forward the image through the network



**dumbbell**



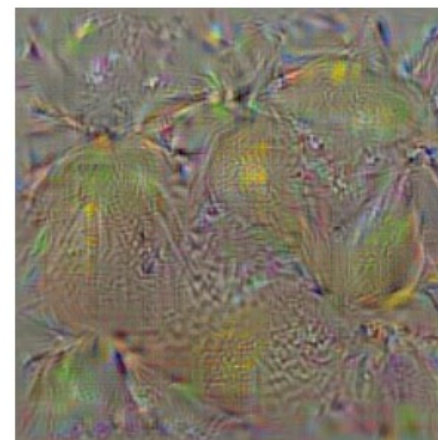
**cup**



**dalmatian**



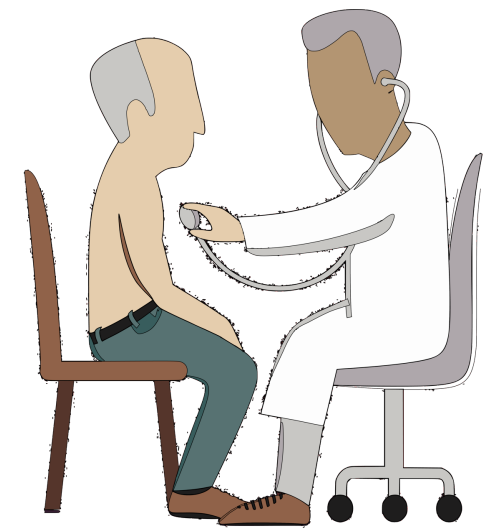
**bell pepper**



**lemon**



**husky**

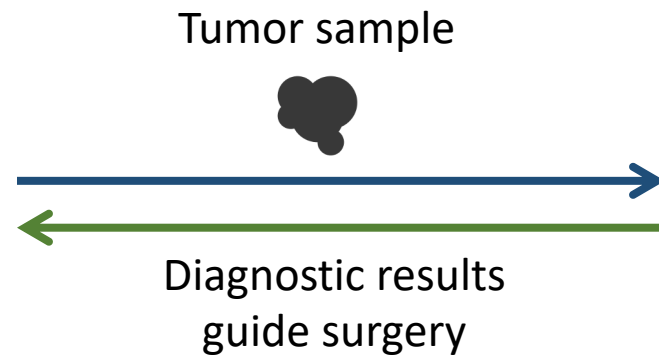


# How Can AI Assist in **Real-World Clinical Settings?**

1. Real-time brain cancer evaluation during surgery
2. Multi-omics prediction for personalized colorectal cancer treatments
3. Multi-task AI for genomic profile identification

# Example 1: The Challenge of Intra-Operative Neuropathology Diagnosis

Brain cancer: 204,000 death/year



**Costly**

**Human Error**

**Physician Burnout**

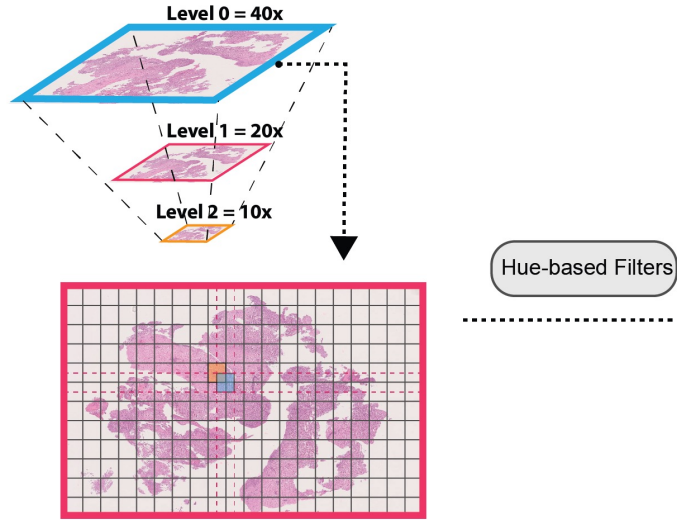
“Frozen Section” Diagnosis



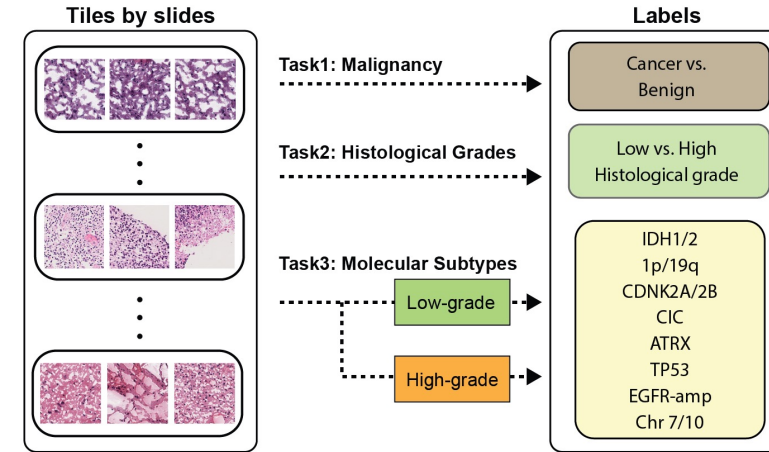


# AI-Based Cryosection Histopathology Assessment and Review Machine (CHARM)

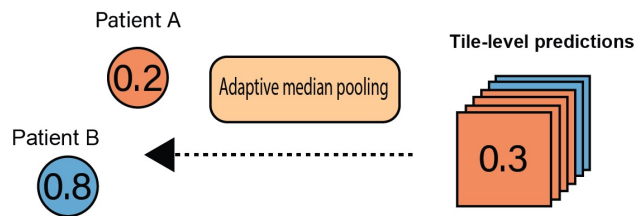
A. Tile the whole slide cryosection images



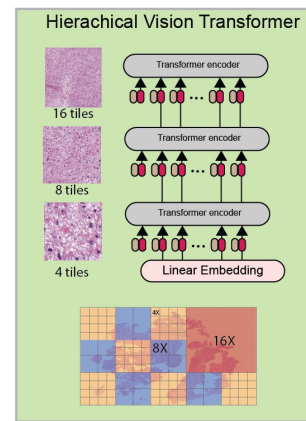
B. Identify 2021 WHO Classification using pathology and genomic profiles



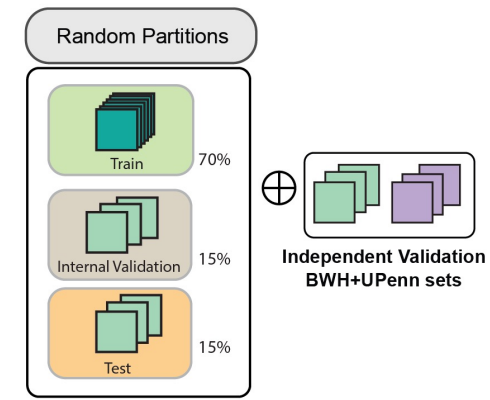
E. Aggregate tiles to patient-level predictions



