GMR- 4234 — Evaluating Instance Segmentation Models on Histopathology Datasets

Project Description

This project surveys instance segmentation models for histopathology image analysis, evaluating models like Mask R-CNN, Detectron2, YOLOv8, YOLOv9, and HoverNet. Experiments focus on PanNuke and NuCLS datasets, covering diverse nuclear classes and tissue types. The study explores preprocessing impacts, such as color normalization, on model performance, aiming to guide researchers and clinicians in model selection for improved diagnostic accuracy in digital pathology.

Introduction

Instance segmentation is transforming digital pathology by enhancing the speed and accuracy of tissue analysis. Whole Slide Imaging (WSI) converts microscope slides into high-resolution digital formats, enabling detailed examination. This study surveys state-of-the-art segmentation models, including Mask R-CNN, Detectron2, YOLOv8, YOLOv9, and HoverNet, applied to two major histopathology datasets: PanNuke and NuCLS. NuCLS, with over 220,000 annotated nuclei from breast cancer samples, supports multiclass segmentation across 13 nuclear classes. PanNuke, containing 205,343 labeled nuclei across 19 tissue types, supports both multiclass and binary segmentation for five cell types.

Analysis

Data Collection:
The study utilized two prominent histopathology datasets:

1. **NuCLS Dataset:**
   - Contains over 220,000 annotated nuclei from breast cancer histopathology images
   - Supports multiclass segmentation across 13 distinct nuclear classes
   - Divided into training, validation, and test subsets
2. **PanNuke Dataset:**
   - Comprises 205,343 labeled nuclei across 19 tissue types
   - Includes five cell types: neoplastic, inflammatory, soft tissue, dead, and epithelial
   - Distributed across 481 visual fields from over 20,000 whole-slide images
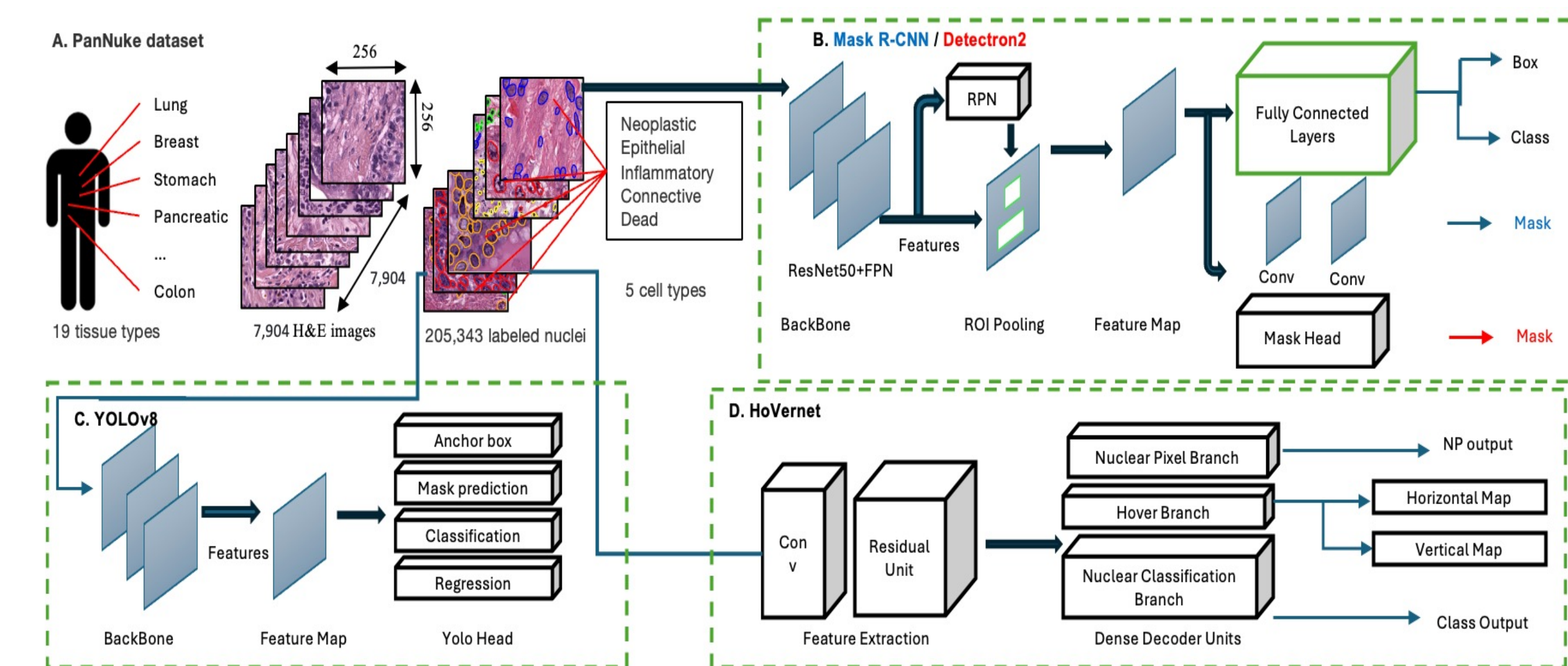

Fig 1: Overview of the PanNuke Dataset and models used in this study.

