

Anomalous dynamics of cell migration

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Cell movement—for example, during embryogenesis or tumor metastasis—is a complex dynamical process resulting from an intricate interplay of multiple components of the cellular migration machinery. At first sight, the paths of migrating cells resemble those of thermally driven Brownian particles. However, cell migration is an active biological process putting a characterization in terms of normal Brownian motion into question. By analyzing the trajectories of wild-type and mutated epithelial (transformed Madin–Darby canine kidney) cells, we show experimentally that anomalous dynamics characterizes cell migration. A superdiffusive increase of the mean squared displacement, non-Gaussian spatial probability distributions, and power-law decays of the velocity autocorrelations is the basis for this interpretation. Almost all results can be explained with a fractional Klein–Kramers equation allowing the quantitative classification of cell migration by a few parameters. Thereby, it discloses the influence and relative importance of individual components of the cellular migration apparatus to the behavior of the cell as a whole.

data analysis | fractional dynamics | non-Brownian motion

Nearly all cells in the human body are mobile at a given time during their life cycle. Embryogenesis, wound-healing, immune defense, and the formation of tumor metastases are well known phenomena that rely on cell migration. Extensive experimental work revealed a precise spatial and temporal coordination of multiple components of the cellular migration machinery such as the actin cytoskeleton, cell-substrate and cell–cell interactions, and the activity of ion channels and transporters (1–4). These findings are the basis for detailed molecular models representing different microscopic aspects of the process of cell migration such as the protrusion of the leading edge of the lamellipodium, or actin dynamics (5). Mathematical continuum models, in contrast, focus on collective properties of the entire cell to explain requirements for the onset of motion and some typical features of cell motility (6). These models are usually limited to small spatiotemporal scales. Therefore, they provide little information about how the integration of protrusion of the lamellipodium, retraction of the rear part, and force transduction onto the extracellular matrix lead to the sustained long-term movement of the entire cell. This process is characterized by alternating phases of directed migration, changes of direction, and polarization. The coordinated interaction of these phases suggests the existence of intermittency (7) and of strong spatio-temporal correlations. It is therefore an important question whether the long-term movement of the entire cell can still be understood as a simple diffusive behavior like usual Brownian motion (8, 9) or whether more advanced concepts of dynamic modeling have to be applied (10, 11).

Results and Discussion

We performed migration experiments and analyzed the trajectories of two migrating transformed renal epithelial Madin–Darby canine kidney (MDCK-F) cell strains: wild-type (NHE⁺) and NHE-deficient (NHE⁻) cells (12). The cells were observed for up to 1,000 min. Fig. 1*a* depicts the contours and the path of a migrating MDCK-F NHE⁺ cell monitored for 480 min. At first sight, the cell's trajectory resembles those of normal Brownian

particles. Brownian motion in terms of the Ornstein–Uhlenbeck process (13, 14) is characterized by a mean squared displacement, msd (for definition, see Eq. 1), proportional to $\sim t^2$ at short times corresponding to ballistic motion and $\sim t$ for long time intervals designating normal diffusion. Our experimental data show that both types of MDCK-F cells behave differently. Consistent with earlier observations, MDCK-F NHE⁻ cells move less efficiently than NHE⁺ cells (12, 15, 16), resulting in a reduced msd for all times. As displayed in Fig. 1*b*, their msd exhibits a crossover between three different dynamical regimes. For short times (<4 min; phase I), the increase of the msd differs from a ballistic t^2 scaling. The logarithmic derivative of the msd (Eq. 2) shown in Fig. 1*c* characterizes this first region with an exponent $\beta(t)$ below ≈ 1.8 . In the subsequent intermediate phase II (up to ≈ 20 min), the msd reaches its strongest increase with a maximum exponent of $\beta(t) \approx 1.8$. When the cell has approximately moved beyond a squared distance larger than its mean squared radius, r (indicated by arrows in Fig. 1*b*), the exponent $\beta(t)$ of the msd gradually decreases below 1.5.

