

August 22, 2024

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# Expression-Based Molecular Subtyping & Classification of Bladder Cancer TCGA Data

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Artificial Intelligence in Medicine (AIM) Lab

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# A Consensus Molecular Classification of Muscle-Invasive Bladder Cancer (MIBC)

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European Association of Urology (EAU).

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# Overview

## **Bladder Cancer:**

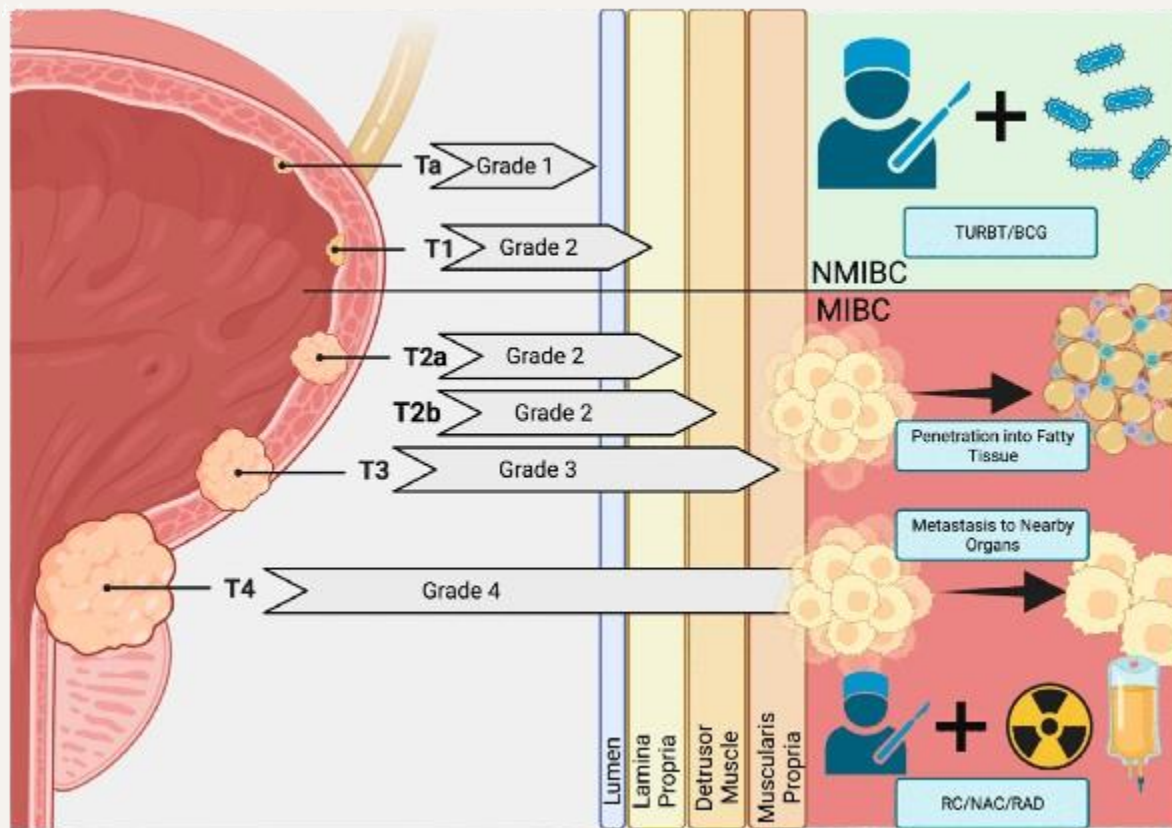
Urothelial Carcinoma Originating in Tissues of the Urinary System

