Anomalous versus Slowed-Down Brownian Diffusion in the Ligand-Binding Equilibrium

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ABSTRACT Measurements of protein motion in living cells and membranes consistently report transient anomalous diffusion (subdiffusion) that converges back to a Brownian motion with reduced diffusion coefficient at long times after the anomalous diffusion regime. Therefore, slowed-down Brownian motion could be considered the macroscopic limit of transient anomalous diffusion. On the other hand, membranes are also heterogeneous media in which Brownian motion may be locally slowed down due to variations in lipid composition. Here, we investigate whether both situations lead to a similar behavior for the reversible ligand-binding reaction in two dimensions. We compare the (long-time) equilibrium properties obtained with transient anomalous diffusion due to obstacle hindrance or power-law-distributed residence times (continuous-time random walks) to those obtained with space-dependent slowed-down Brownian motion. Using theoretical arguments and Monte Carlo simulations, we show that these three scenarios have distinctive effects on the apparent affinity of the reaction. Whereas continuous-time random walks decrease the apparent affinity of the reaction, locally slowed-down Brownian motion and local hindrance by obstacles both improve it. However, only in the case of slowed-down Brownian motion is the affinity maximal when the slowdown is restricted to a subregion of the available space. Hence, even at long times (equilibrium), these processes are different and exhibit irrec-
ocircumflex;oncible behaviors when the area fraction of reduced mobility changes.

INTRODUCTION

The structural elements of living cells (e.g., membranes, cytoplasm, nucleus, and mitochondria) exhibit disorder, heterogeneity, and obstruction typical of poorly connected media (1). For instance, cell membranes are heterogeneous collections of contiguous spatial domains with various length scales and timescales (e.g., fences, lipid rafts, and caveolae) (2) that spatially modulate the diffusion of proteins (3–5). This defines a spatially heterogeneous diffusion problem with a position-dependent diffusion coefficient (4,7–10). On the other hand, the movement of biomolecules such as proteins in the membranes of living cells has consistently been reported to exhibit anomalous diffusion, whereby the mean-squared displacement (MSD) scales sublinearly with time, \( \langle r^2(t) \rangle \propto t^\alpha \) with \( \alpha < 1 \) (11–14). This anomalous diffusion phenomenon (also coined subdiffusion) is a hallmark of diffusion obstruction by obstacles (15) or random walks with heavy-tailed residence time distributions (15,16) (for the sake of conciseness, we will not consider here fractional Brownian motion (fBM) as a model of crowding-induced anomalous diffusion (17)).

The influences of such deviations from simple Brownian motion on the biochemical reactions that take place in these media are just starting to be explored. The fundamentally heterogeneous spatial organization of the cell membrane is believed to locally favor the oligomerization of membrane receptors and prolong their local residence times, thus affecting signal transduction in the plasma membrane (5).

However, careful investigations by Monte Carlo simulations hint that complex or counterintuitive behaviors can generically be expected (18,19).

The effects of anomalous diffusion on the dynamics of simple elementary reactions of biological interest have recently attracted the interest of several groups (20–23) (see Ben-Avraham and Havlin (24) for a book on elementary irreversible reactions). In the case of the binary reaction \( A + B \rightarrow \text{products} \), for instance, anomalous diffusion alters the overall reaction kinetics (25–27) and may favor the search of target DNA sequences by transcription factors (28,29) or reduce the time needed by an enzyme to reach its substrate (30). Anomalous diffusion has also been proposed as a key regulator of the spatiotemporal dynamics of Michaelis-Menten enzyme reactions (E+S ⇌ C ⇌ E + P) (31,32).

The case of reversible reactions, such as the ubiquitous ligand-binding equilibrium,

\[
L + R \xrightleftharpoons[k_{on}]{k_{off}} C
\]

(1)

(where \( L \) is the ligand, \( R \) its free receptor, and \( C \) the bound complex), has received less attention. Reversible reactions are expected to converge at long times to equilibrium, thus permitting investigators to study the influence of anomalous or position-dependent diffusion not only on transient regimes but also on long-time equilibrium properties. Indeed, from standard mass-action laws (33), the concentration of complex \( C \) in reaction Eq. 1 evolves according to \( dC(t)/dt = k_{on}L(t)R(t) - k_{off}C(t) \), where \( X(t) \) is the
concentration of species X at time t. At equilibrium 
\((dC/dt = 0)\), assuming that the total amount of L molecules, 
\(L_0\), is much larger than that of \(R, R^\prime\), these mass-action laws yield 
\(C_{eq} = L_0 R f/(K_{dp} + L f)\), where the equilibrium constant 
\(K_{dp}\) is the ratio of the reaction affinity (the smaller the 
curves (the equilibrium amounts of ligand) with equilibrium constant, 
\(K_{dp}\), a measure of the reaction affinity (the smaller the 
\(K_{dp}\), the larger the affinity). 

