

# MU-HRMNet: High Resolution Dual-Stream Marker Based Network for Cell Segmentation and Tracking

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Platform: Linux

Prerequisites: Python with PyTorch

## ***MU-HRMNet: SUMMARY***

Our method is a two-stage method, as shown in Figure.1. The pipeline consists of two main modules: cell segmentation and cell tracking. The cell segmentation is designed to localize different cells, and the tracking algorithm to used to track cells across frames.

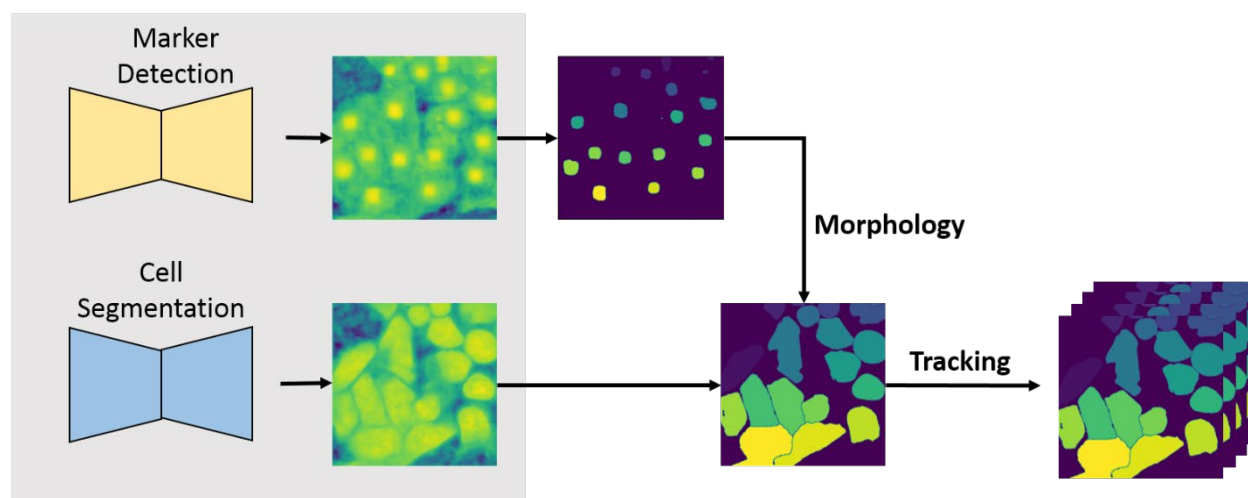


Figure.1 MU-HRMNet for cell detection, segmentation, and tracking

## ***MU-HRMNet: SEGMENTATION***

There are two networks in our algorithm, one network is designed for cell centroids(markers) detection, and the other is designed for mask detection. We use the HRNet [4] as the CNN model to learn the centroid localization and cell segmentation mask. Transform distance maps are computed in training and used for penalizing the boundary region for accurate cell segmentation. Centroids are used to locate the cells and segment the segmentation mask to multiple cells.

The input images are pre-processed contrast adjustments with z-score distribution. For the training process, marker localization is trained with centroid supervision, and segmentation mask is supervised by silver truth of annotations. Both the marker localization network and cell segmentation network are trained on eight 2D datasets and five 3D datasets with an input size of  $256 \times 256$  with distance penalty loss. During training, regular data augmentation strategies including rotation, flip, and scale from 0.8 to 1.5 are applied for each sample. During inference, both centroids and segmentation masks are generated, and then the morphology operations are used to split cells guided by our generated centroids.

### ***MU-HRMNet: TRACKING***

The cell tracking pipeline is based on adapting our computer vision based multi-object tracking algorithms [1, 2] for biological cell tracking. Multi-cell tracking is used to track the detected cells produced by the above segmentation network. Data association using the linear assignment approach is applied to link the cells in consecutive frames. Data association criteria uses the bounding box IOU score or the mask IOU score combined with a generalized Hungarian optimization algorithm [3]. The tracking procedure adds several design modules for robust tracking including (a) gating strategy for reducing assignment complexity of ids by pruning improbable assignments, and (b) Kalman filter for recovering from miss-detections. With these modules, tracks for new cells entering or old cells exiting the field of view are explicitly handled. For more details of the tracking algorithm, please refer to [1, 2].

### REFERENCES

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4. Sun, Ke, et al. Deep high-resolution representation learning for human pose estimation. Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition. 2019