

Random walk models of eukaryotic cell migration

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Abstract

Introduction:

Cell migration through extracellular matrices is critical to the normal development of tissues and organs and in disease processes.

Random walk models are often applied in biology to investigate movement of particles, cells or whole organisms.

Methods: The mode of migration has been described in terms of various types of random walks. To understand the details of the migratory behavior we rely on mathematical models and their calibration to experimental data.

To distinguish different types of random walk, such as Brownian motion, biased random walks or correlated (persistent) random walks, the most commonly used summary statistics are the distribution of step lengths, the mean square displacement and the autocorrelation function of the turning angles, however we need to combine several such simple models to form more realistic hybrid models such as transition matrices (TMs). Superstatistical approach aim to analyze and model heterogeneous random walks of individual cells.

Results and discussion: we need to develop methods to discriminate cell migration strategies in different conditions and environments such as absence or existence of a chemotactic signal. Resulting insights should be used to design simple and meaningful models of cell migration and movement.

Conclusion: Anomalous features of cellular random walks have been reported, and a variety of models have been proposed in the literature to account for those anomalies.

Keywords: *cell migration, Random Walks, statistical modeling, anomalous diffusion*

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