Methods:
1. **Models Evaluated:**
   - Mask R-CNN with ResNet-101 backbone
   - Detectron2 with ResNet50 backbone and Feature Pyramid Network
   - YOLOv8 with EfficientRep backbone
   - YOLOv9 with PGI and Reversible Functions
   - HoverNet with dual-branch architecture
2. **Segmentation Approaches:**
   - Binary instance segmentation
   - Multiclass instance segmentation

Results

Our study evaluated the performance of various deep-learning models for semantic image segmentation on the PanNuke and NuCLS datasets, revealing significant insights into their capabilities across different tissue types and cell categories.

For the PanNuke dataset, we conducted both multi-class and binary instance segmentation experiments. In multi-class segmentation, HoverNet outperformed Mask R-CNN across all metrics. For binary segmentation, YOLOv8 emerged as the top performer among Mask R-CNN, Detectron2, YOLOv8, and YOLOv9, demonstrating superior performance in many categories, particularly excelling in segmenting neoplastic cells across various tissue types.
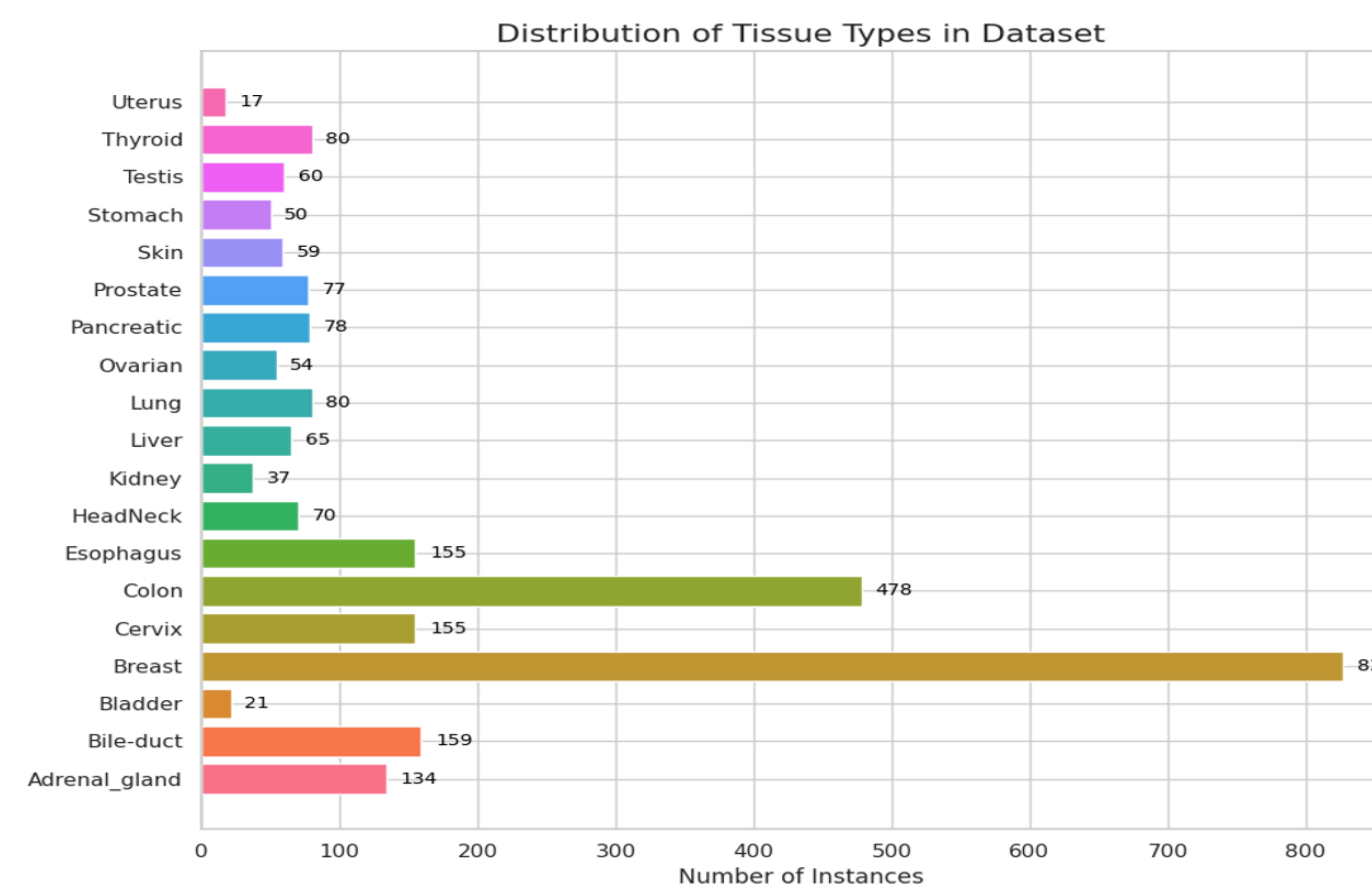

