

CALCULATION OF MOUSE FIBROBLAST CELL LINE PRESENTED ON CONTRAST MICROIMAGES

Ponomarov, Y. V.¹, Ipatko, K. O.¹, Danylov, H. O.¹, Bozhok, G. A.²

¹*National Technical University «Kharkiv Polytechnic Institute», Kharkiv*

²*Institute of Problems of Cryobiology and Cryomedicine, Kharkiv*

The process of calculating fibroblast cells when analyzing contrast microscopy images is an essential part of nearly any biological research study. However, it has been well known for the large amount of time required for it. That is why automating this process [1] would be a significant innovation, since it would allow to speed up the calculations enormously, while keeping the error rate low enough, too.

The object of the research is calculating mouse fibroblast cells of L929 cell line presented on given contrast microscopy images. Structural schema of the algorithm are shown in Fig. 1.

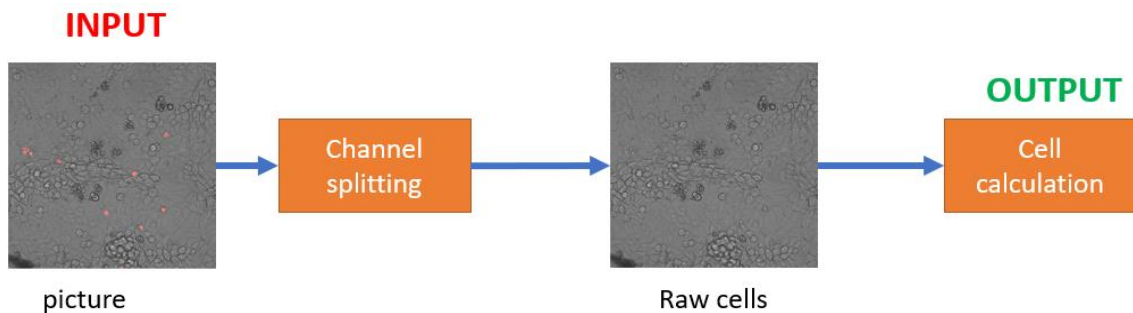


Figure 1 – Structural schema of algorithm for calculating epidermis cells process

In this paper existing approaches in the field of deep neural networks have been reviewed. Apparently, none of the existing standard approaches [2] can be used from scratch due to both the specificity of the target images and the architectural limitations of most neural networks. For example, modern neural networks of object detection or instance segmentation can detect no more than 300 objects per image, while microscopy images usually contain 500-700 cells on average.

Another significant challenge to consider is the amount of data – just several thousands of images in our case, but very often there are fewer than 1,000 images available. That is why augmentation techniques are extremely important, as well as developing new datasets in this area.

It can be concluded that the challenge of calculating epidermis cells on contrast microscopic images still remains unsolved. However, recently new steps in the area have been made towards achieving better results by both developing new deep machine learning models and creating new sets of data.

References:

1. Prem Krishna Shrestha, Nicholas Kuang, Ji Yu, Efficient end-to-end learning for cell segmentation with machine generated weak annotations, 2023.
2. Nabeel Khalid, Rickard Sjogren, Andreas Dengel, Sheraz Ahmed, DeepCeNS: An end-to-end Pipeline for Cell and Nucleus Segmentation in Microscopic Images, 2021.