

IMCB-SG (1)

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Platform: Windows

Prerequisites: MATLAB Compiler Runtime 2012a (x64)

IMCB-SG (1): SUMMARY

The 2D+t datasets are classified into fluorescent and phase contrast types. For 2D+t cell tracking, we use an approach of performing tracking first then followed by segmentation. Tracking is realized by directly tracing the seeds.

IMCB-SG (1): TRACKING

First, a Gaussian filter is used to smooth the images in spatial domain for two purposes. One is to remove noise and the other is to highlight the region of the interested objects. Window size and standard deviation are two parameters of the Gaussian filter that are set based on the structure of cells or nuclei in the images. Morphology operations are used to further remove background noise. For low contrast images, we use histogram equalization and contrast adjustment techniques to enhance the images. Second, we align the 2D images into 3D stacks such that the third dimension represents time. After the alignment, we use a convolution based Gaussian filter to smooth the images along time. The purpose we perform this step is to recover missing objects caused by low temporal resolution, weak or corrupted signal, or fast movement of cells or nuclei. After the first two steps, we use extended maxima transform to locate seeds based on image gradient. The extended maxima transform is a local maxima searching algorithm which can have different image features as input. We have tried both the distance function based on obtained binary images and image gradient as input, and the result shows that image gradient performs better on most data sets. In the last step of the tracking, the trace of the above-mentioned 2D seeds forms 3D segments which are our sought tracking trajectories. We apply a morphological opening operation to remove some small 3D segments that are considered as noise or artifacts caused by the processing. Tracking is realized by tracing the trajectories of the remaining 3D segments. Cell movement and mitotic events are all incorporated in the trajectories.

IMCB-SG (1): SEGMENTATION

In the segmentation stage, a thresholding technique is applied to obtain binary images for each 2D time frame. A global image threshold value by Otsu's method is used to conduct thresholding. After thresholding, we use morphological opening to remove spurious objects. Based on the binary images obtained, we combine 2D seeds in each time frame and image gradient after Gaussian smoothing in both spatial and temporal domains to use the watershed algorithm to obtain final segmentation. The main purpose of using the seed controlled watershed algorithm is to solve the touching cell segmentation problem. In addition, for phase contrast images we use a linear imaging model to restore artifact free images by removing halos and shade-off from phase contrast images [1]. After the restoration, the artifact free images are used as input of our algorithms and the rest of the processing for segmentation and tracking is the same.

REFERENCES

1. Yin Z, Kanade T, Chen M. Understanding the phase contrast optics to restore artifact-free microscopy images for segmentation. *Medical Image Analysis* **16**, 1047-1062 (2012).