

August 22, 2024

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

Artificial Intelligence in Medicine (AIM) Lab



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

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European Association of Urology (EAU).

Overview

Bladder Cancer:

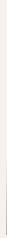
Urothelial Carcinoma Originating in Tissues of the Urinary System

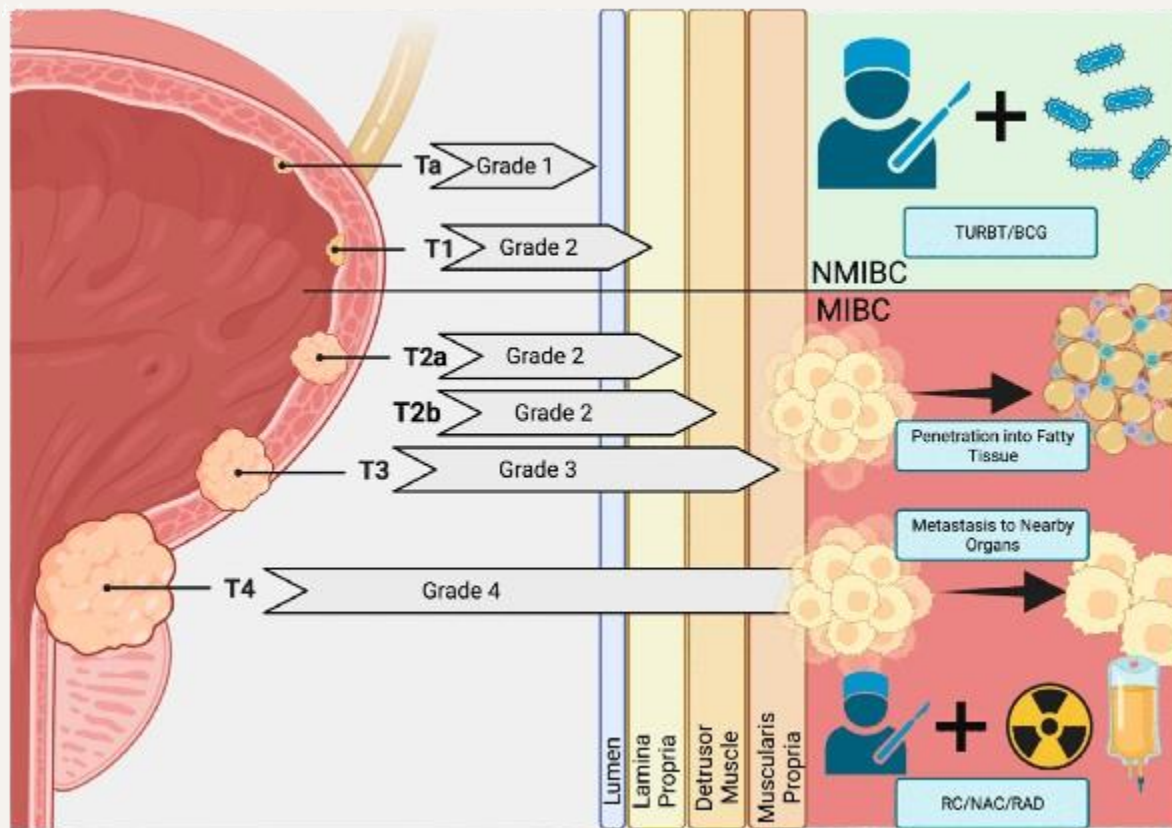
Non-Muscle Invasive Bladder Cancer

Superficial Cancer Confined to
Mucosa Layer

Muscle-Invasive Bladder Cancer

Aggressive Cancer Penetrating
Muscle Layer





Introduction

Existing Classification Systems:

Diversity of Molecular Subtypes Impedes Clinical Application



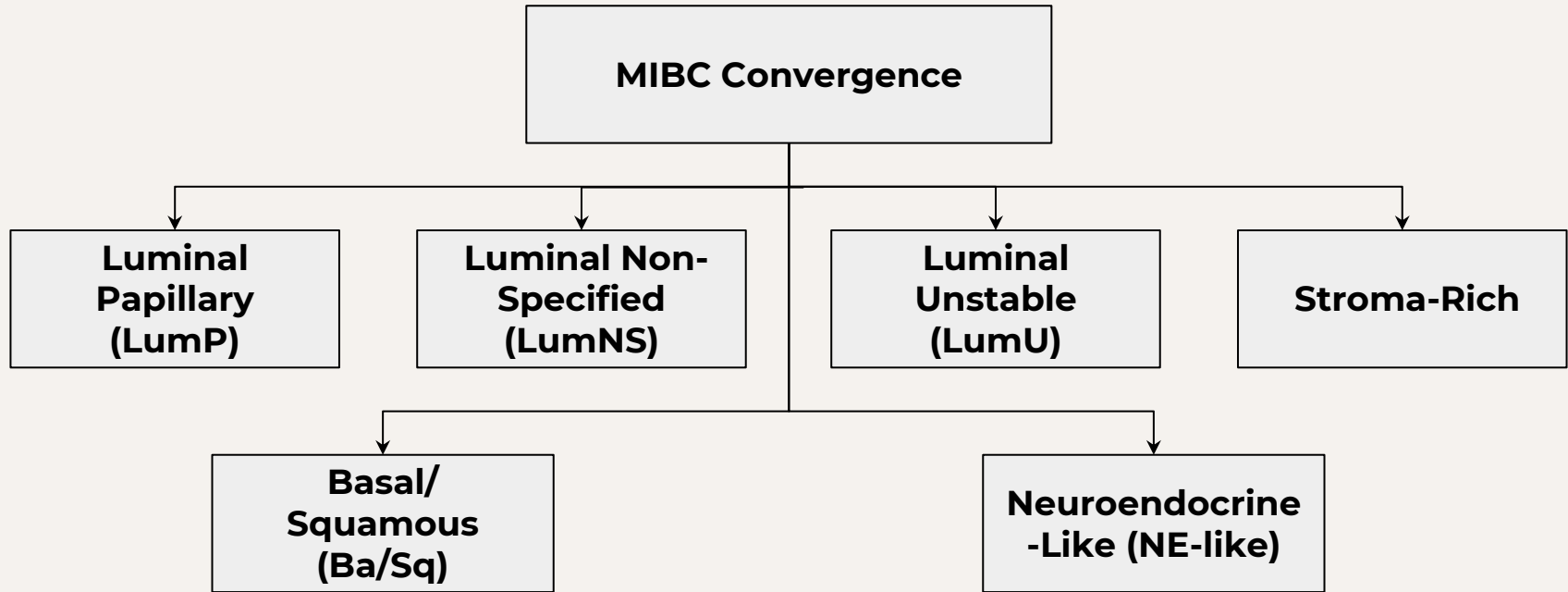
Lack of Naming Convention + Data Variability

Research Objective:

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

Consensus Classification

Implementation: Nearest-Centroid Transcriptomic Classifier in R



Analytical Workflow

Patch Extraction



Feature Extraction



Multiple Instance Learning (MIL)



