DESU-US

Authors: Yibing Wang, Hector Miranda, Saujanya Annasamudram, Keni Zheng, Sokratis Makrogiannis

Email: smakrogiannis@desu.edu

Platform: Windows (x64)

Prerequisites: Matlab Compiler Runtime 2019b (x64)

DESU-US: SUMMARY

Our approach focuses on cell segmentation and tracking in video sequences by nonlinear diffusion PDE modeling [1] extended to the joint spatio-temporal domain, and region-based level-set optimization approach for cell segmentation. Cell tracking uses local-global optical flow for cell matching and linking. We perform cell event detection using graph processing.

DESU-US: PREPROCESSING

Our method performs frame intensity standardization by histogram transformation with no user interaction [2]. The purpose is to reduce intensity variability that complicates frame-to-frame analysis in differential techniques. We estimate the cumulative distribution function (CDF) of pixel intensities in the complete sequence, compute the global intensity minimum and maximum, and set a CDF reference point at a given reference percentile. Then for each frame and its neighbors, we find a CDF test point at the reference percentile. We map the pixel intensities of the frame triplet on to the standardized domain using the reference and test intensities, and the global minimum and maximum.

DESU-US: SEGMENTATION

We pursue a solution of the cell detection problem in the joint spatio-temporal domain to overcome weaknesses of techniques that operate only on the spatial domain. We employ a PDE-based formulation of spatio-temporal motion diffusion to detect the cell motion [2]. We compute a probabilistic edge map on the diffused frame, apply the H-minima transform, and impose the regional minima onto the edge map. We then employ watershed-based segmentation to delineate the cells. We utilize a motion activity measure of diffusion as a criterion to identify the moving cells. To refine cell delineation accuracy produced by motion diffusion-based segmentation, we use energy minimizing geometric active contours that assume a piece-wise constant image region model as a special case of the Mumford-Shah segmentation framework. Furthermore, we perform temporal linking of the region-based level sets toallow for faster convergence and to resolve non-convexity that affects energy-based minimization that

is typical in image analysis inverse problems. We perform cell separation by applying the signed distance transform to the cell segmentation, reducing spurious local minima, and finding the watershed ridges.

DESU-US: TRACKING

We use a method for automated tracking of biological cells in time-lapse microscopy by motion prediction and minimization of a global probabilistic function for each set of cell tracks [3]. We first compute cell characteristics related to intensity, shape and size, to be used for probabilistic cell matching and cell quantification. We estimate the cell motion by use of a variational multi-scale optical flow technique. Next, we apply the motion field to calculate warped cells and use a maximum likelihood decision function to find cell correspondences. We then construct the cell linked lists to represent cell tracks, and we backtrace the lists to detect overlapping tracks, and identify and handle the cell events. After finding all cell events, we construct the cell lineage tree that stores and visualizes the cell events. In addition, we calculate dynamic cell characteristics to perform quantitative analysis and visualization.

DESU-US: POST-PROCESSING

No post-processing step has been taken after tracking.

REFERENCES

1. Weickert J. Anisotropic Diffusion in Image Processing. Stuttgart: Teubner, 1998.
2. Boukari F, Makrogiannis S. Joint level-set and spatio-temporal motion detection for cell segmentation. *BMC Medical Genomics* **9,** 179-194 (2016).
3. Boukari F, Makrogiannis S. Automated cell tracking using motion prediction-based matching and event handling. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* **17**, 959-971 (2020).