

MU-Ba-US

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Platform: Linux

Prerequisites: Python 3.6 with PyTorch

MU-Ba-US: SUMMARY

Our method is a two-stage method that follows the tracking by detection paradigm. 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.

MU-Ba-US: PREPROCESSING

The input images are preprocessed using contrast adjustments with z-score distribution.

MU-Ba-US: SEGMENTATION

There are two networks in our algorithm, one network is designed for cell centroid (marker) detection, and the other is designed for mask detection. We use HRNet [1] 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. For the training process, marker localization is trained with centroid supervision, and segmentation mask is supervised by silver truth. Both the marker localization network and cell segmentation network are trained on eight 2D+t datasets and five 3D+t datasets with an input size of 256×256 with the 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 the mathematical morphology operations are used to split cells guided by our generated centroids.

MU-Ba-US: TRACKING

The cell tracking pipeline is based on adapting our computer-vision-based, multi-object-tracking algorithms [2, 3] 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

intersection-over-union score or the mask IOU score combined with a generalized Hungarian optimization algorithm [4]. 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 missdetections. With these modules, tracks for new cells entering or old cells leaving the field of view are explicitly handled.

MU-Ba-US: POST-PROCESSING

No post-processing step was taken.

REFERENCES

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