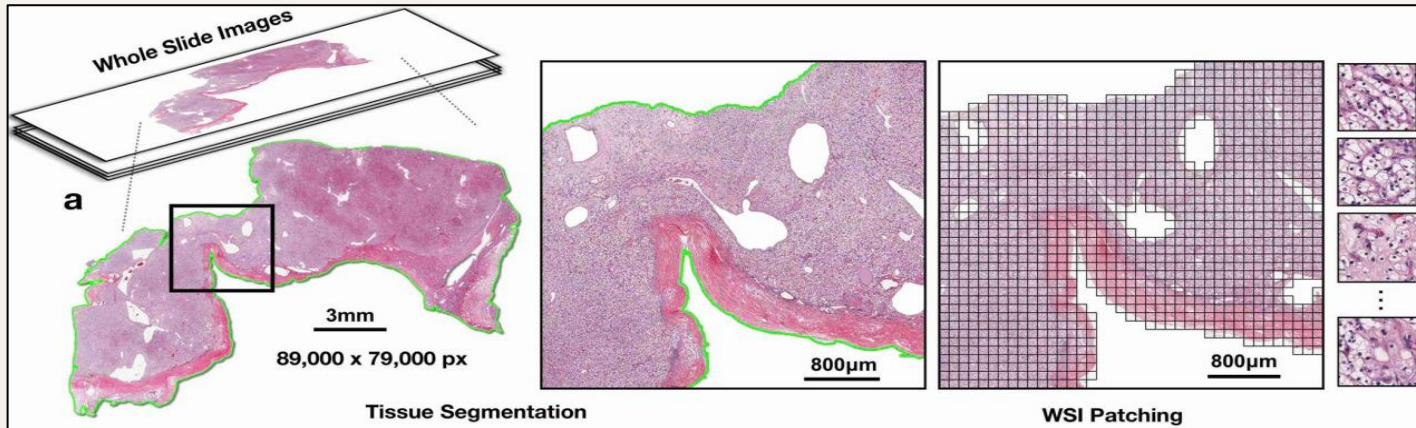
Information Visualization

Patch Extraction

Purpose: Facilitate Localized Deep Learning

Input: Masks Pre-Selected from HistoQC

Output: 1,500 Patches Per Whole Slide Image

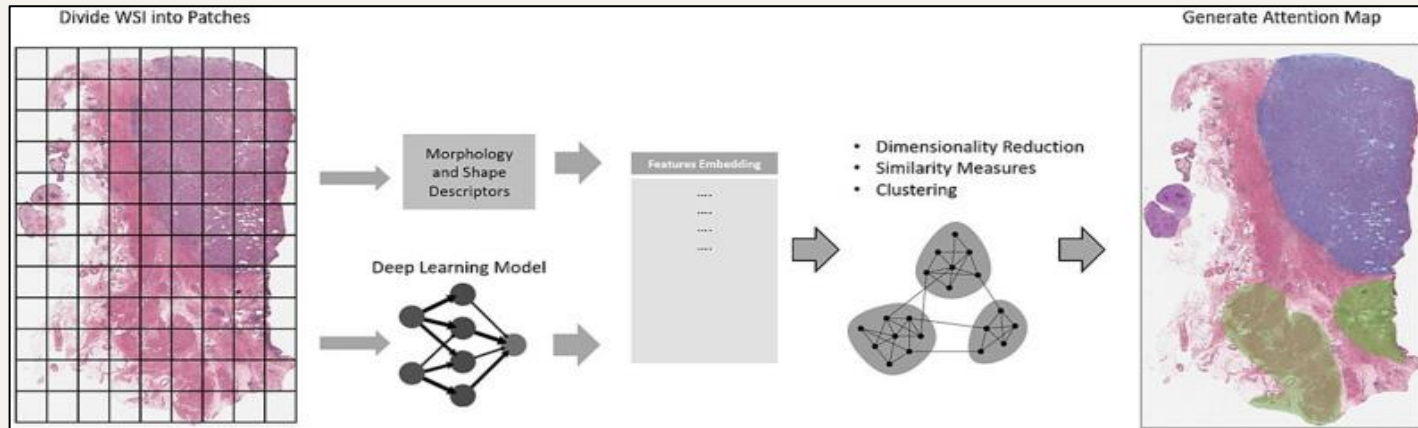


Feature Extraction

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

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:

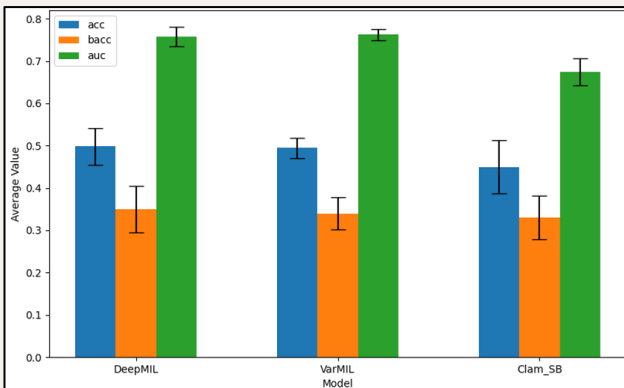
1. Accuracy
2. Bal. Accuracy
3. AUC

Others:

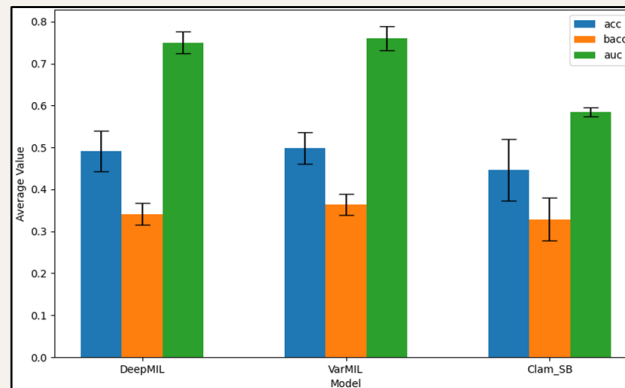
1. Time
 2. Recall
 3. Precision
 4. F1-Score
-

DIAGNOSTIC

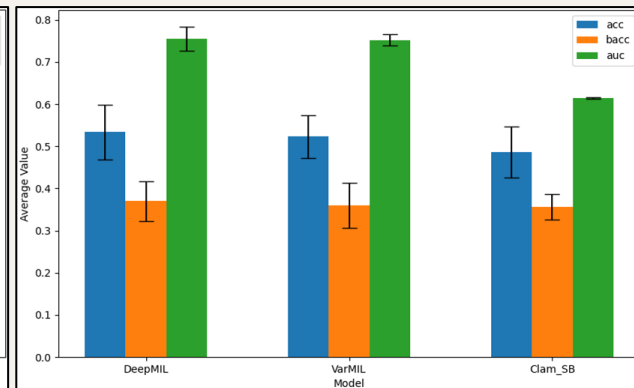
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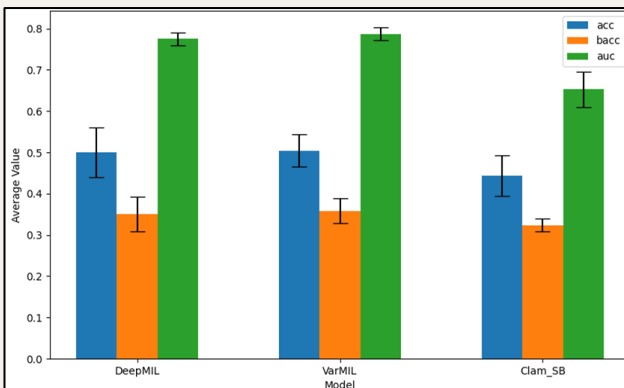
Phikon



