Untangling cell tracks: Quantifying cell migration by time lapse image data analysis.

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Abstract

Automated microscopy has given researchers access to great amounts of live cell imaging data from in vitro and in vivo experiments. Much focus has been put on extracting cell tracks from such data using a plethora of segmentation and tracking algorithms, but further analysis is normally required to draw biologically relevant conclusions. Such relevant conclusions may be whether the migration is directed or not, whether the population has homogeneous or heterogeneous migration patterns. This review focuses on the analysis of cell migration data that are extracted from time lapse images. We discuss a range of measures and models used to analyze cell tracks independent of the biological system or the way the tracks were obtained. For single-cell migration, we focus on measures and models giving examples of biological systems where they have been applied, for example, migration of bacteria, fibroblasts, and immune cells. For collective migration,

we describe the model systems wound healing, neural crest migration, and *Drosophila* gastrulation and discuss methods for cell migration within these systems. We also discuss the role of the extracellular matrix and subsequent differences between track analysis in vitro and in vivo. Besides methods and measures, we are putting special focus on the need for openly available data and code, as well as a lack of common vocabulary in cell track analysis.

Involved units

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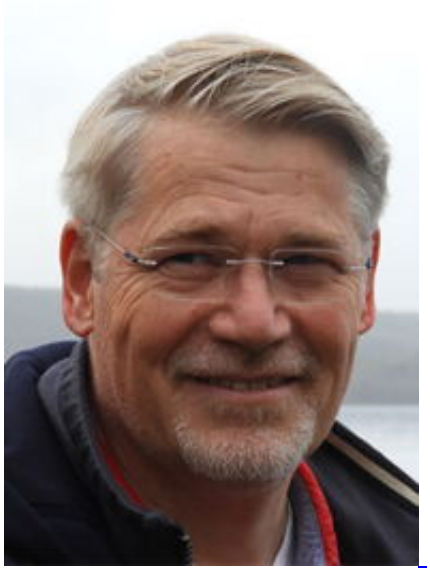

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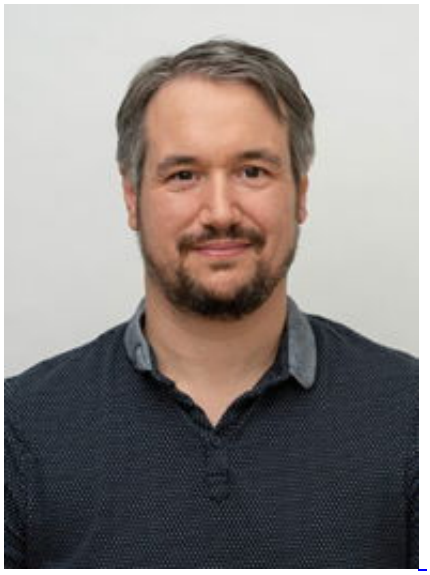

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