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

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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:

- 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

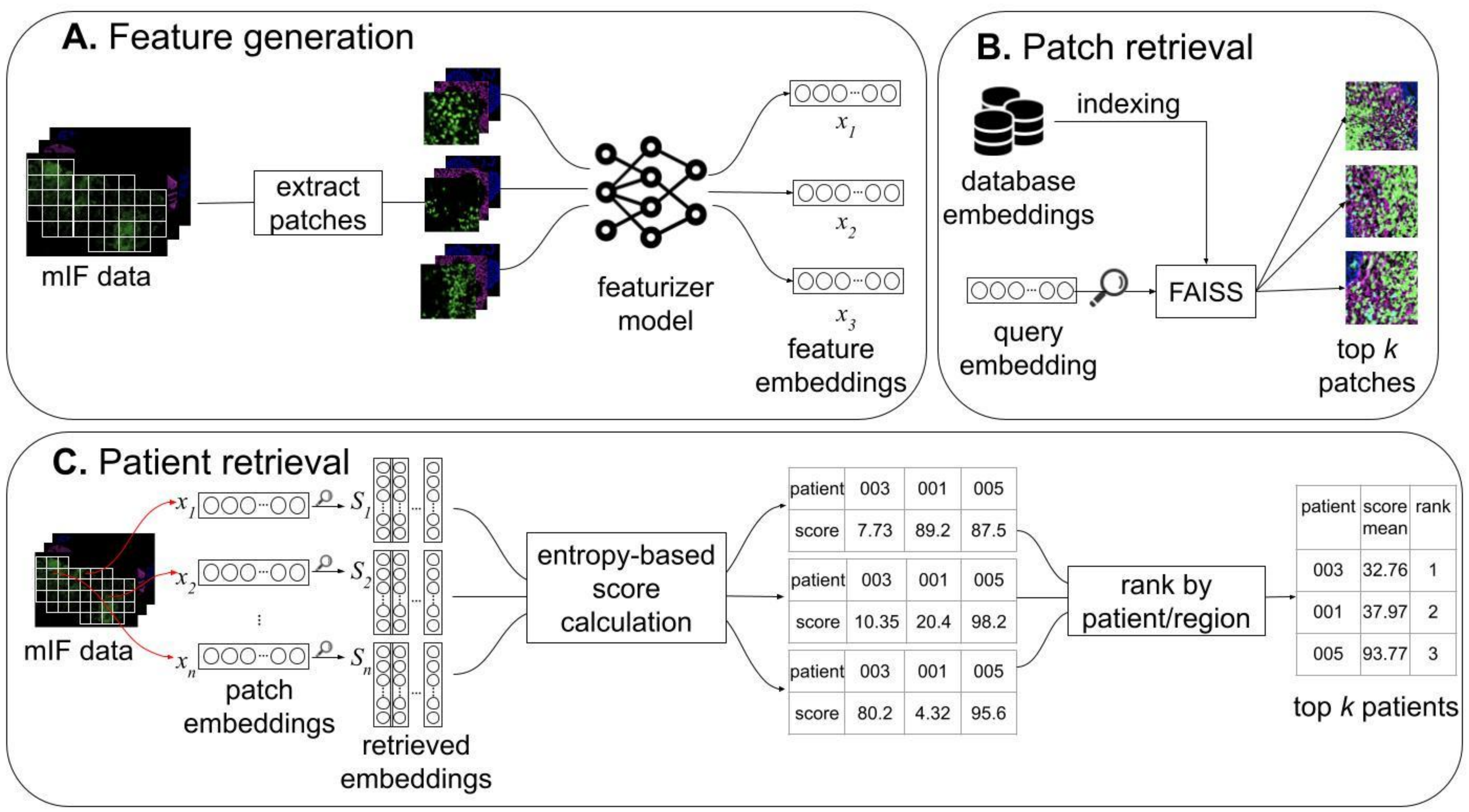