We next extracted the probability that the cells reach a given position x at time t from the experimental data. This corresponds to the temporal development of the spatial probability distribution function $p(x, t)$ delivering information beyond the msd . Fig. 2*a* and *b* reveals the existence of non-Gaussian $p(x, t)$ distributions for different points in time. The transition from a peaked distribution at short times $t = 1$ min to rather broad distributions at long times $t = 120$ min and $t = 480$ min in Fig. 2*a* and *b* suggests again the existence of distinct dynamical processes acting on different time scales. The shape of the distributions can be quantified by calculating the kurtosis according to Eq. 5, which is displayed as a function of time in Fig. 2*c*. The kurtosis rapidly decays from values of ≈ 7 – 9 to reach a constant value of ≈ 2.3 for both cell types in the long time limit. Such a behavior implies a transition of $p(x, t)$ from a peaked to a flat form also visible from Fig. 2*a* and *b*. The time-dependent deviation of the kurtosis from the value of 3, which would correspond to a Gaussian distribution (as, e.g., for the Ornstein–Uhlenbeck process), is another strong manifestation of the anomalous nature of cell migration.

To gain further insight into the origin of the anomalous dynamics, we calculated the velocity autocorrelation function $v_{ac}(t)$ (defined in Eq. 4) that characterizes the correlation of the velocity (Eq. 3) at time t with its value at time $t = 0$ (Fig. 3). As for the msd in Fig. 1*b*, the double-logarithmic plot displays transitions between three regimes characterized by different time scales for both cell types. After a pronounced dip at short times, the autocorrelation function shows a gradual transition during intermediate times to a power-law-like decay at long times. In contrast, the Ornstein–Uhlenbeck realization of Brownian motion would imply a purely exponential decay of the

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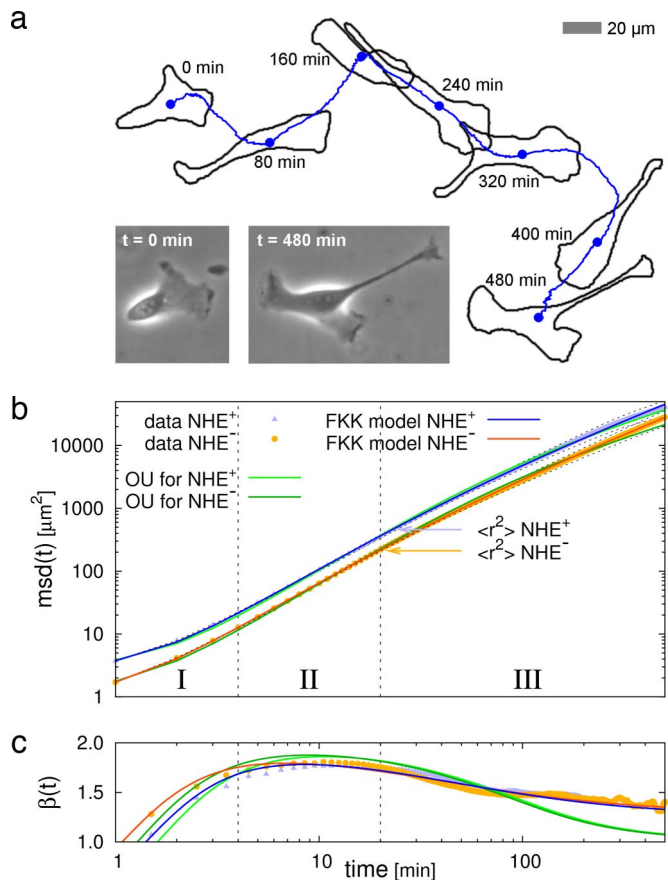