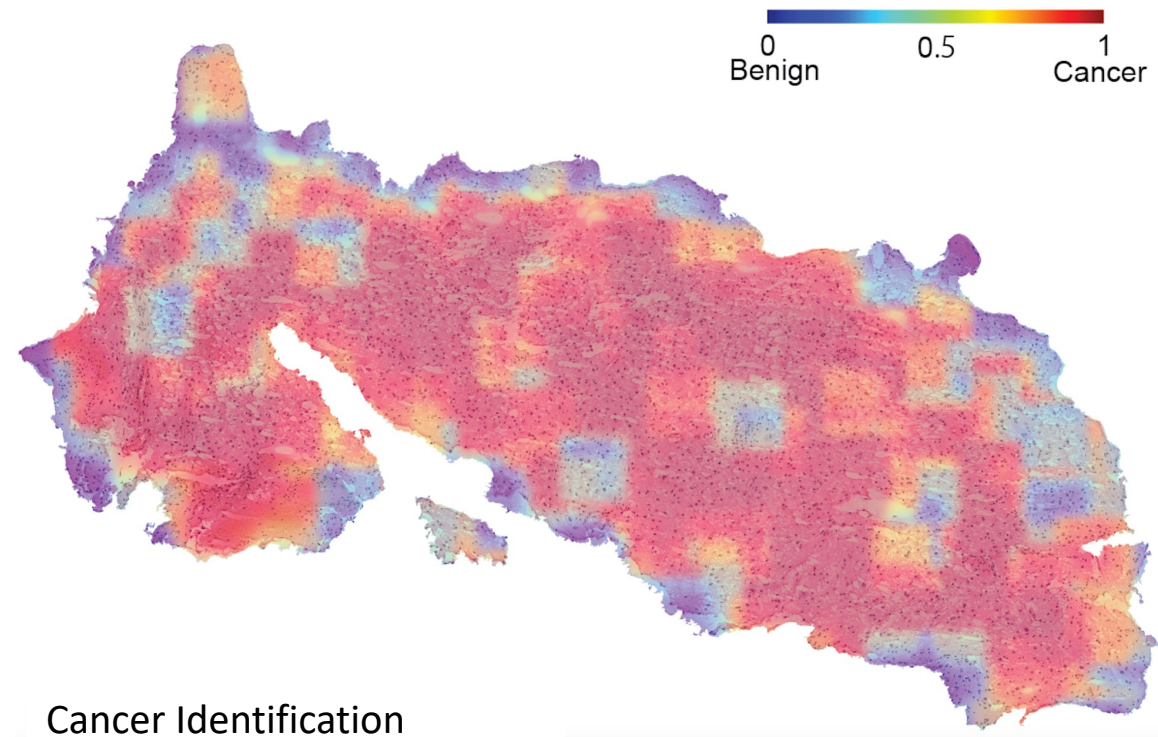
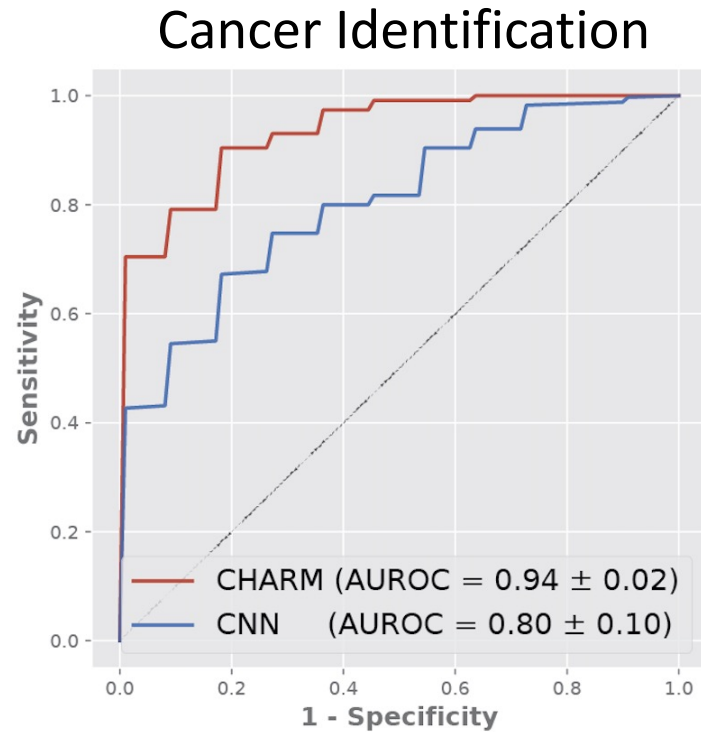
D. Train and validate the models



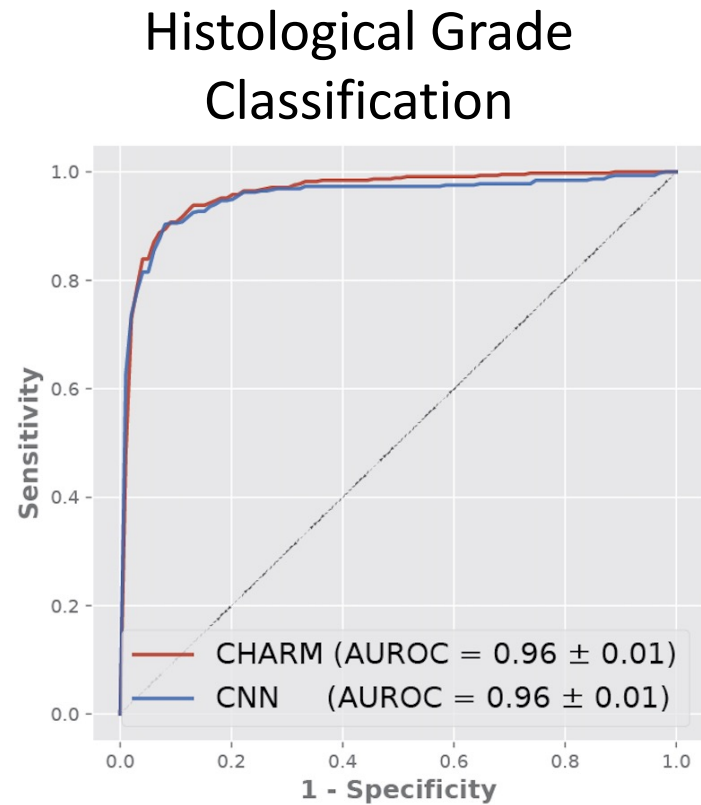
C. Partition the datasets



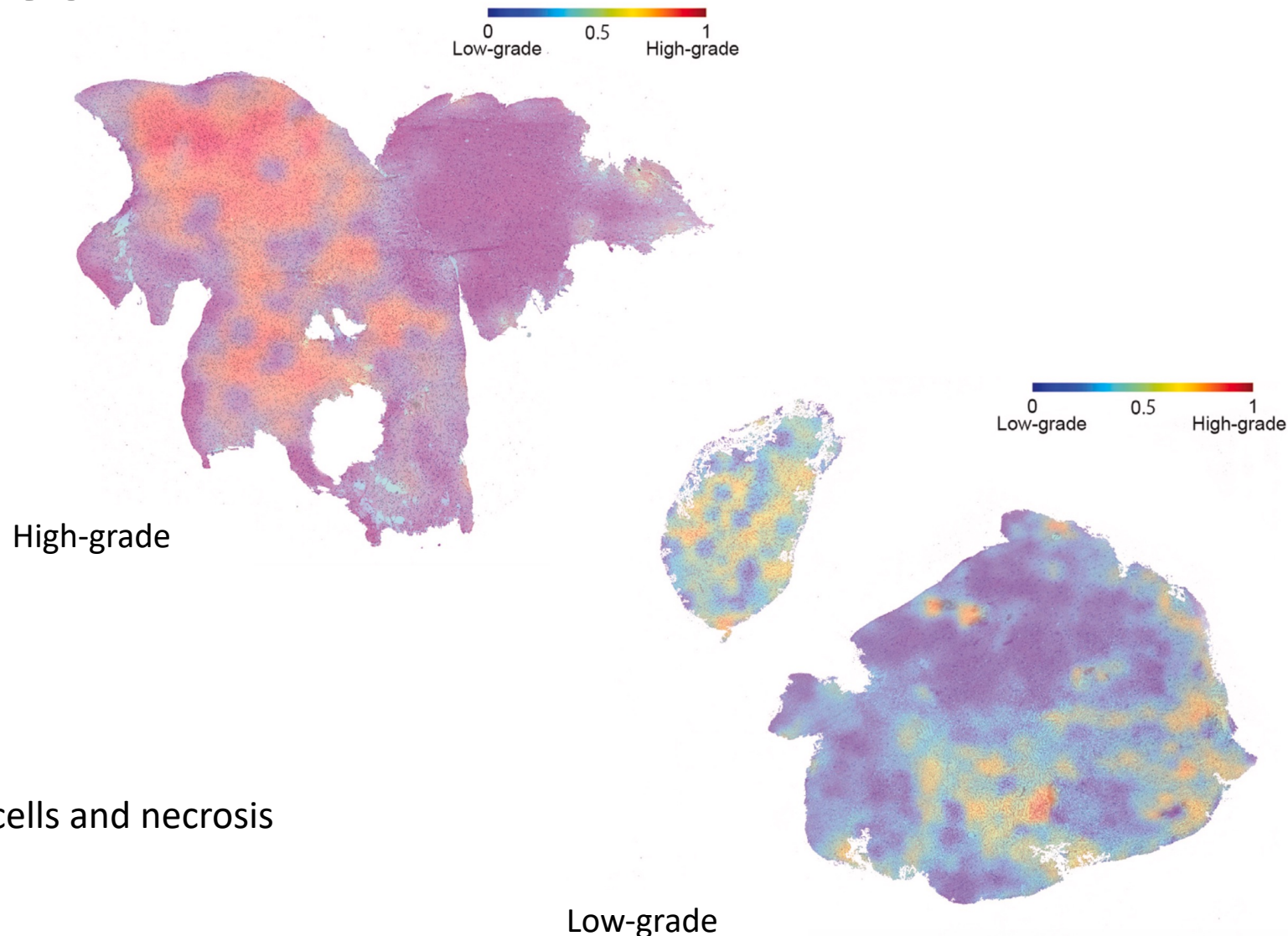
# Identifying Malignant Cells in Cryosection Samples



# CHARM Successfully Differentiated Histological Grades



**High histological grade:** dense glioma cells and necrosis



# However, the updated WHO Classification Included **Molecular Profiles** in the Definition of Glioma Grades

## Neuro-Oncology

XX(XX), 1–21, 2021 | doi:10.1093/neuonc/noab106 | Advance Access date 29 June 2021

### The 2021 WHO Classification of Tumors of the Central Nervous System: a summary

David N. Louis, Arie Perry, Pieter Wesseling<sup>®</sup>, Daniel J. Dominique Figarella-Branger, Cynthia Hawkins, H. K. I. Riccardo Soffietti, Andreas von Deimling, and David W

Can AI infer IDH mutation status from pathology images?

