

Statistical analysis of NIH 3T3 fibroblasts motility

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In recent years, in connection with the current problems of bio-engineering, much attention was paid to the analysis of the movement of bacteria and cells. An approach to cell motility as a random motion is well-known and fruitful [1]. It enables, applying powerful methods related to the theory of random processes, to understand more deeply very slow motion of these biological objects and, as a result, be able to control it. Undoubtedly, such models should adequately describe the available experimental results. The statistical analysis of cell motility on a homogeneous surface was performed in the report. Namely, based on experimental data for coordinates of thirty cells (NIH 3T3 fibroblasts) with the time-lapse of 5 minutes, we found the correlation functions of velocity projections and the mean-square displacement (MSD) using averaging over ensemble of cells and time. The velocity correlation function has two significantly different time scales and represents approximately the sum of two exponentials [2,3]. The MSD of cells demonstrates two different regimes: the ballistic diffusion at small time scales transforms to Brownian diffusion in asymptotic. At the same time, we observed only one small time scale in the correlation function of velocity modulus. Based on the results of statistical analysis processing of time series the theoretical model of cell motility is proposed. Specifically, the cell velocity is governed by linear integro-differential Langevin equation with exponential memory function and additive white Gaussian noise having two statistically independent components. Using the Laplace transform we solve this equation and obtain the exact formula for the spectral power density of velocity. Then, applying the Fourier transform we find the velocity correlation function and mean-square displacement. Our model contains some parameters, which can be determined from the experimental data for the velocity correlation function and asymptotic of the mean-square displacement. The velocity correlation function graph for both projections, reproduced from experimental data, is in a good agreement with theoretical predictions. At the same time, analysis of high-order moments of cell velocity indicates non-Gaussian nature of considered random processes.

[1] D. Selmeczi et al, *Biophys. J.* **89**, 912 (2005).

[2] D. Selmeczi et al, *Eur. Phys. J. ST* **157**, 1 (2008).

[3] L. Li, et al, *Phys. Biol.* **8**, 046006 (2011).