

A Multi-Granularity Approach to Similarity Search in Multiplexed Immunofluorescence Images

Jennifer Yu^{1,2}, Zhenqin Wu¹, Aaron T. Mayer¹, Alexandro Trevino¹, James Zou^{1,3,4,5}

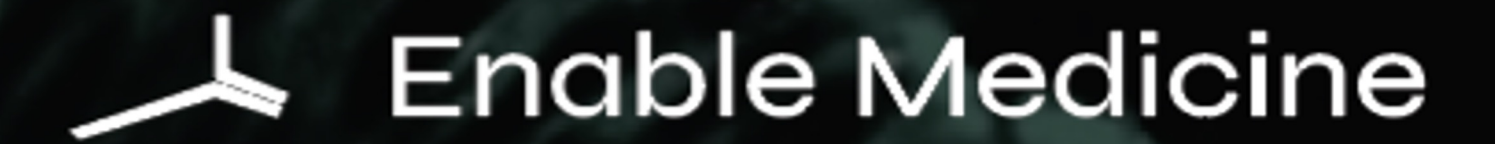
¹Enable Medicine, Menlo Park, CA 94025, USA

²Department of Computer Science, University of Toronto Toronto, ON M5S 2E4, Canada

³Department of Electrical Engineering, Stanford University, Stanford, CA 94305, USA

⁴Department of Computer Science, Stanford University, Stanford, CA 94305, USA

⁵Department of Biomedical Data Science, Stanford University, Stanford, CA 94305, USA



INTRODUCTION

Recent advancements in AI, particularly in self-supervised learning, have shown significant promise in extracting meaningful features from medical images for tasks like classification and similarity search. State of the art models excel in retrieving hematoxylin and eosin stain (H&E) images. However, there is a lack of a specialized image search pipeline for multiplex immunofluorescence (mIF) images. Although mIF image is also microscopic like H&E, it is more challenging because of:

- High dimensionality
- Domain-specificity
- Complex molecular information

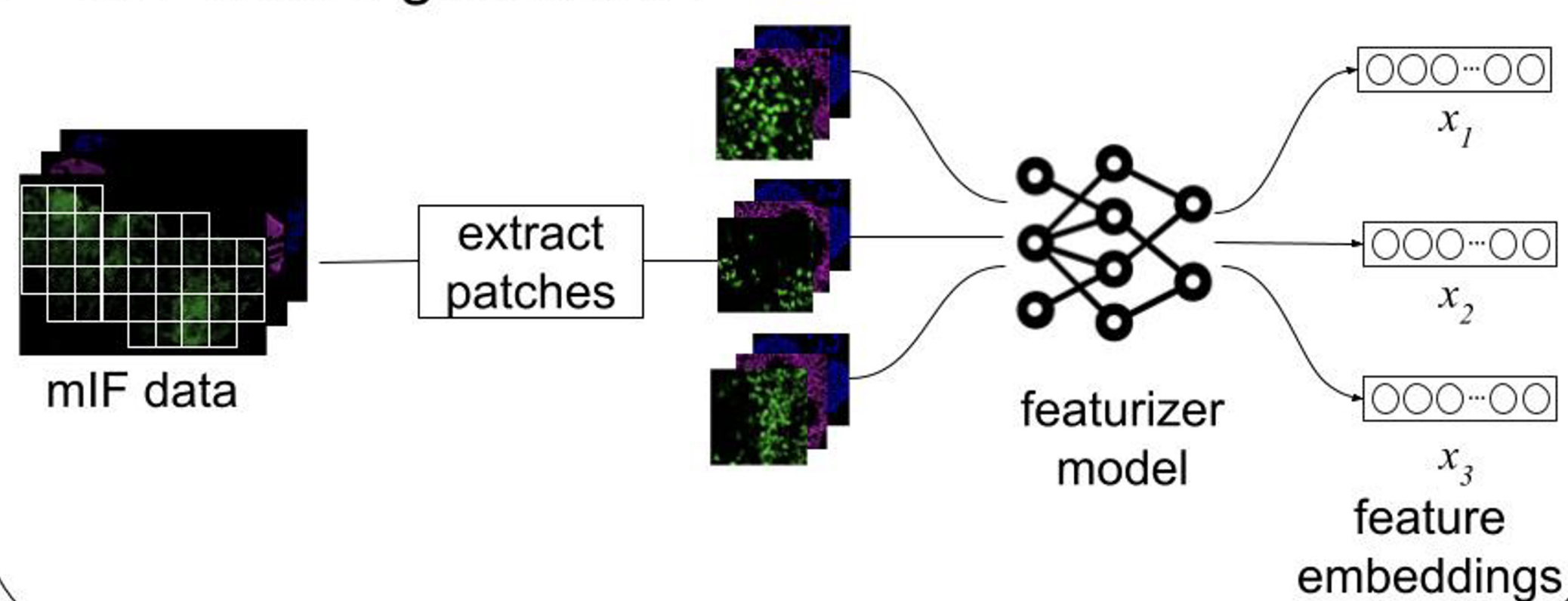
OBJECTIVE

Our objective is to not only identify similar patches but also to aggregate patch-level results for a more multi-level search. This requires a sophisticated similarity search pipeline that can pinpoint similarities across various granularities, providing numerous clinical advantages:

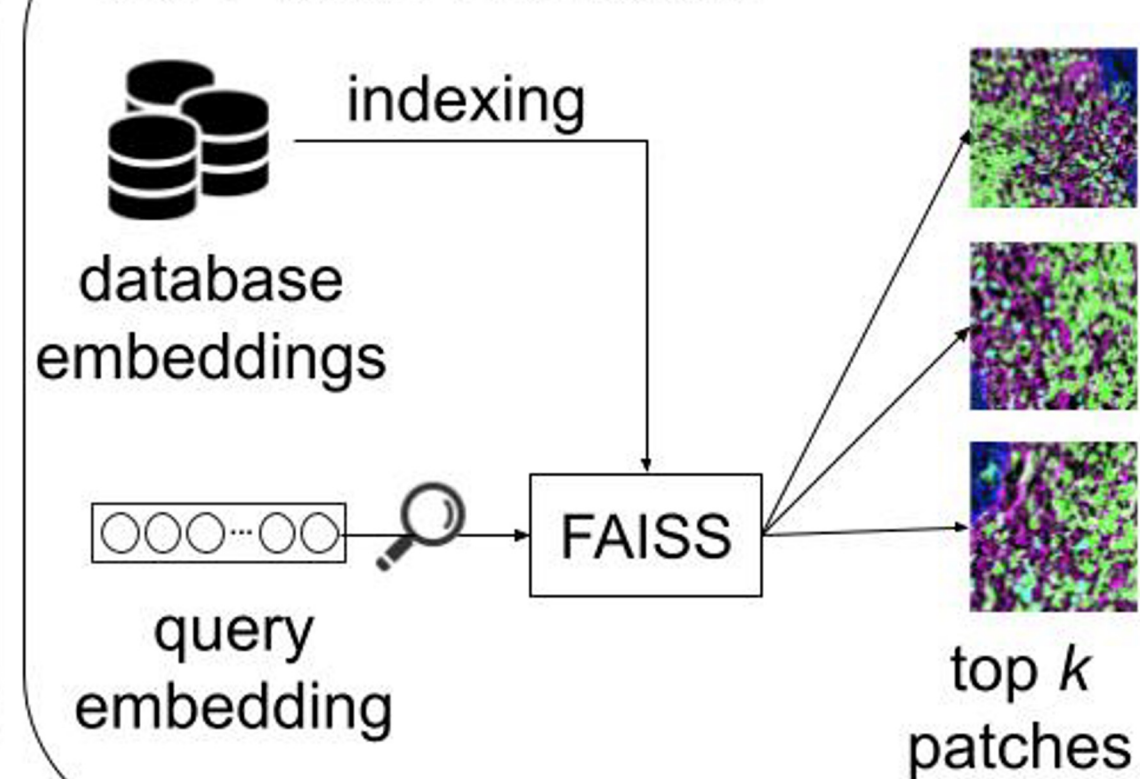
- Accelerate data labeling process
- Enable a more holistic clinical analysis, like retrieving diagnoses or tissue states
- Determine patient outcomes
- Develop new biomarkers