Figure 1: The MIISS framework overview

RESULTS

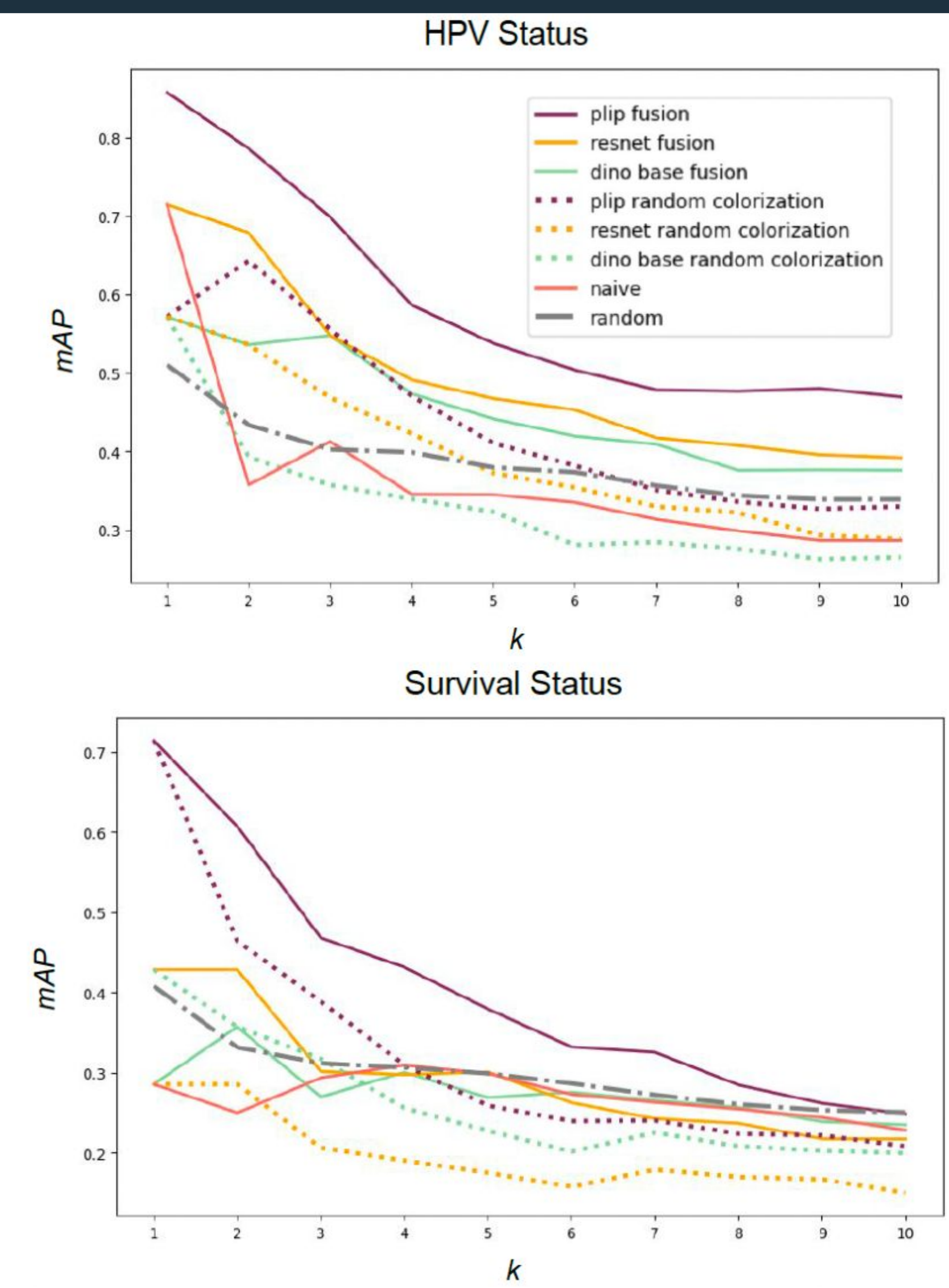

Figure 2: Cross-study evaluation on patient-level: PLIP outperformed other models in retrieving patients of the same clinical outcomes.

