Tailoring nnUNet to pathology: A use case on quantifying TILs for immunotherapy treatment response prediction and survival analysis

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Abstract

Image segmentation is at the core of many tasks including the engineering of many computational biomarkers. However, deep learning-based segmentation models can be difficult to configure, especially in the case of multi-class segmentation. The self-configuring nnUNet framework helped a lot for image segmentation tasks for radiology but is not explored much for pathology applications. We found that the default nnUNet does not fully consider certain pathology data-specific qualities, such as the sheer size of whole slide images, the high variety of cell morphologies, and staining variabilities. Here we present nnUNet for pathology, we tailor the framework to a pathology use case and show its application to a computational biomarker. We train nnUNet on HE-stained biopsies and resections from NSCLC patients for a multi-class segmentation task containing 13 tissue classes. We evaluated performance on segmentation and a downstream task on tumor-infiltrating lymphocyte quantification on the Pembro-RT dataset. We identified critical improvements in the normalization approach, and related batch and patch size configurations, and the addition of pathology augmentations. Furthermore, we added a whole slide inference pipeline, and added an uncertainty extraction approach that proves helpful in the biomarker engineering pipeline. All code is made available at -link-.

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