Fig. 1. Summary of migration experiments. (a) Overlay of a migrating MDCK-F NHE⁺ cell with its path covered within 480 min. The cell frequently changes its shape and direction during migration. (b) Double-logarithmic plot of the mean squared displacement (*msd*) as a function of time. Experimental data points for both cell types are symbolized by triangles and circles. Different time scales are marked as phases I, II, and III as discussed in the text. The solid blue and orange lines represent the fit to the *msd* of the fractional Klein–Kramers (FKK) equation including a noise term (Eq. 10). Green lines show the results of the Ornstein–Uhlenbeck (OU) model plus noise (Eq. 11). The corresponding parameters of the theoretical models are given in Tables 1 and 2. The dashed black lines indicate the uncertainties of the *msd* values according to Eq. 15. (c) Logarithmic derivative $\beta(t)$ (Eq. 2) of the *msd* for MDCK-F NHE⁺ and NHE⁻ cells. Data and model curves are marked as in b.

velocity autocorrelation function for all times. The nontrivial behavior of the velocity autocorrelation function stresses the existence of long-range correlations in time of the underlying dynamical process of cell migration. We would like to emphasize at this point that no chemotactic or other physical gradients were imposed on the cells examined in our study. Thus, our analysis shows that the so-called “random migration” does actually not proceed as randomly as one might expect.

To generalize the interpretation of our data, we sought an integrative mathematical model. The experimental results posed extensive constraints on the choice of such a model. A full theory should generate a power-law behavior of the *msd* including transitions between different time scales, non-Gaussian probability distributions, and a velocity autocorrelation function with a power-law decay for long times. Conventional Langevin, Fokker–Planck, and Klein–Kramers equations (17) provide descriptions of ordinary Brownian motion [e.g., the Ornstein–Uhlenbeck process (13, 14)] that do not match these constraints. The anomalous nature of cell migration demands for the inclusion of temporal memory in the above equations that can be achieved by introducing fractional derivatives (18–21). We

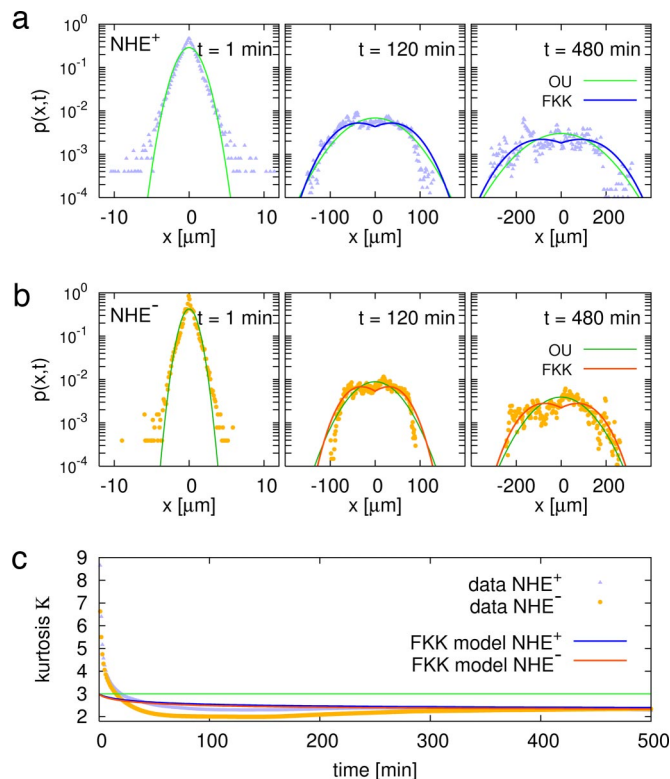


Fig. 2. Time-dependent development of the spatial probability distribution $p(x, t)$. (a and b) Experimental data for NHE⁺ and NHE⁻ cells, respectively, at different time points $t = 1, 120,$ and 480 min in a semilogarithmic representation. The continuous blue and orange lines show the solutions of the fractional diffusion equation as given in Eq. 9 with the parameter set obtained by the *msd* fit in Table 1. Analogously, the green lines depict the Gaussian Ornstein–Uhlenbeck functions. For $t = 1$ min, the probability distribution of the data points shows a peaked structure clearly deviating from a Gaussian form. (c) The kurtosis of the distribution function $p(x, t)$ varies as a function of time and saturates at ≈ 2.3 for long times. Being different from the value of 3 (green line, OU), the kurtosis confirms the deviation from a Gaussian (Ornstein–Uhlenbeck) probability distribution. The continuous blue and orange lines (FKK) represent the kurtosis modeled with the fractional Klein–Kramers equation including a Gaussian noise term.

