Anomalous dynamics of migrating biological cells

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Nearly all biological cells cover larger distances during their life cycle. Embryogenesis, wound-healing, immune defense, and the spreading of tumor metastases are well-known phenomena in the human body that rely on cell migration. On the molecular level the intrinsic cell migration machinery involves a spatially and temporally coordinated interplay of the actin cytoskeleton, cell-substrate and cell-cell interactions, and the activity of ion channels and transporters.

Laboratory experiments with isolated single cells crawling on a two-dimensional substrate show an impressive variety of dynamical processes under the microscope. The moving cells display certain non-periodic phases alternating between resting and directed motion. The migration process is accompanied by changes of the cell structure such as protrusions at the leading edge or retractions at the rear part. The experimental observation with time lapse movies already indicates, that cellular migration dynamics is a complex process that can hardly be put into a 'single number' or 'simple model'.

In this work sequences of microscopic phase contrast images of different variants of renal epithelial MDCK-F cells are acquired for periods of up to 15 hours, recorded at time intervals of one minute. Starting from the well-defined cell contour, the corresponding cell center reflects influences of structural changes and of 'rigid' movements. Depending on the cell type, cells display forms with a typical diameter of 20 – 30 μm. The cell center performs steps of the order of ~ 1 μm within one minute. The duration of resting and moving phases is of the order of one hour.

To further classify the dynamical process, we use ensembles of 20 to 30 cells to calculate dynamical properties from the cell paths. The mean square displacement shows a characteristic transition from a nearly ballistic behavior at small times to an anomalous super-diffusive increase for larger times. In addition, the probability density function p(x,t) exhibits a non-Gaussian behavior changing from a spiky form at small times to a flat distribution at longer times. This transition is in agreement with the time dependence of the kurtosis decreasing from values above 3 to values below as time increases. The framework of fractional Langevin equation and fractional diffusion equation seems to capture the characteristic features of the experimental data. Bayesian data analysis techniques are applied to extract the parameters of the model equations with respect to the experimental data. It is quite remarkable that cells consisting of an uncountable number of molecular components perform a collective motion which is consistent with a fractional dynamics.