

Foundation model based prostate cancer segmentation on whole mount digitized H&E radical prostatectomy section

Prostate needle core biopsies are the clinical standard for prostate cancer (PCa) diagnosis, but their limited sampling often fails to capture the full spatial extent of disease. Some intermediate/high risk patients undergo Radical Prostatectomy (RP) and whole mount processing of RP specimens provides a comprehensive view of tumor spatial architecture and heterogeneity but are rarely annotated at scale. In this study, we evaluate whether a foundation model trained exclusively on biopsy whole-slide images (WSIs) can generalize to segment cancer in whole mount RP WSIs, despite the domain shift introduced by differences in tissue scale and spatial distribution.

In our study, we use UNI[1], a state-of-the-art pathology foundation model pretrained via self-supervised learning, to extract 1,536-dimensional feature embeddings from image patches. The training dataset (D1) comprises over 10,000 biopsy WSIs from 2,113 patients in the PANDA challenge dataset [2], annotated with Gleason pattern masks. Using WSITools [3], we segmented tissue regions and extracted ~ 4.9 million 224×224 patches at $20\times$ magnification ($0.5 \mu\text{m}/\text{pixel}$). Patch labels were assigned based on $>50\%$ overlap with annotated Gleason $\geq 3+4$ cancer regions, merged into a single clinically significant PCa class. Color normalization was applied using the torchstain[4] library with a pathologist-approved reference patch.

A logistic regression classifier was trained on these patch-level embeddings in a one-shot linear probe setup to predict cancer presence. For evaluation (D2), we used 48 whole mount H&E-stained RP WSIs from an institutional dataset, resulting in ~ 3.5 million patches, based on expert-provided WSI cancer masks as ground truth. On D2, our model achieved a sensitivity of 0.76, specificity of 0.93, and AUROC of 0.92, demonstrating strong generalization to the RP domain. Patch-level predictions were stitched to reconstruct slide-level segmentation masks. To obtain a more spatially refined prediction segmentation mask, morphological post-processing was applied to remove noise and close gaps between segmented regions, which significantly improved the Dice score from 0.59 to 0.81

This study demonstrates that self-supervised pathology encoders trained solely on biopsy WSIs can transfer effectively to full-context segmentation tasks in whole mount RP tissue. This biopsy-to-RP generalization suggests that foundation models can serve as scalable, label-efficient backbones for downstream computational pathology applications such as tumor quantification and spatial biomarker discovery.

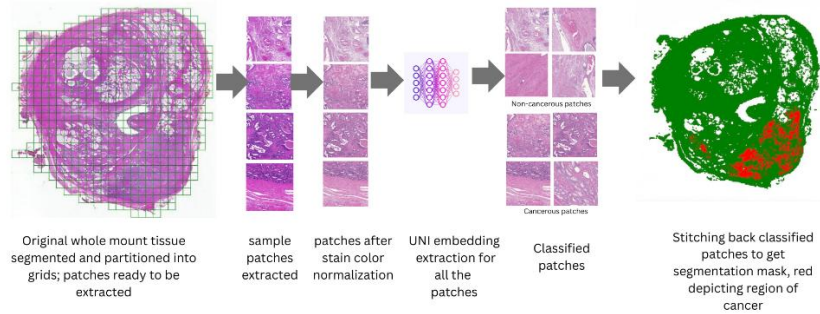


Figure: Overview of the implemented pipeline for whole mount RP image analysis, from preprocessing to cancer region segmentation.

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