METHOD

A. Feature generation



B. Patch retrieval



C. Patient retrieval

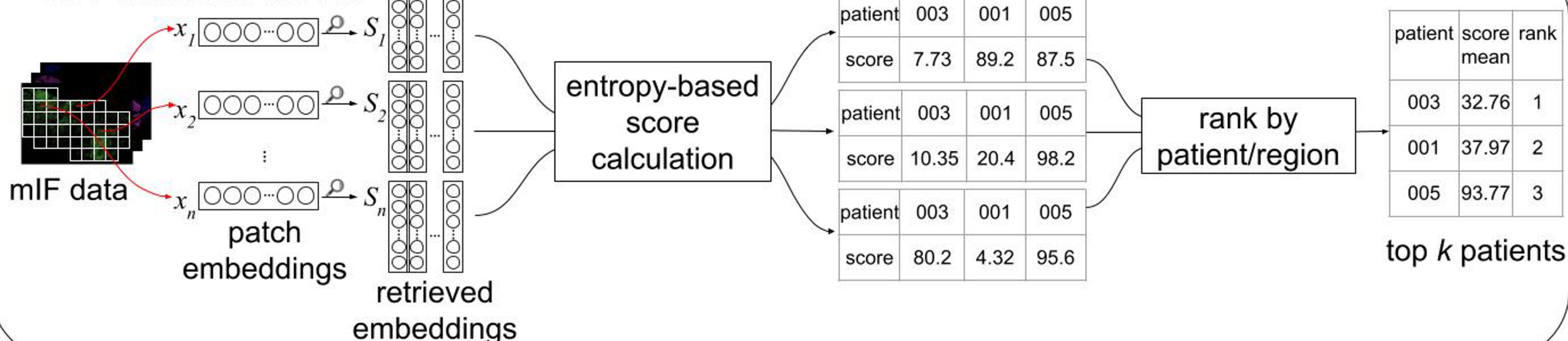


Figure 1: The MISS framework overview

RESULTS

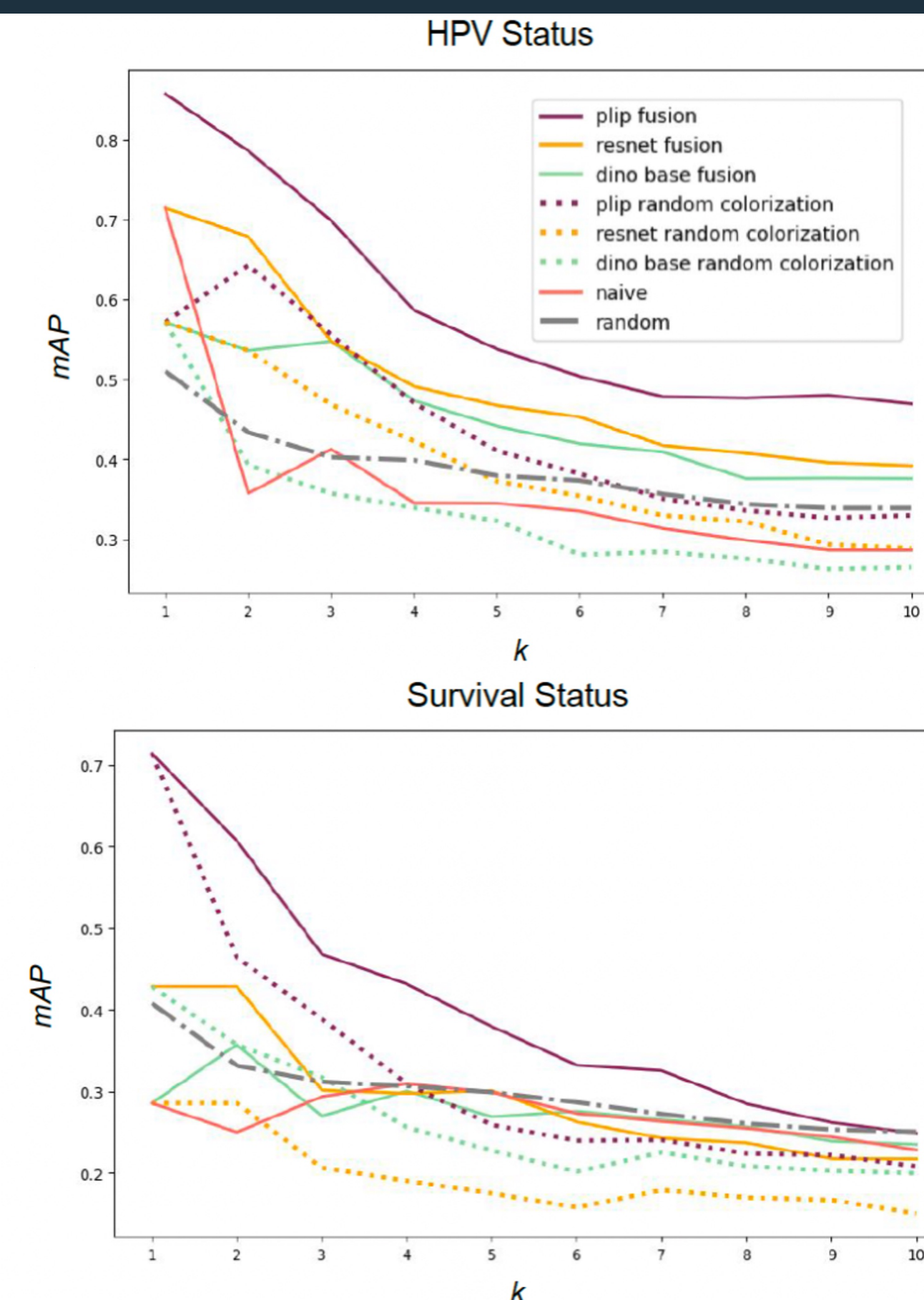


Figure 2: Cross-study evaluation on patient-level: PLIP outperformed other models in retrieving patients of the same clinical outcomes.