However, the significance of anomalous diffusion for 
equilibrium properties is questionable because in many 
experimental data (34–37), the anomalous regime is only 
transient: at long times, the MSD crosses over to normal 
(Brownian) diffusion, with \(\alpha = 1\) but a reduced apparent 
diffusion coefficient. Such transient behaviors are obtained, 
e.g., when the density of obstructing obstacles is below the 
percolation threshold (38–40) or the residence time is 
power-law distributed with a cutoff (37,41). Fig. 1A illustrates 
this transitory behavior with a Monte Carlo simulation 
of two-dimensional (2D) random walks on a square lattice in 
the presence of immobile obstacles (obstacle density 
\(\rho = 0.35\)). For very short simulation times, the distance 
traveled by the molecules is less than the typical distance 
between obstacles, so the movement converges to a Brownian 
regime without obstacles (with microscopic diffusion coeffi-
cient \(D_0\)). The movement then crosses over to the anomalous 
subdiffusive regime at longer times, with the MSD \(\langle R^2(t) \rangle\) 
scaling sublinearly with time (roughly \(\sim t^{0.8}\) in the figure). 
However, the anomalous regime is transitory because at 
longer times, the movement crosses over to a second Brown-
nian regime with a smaller apparent macroscopic diffusion 
coefficient, \(D_M\). A similar behavior is observed when mole-
cule movements are due to a continuous-time random walk 
(CTRW), in which the residence time \(\tau\) between two succes-
sive jumps has a power-law distribution 
\((\phi(\tau) \propto \tau^{-(1+\alpha)})\) with 
\(0 < \alpha < 1\) (15,16). When the residence time is upper-bounded 
by a cutoff \(\tau_c\) (Fig. 1B), the (ensemble-averaged) MSD scales 
anomalously \((\langle R^2(t) \rangle \propto t^\alpha\) for \(t < \tau_c\) and then crosses over to 
a Brownian regime with reduced diffusion coefficient at 
longer times. In both cases in Fig. 1, the transient anomalous 
behavior transforms to a slowed-down Brownian motion at 
long times. This asymptotic slow-down Brownian regime 
could be considered a macroscopic (homogenized) representation 
of the underlying microscopic anomalous diffusion. Following 
this line of reasoning, it is tempting to assume that 
the long-time (or equilibrium) behavior of a molecule 
undergoing transient anomalous diffusion can be captured 
by a slowed-down Brownian motion. 

Here, we questioned the validity of this assumption, i.e., 
that slowed-down Brownian motion can capture transient 
anomalous diffusion at long times. We studied the equilib-
rium properties of the ubiquitous ligand-binding equilibrium 
(Eq. 1) when diffusion was transiently anomalous due to

![Image of Figure 1](image-url)

**FIGURE 1** Transient anomalous diffusion as a transitory behavior in a macroscopic slowed-down Brownian regime. Time evolutions (log-log scales) of the 
MSD, \(\langle R^2(t) \rangle\) (top) and the corresponding evolution of the ratio \(\langle R^2(t) \rangle/t\) (bottom) during transient subdiffusive anomalous diffusion due to obstacle hind-
rance (A) or power-law distributed residence times (CTRW) (B) are shown. Thick lines show the (ensemble) average, and the light swaths indicate +1 SD. In the top panels, Brownian motion manifests as a straight line with unit slope and a y-intercept set by the diffusion coefficient (thin dashed orange lines). The anomalous regime is observed as a transitory behavior, with slope \(\alpha = 0.80\) in (A) or \(\alpha = 0.80\) in (B) (dotted lines), crossing over to an effective macroscopic Brownian regime with diffusion coefficient \(D_M\). For panel A, one gets \(D_M \approx 0.125\), whereas \(D_M \approx 0.032\) in B. In the bottom panels, Brownian motion manifests as a horizontal straight line with the y-intercept set by the diffusion coefficient and the anomalous regime as straight lines with slope \(1 - \alpha\). Parameters: \(w = 1\), \(\Delta x = 2\) and \(D_0 = 1\), domain size \(w = 10^6\). Data are averages of \(10^4\) independent trajectories (A) obstacle density \(\rho = 0.35\), (B) CTRW exponent \(\alpha = 0.8\), cutoff time \(\tau_c = 5 \times 10^4\).
either obstacles (below the percolation threshold) or power-law-distributed residence times, or when normal space-dependent Brownian diffusion took place. Using Monte Carlo simulations and theoretical arguments, we show that this approximation fails even for equilibrium properties, if diffusion conditions are heterogeneous in space.

MATERIALS AND METHODS

Brownian motion

To simulate diffusion, we initially position L and R molecules uniformly at random on a $S = w \times w$ 2D square lattice with reflective boundaries. Each lattice site $(i,j)$ is associated with a diffusion coefficient $d(i,j)$ (all molecules here have identical diffusion coefficients). At each time step $\Delta t$, every molecule is allowed to leave its current location $(i,j)$ with jump probability $p(i,j) = 4 \Delta t / (\Delta x)^2 d(i,j)$, where $\Delta x$ is the lattice spacing. The destination site is chosen uniformly at random from the four nearest neighbors $(i \pm 1, j \pm 1)$. If the jump of the molecule to its destination site results in the formation of an $(L,R)$ couple on the same lattice site, a binding event may occur, i.e., the $(L,R)$ couple may be replaced by a single C molecule at the site, with probability $p_{br}$. Finally, at each time step, every C molecule can unbind, i.e., the C molecule is replaced by an $(L,R)$ couple at the same site, with probability $p_{bu}$.

Immobile obstacles

To simulate anomalous diffusion due to obstacles, we position obstacles at random locations (with uniform distribution) at the beginning of the simulation. The obstacles behave as a separate type of molecules that are kept unreactive and immobile, whereas the other molecules (L, R, and C) move as indicated above. Obstacles exclude the lattice site they occupy: when the destination site of a moving L, R, or C molecule contains an obstacle, the molecule is reflected back to its origin site (the destination site becomes the origin position). Reaction is modeled as described above for Brownian motion.