therefore modeled our *msd* data with the fractional Klein–Kramers equation in Eq. 6 (18), which includes the Ornstein–Uhlenbeck process as special case ($\alpha = 1$). The inclusion of an uncorrelated noise term delivers the formula for the *msd* as given in Eq. 10. The continuous blue and orange lines in Fig. 1b represent the resulting fits with parameter values as given in Table 1 for MDCK-F NHE⁺ and NHE⁻ cells. There is excellent agreement of data and model for all times. The shallow initial slope of the *msd* curve is due to the estimated noise level $\eta \approx 0.78 \mu\text{m}$ and $0.47 \mu\text{m}$ for NHE⁺ and NHE⁻ cells, respectively. The values of η are much larger than the measurement uncertainty of $\sigma_{\text{pos}} \approx 0.1 \mu\text{m}$ showing the influence of “biological noise” generated by lamellipodial activity. The time scale $\tau_{\alpha} = (1/\gamma_{\alpha})^{1/\alpha}$ (Table 1 and Eqs. 6–8) characterizes the transition of the Mittag-Leffler function from stretched exponential to power-law behavior for $t \gg \tau_{\alpha}$. The resulting time scales $\tau_{\alpha} = 18.7$ min for NHE⁺ and $\tau_{\alpha} = 15.2$ min for NHE⁻ are comparable with the times at which the cells cross their mean squared radii ($458 \mu\text{m}^2$ and $211 \mu\text{m}^2$ for NHE⁺ and NHE⁻ cell, respectively). For larger times, the *msd* shows a transition to a power law of $\sim t^{2-\alpha}$ (see Eq. 8) thus describing superdiffusion of $\sim t^{1.25}$ for NHE⁺ and $\sim t^{1.28}$ for NHE⁻ cells. The enhanced thermal velocity, v_{th}^2 , and the slightly reduced value of γ_{α} generate a diffusion coefficient

Table 2. Parameter estimation: Ornstein–Uhlenbeck process

Cell type	Parameter					
	$\alpha, 1$	$\gamma_1, 1/\text{min}$	$v_{\text{th}}^2, \mu\text{m}^2/\text{min}^2$	$\eta, \mu\text{m}$	τ_1, min	$D_1, \mu\text{m}^2/\text{min}$
NHE ⁺	1 ± —	0.028 ± 0.001	0.549 ± 0.019	0.830 ± 0.007	36.22 ± 0.70	19.88 ± 0.95
NHE ⁻	1 ± —	0.029 ± 0.001	0.339 ± 0.012	0.522 ± 0.005	34.09 ± 0.70	11.57 ± 0.58

Parameters and their uncertainties (SD) were estimated with Bayesian data analysis applied to the Ornstein–Uhlenbeck (OU) result in Eq. 11, for both cell types MDCK-F NHE⁺ and NHE⁻. The missing anomalous features of the Ornstein–Uhlenbeck process imply the modification of the parameters.

framework that allows the classification of the dynamics of cell migration with a few physical parameters that can be calculated from the cells' trajectories. These can be compared for different cell types and under different experimental conditions. We probed our model by comparing migration of wild-type and NHE-deficient MDCK-F cells. The defect in directional migration induced by NHE deficiency (12, 15) can clearly be detected by analyzing the dynamics of MDCK-F cell migration. However, it is remarkable that the general pattern of anomalous dynamics is not changed by NHE deficiency. This observation indicates that the dynamics of cell migration is organized on a level of complexity that is above that of individual components of the cellular migration machinery. However, our model may allow the identification of those components of the cellular migration apparatus that govern the long-term behavior of migrating cells.

