IA-45

Enhanced Detection of Unstained Cells in an Existing Segmentation and Tracking Framework

N. Al-Zaben, A. Medyukhina, M. T. Figge

01/03/2017

Enhanced Detection of Unstained Cells in an Existing Segmentation and Tracking Framework

Naim Al-Zaben[1,2,3], Anna Medyukhina[1], Marc Thilo Figge[1,2]
1) Applied Systems Biology, Leibniz Institute for Natural Product Research and Infection Biology - Hans Knöll Institute
2) Friedrich Schiller University Jena, Germany
3) Jena School for Microbial Communication (JSMC)

Introduction

During the last decade, various areas in the biological sciences experienced a tremendous boost owing to the application of live cell imaging techniques that allow visualizing biological processes in real-time. Today, time-lapse microscopy experiments are routinely performed in biological research, however, in many cases the acquired image data are eventually used for illustrative purposes only. This disregard of quantitative information on dynamical, functional and morphological aspects of the biological system under consideration is due largely to the lack of systematic strategies for the appropriate processing and for the statistical analysis of image data.
We present enhancements to an existing automated segmentation and tracking framework for videos from live cell imaging [1]. The framework handles highly variable cell shapes and does not rely on any cell staining. The segmentation approach is based on a combination of spatial and temporal image variations in pixel intensities to detect moving cells in the microscopy videos. Although the existing framework performs well in detecting and tracking cells, it fails to do so in cases where some of the cells become undetectable due to a low spatial variance. This mostly happens for flattening cells causing transient failures in the track detection associated with a fragmentation of cell tracks.

Prevoius work

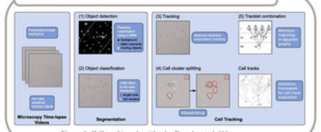

Figure 1: Cell tracking algorithm by Brandes et al. [1]

Enhancements

We enhanced the detection of cells by revising the class of "static elements" and correcting for misclassified PMNs. The PMN that were previously falsely detected as static elements, are now captured and integrated into the subsequent tracking procedure.

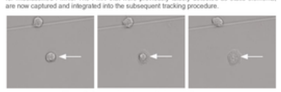

Figure 2: Time point where cells become flat

To avoid over-detection, we consider only tracks of flat cells that can be combined with previously existing tracks. This enhancement results into improved continuous tracking of cells with considerably less track fragmentation.

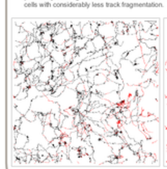

Figure 3: Existing tracks (Black) and added tracks/corrections (Red)

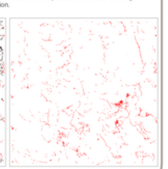

Figure 4: Added tracks and corrections

Results

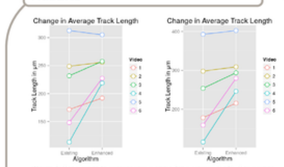

Figure 5: The change in average track length for all tracks (Left). The change in average track length without identical and newly added tracks (Right).

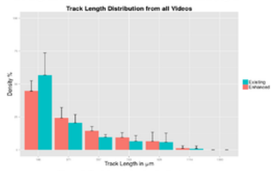

Figure 6: Track length density distribution

Figure 7: The change in TFE (Left) and ME (Right) in comparison to the GT (Videos 1-3)
- GT (Ground-truth Tracks)
- TFE (Track Fragmentation Error) – avg. number of fragments per GT
- ME (Merging Error) – avg. number of track mergings

References
[1] S. Brandes et al., Medical Image Analysis (2015) 20, 34-51

naim.al-zaben@hki-jena.de

This work is financially supported by the excellence graduate school Jena School for Microbial Communication (JSMC).