### **Non-Muscle Invasive Bladder Cancer**

Superficial Cancer Confined to  
Mucosa Layer

### **Muscle-Invasive Bladder Cancer**

Aggressive Cancer Penetrating  
Muscle Layer



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# Introduction

## **Existing Classification Systems:**

Diversity of Molecular Subtypes Impedes Clinical Application



Lack of Naming Convention + Data Variability

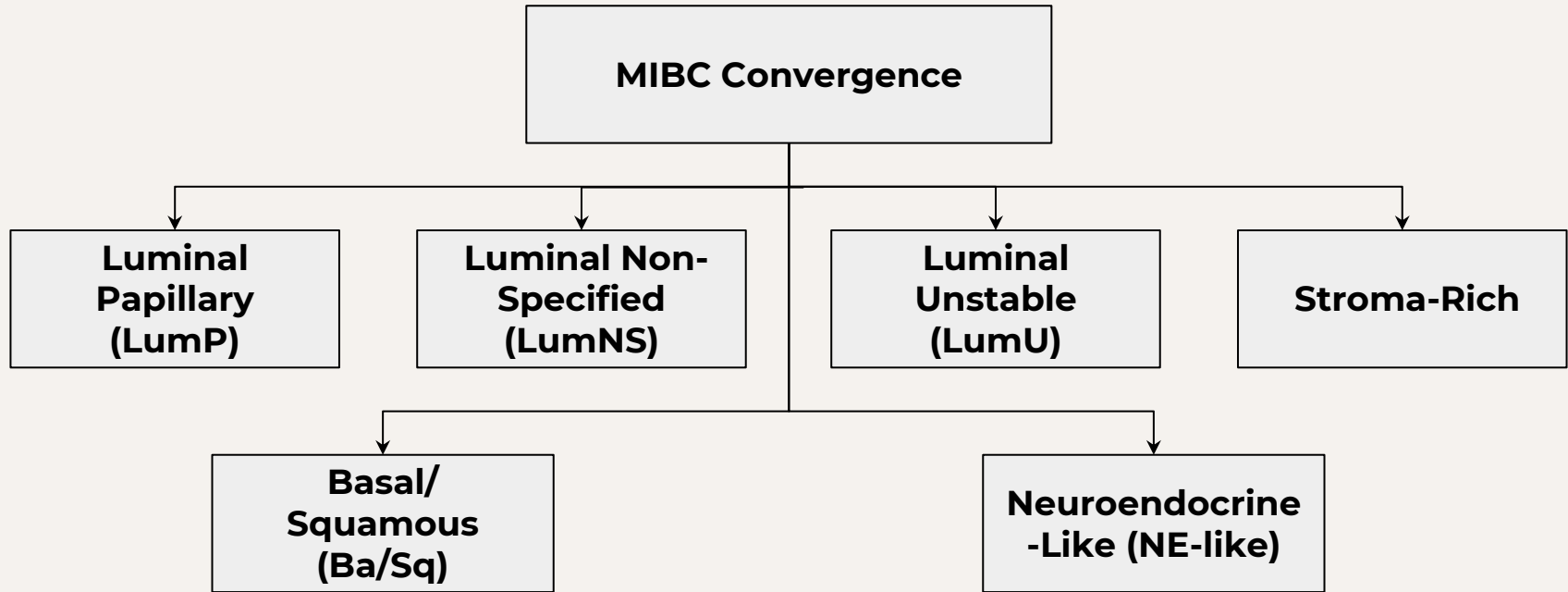
## **Research Objective:**

“Achieve International Consensus of MIBC Molecular Subtypes that Reconciles Published Classification Schemes”

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# Consensus Classification

**Implementation:** Nearest-Centroid Transcriptomic Classifier in R



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# Analytical Workflow

**Patch Extraction**



**Feature Extraction**



**Multiple Instance Learning (MIL)**



**Information Visualization**

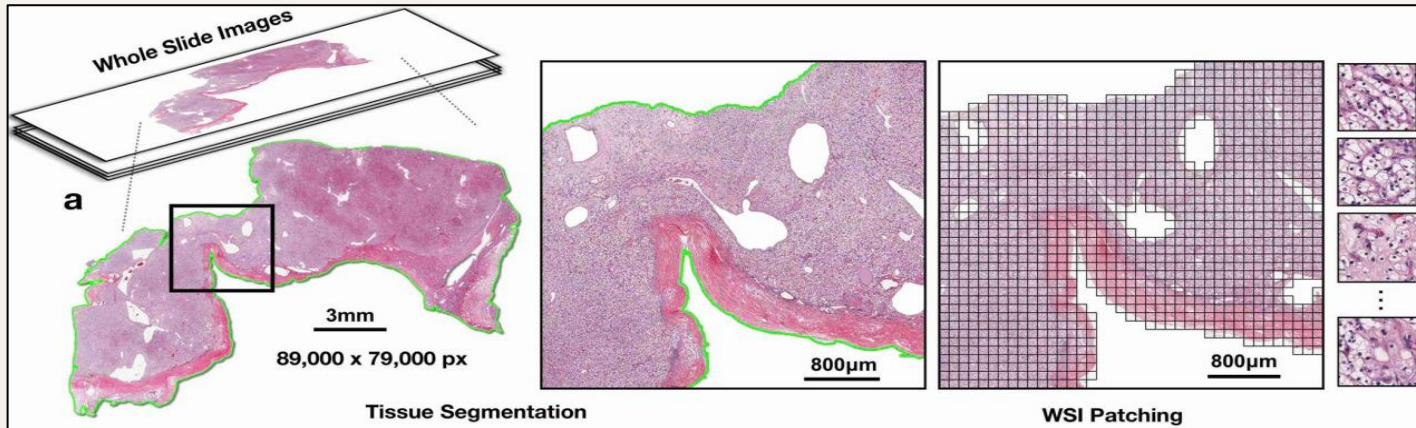
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# Patch Extraction

