

## **MSU-RU**

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Platform: Linux

Prerequisites: Python 3.9

### *MSU-RU: SUMMARY*

We use a weakly-supervised approach that extends the amount of segmentation training data for image sequences where only a couple of frames are annotated [1]. The approach uses the tracking annotations as weak labels and image registration to extend the segmentation annotation to the neighboring frames. This technique was applied to cell segmentation step in the cell tracking problem.

### *MSU-RU: PREPROCESSING*

Whereas the contrast limited adaptive histogram equalization (CLAHE) followed by a Gaussian filter with the standard deviation of  $\sigma$  is applied to each frame of **Fluo-N2DH-GOWT1**, the gamma correction with the brightness parameter  $\gamma$  is applied to each frame of **Fluo-C2DL-Huh7**. All the data is normalized between minimum and maximum of each frame into  $[0, 1]$  range. The each side of the image should be divided by 32, thus the images are zero-padded, if needed.

### *MSU-RU: SEGMENTATION*

For segmentation, we used U-Net [2] with a pretrained ResNet34 backbone and several custom modifications. We trained the network on image crops instead of resizing the single frame. Instead of single output, we also predicted markers of connected components in cell masks. We exploited this idea from [3] as it solves the problem of adjacent cell masks fusion very well. In addition, since the registration-based generated cell masks could still contain some errors caused by wrong registration, we use different weights in the loss function for generated cells masks and gold truth cell masks. We also generate the standard U-Net weights to better divide the adjacent cells and add it to the weight maps.

### *MSU-RU: POST-PROCESSING*

The last step is the application of the watershed segmentation with seeds defined by the network output. The predicted masks and markers are post-processed before the watershed application. All the post-processing parameters are adapted to each dataset using the *Optuna* python package for

parameter optimization. We adapt  $T_{\text{best}}$  for the best predicted segmentation map binarization and  $size$  to remove small objects using morphological operations. Then, we use  $T_{\text{strong}}$  to binarize markers and  $T_{\text{soft}}$  to add missing markers with smaller confidence. Finally, we apply watershed segmentation and get the instance masks.

## REFERENCES

1. Anoshina NA, Sorokin DV. Weak supervision using cell tracking annotation and image registration improves cell segmentation. In *Proceedings of the 11th IEEE International Conference on Image Processing Theory, Tools and Applications* (2022).
2. Ronneberger O, Fischer P, Brox T. U-net: Convolutional networks for biomedical image segmentation. In *Proceedings of Medical Image Computing and Computer-Assisted Intervention*, 234-241 (2015).
3. Lux F, Matula P. DIC image segmentation of dense cell populations by combining deep learning and watershed. In *Proceedings of the 16th IEEE International Symposium on Biomedical Imaging*, 236-239 (2019).