CTRW

Molecule motion by CTRW is modeled as for Brownian motion except that upon each jump to its destination site, the molecule is attributed a new residence time $\tau$ sampled from the power-law distribution $\phi(\tau) = \tau^{-\alpha} \phi(\tau) = 1$. Hence $\Delta t$, the simulation time step, is the smallest residence time possible, and $\tau_c$, the cutoff time, sets its maximal value. Therefore, the next jump of this molecule will not take place before $\tau_c$ time units have elapsed. Reactions are modeled exactly as for the Brownian case above, with the additional property that molecules can react during residence (i.e., between jumps, whenever they are located at the same location). Moreover, every new molecule resulting from a reaction samples a new residence time. Because microscopic details can have a crucial effect on CTRW-based reactions (21,42-43), we checked in a subset of simulations that the latter does not impact qualitatively our simulation results.

Simulation parameters

In a typical simulation, we start with $r(0) = r_f$ R molecules and $l(0) = l_f$ L molecules (where $xy$ refers to the total number of molecules X), and no C, and run the simulation until the density of bound receptors C reaches a steady state, $C_{eq}$. We used standard parameter values throughout this study unless otherwise specified, i.e., lattice size $w = 800$, $r_f = 100$, $\Delta t = 1$, $\Delta x = 2$, $p_{br} = 0.1$, $p_{bu} = 10^{-3}$, and diffusion coefficient $D_0 = 1$. The ligand dose, $l_f$, was varied to obtain dose-response curves. Data were averaged over 20 independent simulations.

Depending on simulation conditions, equilibrium was typically reached after at most $10^5$ (obstacles) to $5 \times 10^5$ (slow-down Brownian diffusion) time steps. The equilibrium value of $C_{eq}$ was therefore computed as the time average of $C(t)$ for $t \in [4.5,5.0] \times 10^5$ (obstacles) or $[9.5,10.0] \times 10^5$ (slow-down Brownian). With CTRW, the time needed to establish equilibrium is much longer than the cutoff $\tau_c$. In all of our simulations for $\tau_c \leq 10^3$, we observed that equilibrium was reached before $t = 9.5 \times 10^5$, so we used the values for $t \in [9.5,10.0] \times 10^5$ to compute the equilibrium value.

RESULTS

Reaction in spatially homogeneous conditions

We first studied Eq. 1 in spatially homogeneous conditions, i.e., in conditions where the diffusion coefficient or local obstacle density is the same everywhere in space.

Fig. 2A shows typical time courses of the bound fraction $C(t)/R_f$ for different values of the diffusion coefficient $D$ (no obstacles). Although the time needed to reach equilibrium increases with smaller diffusion coefficients, all curves seem to converge to long times at similar levels, thus suggesting that the equilibrium concentration of bound receptor $C_{eq}$ does not depend on the diffusion coefficient. This is of course an expected result from standard thermodynamics: equilibrium configurations should in principle be independent of dynamics, i.e., values of transport coefficients such as diffusion coefficients. The situation is different when the molecule movement exhibits transient anomalous diffusion due to immobile obstacles randomly spread over the whole lattice. At long times (Fig. 2B), the reaction also converges to equilibrium. In this case, though, the convergence time to this equilibrium does not seem to be affected by the density of hindering obstacles, but the concentration of bound receptor at equilibrium seems to vary with the obstacle density in a nontrivial fashion.

Fig. 3A shows the dose-response curve for an obstacle density $\rho = 0.35$ (upper thick green line), for which molecule motion exhibits the transient anomalous diffusive behavior due to obstacles shown in Fig. 1A (thick green line). With immobile obstacles, the bound fraction for all doses is found to be significantly larger than the dose-response curve obtained in the absence of obstacles (solid black circles). This confirms the observation of Fig. 2B that obstacle hindrance alters the bound fraction at equilibrium. Because the molecule movement for $\rho = 0.35$ converges at long times to Brownian diffusion with the effective macroscopic diffusion coefficient $D_M = 0.125$ (Fig. 1A), we compared these results with the dose-response curve obtained when the molecules moved by a Brownian motion (no obstacles) with diffusion coefficient $D = 0.125$ (thick orange line). In agreement with the observation...
made above, and standard thermodynamics, the corresponding dose-response curve was not significantly different from the curve obtained with $D = 1$ (solid black circles). This confirms that the macroscopic slowed-down Brownian regime reached at long times during transient anomalous diffusion does not adequately account for the equilibrium properties of Eq. 1.

The dose-response curves for anomalous diffusion due to obstacles maintain a shape that is compatible with the classical dose-response equation ($C_{eq}/R_T = L_T/(K_D + L_T)$). Therefore, we can fit them using this equation and retrieve for all obstacle densities the corresponding apparent equilibrium constant $K_D$. Fig. 3 B displays $K_D$ values for several values of the diffusion coefficient reduction $\gamma = 1 - D$ in the absence of obstacles (B1) and for several obstacle densities $\rho$ (B2). As expected, even a one order of magnitude span for $D$ in the Brownian case does not influence the apparent $K_D$ (B1).

The situation is different for transient anomalous diffusion, though. Far from the percolation threshold ($\rho = 0.41$), $K_D$ decays linearly with obstacle density as $K_D/K_{D0} = 1 - \rho$. This is a simple effect of the excluded volume occupied by the obstacles. Indeed, for a constant number of molecules, the available space decreases when the obstacle density increases. Consequently, the local density of molecules increases with the obstacle density. This gives rise to the measured decrease of the apparent constant $K_D$. In agreement, the decay of $K_D$ far from the percolation threshold disappears if the concentrations are computed on the basis of the accessible space, $1 - \rho$, instead of the whole space. Therefore, hindered diffusion due to obstacles not only decreases molecule mobility but also increases the affinity ($\sim 1/K_D$) of the reaction. This trend, however, reverses close to the percolation threshold, where $K_D$ increases. This behavior is due to the competition between two effects: with increasing obstacle densities, the mean
first-collision time increases because the macroscopic diffusion coefficient is slower (the first encounter between two distant molecules takes increasingly longer). On the other hand, the recollision time decreases because recollisions imply that molecules are initially close by (as a consequence of failed binding attempts or unbinding events), and anomalous diffusion favors recollisions (25,29). Close to the percolation threshold, the increase of the first-collision time overcompensates (by far) for the decrease of the recollision time (not shown). As a result, the forward reaction rate, \( k_{\text{on}} \), and the apparent affinity strongly decrease close to the threshold.