**Table 1** 2021 WHO Classification of Tumors of the Central Nervous System. Provisional Entities are in Italics

#### World Health Organization Classification of Tumors of the Central Nervous System, fifth edition

##### Gliomas, glioneuronal tumors, and neuronal tumors

###### Adult-type diffuse gliomas

Astrocytoma, IDH-mutant

Oligodendroglioma, IDH-mutant, and 1p/19q-codeleted

**Glioblastoma, IDH-wildtype**

Low grade

High grade

###### Pediatric-type diffuse low-grade gliomas

Diffuse astrocytoma, *MYB*- or *MYBL1*-altered

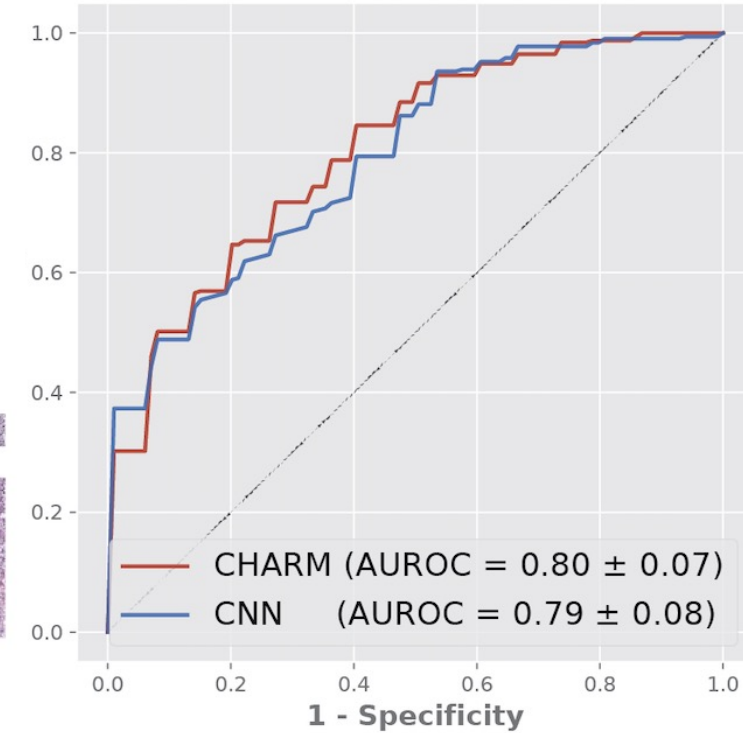
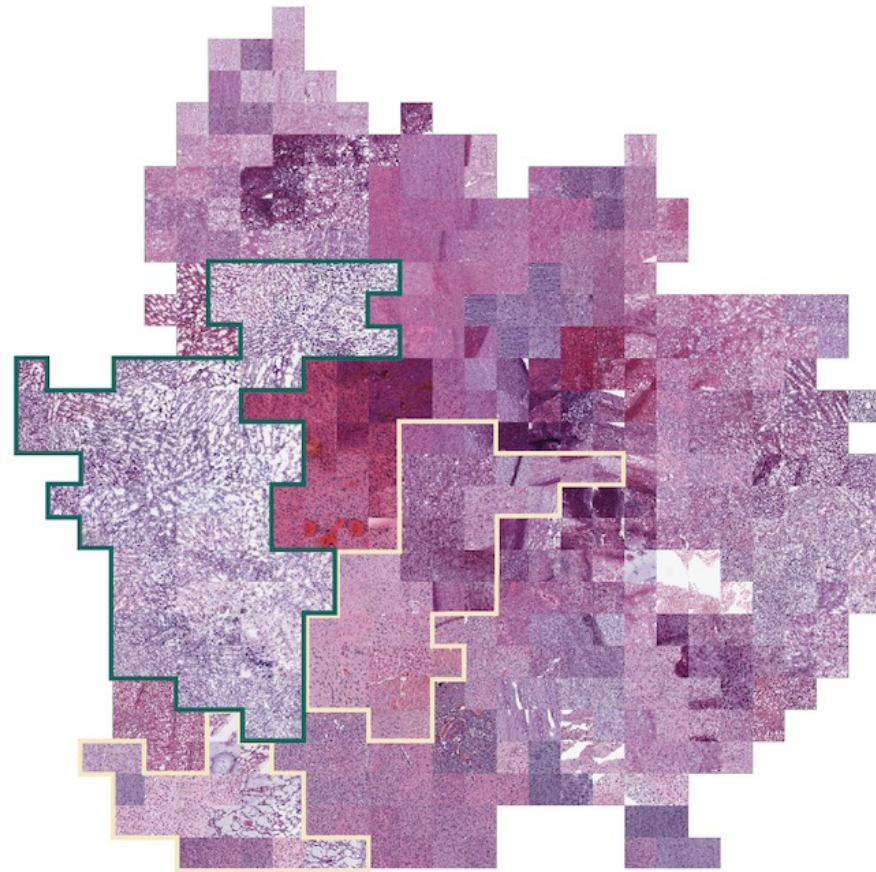
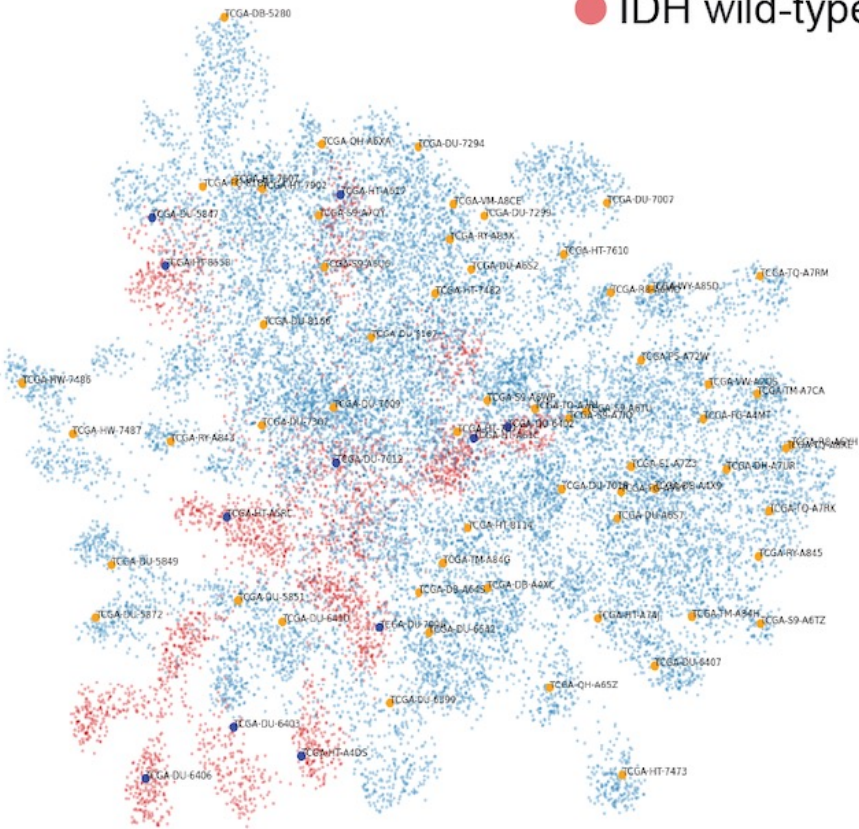
Angiocentric glioma