Fig 2: Distribution of Tissue Types in the PanNuke Dataset.

On the NuCLS dataset, which focused on multi-class instance segmentation, YOLOv8 again outperformed the other models, with Mask R-CNN and YOLOv9 showing comparable results. Mask R-CNN performed well in certain scenarios, especially in segmenting inflammatory cells in some tissue types, while Detectron2 excelled in specific tissue types and cell categories, showing strong performance in segmenting neoplastic cells in tissues like skin and bile-duct. YOLOv9, while generally not the top performer, showed competitive results in some categories, particularly in mAP scores for certain tissue types.
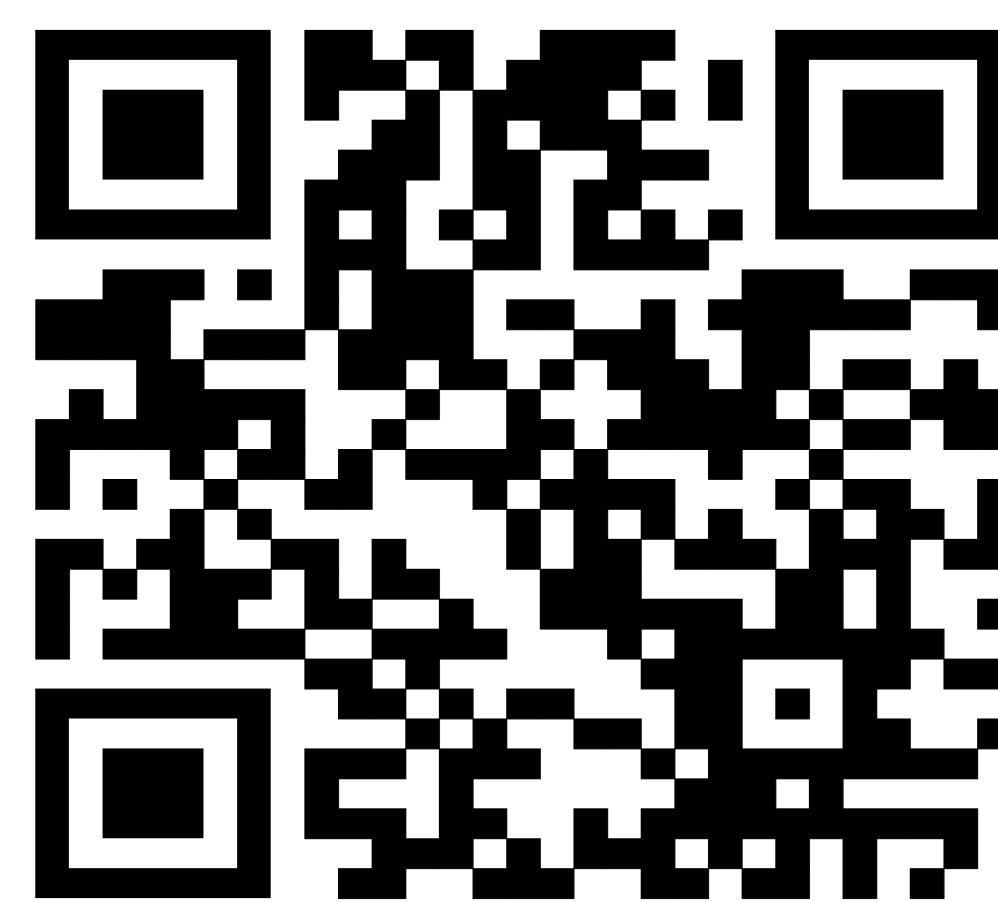
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The performance varied across different tissue types and cell categories, highlighting the importance of model selection based on specific histopathology tasks. These findings provide valuable insights into the strengths and limitations of different deep learning models for semantic image segmentation in digital pathology, potentially guiding researchers and clinicians in model selection for improved histopathology image analysis.