When anomalous diffusion is due to CTRW, the kinetics of the reaction shows a very different picture (Fig. 2, C and D). For anomalous diffusion due to obstacles, the obstacle density sets both the (apparent) scaling of the MSD with time in the anomalous regime and the duration of this regime. In the CTRW case, though, both quantities (the anomalous exponent \( \alpha \) and the crossover time \( \tau_c \)) are parameters that we can fix separately. Similarly to obstacle-induced anomalous diffusion, the convergence time is not much affected by the value of the cutoff time (Fig. 2 C) or that of the anomalous exponent (Fig. 2 D). However, the concentration of bound receptors at equilibrium varies widely with the CTRW parameters. In general, the equilibrium values obtained with CTRW are much lower than those observed with Brownian motion and obstacle-induced anomalous diffusion. This reduction of equilibrium binding by CTRW progressively attenuates as the cutoff time decays to very low values (Fig. 2 C) or the anomalous exponent increases (Fig. 2 D), i.e., when diffusion is increasingly less anomalous and the motion tends to Brownian. Note that the largest cutoff used in this figure \( (\tau_c = 10^6) \) equals the total simulation time, so that, in effect, \( \tau_c = 10^6 \) corresponds to a permanent CTRW regime (no crossover back to the Brownian regime within the simulation time). In this case, equilibrium cannot be reached during the simulation time (CTRW is then a nonequilibrium process).

This strong reduction of equilibrium binding with CTRW is even more obvious in the dose-response curve in Fig. 3 A. Note that the parameters for CTRW in this panel (blue curve) are those illustrated in Fig. 1 B (thick blue line). For a given ligand dose, the bound fraction at equilibrium with CTRW is much smaller (up to ~2-fold) than the response curve with Brownian motion, whatever the slowdown (thick orange line). Here as well, since the overall shape of the CTRW dose-response curves is compatible with the classical form \( (C_{eq}/R_T = L_T/(K_D + L_T)), \) they can be fitted to estimate the apparent equilibrium constant \( K_{eq} \). Fig. 3 B shows that when diffusion becomes increasingly anomalous (the anomalous exponent \( \alpha \) decreases from 1.0 downward), the equilibrium constant increases up to very high values. Therefore, the ligand-binding reaction at (long-time) equilibrium with CTRW-based or obstacle-based transient anomalous diffusion appears to be incompatible with slowed-down Brownian motion. However, in contrast to obstacle-based anomalous diffusion, CTRW-based anomalous diffusion strongly impairs the bound fraction at equilibrium and, more generally, the affinity of the ligand-binding equilibrium itself.

**Space-dependent Brownian diffusion yields accumulation at equilibrium**

The results presented so far consider spatially homogeneous conditions, i.e., \( D(i,j) = D, \forall i,j \). However, in living cells,
the conditions are usually spatially heterogeneous: spatial domains (e.g., lipid rafts and caveolae) give rise to position-dependent values of $D$. In the experiments discussed below, we addressed this situation by restricting the region of space where diffusion is modified to a central square patch of variable spatial extent. We simulated spatial arrangements in which diffusion is Brownian with coefficient $D_0$ outside the patch and reduced within the central patch by imposing a reduced diffusion coefficient $D_1$ inside the patch.

Before addressing the ligand-binding equilibrium (Eq. 1) in these conditions, we first investigate diffusion in the absence of reaction. We use a central patch whose surface area is 25% of the whole space and simulate the diffusion of nonreactive molecules until they reach equilibrium. Once equilibrium is reached, we perturb it by the addition of supplemental nonreactive molecules in the center of the patch, and measure the characteristic time it takes to reach a new equilibrium and the concentration of molecules inside the patch at this new equilibrium. Because reduced diffusion in the patch slows down the characteristics, it takes to converge back to equilibrium increases when diffusion is reduced in the patch (Fig. 4 A). More intriguingly, when we measure the concentration of molecules in the patch (relative to the exterior) at equilibrium, we observe an increasing accumulation of molecules within the patch when diffusion is slowed down therein (Fig. 4 B). We emphasize here that these are equilibrium conditions.

Although it is surprising, this equilibrium effect can be directly predicted in our system. A first intuitive approach is obtained from the detailed balance condition. A condition for our system to reach (thermodynamic) equilibrium it to respect detailed balance. Consider two states, $A$ and $B$, of a Markov process. Note $A$ the probability to observe state $\eta_A$ the transition probability from $A$ to $B$, the detailed balance condition reads $\eta_A \pi(A \rightarrow B) = \eta_B \pi(B \rightarrow A)$. Consider now two lattice sites, $s_{\text{patch}}$ and $s_{\text{out}}$, located on either side of the frontier separating the central patch from the rest of the lattice. The detailed balance in this case reads $\rho(s_{\text{patch}}) = \pi(s_{\text{out}} \rightarrow s_{\text{patch}})/\pi(s_{\text{patch}} \rightarrow s_{\text{out}})$, where $\rho(x)$ is the concentration of molecules at node $x$. To emulate position-dependent diffusion (see Materials and Methods), our simulation algorithm states that the jump probability between two lattice sites depends exclusively on the diffusion coefficient at the node of origin. The detailed balance thus becomes $\rho(s_{\text{patch}})/\rho(s_{\text{out}}) = D_0/D_1 > 1$ (where $D_0$ and $D_1$ are the diffusion coefficients outside and inside the patch, respectively). This predicts accumulation inside the patch at equilibrium. A more formal approach can be applied, based on the master equation. This approach, detailed in the Supporting Material (section A), predicts that the total number of molecules at equilibrium in the patch $N_{\text{inside}}$ relates to the total number $N_{\text{total}}$, the surface fraction of the patch $\phi$, the total surface $S$, and the diffusion coefficient according to