Polymorphous low-grade neuroepithelial tumor of the young

Diffuse low-grade glioma, MAPK pathway-altered

# Predicting IDH Mutation Status

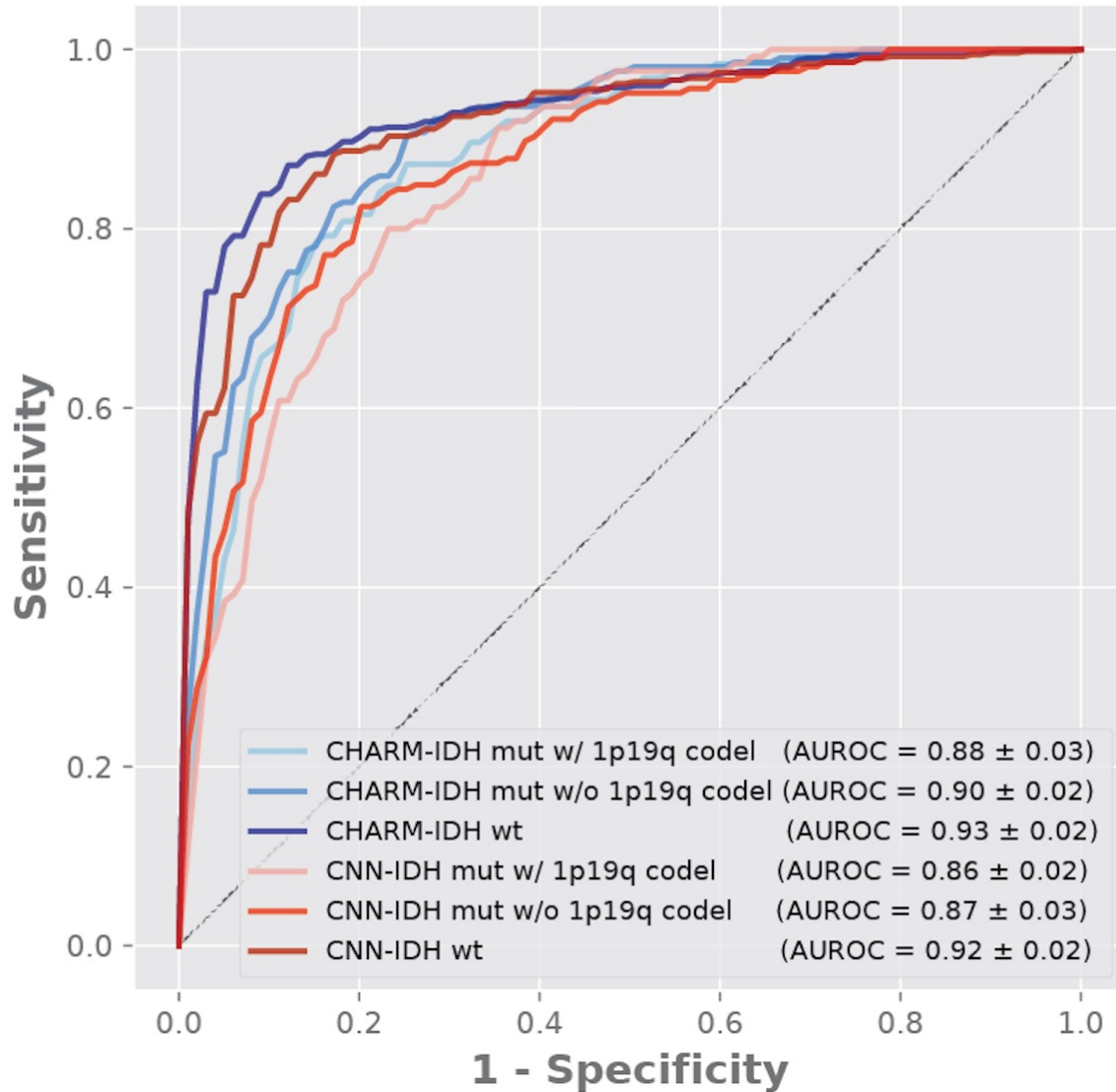
- IDH mutant
- IDH wild-type



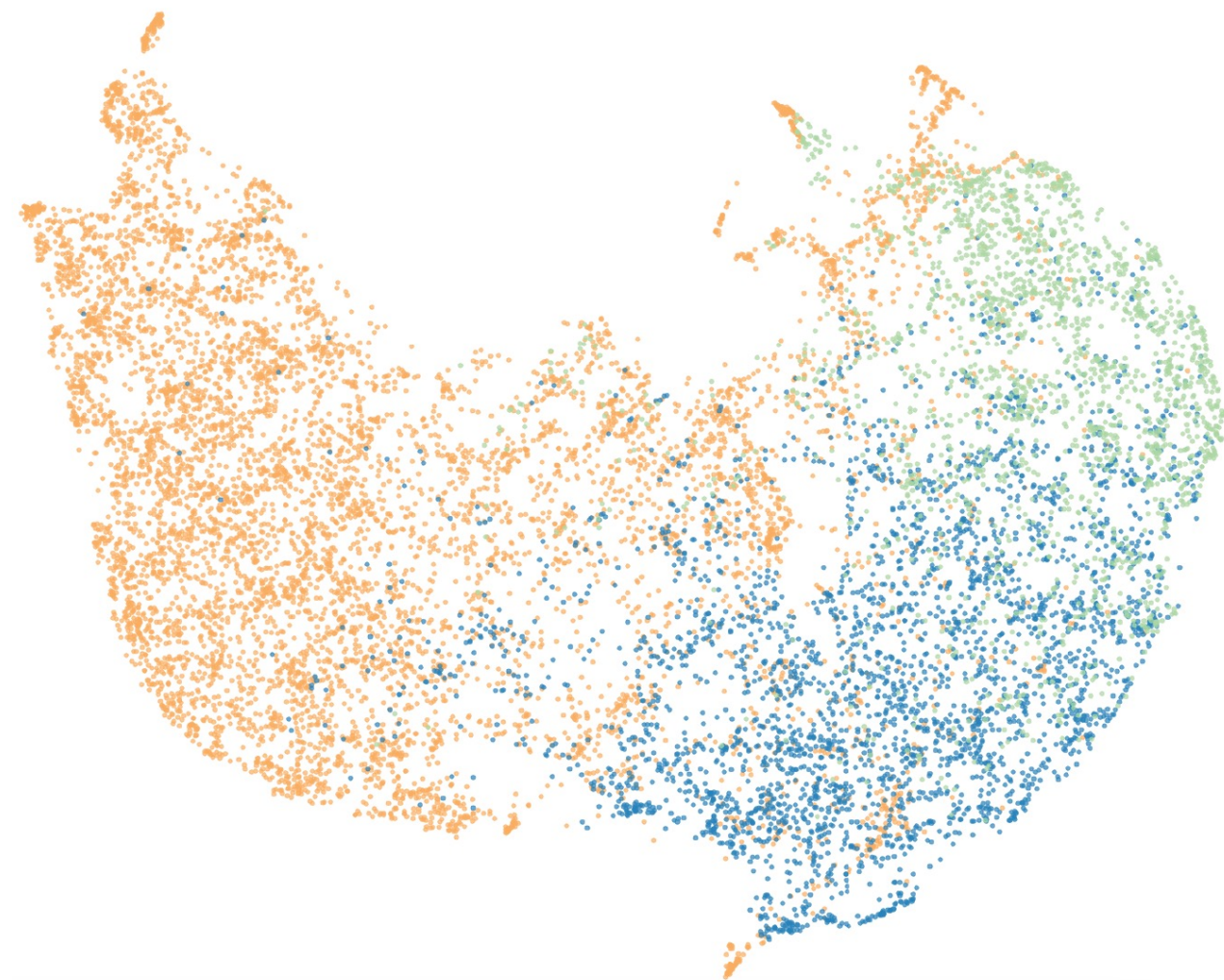
**IDH mutant:** highly edematous specimens with lower cellularity