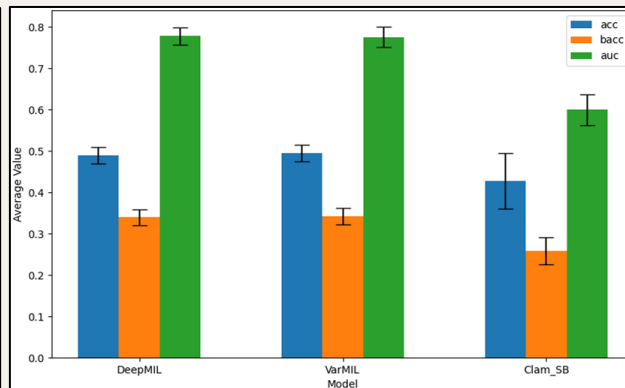
UNI



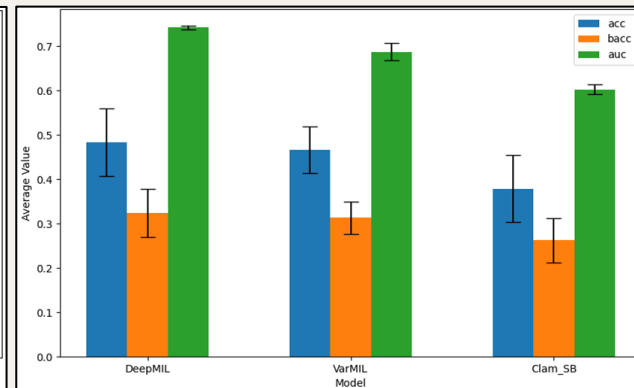
Lunit-Dino



PLIP

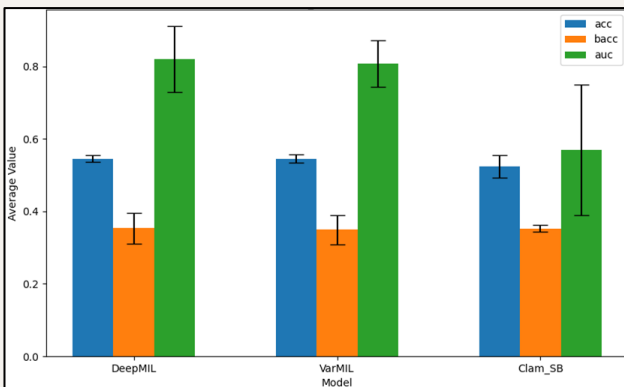


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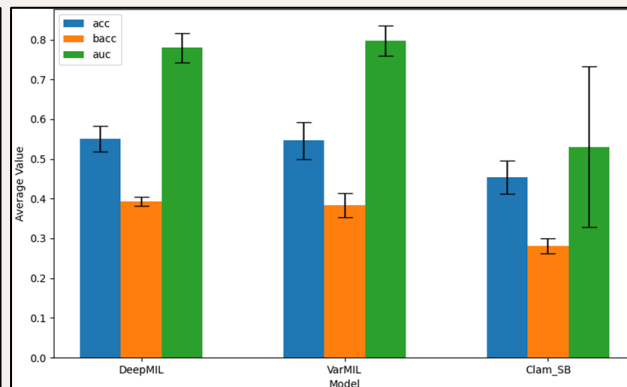


FROZEN

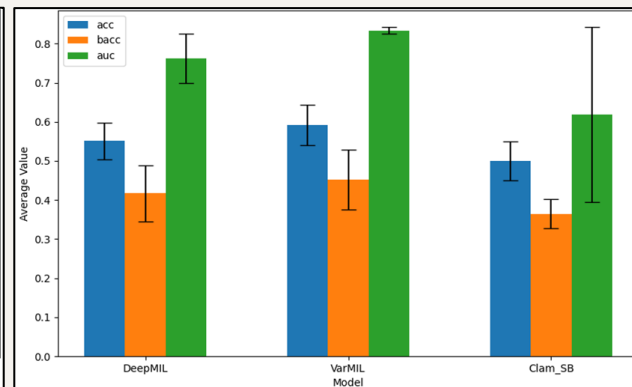
CTransPat



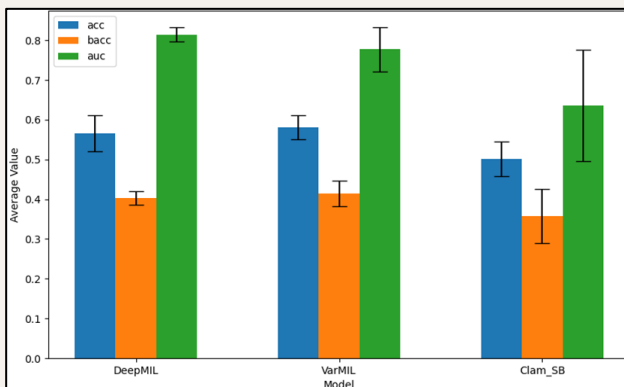
Phikon



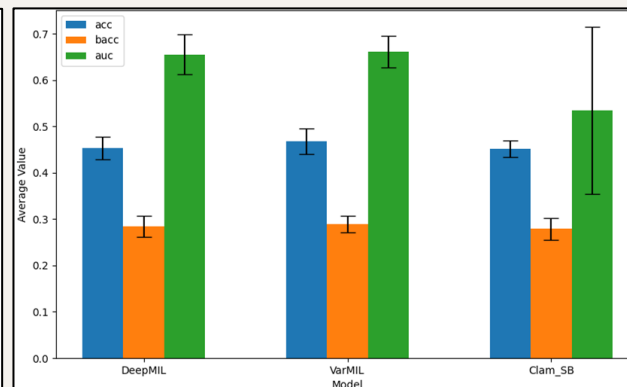
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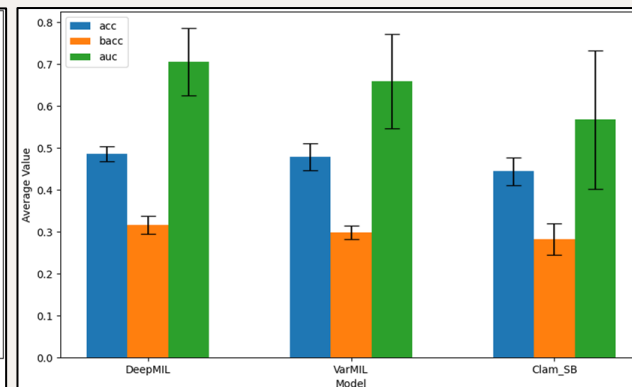
Lunit-Dino