$$N_{\text{inside}} = S\phi N_{\text{total}} \frac{\mathcal{H}(D)}{D_1}, \quad \mathcal{H}(D) = \left[ \frac{\phi}{D_1} + 1 - \phi \right]^{-1} (2)$$

We tested the theoretical prediction of Eq. 2 against our Monte Carlo simulation results shown in Fig. 4 B. The agreement between theoretical prediction (thick dashed line) and simulation results (open diamonds) is very good. This confirms that slowed-down Brownian motion in the patch leads to a larger concentration inside the patch than outside at equilibrium.

Note that our diffusion algorithm, in which the jump probability depends only on the diffusion coefficient at the node of origin, corresponds to solving the Brownian motion with Ito’s stochastic calculus. Using Stratonovich’s rules instead would preserve accumulation within the patch, but
with reduced intensity (3,19). To determine which algorithm is the correct one, one must know the microscopic quantities that cause the observed change of diffusion coefficient at macroscopic scales (3,44).

**Reaction in spatially heterogeneous conditions**

The accumulation phenomenon described above is likely to modify the reaction in the spatially heterogeneous diffusion case. Using several area fractions for the patch, we computed the values of the apparent equilibrium constant $K_D$. With anomalous diffusion due to obstacles (Fig. 5 A), the behavior reported in Fig. 3 B2 is roughly conserved for all patch area fractions $\phi$: $K_D$ decreases linearly with the obstacle density $\rho$ far from the percolation threshold and then increases back close to it. The amplitude of this decay increases with the patch area (as the total space occupied by obstacles increases). Considering the behavior observed in spatially homogeneous conditions (Fig. 3 B2), one would expect that far from the percolation threshold, $K_D = K_{D0}(1 - \phi) + K_{D0}(1 - \rho)\phi$, yielding $K_D/K_{D0} = 1 - \rho \phi$. Indeed, we found that the latter is a very good approximation for the simulation results of Fig. 5 A. Close to the percolation threshold, the apparent affinity reverses and starts to decrease because of the strong increase of the first-collision time (see above).

**FIGURE 5** Equilibrium properties of reaction Eq. 1 in space-dependent conditions. Molecules move with Brownian motion outside the central patch. Inside the central patch, molecule motion is due to (A) transient anomalous diffusion due to obstacles, (B) slowed-down Brownian motion or CTRW with (C) $\alpha = 0.40$ or (D) 0.60. (A–D) The panels show the apparent equilibrium constant $K_f/K_{f0}$ as a function of the area fraction occupied by the patch $\phi$ and the obstacle density $\rho$ (A), the amount of diffusion reduction in the patch, $\gamma = 1 - D_f/D_0$ (B), or the cutoff time $\tau_c$ (C and D; note that $C$ and $D$ show $\log_{10}(K_f/K_{f0})$). The inset in B shows the value of $\phi$ that yields maximal affinity (solid circles) and the corresponding theoretical prediction (Eq. 3, solid line). Other parameters were set according to the standard set (see Materials and Methods).
The situation is quite different for space-dependent Brownian diffusion (Fig. 5 B). Whatever the patch area, we also observe that $K_D$ decreases, but in this case, this is the result of the accumulation phenomenon reported above (Fig. 4 B). Moreover, in this case, $K_D$ exhibits a nonmonotonous dependency with respect to the area fraction $\phi$, with a marked minimum. Hence, for a given value of diffusion reduction in the patch, $\gamma = 1 - D_1/D_0$, our Monte Carlo simulations show that there exists an optimal value of the patch surface area that yields the highest affinity (Fig. 5 B, inset). Using Eq. 2 above for both $R$ and $L$, we can estimate this optimal value analytically. Our theoretical analysis, given in the Supporting Material (section B), indeed shows the existence of an optimal surface area $\phi^*$ that maximizes the apparent reaction affinity. When the size of the space domain $S \gg ((l_1D_0)/(D_1K_D)$ (which is always valid in the simulations shown in this work, given $S = 800^2$), $\phi^*$ is predicted to depend on $\gamma$ according to

$$\phi^* = \frac{1 - \gamma}{2 - \gamma}$$  \hspace{1cm} (3)

In the limit of large slowdowns $\gamma \to 1$, Eq. 3 gives $\phi^* \to 0$: the larger the slowdown, the smaller the optimal patch area. This prediction is in general qualitative agreement with the simulation results of Fig. 5 B, which do not depend in a monotonous way on $\gamma$ and $\phi$, but present extrema along the $\phi$-axis that shift leftward with increasing $\gamma$. In the limit of no-slowdown $\gamma \to 0$, Eq. 3 predicts $\phi^* = 0.5$, but then, in this case, the apparent affinity does not depend on $\phi$ anymore (see the Supporting Material, section B), and thus no extrema are observed. For a quantitative test of Eq. 3, we plotted the relationship between $\gamma$ and the value of $\phi$ that exhibited the smallest $K_D$ in our simulations (Fig. 5 B, inset, open circles). These values were found to align nicely with the prediction of Eq. 3 (inset, solid line), thus validating this prediction quantitatively.