**IDH wild-type:** greater cellularity and atypia

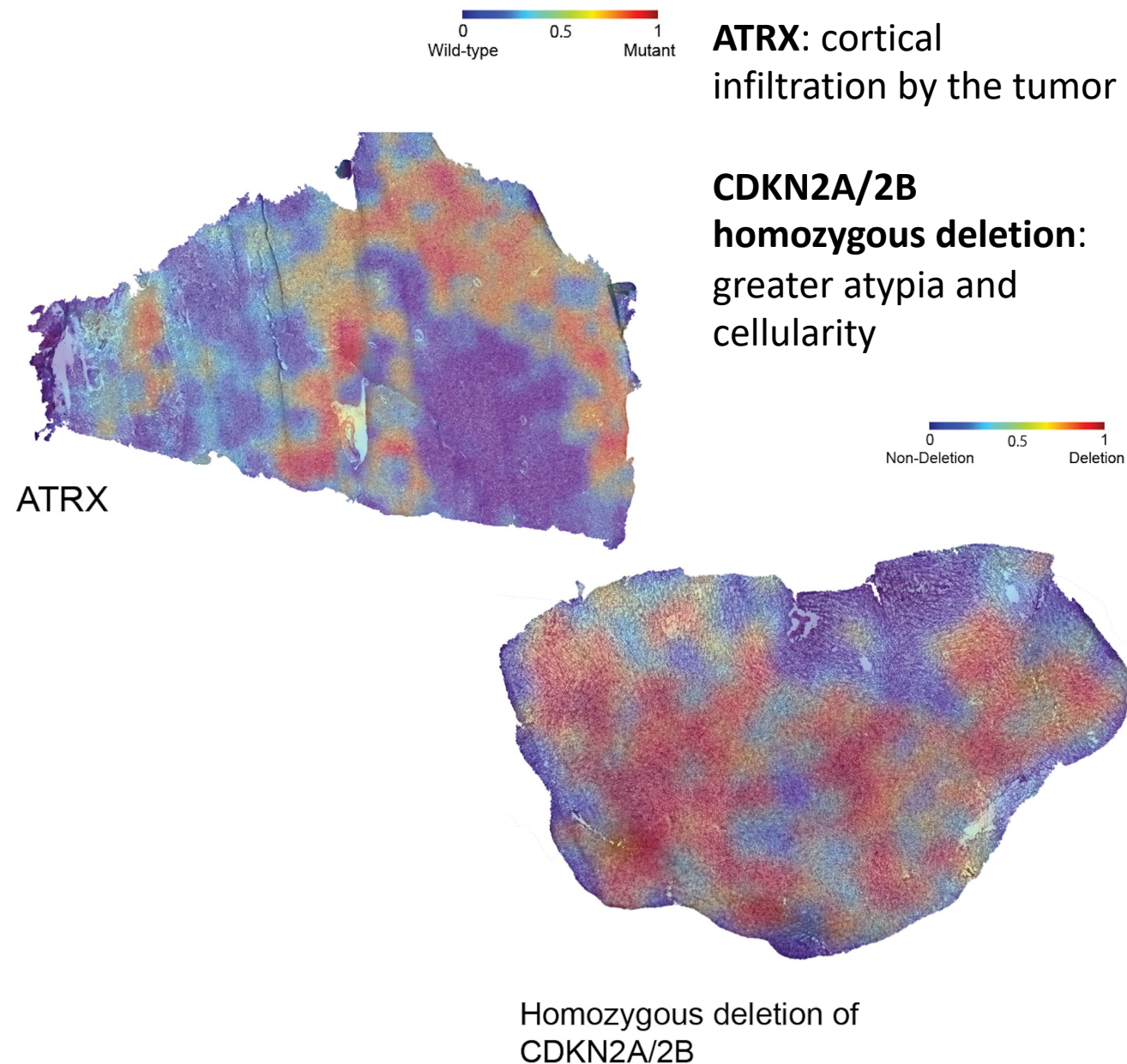
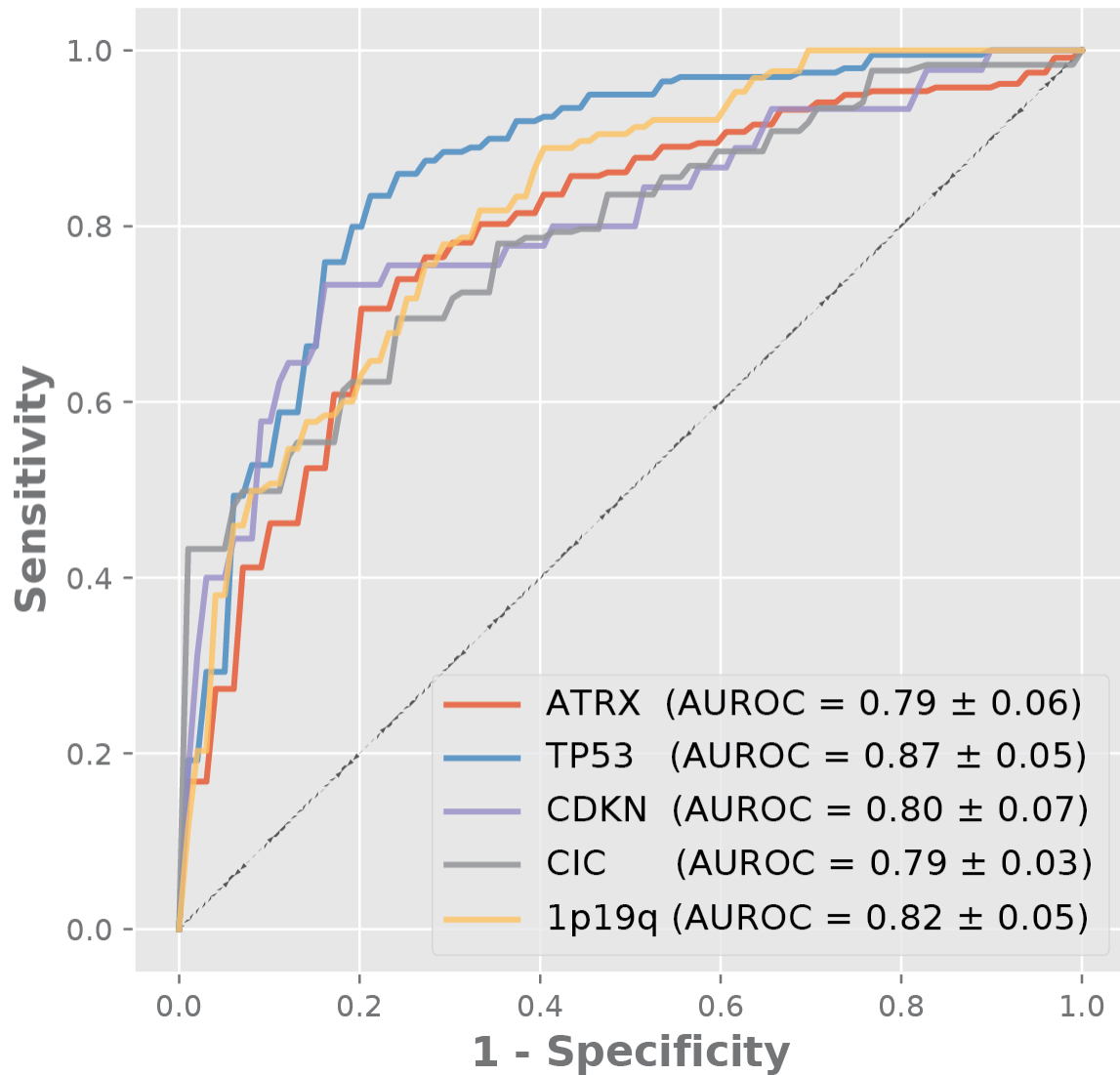
# Predicting WHO CNS5 Classification



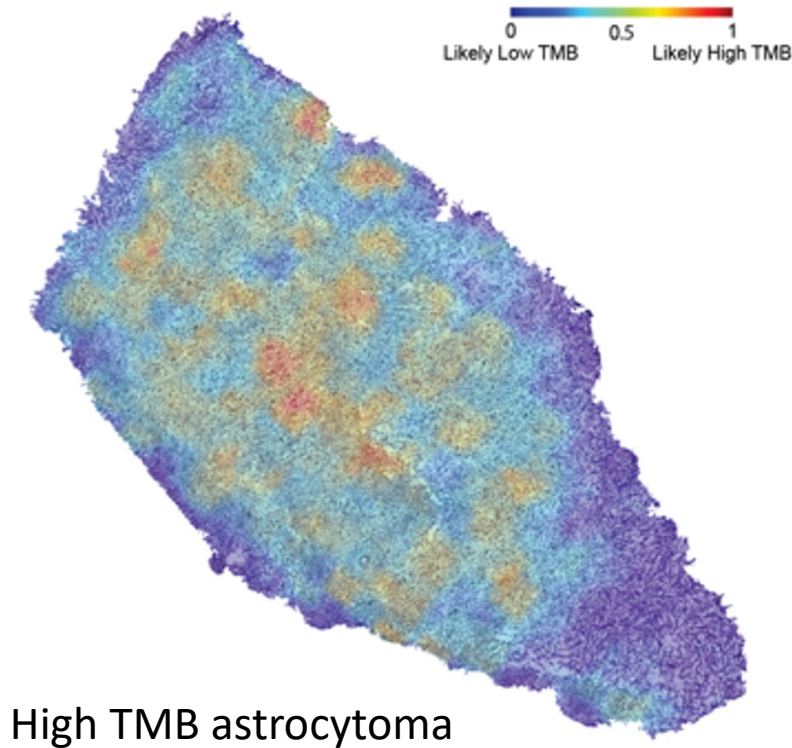
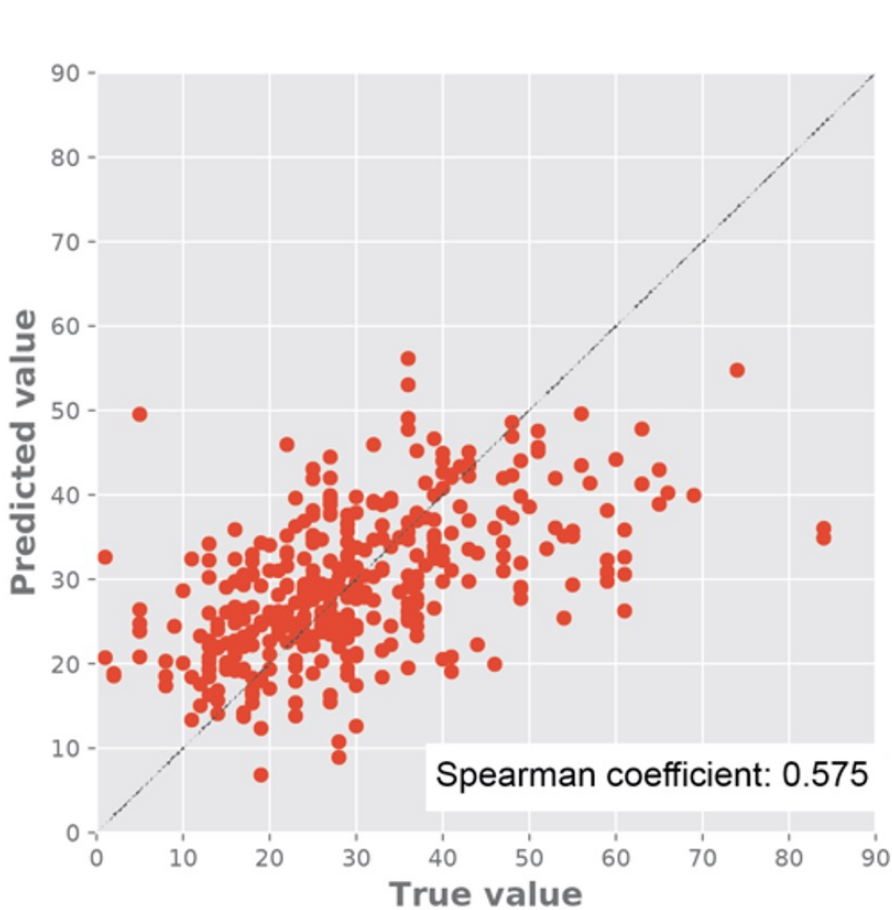
- IDH Mut w/ 1p/19q codel
- IDH Mut w/o 1p/19q codel
- IDH Wildtype