Materials and Methods

Cell Culture. Experiments were carried out on transformed Madin–Darby canine kidney (MDCK-F) cells and on NHE-deficient MDCK-F cells (12) referred to as NHE⁺ and NHE⁻ MDCK-F cells. Cells were kept at 37°C in humidified air containing 5% CO₂ and grown in bicarbonate-buffered minimal essential medium (MEM) (pH 7.4) with Earle's salts (Biochrom) supplemented with 10% FCS (Biochrom).

Migration Experiments. Cells were seeded at low density (to avoid collisions between cells during the experiment) in tissue culture flasks (Falcon) 1–2 days before the experiments. They were incubated in Hepes-buffered (20 mmol/liter, pH 7.4) MEM supplemented with 10% FCS during the course of the experiments. The flasks were placed in a heating chamber (37°C) on the stage of an inverted microscope equipped with phase-contrast optics (Axiocvert 40; Zeiss). Migration was monitored with a video camera (Hamamatsu) controlled by HiPic software (Hamamatsu). Images were taken in 1-min time intervals during a time range of up to 1,000 min. $N = 13$ trajectories of each cell type were used for the analysis consisting of >10,000 data points for each group.

Data Analysis. Image segmentation was performed with Amira software (Visage Imaging/Mercury Computer Systems). The outlines of individual cells at each time step were marked throughout the entire image stack and taken for all further processing. In addition, we assessed the accuracy of the segmentation by repeated segmentation. The normally distributed experimental uncertainty amounts to $\sigma_{\text{pos}} \approx 0.1 \mu\text{m}$ (data not shown). Quantitative data analysis and calculation of parameters were performed with programs developed by us. The x and y coordinates of the cell center (in micrometers) were determined as geometric means of equally weighted pixel positions within the cell outlines as function of time. The combined trajectories of a cell population allow the calculation of the mean squared displacement, msd , that describes the mean of the squared distances between a common starting point at time t_0 and the actual positions of a cell population at time t ,

$$msd(t) = \langle [x(t + t_0) - x(t_0)]^2 + [y(t + t_0) - y(t_0)]^2 \rangle, \quad [1]$$

where $\langle \dots \rangle$ denotes a combined average over all starting times t_0 and cell paths. The increase of the msd can be quantified by the logarithmic derivative

$$\beta(t) = \frac{d \ln msd(t)}{d \ln t} \quad [2]$$

leading to a time-dependent increase $msd(t) \sim t^{\beta(t)}$.

The velocity of migrating cells in x and y direction [$v_{xy}(t)$ ($\mu\text{m}/\text{min}$)] was calculated from trajectories as the difference quotient of two cell positions at times $t + \Delta$ and t

$$v_x(t) = \frac{x(t + \Delta) - x(t)}{\Delta} \quad \text{and} \quad v_y(t) = \frac{y(t + \Delta) - y(t)}{\Delta} \quad [3]$$

with the observation time interval of $\Delta = 1$ min. These velocities were used to calculate the velocity autocorrelation function

$$v_{\text{ac}}(t) = \langle v_x(t + t_0)v_x(t_0) \rangle + \langle v_y(t + t_0)v_y(t_0) \rangle, \quad [4]$$

where $\langle \dots \rangle$ denotes an average as in Eq. 1.

The position of the cells can also be used to calculate the probability $p(x, y, t)$ of finding a cell at position (x, y) for time t . Because we did not find any correlations between x and y direction in the velocity autocorrelation function (data not shown), we reduced the discussion to $p(x, t)$ given as average of x and y positions.

The kurtosis is defined as the ratio of moments by

$$\kappa = \langle x^4(t) \rangle / \langle x^2(t) \rangle^2. \quad [5]$$

It can be interpreted as shape index of the probability distribution function $p(x, t)$ and takes the value of 3 for Gaussian functions.