Conclusions

Our experimental survey of instance segmentation models on the PanNuke and NuCLS datasets highlights key findings:
- YOLOv8 outperformed other models across both datasets, especially in segmenting neoplastic cells.
- Mask R-CNN and Detectron2 showed strengths in tasks like inflammatory cell segmentation.
- HoverNet achieved high recall and accuracy on the PanNuke dataset.
- Performance varied significantly across tissue types and cell categories, emphasizing the need for tailored model selection.
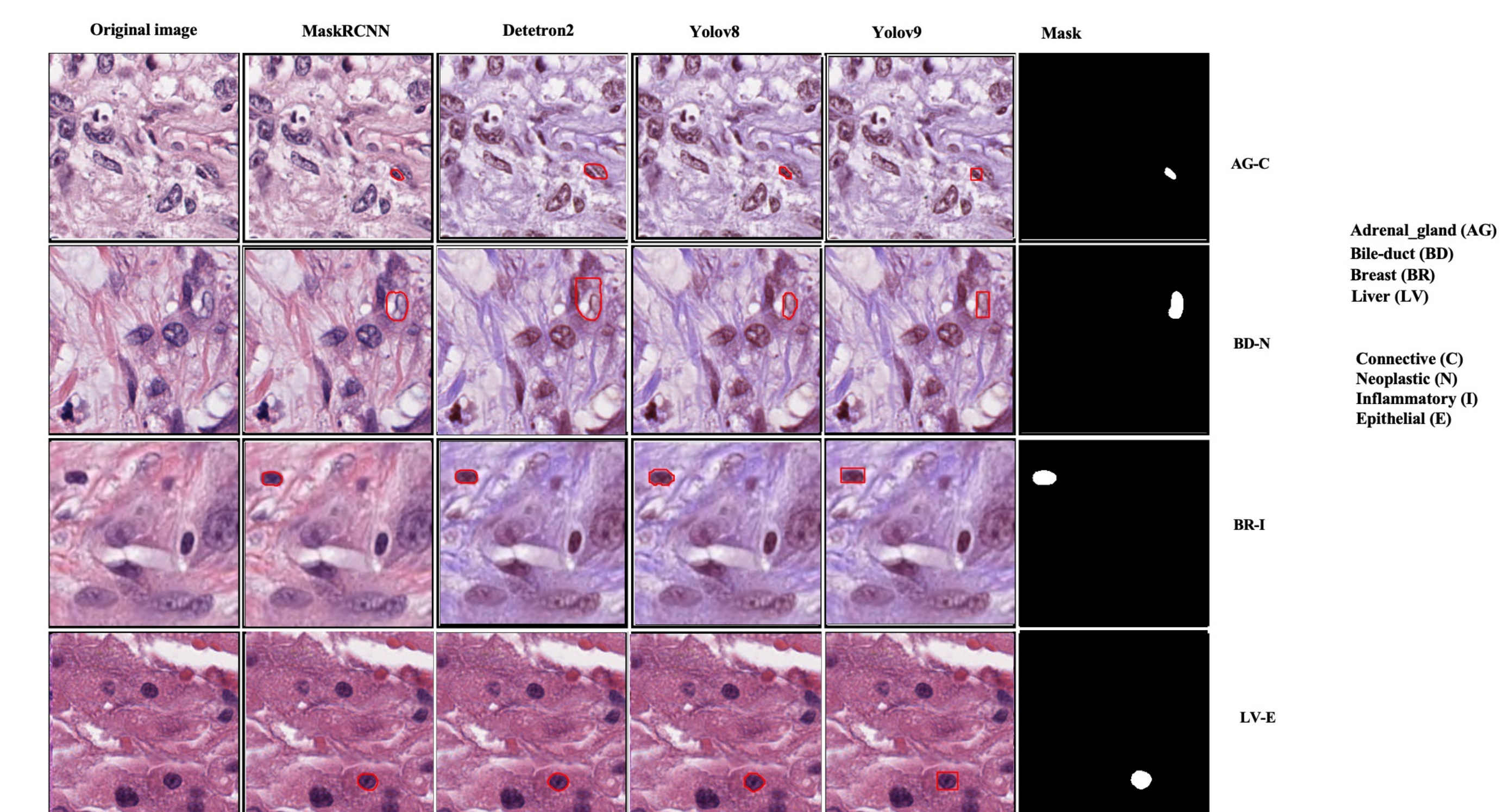

Fig 3: Single Instance Segmentation of PanNuke Dataset using Mask R-CNN, YOLOv8, YOLOv9, and Detectron2.