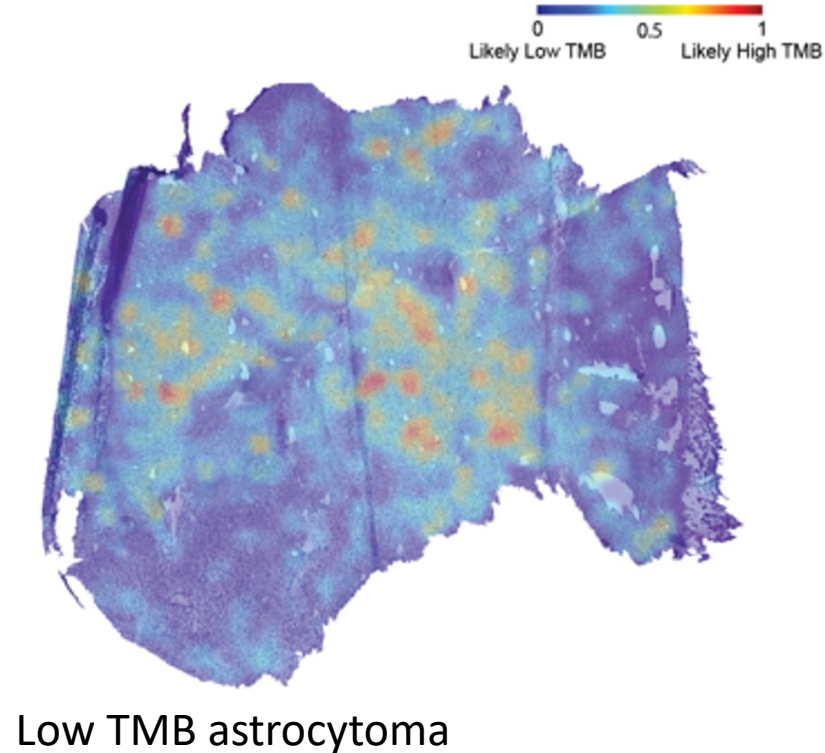
# Predicting Key Genomic Profiles Related to Prognosis



# Associating Histology Findings with Tumor Mutation Burden (TMB)



High TMB astrocytoma

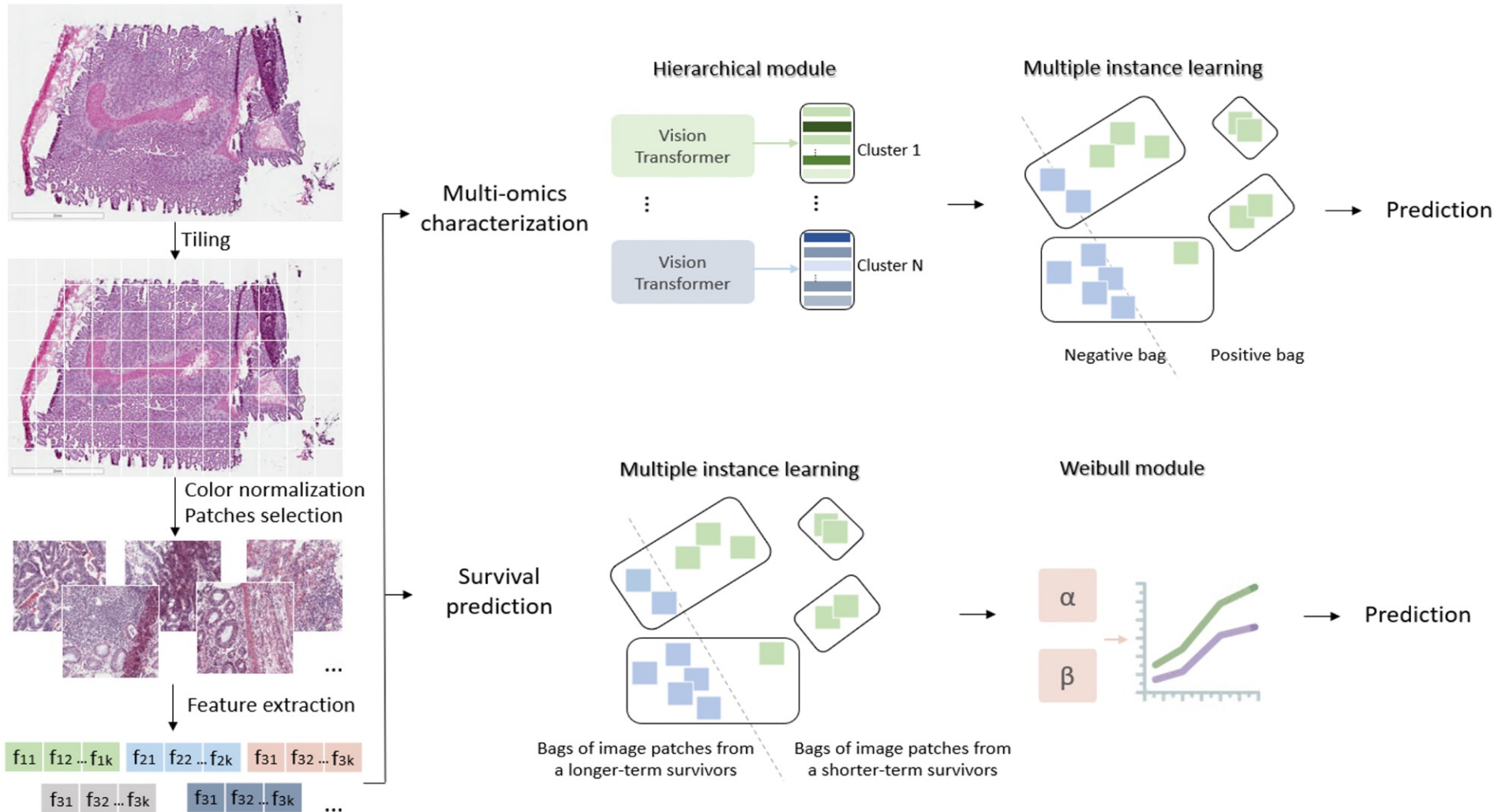


Low TMB astrocytoma

**High TMB:** greater cellularity and atypia, with less edematous regions



# Example 2: Multi-Omics Multi-cohort Assessment (MOMA) Platform for Molecular and Prognostic Prediction



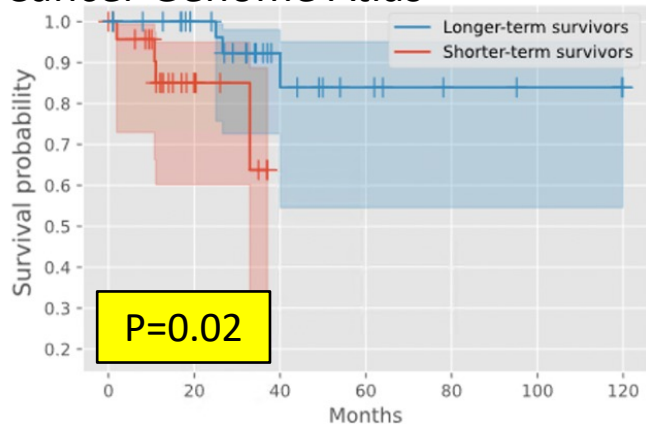
- The Cancer Genome Atlas (TCGA)
- PLCO Cancer Screening Trial
- Nurses' Health Study (NHS)
- Health Professional Follow-Up Study (HPFS)