Fractional Klein–Kramers Equation. The anomalous properties of cell dynamics were assessed with the fractional Klein–Kramers equation (FKK) for the probability distribution $P(x, v, t)$ in position x , velocity v , and time t as proposed by Barkai and Silbey (18) but without external forces:

$$\frac{\partial P(x, v, t)}{\partial t} = -\frac{\partial}{\partial x} [vP(x, v, t)] + \frac{\partial^{1-\alpha}}{\partial t^{1-\alpha}} \gamma_\alpha \left[\frac{\partial}{\partial v} v + \frac{k_B T}{M} \frac{\partial^2}{\partial v^2} \right] P(x, v, t). \quad [6]$$

γ_α denotes the damping term, k_B is the Boltzmann constant, T is the temperature, M is the mass of the particle, and α defines the order of the fractional time derivative of Riemann–Liouville type (see, for example, ref. 20). For $\alpha = 1$, the above equation reduces to the ordinary Klein–Kramers equation (17). The fractional Klein–Kramers equation of Eq. 6 implies that the velocity correlation function is given by the so-called Mittag-Leffler function (22) E_α :

$$\langle v_x(t)v_{x0} \rangle = v_{\text{th}}^2 E_\alpha(-\gamma_\alpha t^\alpha) \Rightarrow v_{\text{ac}}(t)_{\text{FKK-2D}} = 2v_{\text{th}}^2 E_\alpha(-\gamma_\alpha t^\alpha). \quad [7]$$

In the case of the Ornstein–Uhlenbeck limit ($\alpha = 1$), E_α reduces to an exponential decay $\sim \exp(-\gamma_1 t)$. The mean squared displacement of the fractional Klein–Kramers equation is represented by the generalized Mittag-Leffler function (22) $E_{\alpha,\beta}$:

$$msd(t)_{\text{FKK-1D}} = 2v_{\text{th}}^2 t^2 E_{\alpha,3}(-\gamma_\alpha t^\alpha) \sim \frac{2D_\alpha t^{2-\alpha}}{\Gamma(3-\alpha)} \quad \text{for } t \rightarrow \infty. \quad [8]$$

The mean thermal velocity $v_{\text{th}}^2 = k_B T/M$ is related to the generalized diffusion coefficient D_α by the relation $D_\alpha = v_{\text{th}}^2/\gamma_\alpha$. In the limit of large damping ($\gamma_\alpha \rightarrow \infty$), the fractional Klein–Kramers equation reduces to a fractional diffusion

equation (FDE) (19, 20) where the spatial probability distribution functions $p(x, t)$ are given by a Fox function $H(19, 20)$:

$$p(x, t)_{\text{FDE}} = \frac{1}{\sqrt{4\pi D_\alpha t^{2-\alpha}}} H_{12}^{20} \left[\frac{x^2}{4D_\alpha t^{2-\alpha}} \middle| \begin{matrix} (\alpha/2, 2-\alpha) \\ (0, 1) \end{matrix} \middle| \begin{matrix} (1/2, 1) \end{matrix} \right]. \quad [9]$$

Eq. 8 can be extended to include uncorrelated noise of variance η^2 generated by measurement errors (23) or by biological activity; e.g., by the fluctuating lamellipodium ($t > 0$)

$$msd(t)_{\text{FKK-2D+noise}} = 4v_{\text{th}}^2 t^2 E_{\alpha,3}(-\gamma_\alpha t^\alpha) + (2\eta)^2. \quad [10]$$

Eq. 10 reduces to the Ornstein–Uhlenbeck result for $\alpha = 1$ with the noise term

$$msd(t)_{\text{OU-2D+noise}} = \frac{4v_{\text{th}}^2}{\gamma_1^2} (\gamma_1 t - 1 + e^{-\gamma_1 t}) + (2\eta)^2. \quad [11]$$

