IA-13

Automated Characterization of Cell Tracks: Step forward

I. Belyaev, O. Kurzai and M. T. Figge

01/11/2015

Leibniz Institute for Natural Product Research and Infection Biology - Hans Knöll Institute

Automated Characterization of Cell Tracks: Step forward

Ivan Belyaev[1,3], Oliver Kurzai[2,3] and Marc Thilo Figge[1,3]

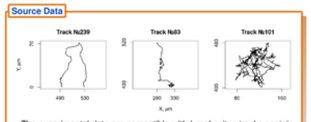
[1]Applied Systems Biology, Leibniz Institute for Natural Product Research and Infection Biology - Hans Knöll Institute
[2]Fungal Septomics, Leibniz Institute for Natural Product Research and Infection Biology - Hans Knöll Institute
[3] Friedrich Schiller University Jena, Germany

Introduction

The focus of this project is on the development of algorithms for (i) automated cell tracking in two and three spatial dimensions and (ii) automated characterization and parameter-free classification of cell tracks. The implementation of these algorithms will be based on our previous work on cell tracking and quantitative track characterization [1]. The main objective is to arrive at classifier models based on dynamic cell properties that allow distinguishing infection scenarios in various species and caused by different pathogens.

This work is part of the project "Whole Blood Imaging" (BLOODi) within the framework of the Leibniz ScienceCampus InfectoOptics. The scientific aim of this project is to combat infectious diseases with advanced optical technologies by establishing the concept of a dynamic hemogram from whole blood infection assays. The dynamic hemogram goes beyond standard blood count examination in that information on the migration and interaction of blood cells is captured. This novel source of information will be investigated for its potential to function as a biomarker in the characterization of whole blood infections caused by various pathogens and in different species. While exciting new insights can certainly be expected at the level of basic research in the fields infection biology and optical technologies, we do envisage right from the start our long-term goal of translating knowledge from bench to bedside.

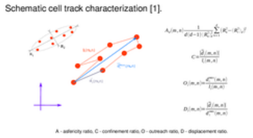
Source Data



The experimental data are compatible with lymphocites tracks containing combinations of random and directed track segments. Due to the rich diversity of cell tracks in general, their classification into different types of migration behavior can be a challenging task.

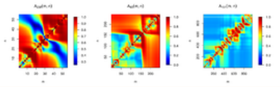
Descriptors: staggered measures

Schematic cell track characterization [1].



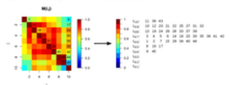
A - asphericity ratio, C - confinement ratio, O - outreach ratio, D - displacement ratio.

The examples of calculated descriptors (matrix form).

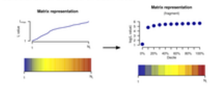


Matrix representation algorithm

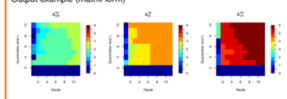
Step I: matrix unfolding and level quantization



Step II: calculation of deciles of each level



Output example (matrix form)



The advantages of algoritm:

- Keep the scale information;
- Produce the feature vectors of the same length;
- The produced vectors are useful for classification.

References

1. Mokhtari at al. PLoS One. 2013 Dec 6;8(12):e80808. doi:10.1371/journal.pone.0080808

Acknowledgements

This project is financially support by Leibniz ScienceCampus InfectoOptics, project BLOODi.

Contact: ivan.belyaev@hki-jena.de