

## **DESU-US**

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Platform: Windows (x64)

Prerequisites: Matlab Compiler Runtime 2019b (x64)

### *DESU-US: SUMMARY*

Our approach focuses on cell segmentation and tracking in video sequences. In the cell segmentation stage, it applies scale generation [1] and differential feature detection in the spatio-temporal domain, and marker-controlled watershed segmentation to delineate and identify the cell candidate regions. It then employs a 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. The executable programs are available online. To modify the algorithm parameters, the user should edit the parameter values provided in the *Challenge\_Parameters.xlsx* spreadsheet.

### *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. In this version, we employ spatio-temporal feature detectors [3] to develop cell region descriptors and separate the watershed regions into cells and background. To refine cell delineation accuracy produced by motion diffusionbased

segmentation, we employ local-intensity-clustering level sets [4]. Furthermore, we perform temporal linking of the region-based level sets to allow for faster convergence and to resolve nonconvexity that affects energy-based minimization that is typical in image analysis inverse problems. We perform cell-cluster separation by applying the signed distance transform to the cell segmentation map, reducing spurious local minima, and finding the watershed ridges.

#### *DESU-US: TRACKING*

We propose 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 [5]. We first compute cell characteristics related to intensity, shape and size, used for probabilistic cell matching and cell quantification. We estimate the cell motion by 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**

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4. Li C, Huang R, Ding Z, Gatenby JC, Metaxas DN, Gore JC. A level set method for image segmentation in the presence of intensity inhomogeneities with application to MRI. *IEEE Transactions on Image Processing* **20**, 2007-2016 (2011).
5. 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).