LEVERAGING INSTANCE SEGMENTATION FOR DESCRIPTIVE STATISTICAL ANALYSIS OF FIBROBLAST CELL AREAS IN BRIGHTFIELD MICROIMAGES

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The analysis of cell areas in brightfield microscopic images is a key step in modern biological research, as cell area is an important characteristic that allows us to assess functional processes, growth level, and the state of cell structures. However, the process of calculating cell area is often time-consuming and thus requires automation to increase research efficiency.

The aim of the study is to develop an automated approach for determining and describing cell areas in brightfield microimages. Our approach is based on YOLO11 model to perform instance cell segmentation using the Sliding Aided Hyper Inference (SAHI) approach. SAHI allows you to divide an image into smaller fragments using a sliding window [1], which provides more accurate cell segmentation even on scaled images. After segmentation, additional rule-based post-processing is applied to extract the descriptive statistics of the cell areas, such as mean, median, and quartiles [2]. Structural schema of the algorithm is shown in Fig.1:
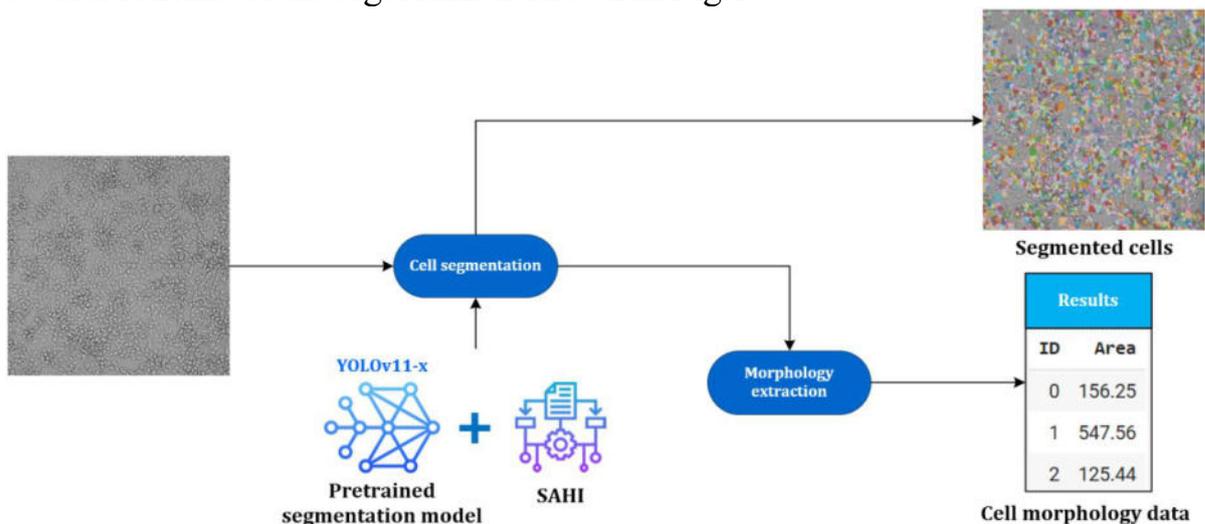

Fig.1 – Structural schema of our algorithm.

The proposed method can be used to further improve cell analysis, including the study of cell behavior under different conditions, and will become an important tool in biomedical research.

References (translated):
1. Minh H.Nguyen, Duong H.Le, Nam T.Nguyen. Sliding Window and Pseudo-labeling techniques for Cellular Segmentation. Proceedings of Machine Learning Research. URL: https://proceedings.mlr.press/v212/nguyen-hai23a.html.
2. Data-analysis strategies for image-based cell profiling / J. C. Caicedo et al. Nature Methods. 2017. Vol. 14, no 9. P. 849–863. URL: https://doi.org/10.1038/nmeth.4397