

## **IMCB-SG (2)**

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Platform: Windows

Prerequisites: MATLAB Compiler Runtime 2012a (x64)

### *IMCB-SG (2): SUMMARY*

We treat low signal to noise ratio (SNR) and highly non-uniform intensity 3D+t data sets separately from normal 3D+t data sets while conducting segmentation. It is performed using a seed controlled watershed approach. Tracking is conducted by frame-to-frame data association according to the minimization of a cost function using the Hungarian algorithm.

### *IMCB-SG (2): SEGMENTATION*

Segmentation is performed differently for normal datasets and for low signal to noise ratio (SNR) datasets with highly non-uniform intensity. During data preparation stage, isotropic 3D image stacks based on linear interpolation are prepared first before segmentation. Severe artifacts appear in data sets with low SNR and highly non-uniform intensity. Therefore, the proposed segmentation is performed separately for normal data sets and artifact data sets. For normal data sets, we apply a 3D Gaussian kernel to smooth the images and parameters are set according to the size of cells or nuclei. After that, we generate a histogram to determine a threshold value and apply thresholding to obtain 3D binary images. Morphological opening is used to remove small objects from the binary images. Furthermore, we use distance transform to compute Euclidean distance. By using the distance function as input, we apply extended maxima transform to find seeds in 3D. According to the seeds and the binary images obtained, the watershed algorithm is used to perform final segmentation. For data sets with low SNR and highly non-uniform intensity, we first use linear interpolation to down-sample image stacks. The main reason for conducting this step is that the following processing steps are very computationally expensive with original resolution. With reduced image resolution, we can perform Gaussian smoothing in 3D spatial domain efficiently. At the same time, we can also perform background removal by using morphological operation and contrast adjustment to enhance the images. After these preprocessing steps, we interpolate the down-sampled images back to their original size. Then, we conduct thresholding to obtain binary images, and use distance function or image intensity as input to detect

seeds by using extended maxima transform. Final segmentation is realized by using a seed controlled watershed algorithm based on distance function and image intensity.

#### *IMCB-SG (2): TRACKING*

For tracking of 3D+t data sets, we have used two approaches to tackling the problem. The first approach is a nearest neighbor search based algorithm. We first define a region corresponding to a cell in the first time frame. According to the number of potential objects in the region of the next time frame, we determine whether it is a migration or mitosis. A recursive tracing technique is used to construct lineage trees of cell mitoses. The second approach is based on global matching using the Hungarian algorithm, which combines both Euclidean distance and overlapping volume. We deal with mapping cases of one-to-one, one-to-many, and many-to-one. For one-to-one case, we consider it as a migration. If it is a many-to-one case, we choose one with the least cost and the rest are considered as termination in this time frame. One-to-many case is considered as a mitotic event and if potential matches are bigger than two then new cell emerging situation is considered.