PLIP



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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
-

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



```
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)

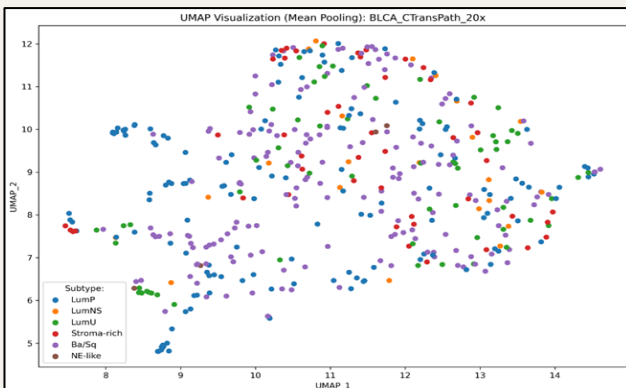
Patch-Level

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

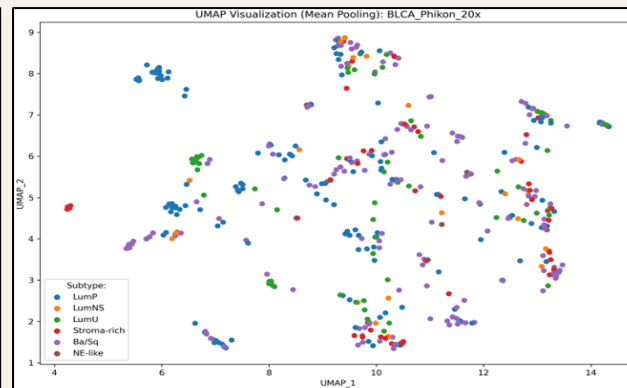
Eg: (1,500, 768) → (150, 768)

DIAGNOSTIC (Slide-Level)

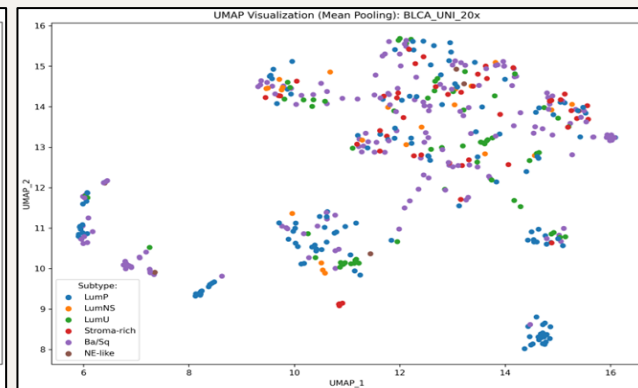
CTransPath



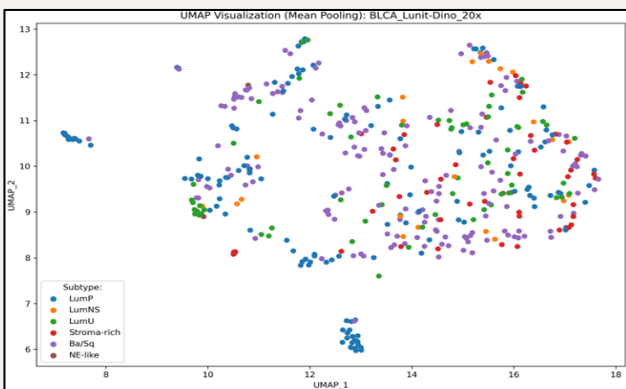
Phikon



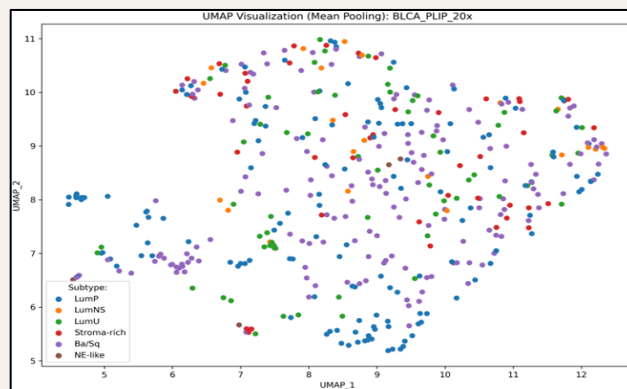