**Purpose:** Facilitate Localized Deep Learning

**Input:** Masks Pre-Selected from HistoQC

**Output:** 1,500 Patches Per Whole Slide Image



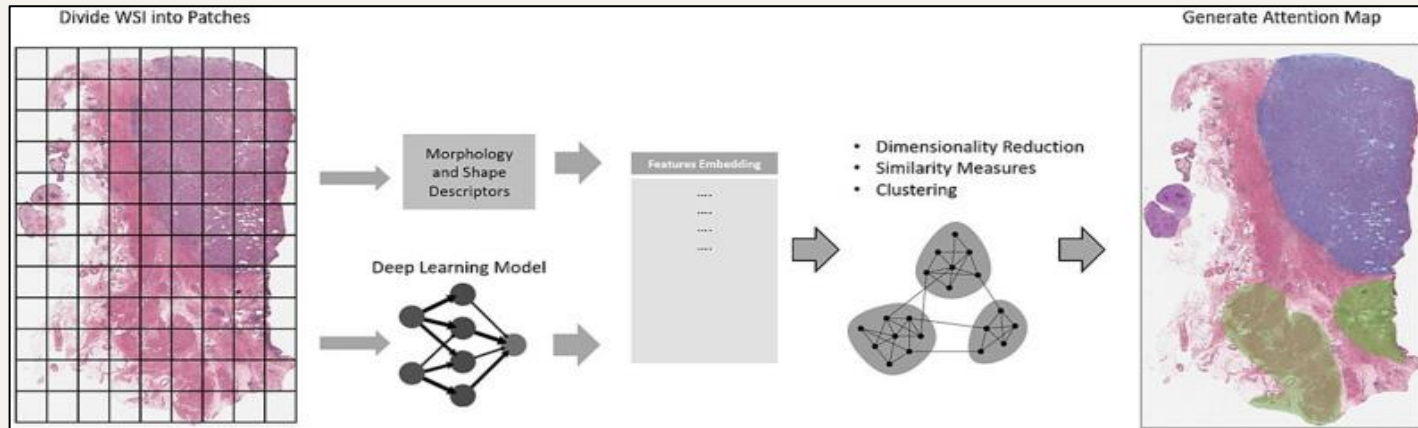


# Feature Extraction

**Purpose:** Meaningfully Represent Tissue Characteristics

**Input:** 1,500 Patches Per Whole Slide Image

**Output:** 458 Diagnostic + 463 Frozen .h5 Files



# Feature Encoders

## **CTransPath**

- Pre-Trained Vision Transformer for Unsupervised Contrastive Learning

## **Lunit Dino**

- Pre-Trained Vision Transformer for Self-Supervised Learning

## **Phikon**

- Pre-Trained Vision Transformer for Self-Supervised Learning

## **PLIP**

- Pre-Trained Vision Transformer for Pathology Image Retrieval

## **UNI**

- Pre-Trained Vision Transformer for Self-Supervised Learning

## **vit**

- Pre-Trained Vision Transformer for Self-Supervised Learning

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# Multiple Instance Learning

**Purpose:** Analyse Extracted Features at Bag-Level

**Input:** 458 Diagnostic + 463 Frozen .h5 Files for 20x Mag

**Output:** 90 Checkpoint + Output .pt Files per Model

## Models:

1. DeepMIL
2. TransMIL
3. ClamSB

## Data Folds:

1. Fold #1
2. Fold #2
3. Fold #3

## Relevant Metrics:

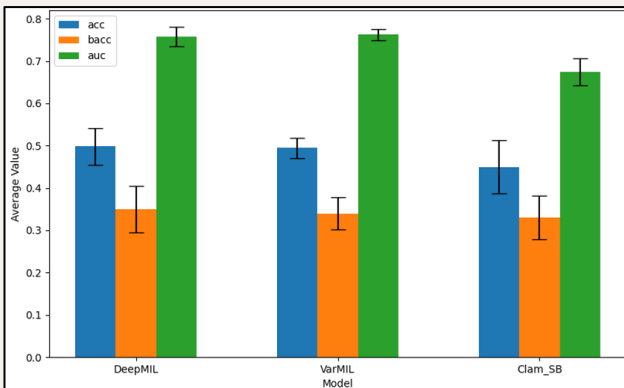
1. Accuracy
2. Bal. Accuracy
3. AUC

## Others:

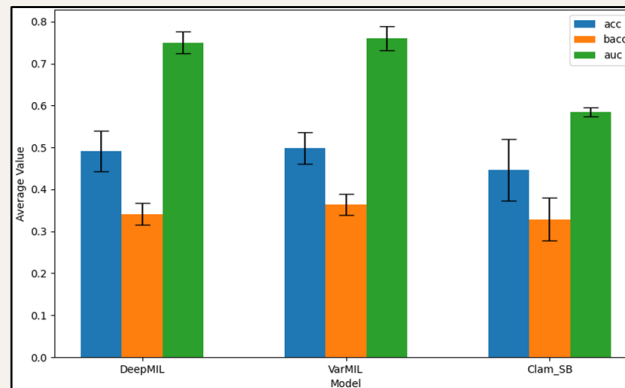
1. Time
  2. Recall
  3. Precision
  4. F1-Score
-

