MU-Ba-US

Authors: Rina Bao, Noor Al-Shakarji, Imad Toubal, Kannappan Palaniappan, Filiz Bunyak

Email: rinabao@mail.missouri.edu, nmahyd@missouri.edu, pal@missouri.edu

Platform: Linux

Prerequisites: Python 3.6 with PyTorch

MU-Ba-US: SUMMARY

Our generalized cell tracking pipeline is a two-stage method that follows the tracking by detection and segmentation paradigm with cell segmentation (DMNet) followed by cell lineage tracking (M2Track). The deep network for cell segmentation is designed to localize cells of different types, appearance, shapes, sizes, and deformation behavior. The multi-object tracking stage is highly scalable using two-step linear sum assignment for data association to track cells across frames generating tracklets followed by tracklet linking and occlusion handling with parent-child lineage associations.

MU-Ba-US: PREPROCESSING

The raw input images are preprocessed using a contrast enhancement approach with trimmed z-score (mean and variance) normalization after outlier removal.

MU-Ba-US: SEGMENTATION

We designed our DMNet [1] using a modified version of HRNet deep architecture [2] to learn both the centroid localization and cell segmentation mask as a multi-head output. There are two streams in the network architecture -- one stream is designed to produce cell centroid (shape marker) detections, and the other is designed to output accurate cell mask segmentations. Transform distance maps are computed during the training stage and used to penalize the boundary region of cells for training the network to generate accurate cell segmentations. When markers reliably localize the cells they are used with the mask stream to jointly improve the segmentation of multiple cells. During the training process, marker localization is trained with centroid supervision, or shape marker computed using masks. Both the marker localization and cell segmentation network streams are trained on eight 2D+t and five 3D+t video microscopy datasets using a distance-based penalty loss function. During training, common data augmentation strategies are applied including rotation, flip, with size scaling from 0.8 to 1.5 applied to each video frame. During inference, DMNet produces both markers and segmentation masks as output images for each frame.

MU-Ba-US: TRACKING

The cell tracking pipeline is based on adapting our computer vision-based, multi-object-tracking algorithm M2Track [3, 4] for biological cell tracking with deformable cell shapes [5, 6, 7]. Multi-cell tracking is used to track the detected and segmented cells produced by DMNet. Data association using linear assignment is used to link detections with tracklets in consecutive frames. The data association criteria includes several user selectable choices including centroid Euclidean distance, bounding box intersection-over-union (IOU) score or a mask-based IOU score combined with a generalized faster version of the Hungarian optimization algorithm [8]. M2Track incorporates several modules for robust tracking including: (i) a gating strategy for reducing assignment complexity by pruning improbable assignments of detections to tracklet IDs, (ii) Kalman filter prediction for recovering from missed detections, (iii) tracklet linking, and (iv) forward-backward association analysis to recover from occlusions and to track mitosis events for lineage linking. Using these tracking modules, tracks for newly entering cells or old cells exiting the field of view are explicitly handled.

MU-Ba-US: POST-PROCESSING

A morphological watershed transform is used to split cells guided by reliable centroids/markers generated by the DMNet segmentation stage.

REFERENCES

1. Bao R, Al-Shakarji NM, Bunyak F, Palaniappan K. DMNet: Dual-stream marker guided deep network for dense cell segmentation and lineage tracking. In *Proceedings of the IEEE International Conference on Computer Vision Workshop on Computer Vision for Automated Medical Diagnosis*, 3354-3363 (2021).
2. Wang J, Sun K, Cheng T, et al. Deep high-resolution representation learning for visual recognition. *IEEE Transactions on Pattern Analysis and Machine Intelligence* **43,** 3349-3364 (2021).
3. Al-Shakarji NM, Bunyak F, Seetharaman G, Palaniappan K. Robust multi-object tracking with semantic color correlation. In *Proceedings of the 14th IEEE International Conference on Advanced Video and Signal Based Surveillance*, 1-7 (2017).
4. Al-Shakarji NM, Bunyak F, Seetharaman G, Palaniappan K. Multi-object tracking cascade with multi-step data association and occlusion handling. In *Proceedings of the 15th IEEE International Conference on Advanced Video and Signal Based Surveillance*, 1-6 (2018).

5. Nath SK, Palaniappan K, Bunyak F. Cell segmentation using coupled level sets and graph-vertex coloring. In *Proceedings of the International Conference on Medical Image Computing and Computer-Assisted Intervention*, 101-108 (2006).
6. Nath SK, Bunyak F, Palaniappan K. Robust tracking of migrating cells using four-color level set segmentation. In *Proceedings of the International Conference on Advanced Concepts for Intelligent Vision Systems*, 920-932 (2006).
7. Palaniappan K, Bunyak F, Nath SK, Goffeney J. Parallel processing strategies for cell motility and shape analysis. In *High-Throughput Image Reconstruction and Analysis*, 39-85 (2009).
8. Crouse DF. On implementing 2D rectangular assignment algorithms. *IEEE Transactions on Aerospace and Electronic Systems* **52,** 1679-1696 (2016).