UNI



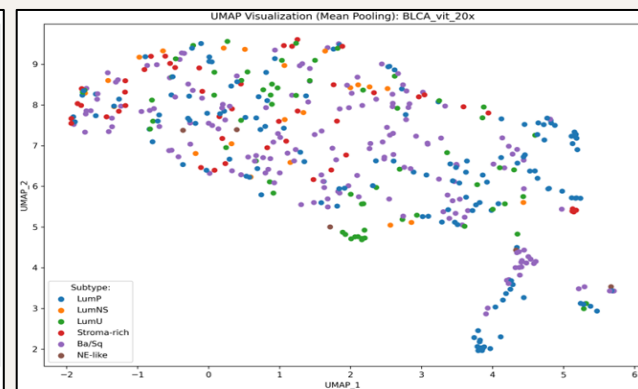
Lunit-Dino



PLIP

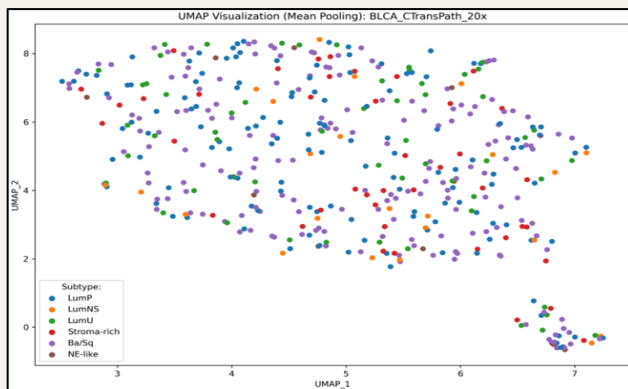


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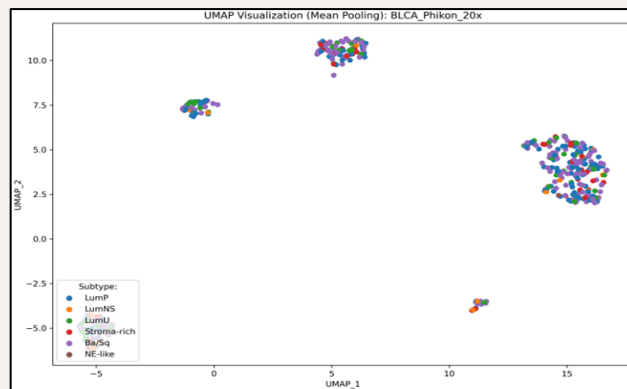


Frozen (Slide-Level)

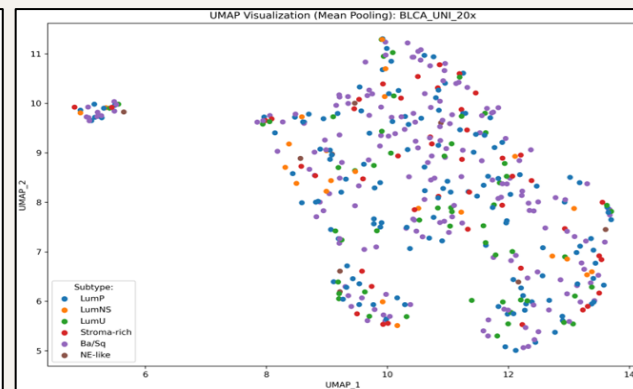
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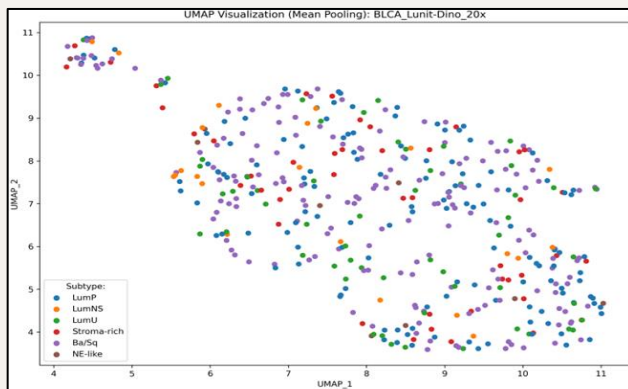
Phikon



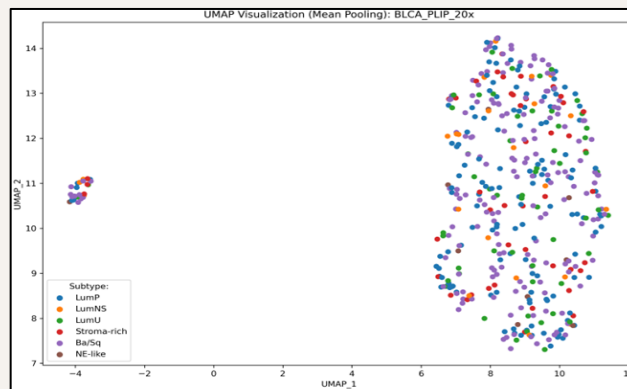
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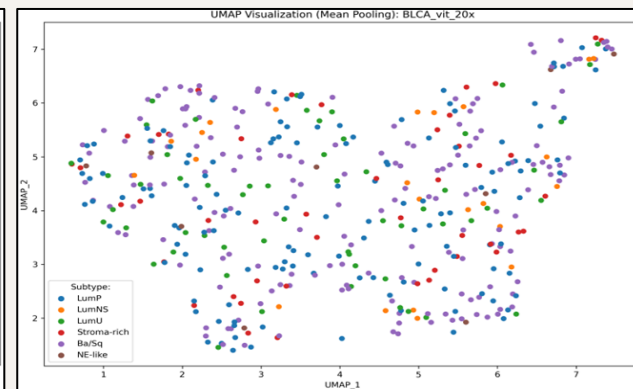
Lunit-Dino



PLIP

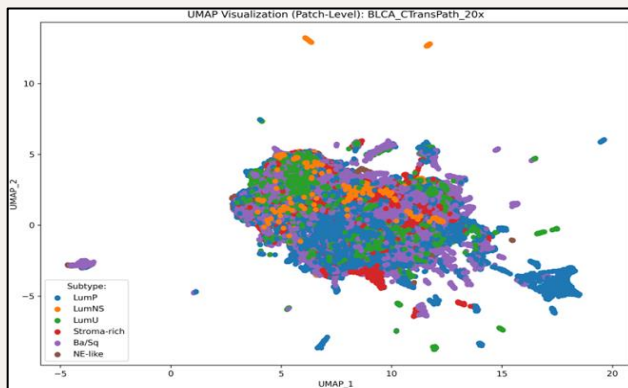