Whole-slide images

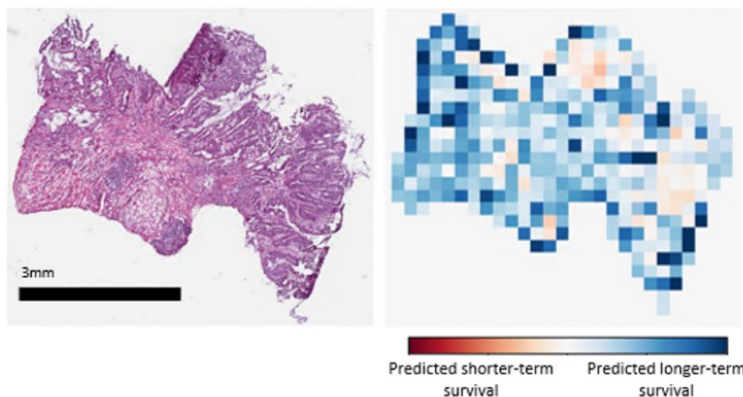
Tissue microarray images

# AI Predicts Overall Survival and Disease-Free Survival of Colorectal Cancer Patients in Multiple Cohorts

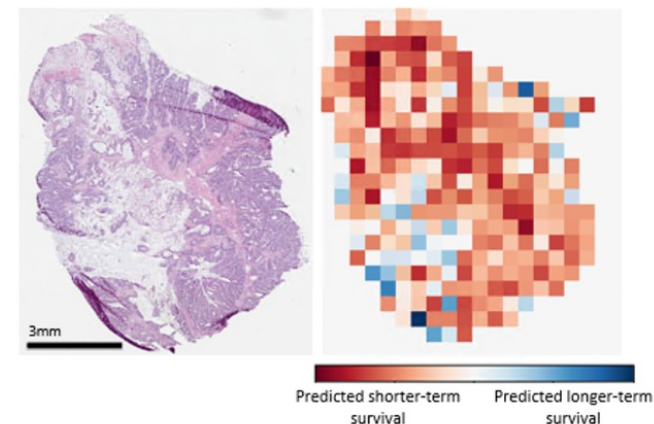
The Cancer Genome Atlas



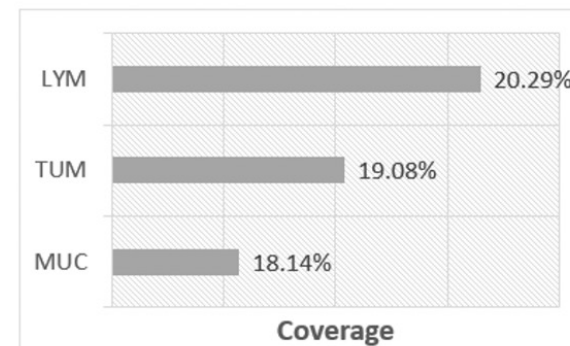
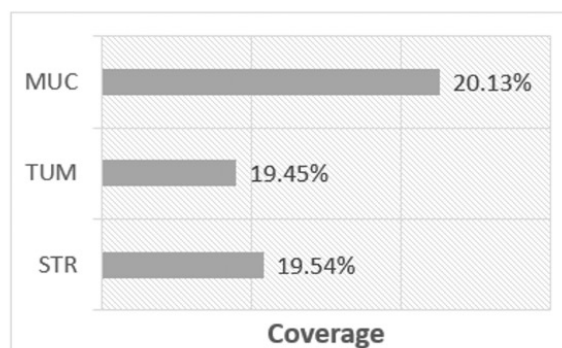
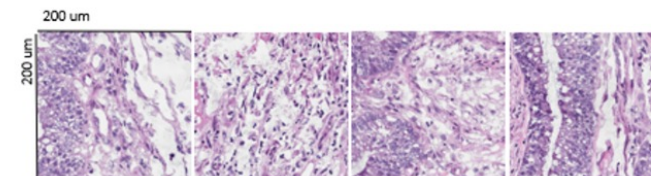
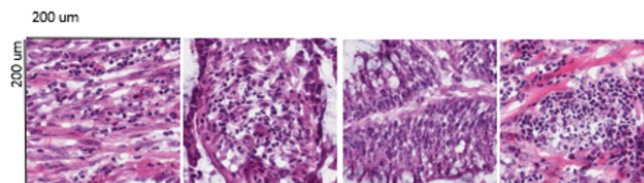
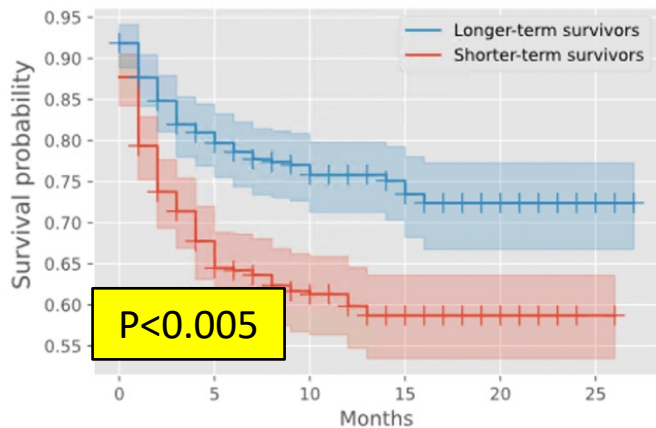
Long-term survivor (124.27 months)



Short-term survivor (2.99 months)



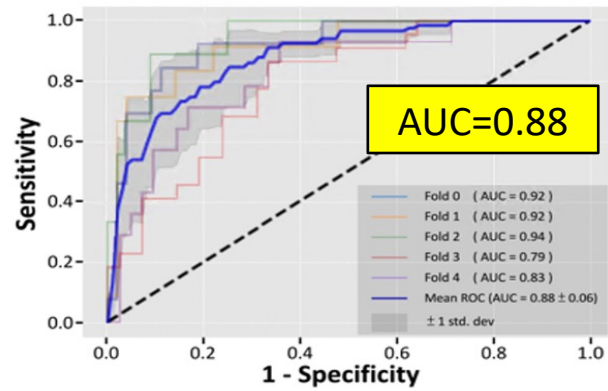
NHS and HPFS



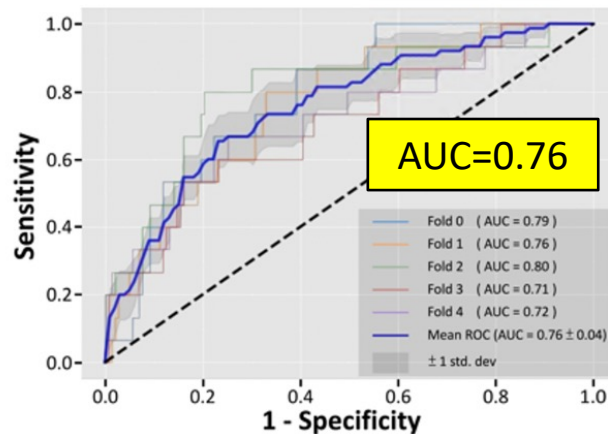
# AI Predicts Multi-Omics Profiles from Pathology Images