Finally Fig. 5, C and D, show the behavior exhibited when anomalous diffusion is due to a CTRW with cutoff time. In agreement with Fig. 3, we note that for almost all of the parameters in these figures, the reaction affinity is massively impaired by CTRW, up to four to six orders of magnitude (note that these curves plot the log of the relative affinity constant). Even for rather short cutoffs (e.g., $\tau_c = 10^3$ time steps), the apparent affinity of the ligand-binding equilibrium is lower with CTRW than with Brownian motion as soon as the patch in which CTRW occurs is wider than one-fourth of the total area. For some parameters, the affinity of the reaction can be larger than Brownian motion. However, this corresponds to very small cutoff times that produce anomalous regimes of very limited duration. In these cases, the CTRW in the patch tends to exhibit Brownian motion with a reduced diffusion coefficient, and thus the system tends to resemble the space-dependent Brownian case illustrated in Fig. 5 B. On the other hand, CTRW is also found to increase the apparent affinity for large cutoff times, but only for small to very small patch area fractions. The biological relevance of these restricted cases is therefore not obvious. Therefore, except for very small patch areas, CTRW-based anomalous diffusion massively impairs the affinity of the ligand-binding equilibrium.

To conclude, we have shown that heterogeneous slowed-down Brownian systems provide an advantage in terms of patchiness: the minimal value of $K_D$ is obtained when the patch occupies a subset of the available space. This is in strong contrast to the equilibrium behavior obtained with transient anomalous diffusion, where the affinity increases or decreases monotonously with the patch area fraction depending on the microscopic origin of the anomalous behavior (obstacles or CTRW, respectively).

**DISCUSSION**

This study was motivated by the concept that, in contrast to the celebrated fluid mosaic model (45), the cellular plasma membrane is not a simple 2D liquid that can be made spatially homogeneous by the rapid lateral diffusion of lipids and proteins. Recent progress in time-lapse imaging (including at the single-molecule scale) has enabled researchers to obtain evidence for the existence of spatial inhomogeneities that form dynamical hierarchical domains at the mesoscale (e.g., fence-picket compartments, raft domains, and protein complex domains) (5). The impact of this organization in hierarchical domains on the signaling reactions that take place on the membrane is still poorly understood. The alteration of the diffusive movements of the proteins in these hierarchical domains may be very important for signaling (18). However, it is not yet entirely clear exactly which parameters of the diffusive movements are modified in which domains. One could think of modulations of the diffusion coefficient (4,7–10) or the confinement distance (46), or a local change from Brownian to non-Brownian diffusion (anomalous diffusion) due to macromolecular crowding or obstacle hindrance (12,47–49). Whether these different scenarios have different effects on biochemical reactions on the membrane is not known.

In this work, we focused on a comparison of three possible scenarios: Brownian diffusion with reduced diffusion coefficient (slowed-down Brownian) and transient anomalous diffusion due to immobile obstacles or power-distributed residence times (CTRW). Indeed, since transient anomalous diffusion converges at long times to a slowed-down Brownian movement, one may be led to consider slowed-down Brownian motion as equivalent to transient anomalous diffusion at equilibrium. In contrast, we have shown here that this assumption fails when diffusion conditions are spatially heterogeneous, since the equilibrium behavior of the three scenarios we contemplated are markedly distinct. When it is due to obstacles, transient anomalous diffusion increases the apparent binding affinity, with
a maximal effect when the obstacles are spread all over the available space. However, when it is based on a CTRW, transient anomalous diffusion strongly decreases the apparent binding affinity. Slowed-down Brownian motion has a very different effect because it increases the apparent affinity in a nonmonotonous way: maximal affinity is reached when the region of reduced diffusion coefficient is restricted to a subdomain of the membrane surface. Therefore, slowed-down Brownian motion in the ligand-binding reaction does not capture the effect of transient anomalous diffusion even at the long times necessary to reach equilibrium.

A main result from our study is that CTRW and hindrance by immobile obstacles lead to very different behaviors at equilibrium even though they yield comparable anomalous scaling of the MSD. This result is in line with the realization that the two processes are fundamentally distinct. For instance, CTRW presents a weak ergodicity breaking (the scaling with time of the time-averaged MSD differs from that of ensemble-averaged MSD) ([37,50] that is not observed with obstacle-based anomalous diffusion. The scaling with time or initial distance of several observables derived from first-passage-time statistics differs notably between the two processes ([51]). Whether the distinct equilibrium behaviors disclosed in our study are related to these differences is currently unknown, but will be investigated in future works. Paradoxically, however, these two processes need not be mutually exclusive and may coexist. For instance, it was recently suggested that the motion of ion channels on the cytoplasmic membrane would be consistent with a CTRW that is restricted to take place on a fractal ([14]). Because hindrance by randomly located immobile obstacles restricts the walker movement to such a fractal geometry (at least close to the percolation threshold) ([38]), such a phenomenon could in principle be studied in our simulations. However, adding the slowdown of the reaction due to obstacles to that due to CTRW may be problematic in terms of simulation times and demand alternative simulation or modeling frameworks.

Recent evidence suggests that fBM (and the associated fractional Langevin equation) is a third possible source of anomalous diffusion, in addition to obstacle hindering and CTRW. fBM is a generalization of classical Brownian motion, where the random increments between two successive locations are not independent (as in Brownian motion) but present long-range temporal correlations ([17]). Like CTRW and hindering by immobile obstacles, fBM gives rise to anomalous diffusion but no weak ergodicity breaking. Most notably, fBM could play an important role in the diffusion of lipids in membranes and be a major source of anomalous diffusion therein ([52–54]). Note, however, that fBM has also been proposed to describe the long-time regime in the transport of lipid granules in Schizosaccharomyces pombe ([37]). Although the impact of fBM on (bio)chemical reactions and on membrane signaling in particular has not yet been thoroughly studied (but see Hellmann et al. ([32])), it may become an important topic if the role of fBM in lipid movements in membranes is confirmed.