In a similar way, uncorrelated noise also influences the velocity autocorrelation function. The fluctuations η_i affect the velocity calculation in Eq. 3 at both positions $x(t)$ and $x(t_i + \Delta)$ separated by the measurement interval Δ . Performing the average for the calculation of the velocity autocorrelation function eliminates all linear terms η_i while quadratic noise terms deliver a modification of the velocity autocorrelation function at times $t = 0$ and $t = \Delta$:

$$v_{\text{ac}}(t)_{\text{FKK-2D+noise}} = v_{\text{ac}}(t)_{\text{FKK-2D}} + \frac{4\eta^2}{\Delta^2} \delta(t, 0) - \frac{2\eta^2}{\Delta^2} \delta(t, \Delta) \quad [12]$$

with the Kronecker delta $\delta(t, t') = 1$ for $t = t'$ and 0 elsewhere. All other times are unaffected, if the noise source is uncorrelated.

Bayesian Data Analysis. The parameters of the FKK model in Eq. 6 and their uncertainties were estimated with Bayesian data analysis (24) (for a recent review, see ref. 25) applied to the corresponding two-dimensional mean squared displacement of Eq. 10 (or Eq. 11 for the Ornstein–Uhlenbeck process). Bayesian data analysis offers a logically consistent link between data and models. It allows a reliable estimation of the model parameters taking the uncertainties of the experimental data into account. The expectation value of the n th moment of the parameters $\hat{\theta} = \{\alpha, \gamma_\alpha, v_{\text{th}}^2, \eta\}$ in Eq. 10 is given by integrating over the posterior probability function for these parameters $p(\hat{\theta} | \text{data})$. The later is proportional to the product of likelihood $p(\text{data} | \hat{\theta})$ and prior function $p(\hat{\theta})$:

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$$\langle \theta_i^n \rangle = \frac{\int \prod_{k=1}^4 d\theta_k \theta_i^n p(\text{data} | \hat{\theta}) p(\hat{\theta})}{\int \prod_{k=1}^4 d\theta_k p(\text{data} | \hat{\theta}) p(\hat{\theta})}. \quad [13]$$

Assuming normally distributed errors, the likelihood function $p(\text{data} | \hat{\theta})$ is given by

$$p(\text{data} | \hat{\theta}) = \left(\prod_{i=1}^N \frac{1}{\sqrt{2\pi\sigma^2(t_i)}} \right) \exp \left\{ -\frac{1}{2} \sum_{i=1}^N \left(\frac{\text{data}(t_i) - msd(\hat{\theta}, t_i)}{\sigma(t_i)} \right)^2 \right\}, \quad [14]$$

where $msd(\hat{\theta}, t_i)$ corresponds to Eq. 10 for the FKK model. A constant prior $p(\hat{\theta})$ was applied because of the lack of advance information about the values of the parameters. The four-dimensional integral in Eq. 13 was evaluated numerically by Markov chain Monte Carlo sampling. Thus, application of Eq. 13 with $n = 1$ delivers the expectation values of the four parameters α (1), γ_α (1/min^α), v_{th}^2 (μm²/min²), and η (μm) based on the available experimental msd data at time points t_i . The error $\sigma(t_i)$ was estimated as

$$\sigma(t_i) = \text{data}(t_i) / \sqrt{NT_{\text{path}}/t_i}, \quad [15]$$

where N is the number of cell paths. The quotient of path length T_{path} (= 500 min) and actual time t_i estimates the number of more or less independent measurement intervals during the calculation of the combined expectation value in Eq. 1 [also see Qian *et al.* (26) for the discussion of statistical errors of the msd]. In addition, Eq. 13 allows for the estimation of the uncertainties of the parameter with $n = 2$ via

$$\delta\theta_k = \sqrt{\langle \theta_k^2 \rangle - \langle \theta_k \rangle^2}. \quad [16]$$

In addition, we applied this formalism to simulated data of the Ornstein–Uhlenbeck process with a number of data that are comparable with the experiments. These simulations showed that the presented Bayesian data analysis delivers an agreement of estimated and actually used simulation parameters within the uncertainties (data not shown).

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