- MSI prediction

The Cancer Genome Atlas

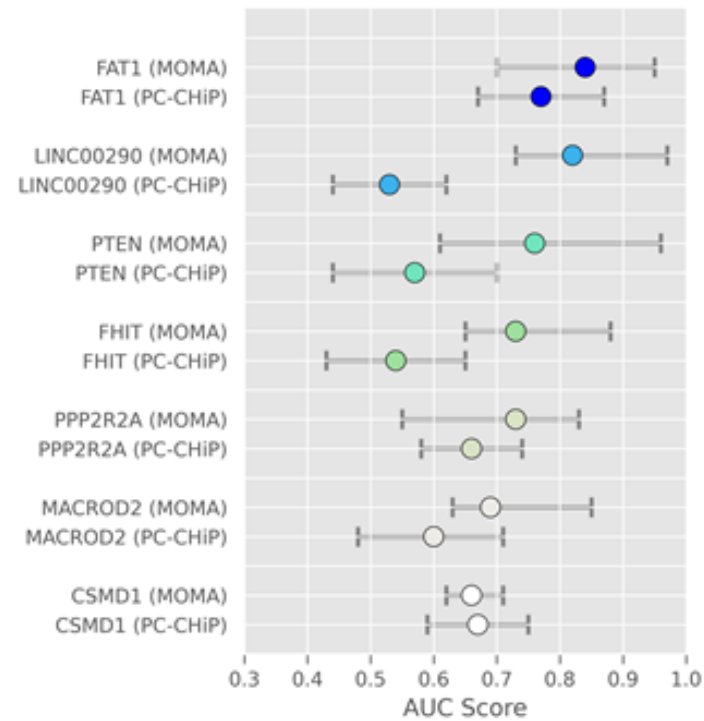


NHS and HPFS

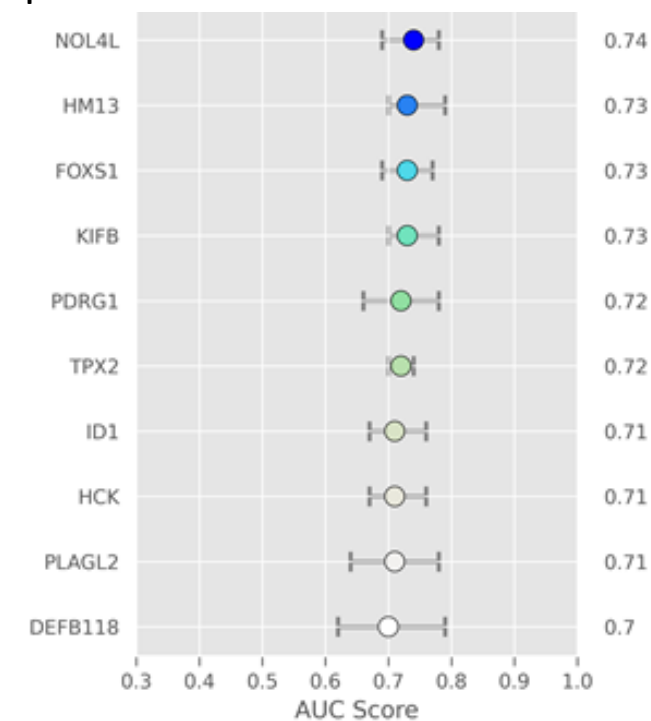


- Copy number alteration

Deletion

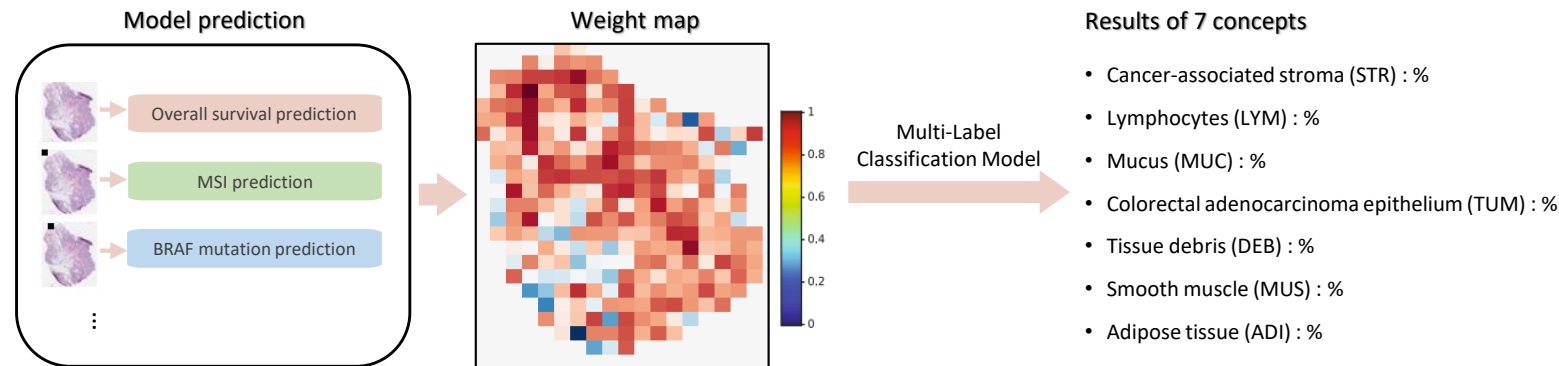


Amplification



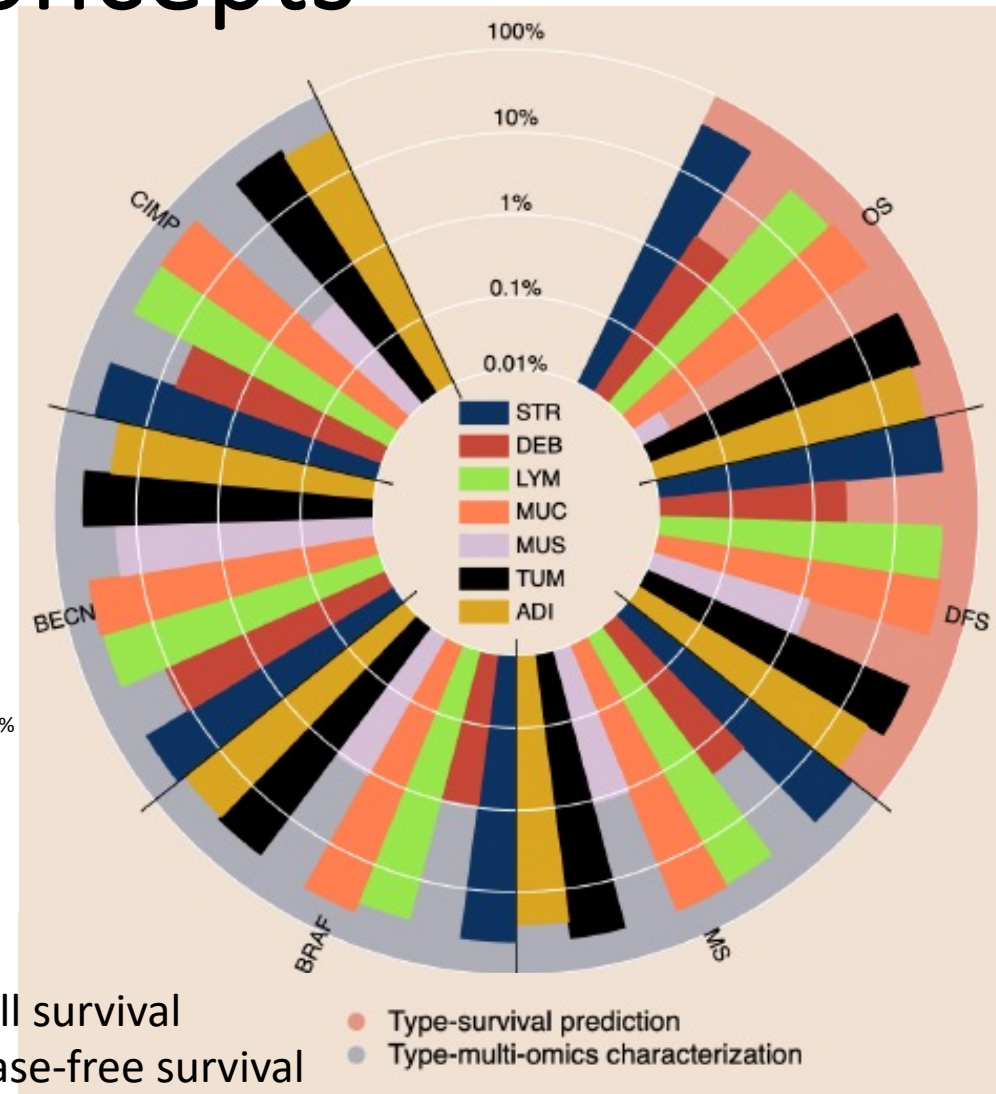
# Explainable AI Describes Novel Imaging Patterns Using Pathology Concepts

- Connecting pathology knowledge with AI-derived features using the weight map



## Results of 7 concepts

- Cancer-associated stroma (STR) : %
- Lymphocytes (LYM) : %
- Mucus (MUC) : %
- Colorectal adenocarcinoma epithelium (TUM) : %
- Tissue debris (DEB) : %
- Smooth muscle (MUS) : %
- Adipose tissue (ADI) : %



OS: Overall survival

DFS: Disease-free survival

MS: Microsatellite instability

● Type-survival prediction

● Type-multi-omics characterization

# Summary

- Human-interpretable features + machine learning
- Deep learning methods
  - Multi-modal foundation models
  - Model interpretation
- Clinical applications in cancer pathology diagnoses