Automated characterization and parameter-free classification of cell tracks based on local migration behavior.

Mokhtari Z, Mech F, Zitzmann C, Hasenberg M, Gunzer M, Figge MT (2013) Automated characterization and parameter-free classification of cell tracks based on local migration behavior. *PLOS ONE* 8(12), e80808.

Details

Abstract

Cell migration is the driving force behind the dynamics of many diverse biological processes. Even though microscopy experiments are routinely performed today by which populations of cells are visualized in space and time, valuable information contained in image data is often disregarded because statistical analyses are performed at the level of cell populations rather than at the single-cell level. Image-based systems biology is a modern approach that aims at quantitatively analyzing and modeling biological processes by developing novel strategies and tools for the interpretation of image data. In this study, we take first steps towards a fully automated characterization and parameter-free classification of cell track data that can be generally applied to tracked objects as obtained from image data. The requirements to achieve this aim include: (i) combination of different measures for single cell tracks, such as the confinement ratio and the asphericity of the

track volume, and (ii) computation of these measures in a staggered fashion to retrieve local information from all possible combinations of track segments. We demonstrate for a population of synthetic cell tracks as well as for in vitro neutrophil tracks obtained from microscopy experiment that the information contained in the track data is fully exploited in this way and does not require any prior knowledge, which keeps the analysis unbiased and general. The identification of cells that show the same type of migration behavior within the population of all cells is achieved via agglomerative hierarchical clustering of cell tracks in the parameter space of the staggered measures. The recognition of characteristic patterns is highly desired to advance our knowledge about the dynamics of biological processes.

Beteiligte Forschungseinheiten

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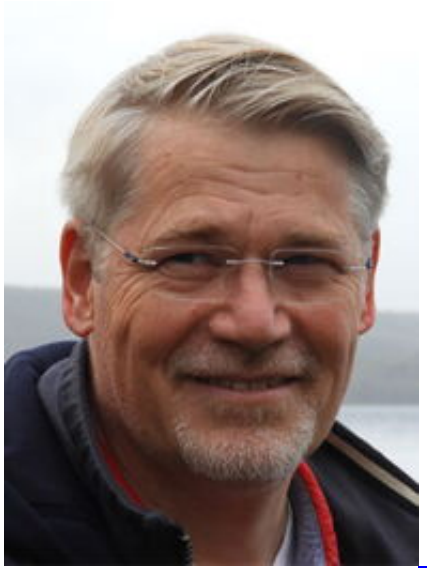

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doi: 10.1371/journal.pone.0080808

PMID: 24324630