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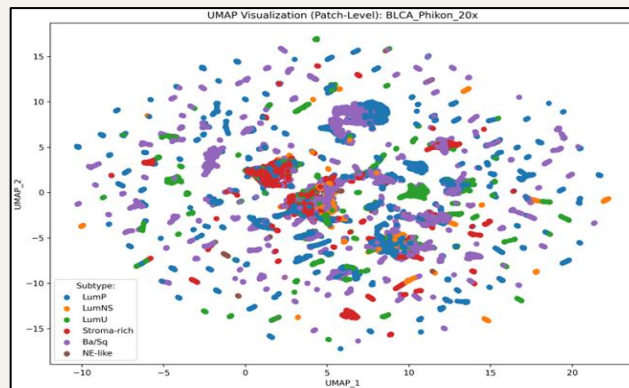


DIAGNOSTIC (Patch-Level)

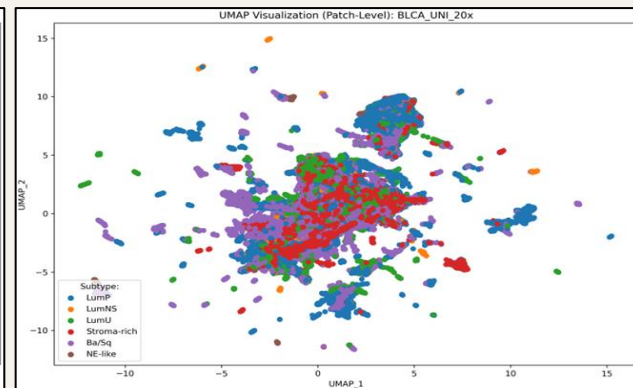
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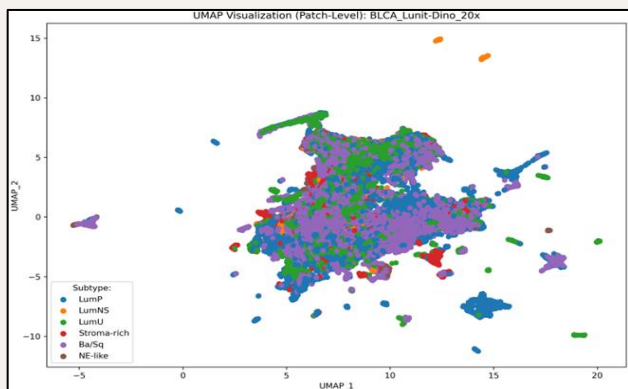
Phikon



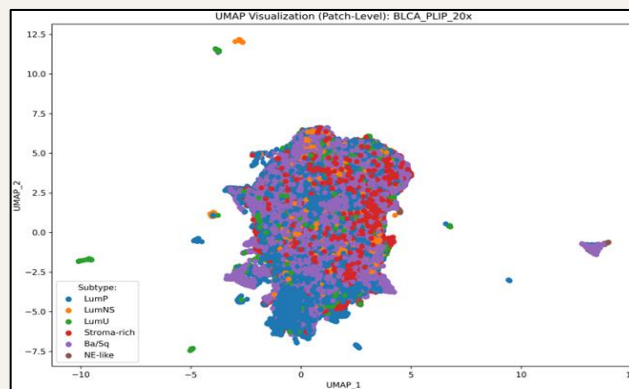
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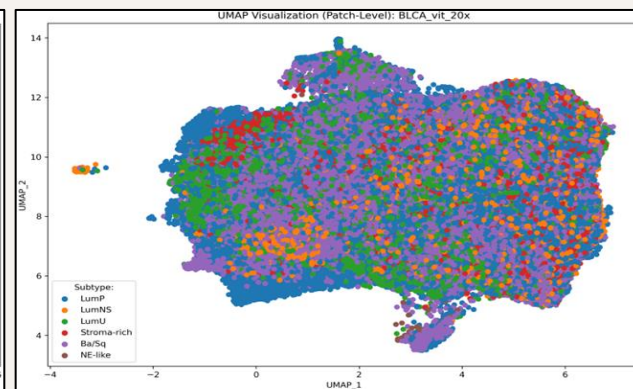
Lunit-Dino



PLIP

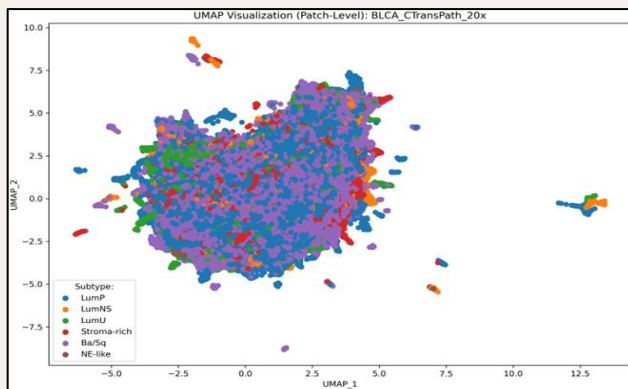


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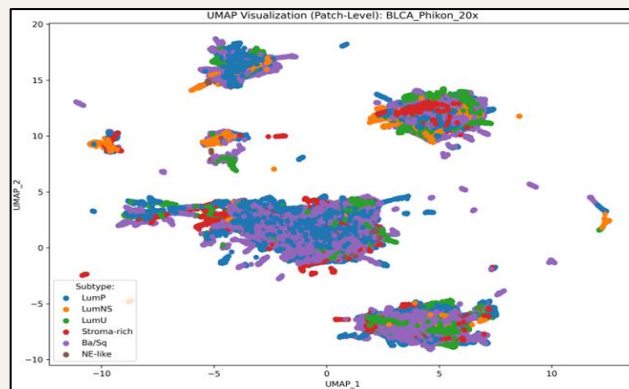


FROZEN (Patch-Level)

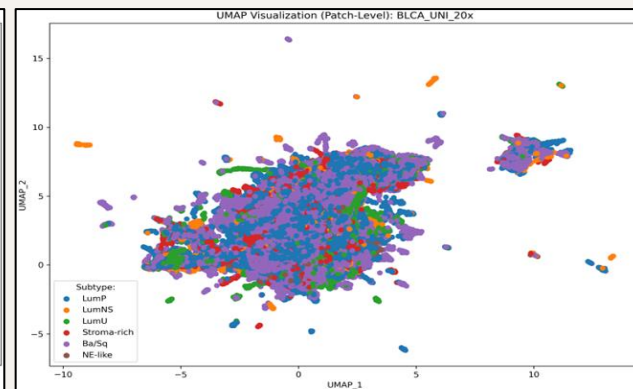
