

Evaluation of parameters of different architectures for segmentation of cell images

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Abstract

Unstained brightfield images pose a significant challenge for image analysis. U-Net architectures are a family of fully convolutional neural network which are used for image segmentation. These architectures are widely used for segmenting biomedical images due to their ability to detect fine spatial details in microscopy data. Understanding the impact different biomaterials have on cell images requires reliable segmentation methods. In this study, different architectures are used to segment brightfield microscopy images to determine cell confluence and assess the impact of various biomaterial concentrations on cell health. Results were compared for different loss functions, batch sizes to identify the optimal parameters for cell segmentation. Manual labelling of the images from an original dataset was conducted under the supervision of the medical practitioners. Among all the trained models, the ones achieving highest accuracy results were chosen for further analysis and cell confluence. Hybrid function with different weights of a combination of binary cross entropy and dice loss was found the best one.

References

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