# DIAGNOSTIC

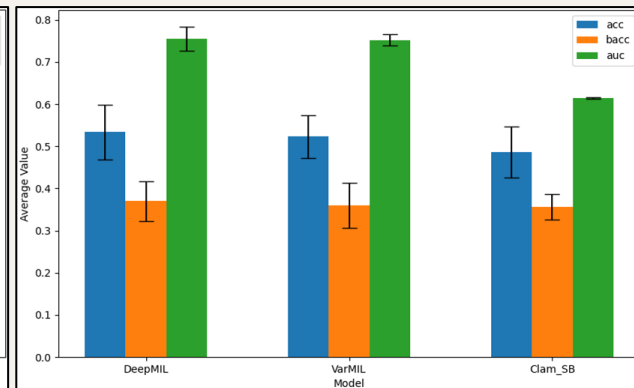
## CTransPath



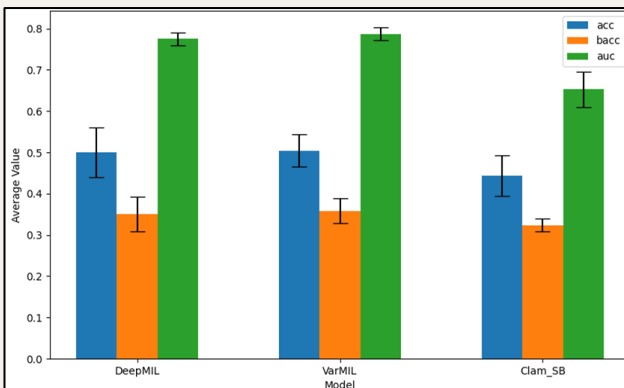
## Phikon



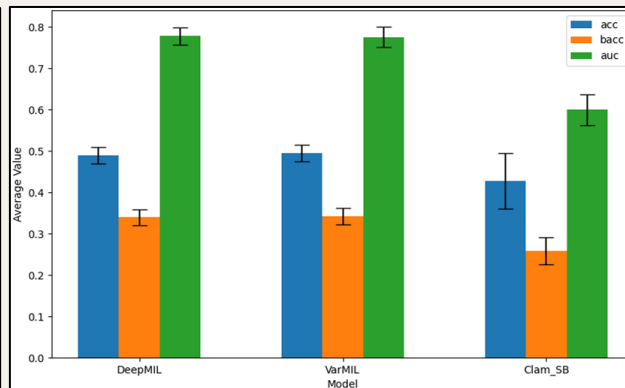
## UNI



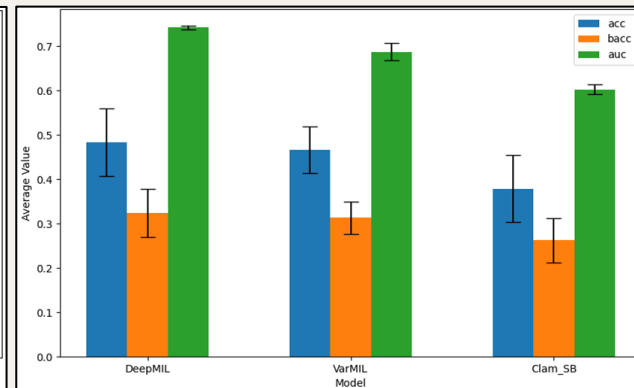
## Lunit-Dino



## PLIP

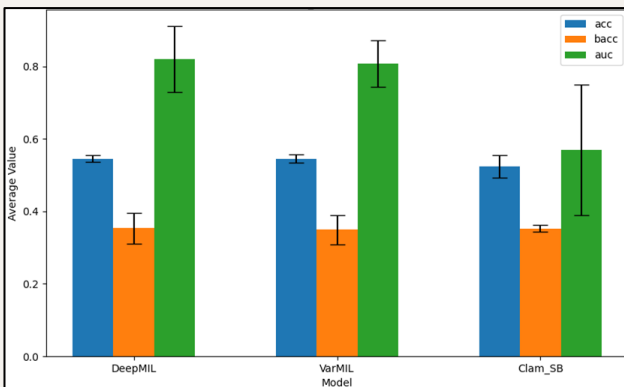


## vit

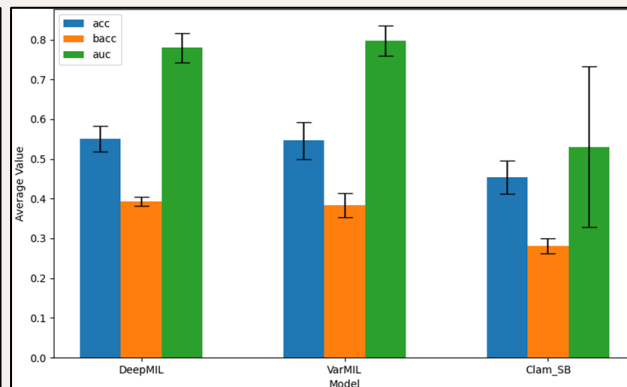


# FROZEN

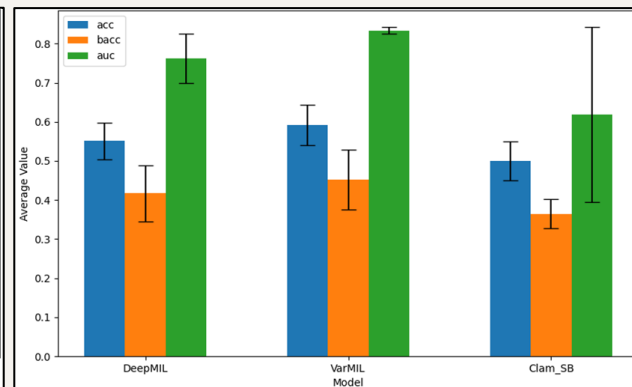
## CTransPat



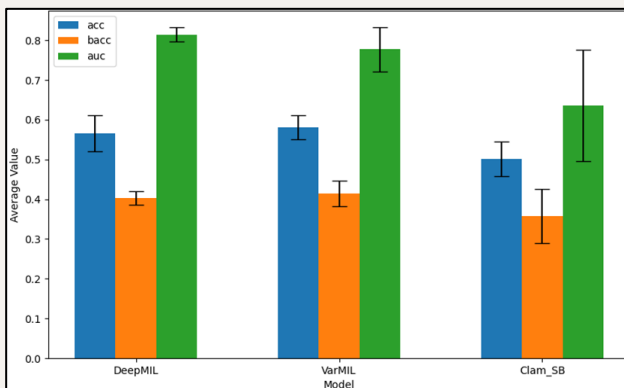
## Phikon



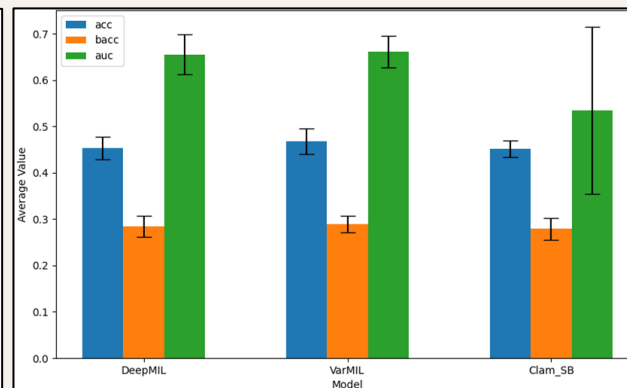
## UNI



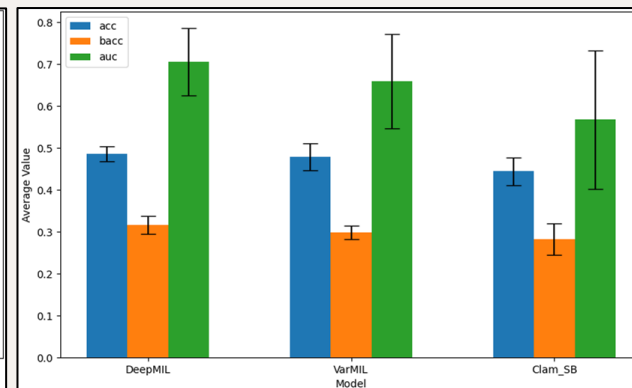
## Lunit-Dino



## PLIP



## vit



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# Summary of Findings

## **Observations:**

- CTransPath, Phikon and UNI were the Highest Performing Encoders
- DeepMIL and VarMIL Consistently Provided the Highest Metrics
- AUC Varied the Most Between Models while BACC Varied the Least

## **Future Work:**

- Implement Hyperparameter Tuning (Learning Rate, Weight Decay etc.)
  - Experiment with Multi-Headed Attention Mechanisms or Hybrid Variants
  - Use Cross-Validation to Prevent Over-Fitting and Increase Robustness
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# Information Visualization

**Purpose:** Determine Relationships Between Subtypes

**Input:** 458 Diagnostic + 463 Frozen .h5 Files for 20x Mag.,  
Manifest File (patient\_id, slide\_id, subtype, slide\_path)

