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Meta Mask Correction for Nuclei Segmentation in Histopathological Image

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Abstract : Nuclei segmentation is a fundamental task in digital pathology analysis and can be automated by deep learning-based methods. However, the development of such an automated method requires a large amount of data with precisely annotated masks which is hard to obtain. Training with weakly labeled data is a popular solution for reducing the workload of annotation. In this paper, we propose a novel meta-learning-based nuclei segmentation method which follows the label correction paradigm to leverage data with noisy masks. Specifically, we design a fully conventional meta-model that can correct noisy masks by using a small amount of clean meta-data. Then the corrected masks are used to supervise the training of the segmentation model. Meanwhile, a bi-level optimization method is adopted to alternately update the parameters of the main segmentation model and the meta-model. Extensive experimental results on two nuclear segmentation datasets show that our method achieves the state-of-the-art result. In particular, in some noise scenarios, it even exceeds the performance of training on supervised data.

Keywords : deep learning, histopathological image, meta-learning, nuclei segmentation, weak annotations
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