MF-Hovernet: An Extension of Hovernet for Colon Nuclei Identification and Counting (CoNiC) Challenge

The most significant morphological characteristic of malignancies, particularly those of the colon, is nuclei identification and counting.

Many deep learning-based approaches have been put forth to address this issue. In this paper, we build an extension the MF-Hovernet problem by using Hovernet for nucleus identification and counting. Our suggested model combines Hovernet architecture with several filer blocks. The current outcome demonstrates the effectiveness of many filter blocks in enhancing the functionality of the first Hovernet model.

In computational pathology, the extraction of interpretable cell-based information that can be employed in later explainable models is made possible by nuclear segmentation, classification, and quantification within Haematoxylin & Eosin-stained histological pictures.

The Colon Nuclei Identification and Counting (CoNIC) Challenge [1] calls for the creation of algorithms that segment, classify, and count six different types of nuclei: connective tissue, lymphocytes, eosinophils, neutrophils, and lymphocytes.

Two tasks are involved in this challenge. In the first task, participants must concurrently divide the tissue's nuclei into groups according to the six categories listed above. Regression analysis is the second task. How many nuclei of each type are present in each input image is the task's output.

In the CoNiC challenge, this article described a method for nuclei detection and counting from pathology images. For segmenting and counting nuclei on pathology pictures, our method incorporates the multiple filter block to Hovernet. The current outcome demonstrates the effectiveness of many filter blocks in enhancing the functionality of the first Hovernet model. In the future, we want to refine our approach and look at how well the CoNiC challenge's test set performed.