**Output:** UMAP Plots



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graph TD; A[Output: UMAP Plots] --> B[Slide-Level]; A --> C[Patch-Level];
```

## Slide-Level

Mean Pooling of 1,500  
Patches + Filtering of  
Features with No Subtypes

Eg: (1,500, 768) → (1, 768)

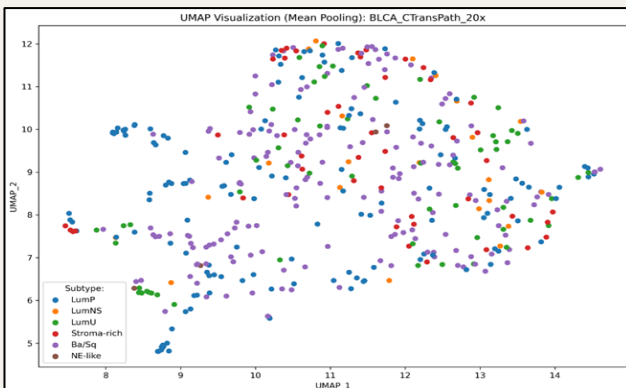
## Patch-Level

Random Selection of 150  
Patches + Filtering of  
Features with No Subtypes

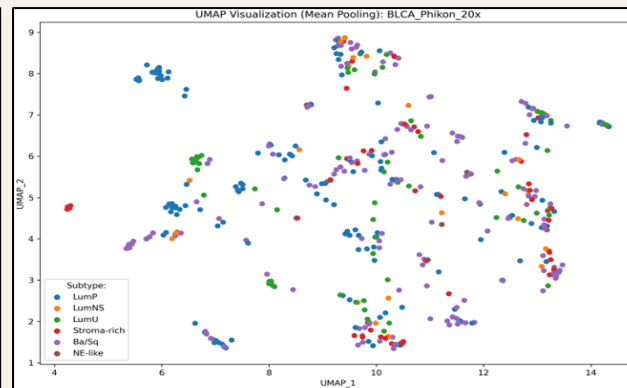
Eg: (1,500, 768) → (150, 768)

# DIAGNOSTIC (Slide-Level)

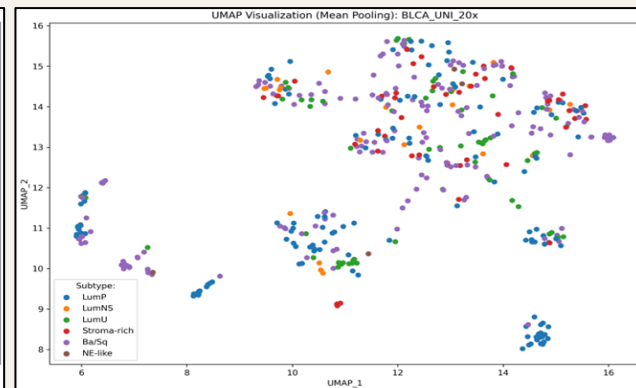
## CTransPath



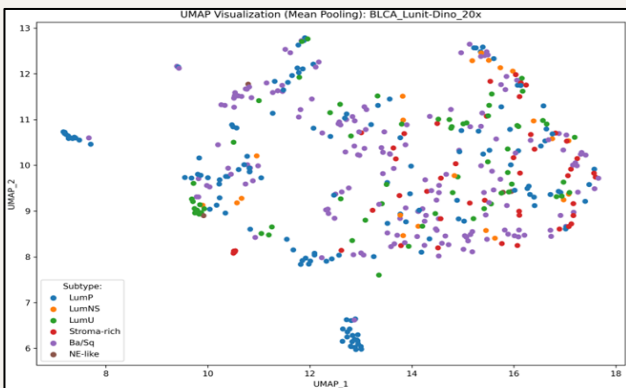