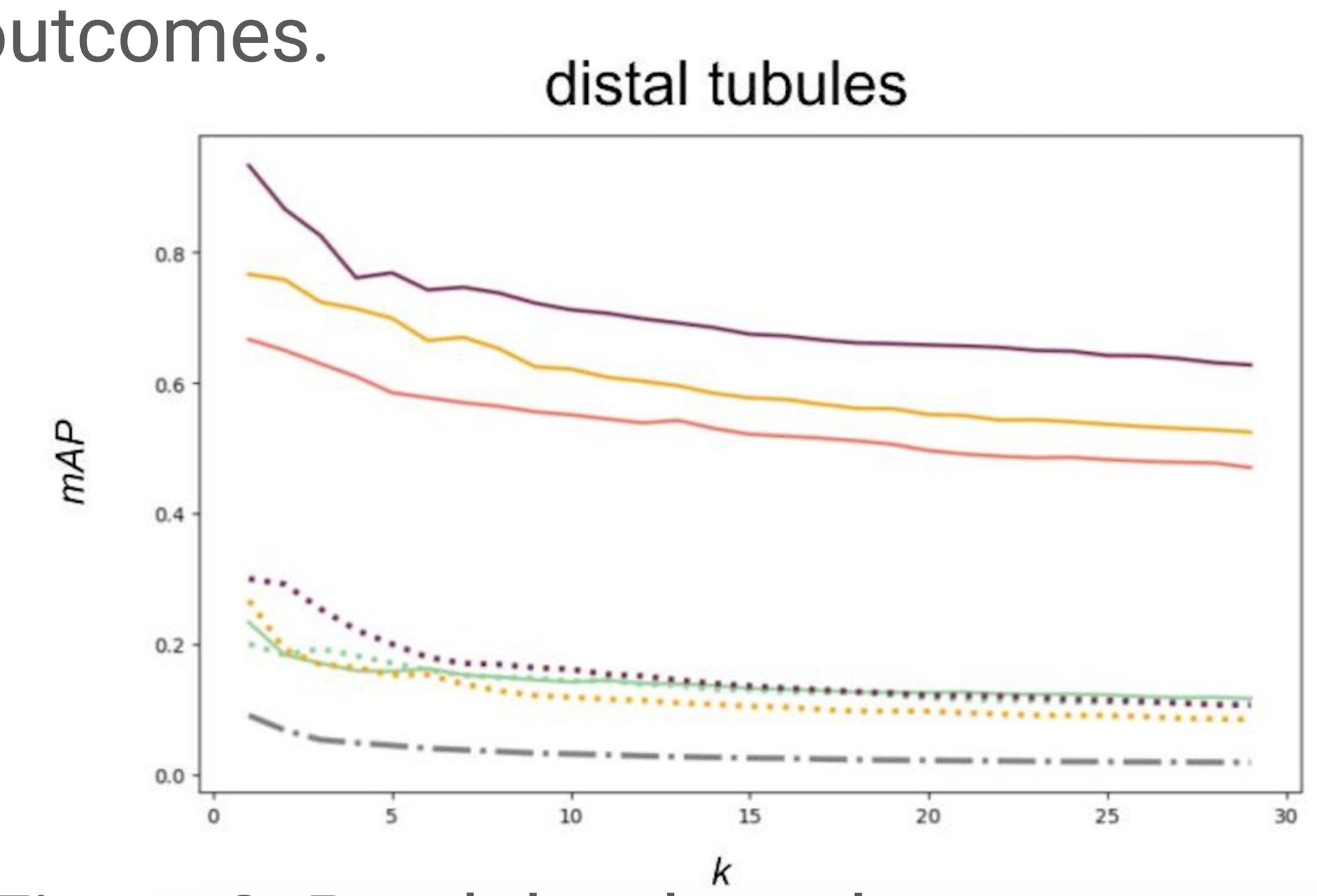

Figure 3: Patch level result

CASE STUDY

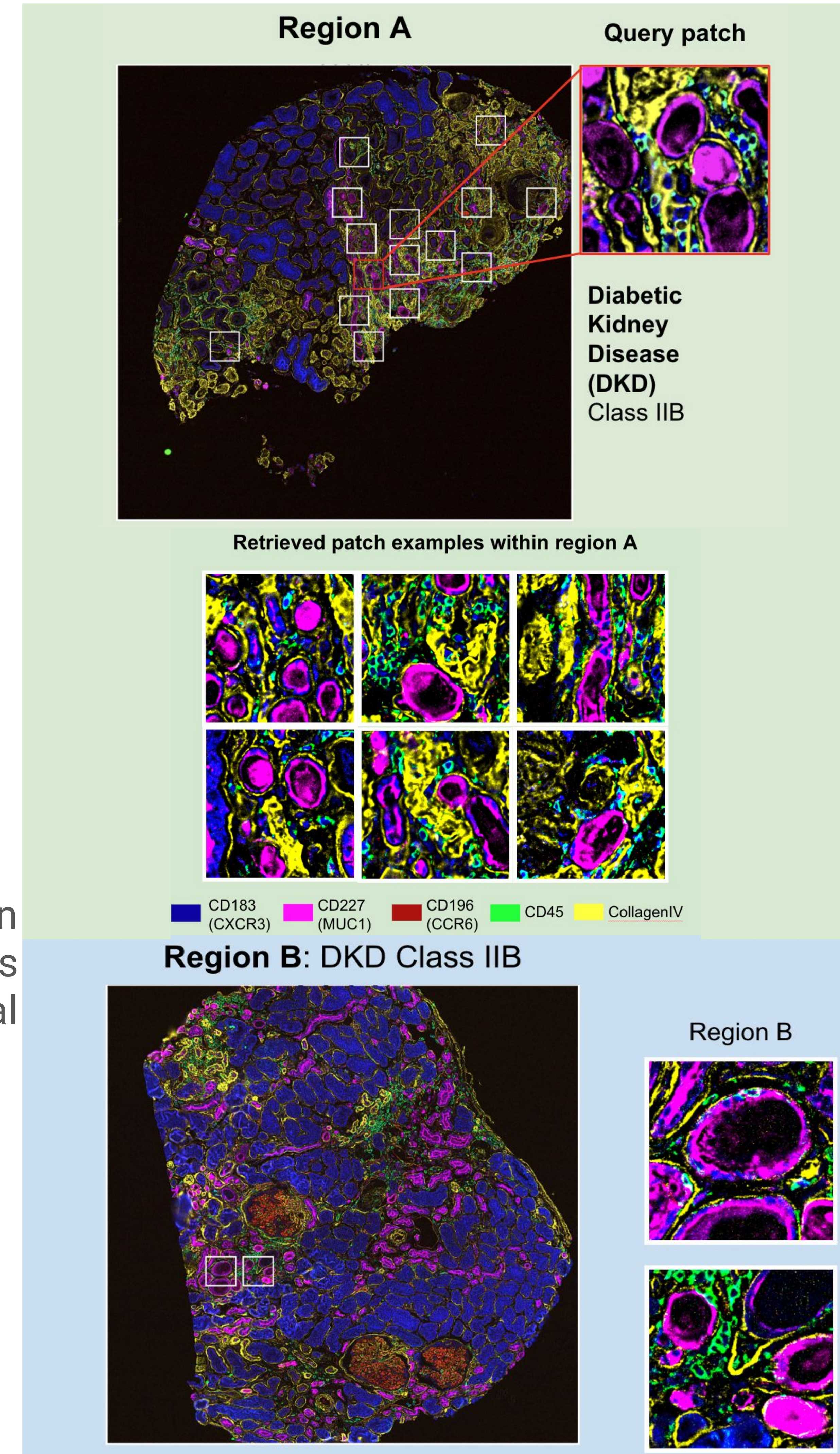

Figure 4: Case study on an example from the DKD Kidney study

CONCLUSION

1. Our evaluations on datasets from different tissues demonstrated the robustness and effectiveness of the MIISS 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.