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Deploying Patch-Based Segmentation Pipeline for Fibroblast Cell Images at Varying Magnifications
(2023) *IEEE Access*, 11, pp. 98171-98181.

DOI: 10.1109/ACCESS.2023.3312232

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Abstract

Cell culture monitoring necessitates thorough attention for the continuous characterization of cultivated cells. Machine learning has recently emerged to engage in a process, such as a microscopy segmentation task; however, the trained data may not be comprehensive for other datasets. Most algorithms do not encompass a wide range of data attributes and require distinct system workflows. Thus, the main objective of the research is to propose a segmentation pipeline specifically for fibroblast cell images on phase contrast microscopy at different magnifications and to achieve reliable predictions during deployment. The research employs patch-based segmentation for predictions, with U-Net as the baseline architecture. The proposed segmentation pipeline demonstrated significant performance for the UNet-based network, achieving an IoU score above 0.7 for multiple magnifications, and provided predictions for cell confluency value with less than 3% error. The study also found that the proposed model could segment the fibroblast cells in under 10 seconds with the help of OpenVINO and Intel Compute Stick 2 on Raspberry Pi, with its optimal precision limited to approximately 80% cell confluency which is sufficient for real-world deployment as the cell culture is typically ready for passaging at the threshold. © 2013 IEEE.

Author Keywords

Cell confluency; deep learning; fibroblast; microscopy segmentation; phase contrast

Index Keywords

Cell culture, Computer architecture, Deep learning, Fibroblasts, Forecasting, Network architecture, Pipelines; Cell confluency, Cell images, Deep learning, Fibroblast cells, Images segmentations, Microscopy segmentation, Patch based, Phase-contrast; Image segmentation

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Publisher: Institute of Electrical and Electronics Engineers Inc.

ISSN: 21693536

Language of Original Document: English

Abbreviated Source Title: IEEE Access

2-s2.0-85171543323

Document Type: Article
Publication Stage: Final
Source: Scopus

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