Preprocessing methods, such as color normalization and data augmentation, were crucial for boosting model performance. These findings reinforce the importance of model selection and preprocessing in histopathology analysis, guiding researchers and clinicians toward improved diagnostic accuracy in digital pathology. Future work should aim to enhance model generalization across diverse tissue types and integrate these segmentation techniques into clinical workflows.
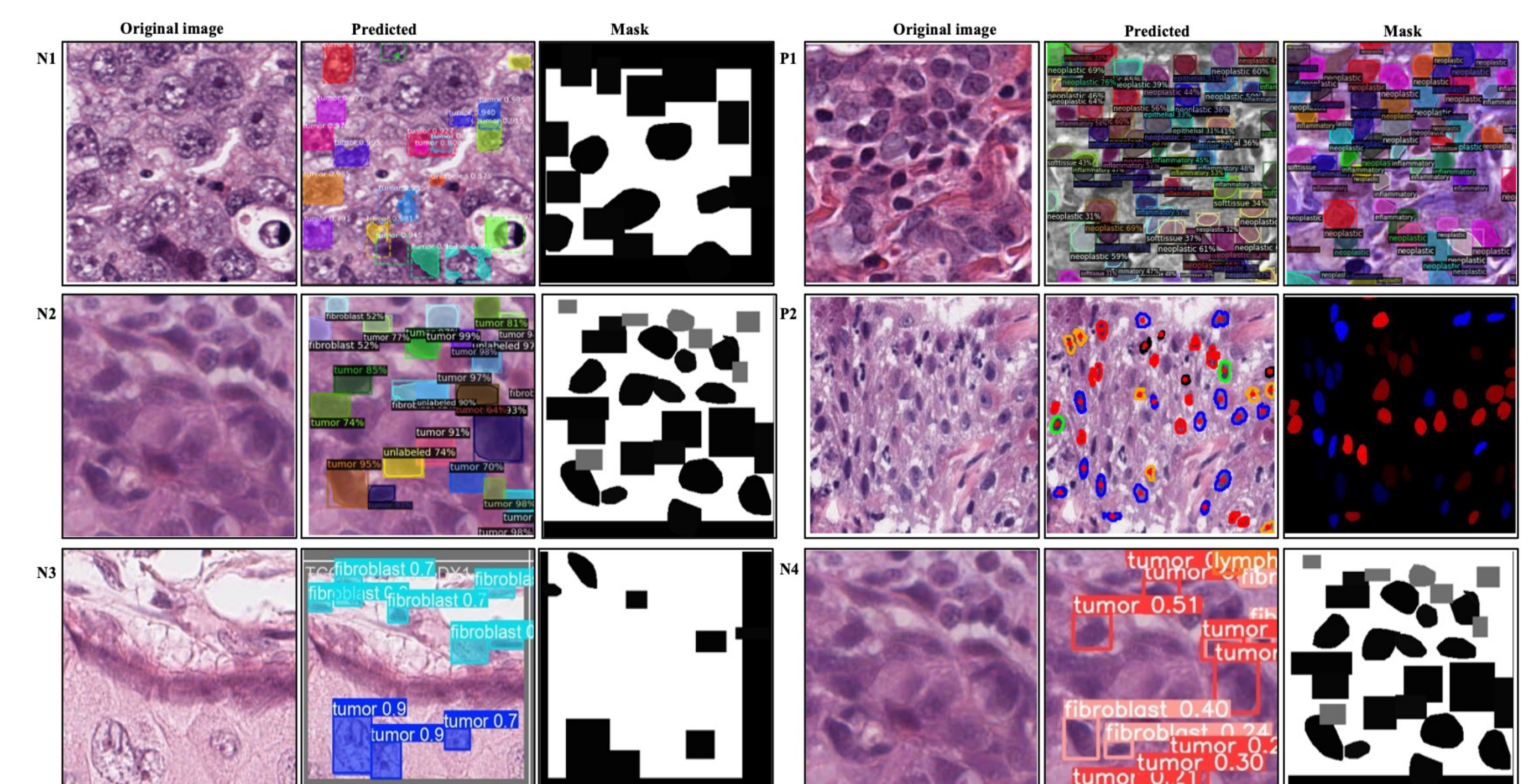

Fig 4: Comparison of Instance Segmentation Models on NuCLS Dataset and PanNuke.

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