Our results for slowed-down Brownian motion suggest that when the membrane is partitioned into two regions only (i.e., the patch, in which diffusion is slowed down, and the rest of the lattice), a surface area for the patch exists that optimizes the apparent reaction affinity. However, this is a very simplified configuration, since there may be several disconnected (slowed-down) patches coexisting in the membrane. It is unknown whether in this case a (total) optimal surface area would still exist or what (if any) type of spatial configuration of the patches would be optimal. In terms of combinatorics, a numerical study of this problem by Monte Carlo simulations would be very challenging because the number of configurations for a given total patch surface area is very large, but it could reveal some very interesting properties for space-dependent Brownian diffusion.

The functional implications of our findings may be important for our understanding of the organization of cell membranes and, more generally, cell spaces. For instance, it is interesting to note that in living cell membranes, slowed-down regions (e.g., rafts) show a very patchy distribution, whereas bulky obstacles seem less systematically clustered in limited regions. Therefore, by controlling the spatial extent of areas with reduced lateral diffusion, cells may be able to control the apparent affinity of the ubiquitous ligand-reaction binding events.

SUPPORTING MATERIAL

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REFERENCES

6. Reference deleted in proof.


A. Space-dependent Brownian diffusion yields accumulation at equilibrium

Let us consider the 1d case for simplicity, and a constant-by-part dependence of the diffusion coefficient \( D(x) = D_1 \), \( \forall x \in [a, b] \) and \( D(x) = D_0 \) outside the patch \([a, b]\). Let us then consider a single molecule and let \( \pi(x,t) \) its probability to be located at position \( x \) at time \( t \):

\[
\pi(x,t+\Delta t) = q(x)\pi(x,t) + \pi(x-\Delta x,t)\left(1-q(x-\Delta x)\right)/2 \\
+\pi(x+\Delta x,t)\left(1-q(x+\Delta x)\right)/2
\]

where \( q(x) \) is the probability not to jump at each time step and is defined, using the jump probability \( \beta(x) = 2\Delta t/(\Delta x)^2 D(x) \) (see Methods), as \( q(x) = 1 - \beta(x) \). Noting \( g(x,t) = (1-q(x))\pi(x,t)/2 \) and developing \( g(x \pm \Delta x,t) \) in series of \( x \), one obtains at order 2

\[
\pi(x,t+\Delta t) = q(x)\pi(x,t) + 2g(x) + (\Delta x)^2 \partial_{xx}g(x) \\
= \pi(x,t) + (\Delta x)^2 \partial_{xx}g(x,t)
\]

Dividing by \( \Delta t \) and taking the limit \( \Delta t \to 0 \), one gets

\[
\partial_t \pi(x,t) = \partial_{xx} (D(x)\pi(x,t)) \tag{SI.3}
\]

where we used the expression of \( \beta(x) \) above to define \( D(x) \). Noting \( u(x,\infty) \) the density of molecules at \( x \) at equilibrium, one expects from eq. (SI.3)

\[
D(x)u(x,\infty) = \mathcal{H}(D) \tag{SI.4}
\]

where \( \mathcal{H}(D) \) is the spatial harmonic mean of the (space-dependent) diffusion function

\[
\mathcal{H}(D) = \left[ \int D^{-1}(x)dx \right]^{-1} \tag{SI.5}
\]

Now, using the constant-by-part function for \( D(x) \) expressed above, this yields \( u(x,\infty) = \mathcal{H}(D)/D_1 \), \( \forall x \in [a, b] \) and \( u(x,\infty) = \mathcal{H}(D)/D_0 \) outside. The equilibrium concentration inside the \([a, b]\) patch thus equals that found outside the patch multiplied by \( D_0/D_1 \). Hence the larger the slowdown of the Brownian motion inside the patch, the larger the accumulation inside it at equilibrium, explaining the simulation results of Fig.4B. In the present 2d case, the total number of molecules in the patch \( N_{\text{inside}} \) relates to total number \( N_{\text{total}} \), the surface fraction of the patch \( \phi \), the total surface \( S \) and the diffusion coefficient according to:

\[
N_{\text{inside}} = S\phi N_{\text{total}} \frac{\mathcal{H}(D)}{D_1}, \mathcal{H}(D) = \left[ \frac{\phi}{D_1} + \frac{1-\phi}{D_0} \right]^{-1} \tag{SI.6}
\]
B. Optimum area for spatially restricted slowed-down Brownian motion

Let us consider a space domain of total area $S = w \times w$, in which molecules move by Brownian motion with diffusion coefficient $D(x) = D_1$ inside the central patch (of surface $\phi S$) and $D(x) = D_0$ in the outer region around this central patch (surface $(1 - \phi)S$). We denote numbers of molecules by lower-case letters to distinguish them from concentrations (denoted by capital letters); $x$ thus expresses the number of X molecules in the domain. Moreover, just like for the diffusion coefficient above, we use indices for each variable to indicate location, i.e. $x_1$ refers to the number of X molecules within the central patch while $x_0$ refers to its value outside the patch. Finally, in the following, all results will relate to equilibrium values, so that we drop the "eq" notation used above for readability.