## Phikon



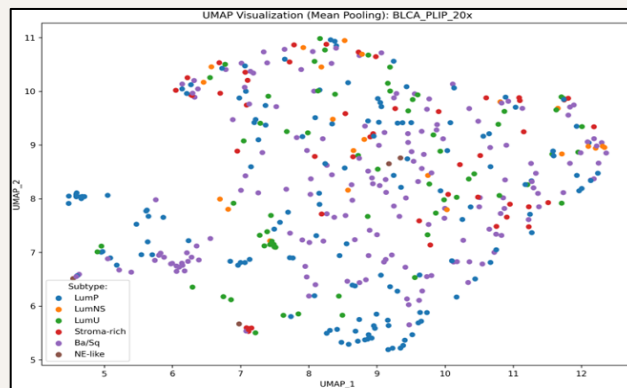
## UNI



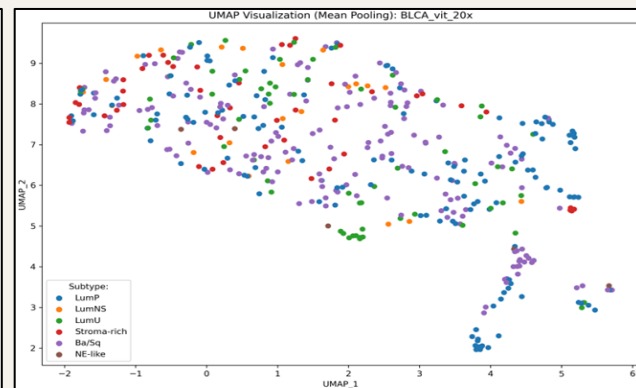
## Lunit-Dino



## PLIP



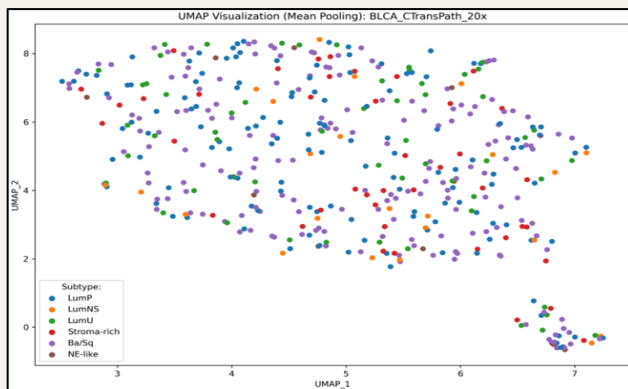
## vit



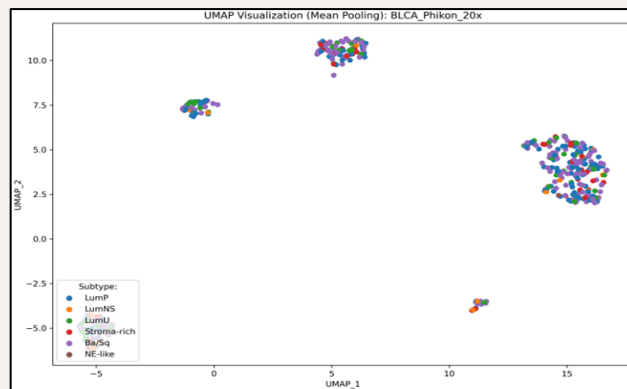


# Frozen (Slide-Level)

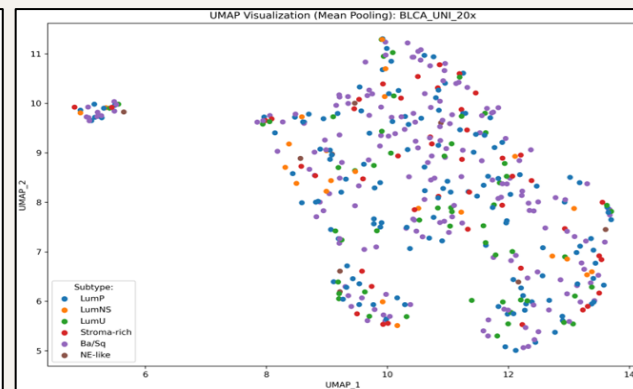
## CTransPath



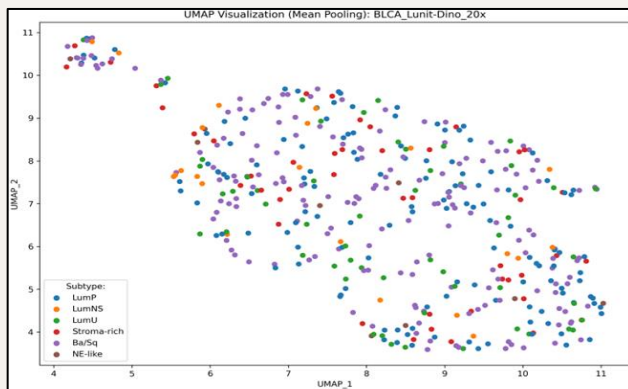
## Phikon



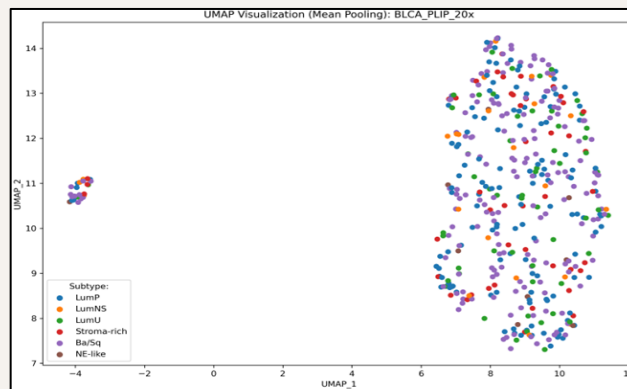
## UNI



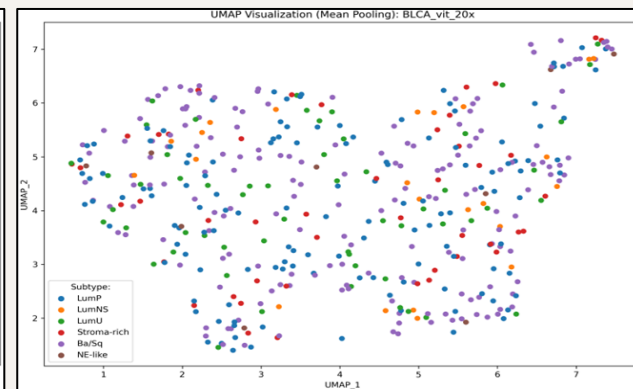
## Lunit-Dino



## PLIP

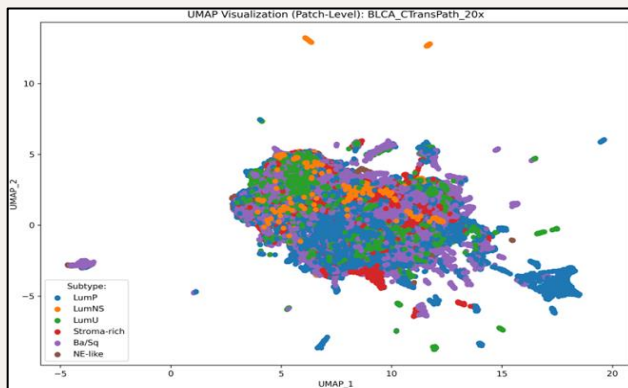


## vit

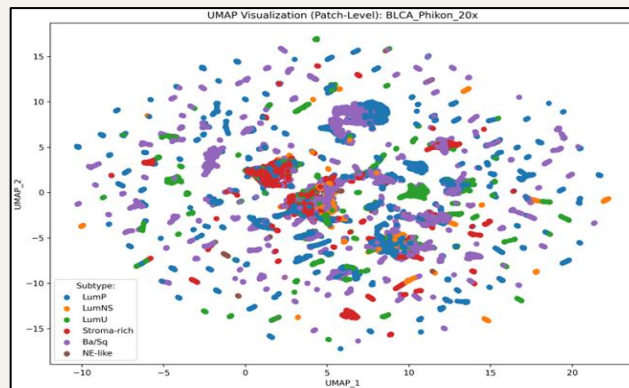


# DIAGNOSTIC (Patch-Level)

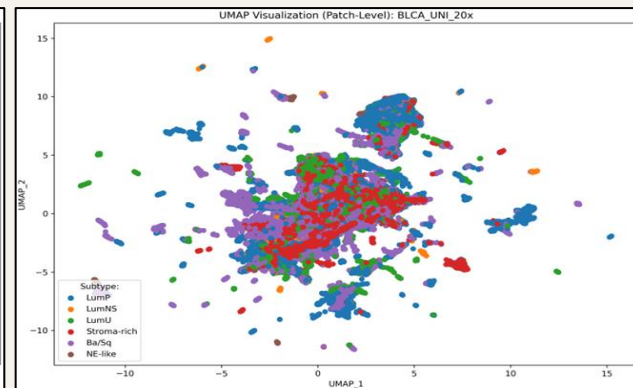
