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

Automated characterization of cell tracks based on local migration behavior

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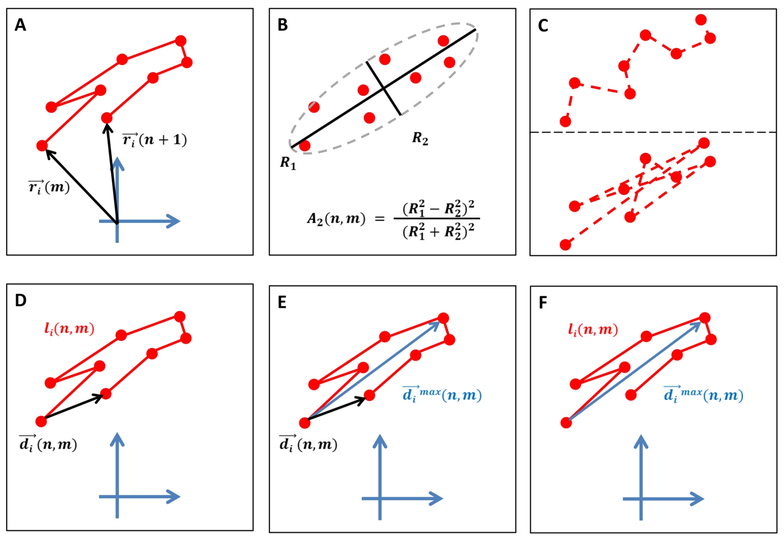
1. Introduction

Cell migration is a critical parameter for a wide variety of physiological and pathophysiological processes. In order to capture important details of a biological process under consideration and to arrive at quantitative predictions, it is generally required that algorithms capable of analyzing the specific experimental data have to be developed first.
We take first steps towards a fully automated characterization and parameter-free classification of cell track data.
We identified the following two requirements to achieve this aim:
(i) computation of staggered measures to retrieve local information from all possible track segments.
(ii) combination of different measures such as the confinement ratio and the asphericity of the cell track volume. We demonstrate that classification of cell tracks can be achieved via hierarchical clustering of cell tracks in the space of the staggered confinement ratio and asphericity.

2. Method

Schematic cell track characterization. (A) Example of a cell track segment. (B) The **volume asphericity**. (C) Track segments with different time-orderings. (D) The **confinement ratio** is determined by the displacement over the length of the cell track segment. (E) The **displacement ratio** is determined by the displacement over the maximal displacement of the cell track segment. (F) The **outreach ratio** is determined by the maximal displacement over the length of the cell track segment.



Staggered volume asphericity:

$$A_d(n,m) = \frac{1}{d(d-1)\langle R_l^2\rangle_d^2} \sum_{k=1}^{d} (R_k^2 - \langle R_l^2\rangle_d)^2 \qquad (1)$$

Staggered confinement ratio:

$$C_i(n,m) = \frac{\left|\vec{d}(n,m)\right|}{l_i(n,m)} \qquad (2)$$

Staggered displacement ratio:

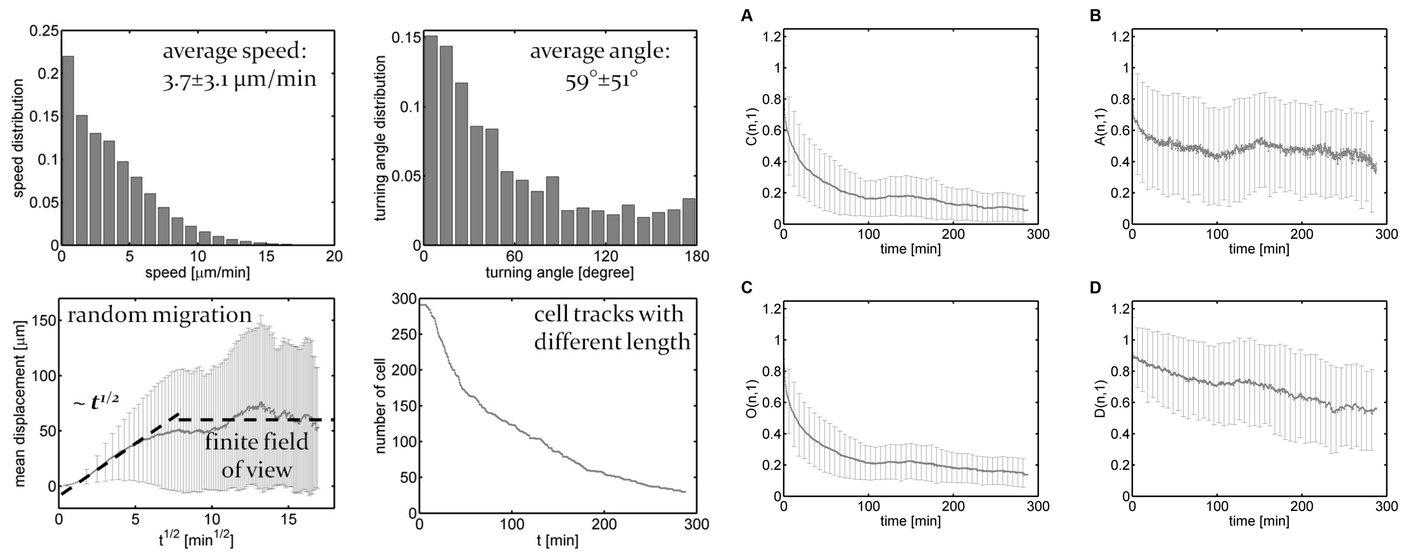
$$D_i(n,m) = \frac{\left|\vec{d}(n,m)\right|}{d_i^{max}(n,m)} \qquad (3)$$

Staggered outreach ratio:

$$O_i(n,m) = \frac{d_i^{max}(n,m)}{l_i(n,m)} \qquad (4)$$

3. Population analysis

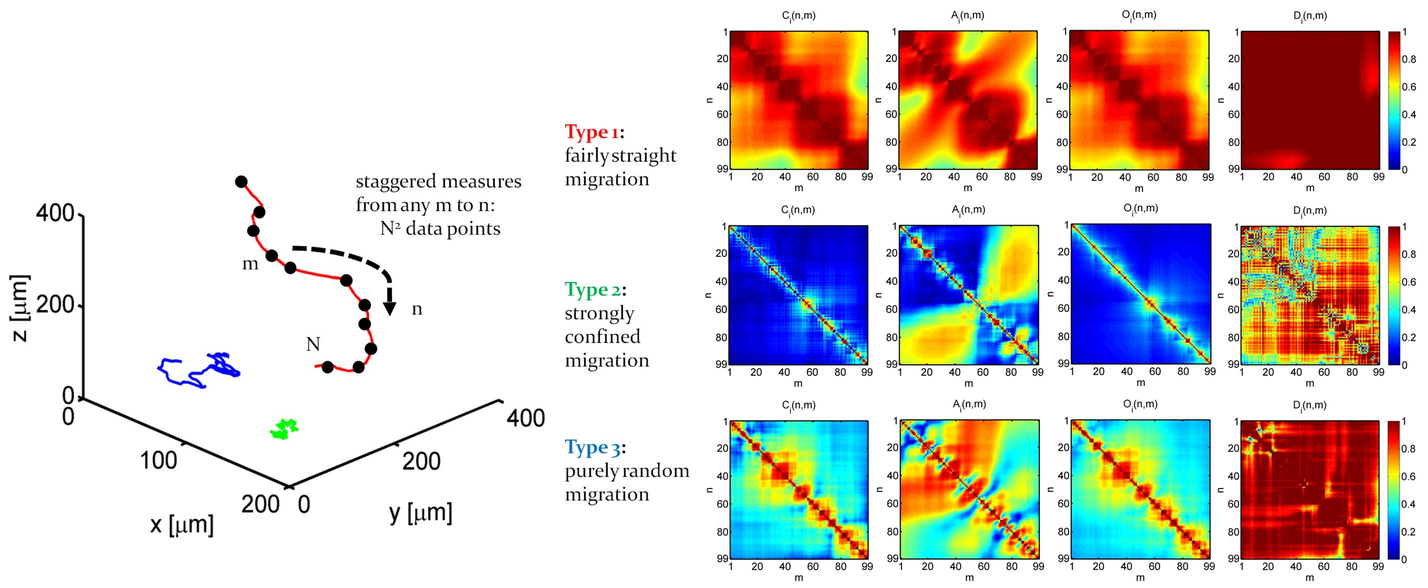
Cell population analyses of cell track data obtained from neutrophil migration