distal tubules

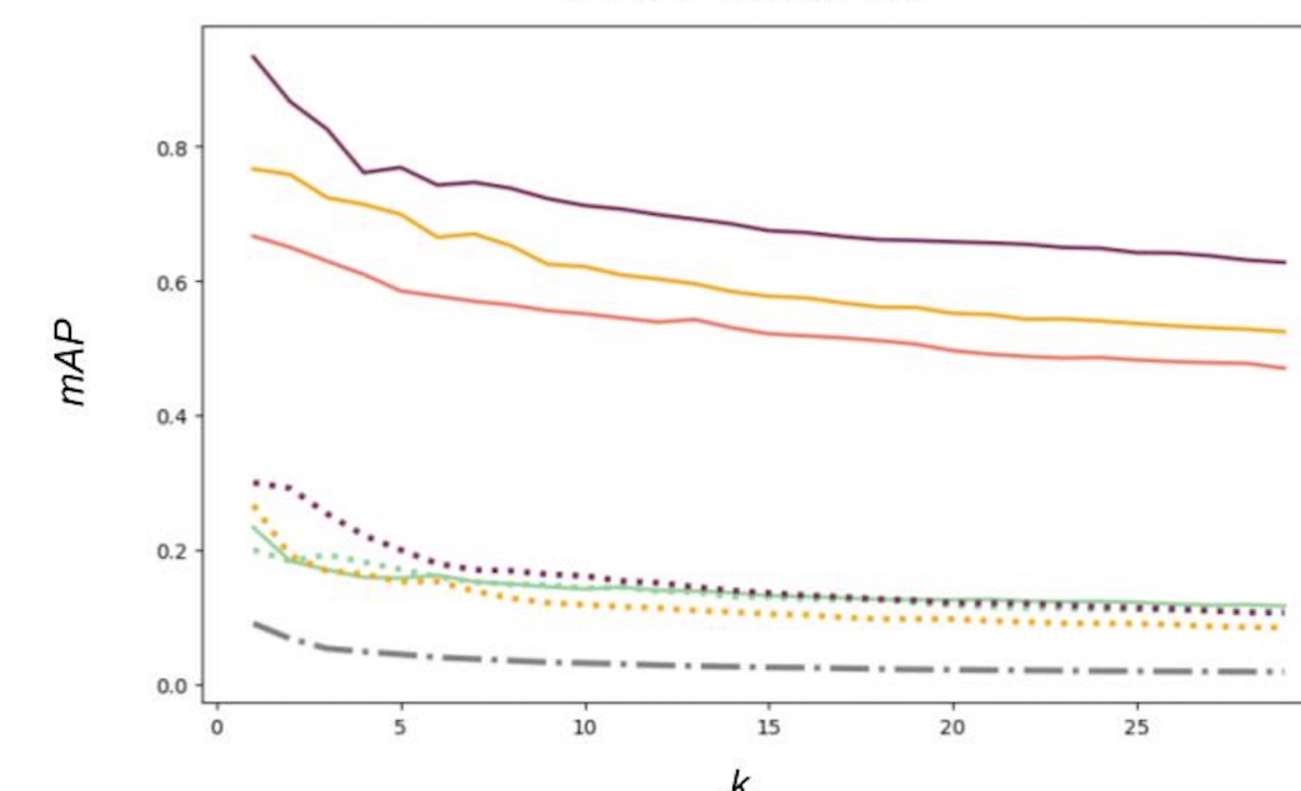


Figure 3: Patch level result

CASE STUDY

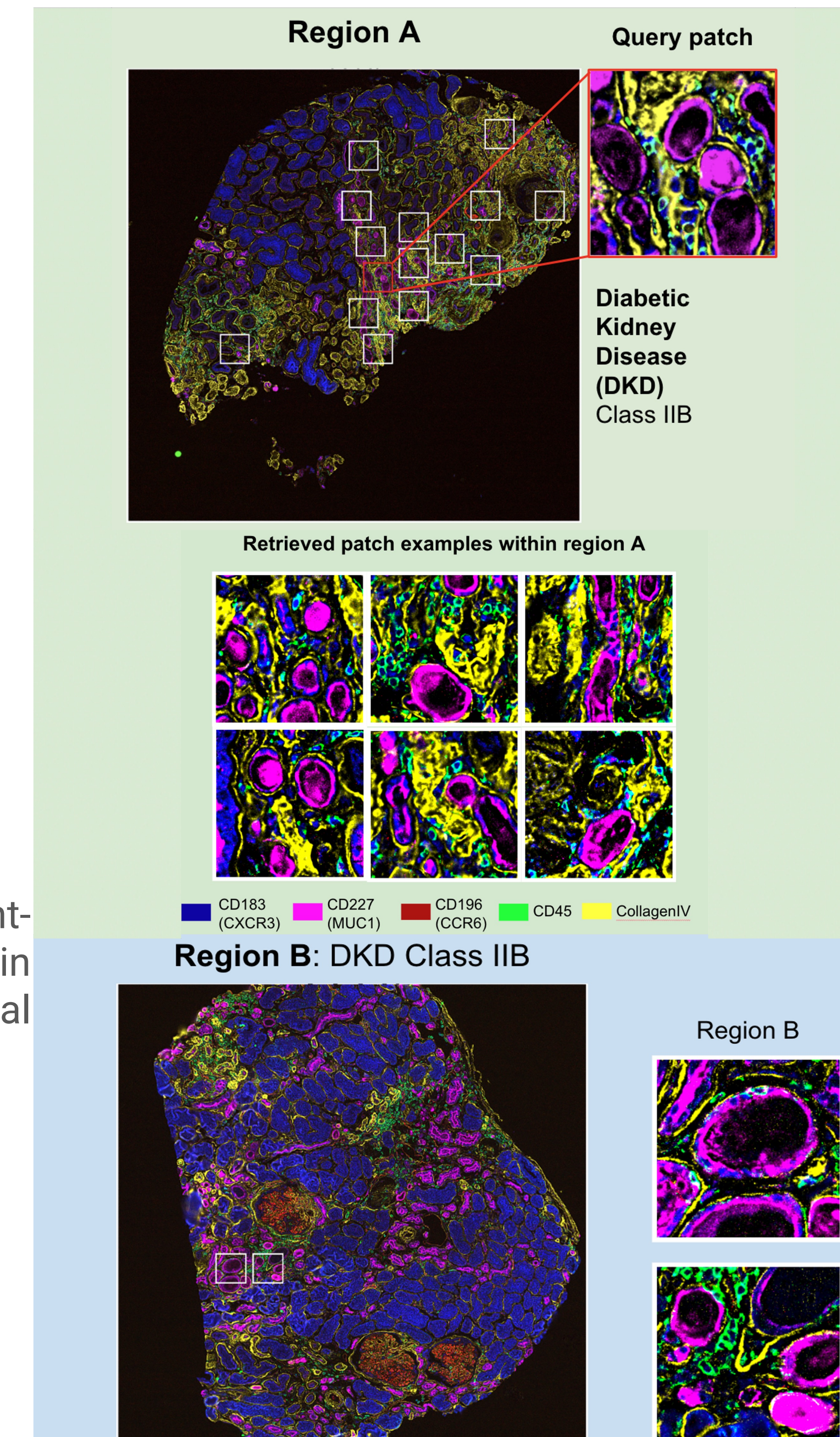


Figure 4: Case study on an example from the DKD Kidney study

CONCLUSION

1. Our evaluations on datasets from different tissues demonstrated the robustness and effectiveness of the MISS framework.
2. **Potential for Specialized Pre-Trained Models on mIF:** PLIP's success in mIF image search suggests the possibility of developing specialized pre-trained models for mIF images.
3. **Future works:** Improve computational efficiency, incorporate uncommon biomarkers, encompass more spatial omics modalities and diseases and develop a user-friendly interface for broader clinical & research applications.