## CTransPath



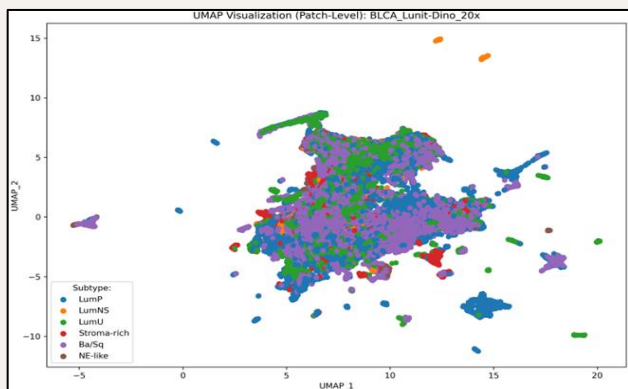
## Phikon



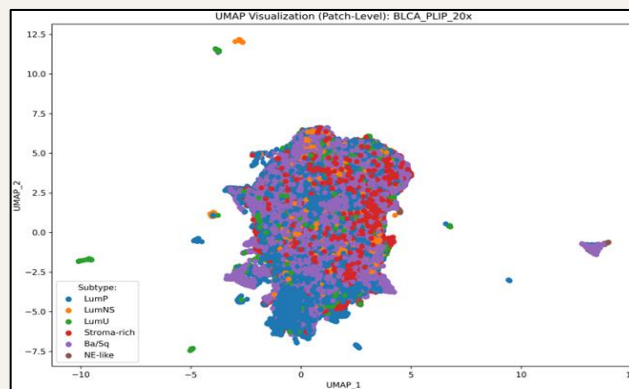
## UNI



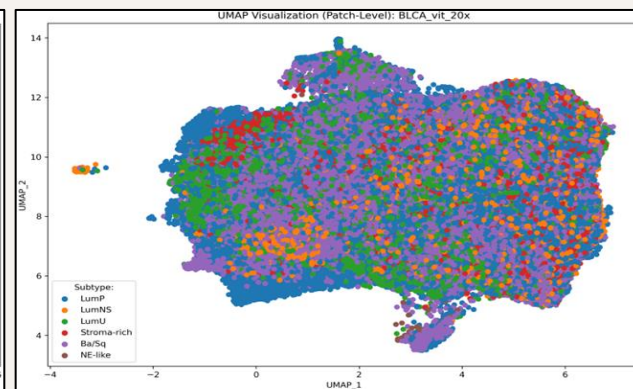
## Lunit-Dino



## PLIP

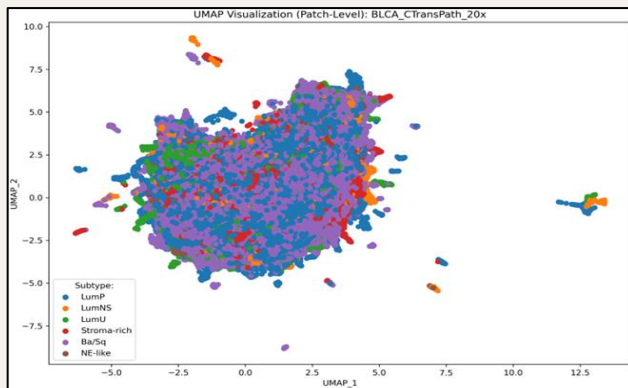


## vit

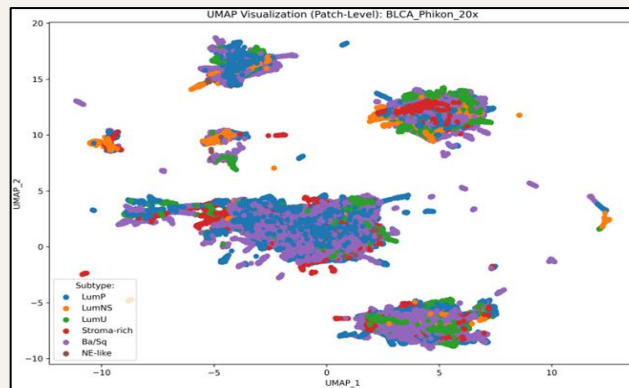


# FROZEN (Patch-Level)

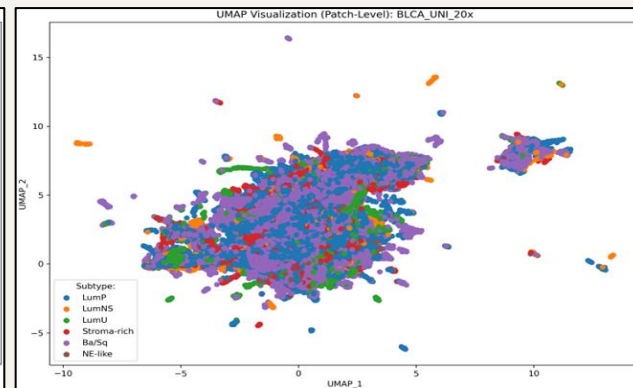
## CTransPath



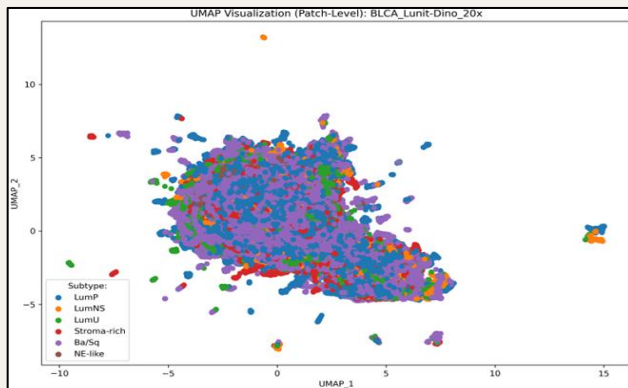
## Phikon



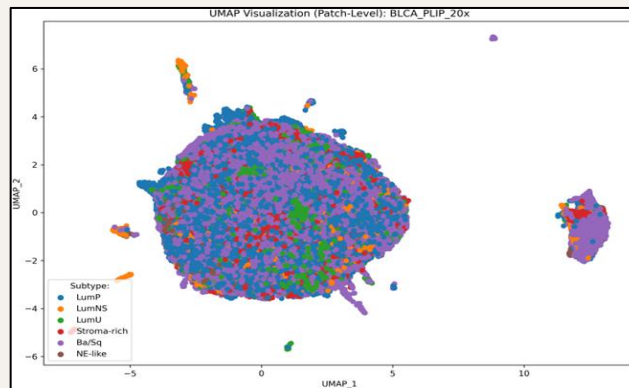
## UNI



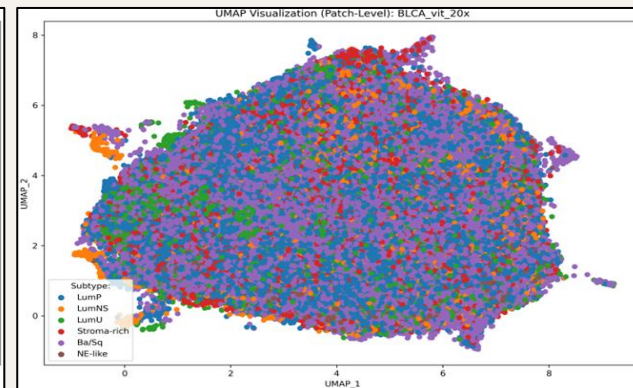
## Lunit-Dino



## PLIP



## vit



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# Summary of Findings

## **Observations:**

- Patch-Level UMAPs Provided Higher Granularity than Slide-Level UMAPs
- Patch-Level UMAPs Capture Data Diversity Better than Slide-Level UMAPs
- Patch-Level UMAPs Retain Local Patterns Better than Slide-Level UMAPs

## **Future Work:**

- Stratified Sampling Based on Patches of Interest + Extract More Samples
  - Implement Weighted Aggregation or Hierarchical Pooling at Slide-Level
  - Perform Dimensionality Reduction (PCA, t-SNE) Prior to UMAP Plotting
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# Acknowledgements

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# Questions?

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