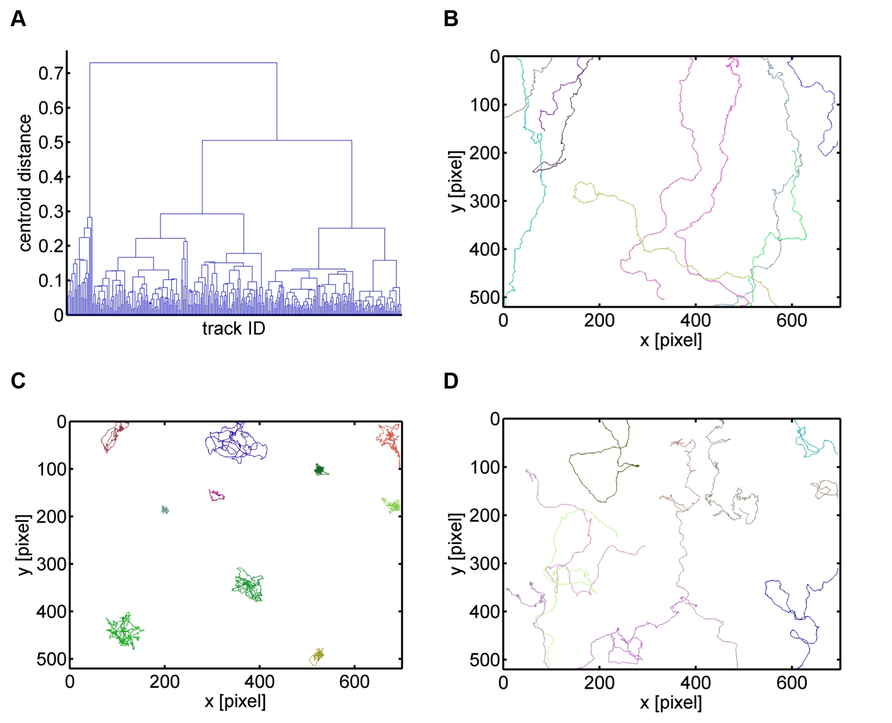
Analyses at the population level do not provide the information required to decompose a cell population into different sub-populations with distinct migration behavior.

4. Single cell analysis

Cell tracks with different types of migration behavior are shown (left). Heat maps of the staggered confinement ratio, staggered volume asphericity, staggered outreach ratio and staggered displacement ratio for the three types of cell tracks are shown (right).



Hierarchical clustering of neutrophil cell tracks in the parameter space of four staggered measures. (A) Dendrogram from the agglomerative hierarchical clustering based on the euclidean distance between the centroids of groups of data points. (B) Representative cell tracks of the cluster with fairly straight cell tracks. (C) strongly confined cell tracks. (D) purely random cell tracks.



5. Conclusion

- Dynamic changes in the migration behavior of single cells can be studied by extracting the information of a staggered measure contained in its heatmap.
- Hierarchical clustering of cell tracks in the parameter space related to staggered measures is applied to map clusters of cell tracks with similar migration behavior back into a system's spatial environment.

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