Our major assumption in the following theoretical analysis is to consider that the reaction proceeds separately in each zone (inside or outside of the patch), independently of each other. Our goal then becomes to determine the value of $c_0 + c_1 = c_T$, the total number of complexes. According to our space separation assumption, one has in each zone $i = \{0, 1\}$:

$$C_i = \frac{R_{i,T}L_{i,T}}{K_{Di} + L_{i,T}} \quad (\text{SI.7})$$

where $R_{i,T} = R_i + C_i$ and $L_{i,T} = L_i + C_i$. In terms of molecule numbers, this translates into

$$c_0 = \frac{r_{0,T}l_{0,T}}{K_{D0}(1 - \phi)S + l_{0,T}} \quad \text{and} \quad c_1 = \frac{r_{1,T}l_{1,T}}{K_{D1}\phi S + l_{1,T}} \quad (\text{SI.8})$$

Now, according to eq. (7) (main text), the relative amount of reactants in each zone is given by

$$\rho(x) = \frac{\mathcal{H}(D)}{D(x)} \quad (\text{SI.9})$$

with $\mathcal{H}$ the (2D) spatial harmonic mean of the diffusion constant $D$

$$\mathcal{H}(D) = \left[ \iint_S D^{-1}(x)dx \right]^{-1} = \left[ S \frac{\phi}{D_1} + S(1 - \phi) \right]^{-1} \quad (\text{SI.10})$$

The amount of reactant outside the central patch thus reads

$$r_{0,T} = r_T \int_{(1 - \phi)S} \rho(u)du = \iint_{(1 - \phi)S} \frac{\mathcal{H}(D)}{D(u)}du$$

so that

$$r_{0,T} = \frac{r_T (1 - \phi) S \mathcal{H}(D)}{D_0} \quad (\text{SI.11})$$

Likewise, inside the patch:

$$r_{1,T} = r_T \int_{\phi S} \rho(u)du = \iint_{\phi S} \frac{\mathcal{H}(D)}{D(u)}du$$

yielding

$$r_{1,T} = \frac{r_T \phi S \mathcal{H}(D)}{D_1} \quad (\text{SI.12})$$

Note that

$$(1 - \phi) S \mathcal{H}(D)/D_0 + \phi S \mathcal{H}(D)/D_1 = 1$$
and the above results stands for $l_{i,T}$ ($i = \{0, 1\}$) as well.

Therefore, noting

$$\alpha = (1 - \phi) S \mathcal{H}(D)/D_0$$

(SI.13)

and

$$1 - \alpha = \phi S \mathcal{H}(D)/D_1$$

(SI.14)

we obtain

$$c_T = c_0 + c_1 = r_T l_T \frac{\alpha^2}{K_{D0}(1 - \phi)S + \alpha l_T} + \frac{(1 - \alpha)^2}{K_{D1}\phi S + (1 - \alpha)l_T}$$

(SI.15)

In particular, in homogeneous conditions ($D_0 = D_1$ and $K_{D0} = K_{D1}$), one has $\mathcal{H}(D) = D_0/S$ and $\alpha = 1 - \phi$ so that eq.(SI.15) reduces to $c_T = r_T l_T/(K_{D0}S + l_T)$ $\forall \phi$, i.e. precisely the classical dose-response curve for homogeneous conditions. Note that except for homogeneous conditions, eq.(SI.15) does not generally display the classical parabolic shape, typical of the homogenous conditions ($y = cx/(d + x)$).

Now, the assumption of space separation between the two zones means that the movement is homogeneous (position-independent) Brownian motion for each zone. In this case we have found on Figure 3B1 (main text) that $K_{D1} \approx K_{D0}$ for all values of $D_1$ tested ($D_0 = 1$). We thus set $K_{D0} = K_{D1} \equiv K_D$ in the following. To find the extremum of eq.(SI.15), we search for the solutions of $dc_T/d\phi = 0$ and get:

$$\phi^* = \frac{S + ad - \sqrt{d(S + ad)(a + Sd)}}{S(1 - d^2)}$$

(SI.16)

where we noted $d \equiv D_0/D_1$ and $a \equiv l_T/K_D$. We remark that in this expression, the value of the optimum area $\phi^*$ depends on the dose, i.e. the total concentration of ligand $L_T = L + R$. This is related to the fact that eq.(SI.15) generally has not a typical parabolic shape. However, eq.(SI.16) greatly simplifies when $S \gg ad$ (which is always valid in the simulations shown in the present article, given $S = 800^2$), to a very simple expression

$$\phi^* \approx \frac{1 - \gamma}{2 - \gamma}, \quad S \gg ad$$

(SI.17)

with $\gamma = 1 - D_1/D_0$. It is remarkable that, in this limit, $\phi^*$ does not depend on the dose $a$ anymore, which in fact relates to the fact that the expression for $c_T$ (eq.(SI.15)) in this case adopts a classical parabolic shape.

Taken together, this simple theoretical analysis predicts the existence of an optimal surface area $\phi^*$ for the affinity, that depends on the value of $D_1$ relative to $D_0$. In the limit of large slowdowns $\gamma \to 1$, eq.(SI.17) gives $\phi^* \to 0$: the larger the slowdown, the smaller the optimal patch area. This prediction is in general qualitative agreement with the simulation results of Figure 5B that do not depend in a monotonous way on $\gamma$ and $\phi$ but presents extrema along the $\phi$-axis that shift leftward with increasing $\gamma$. In the limit of no-slowdown $\gamma \to 0$, eq.(SI.17) predicts $\phi^* = 0.5$ but then, in this case, the value of $c_T$ does not depend on $\phi$ anymore (see above for $D_0 = D_1$), so that no extremum are observed.