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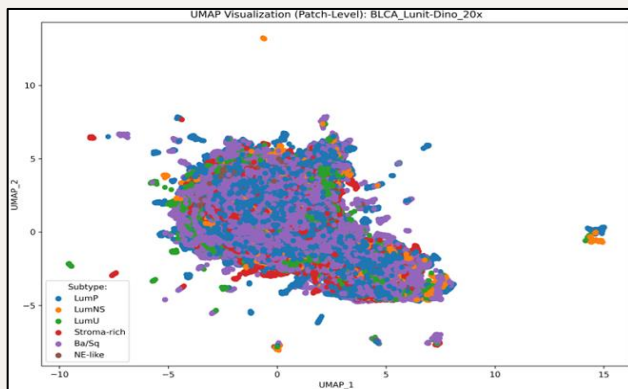
Phikon



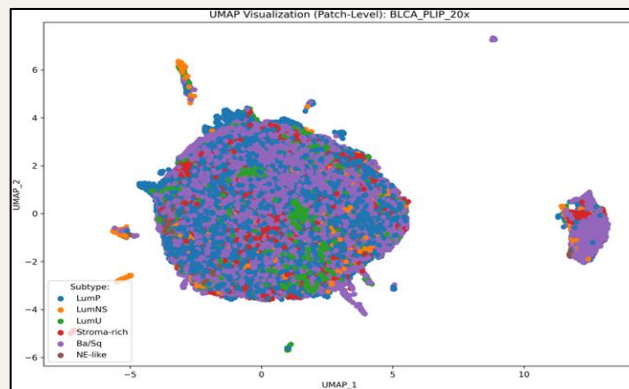
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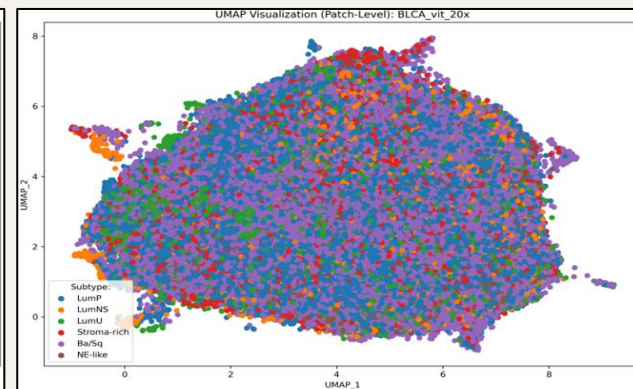
Lunit-Dino



PLIP



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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 Aggression or Hierarchical Pooling at Slide-Level
 - Perform Dimensionality Reduction (PCA, t-SNE) Prior to UMAP Plotting
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Acknowledgements

Questions?
