Diffusion through semi-permeable membranes

Aiyan B.

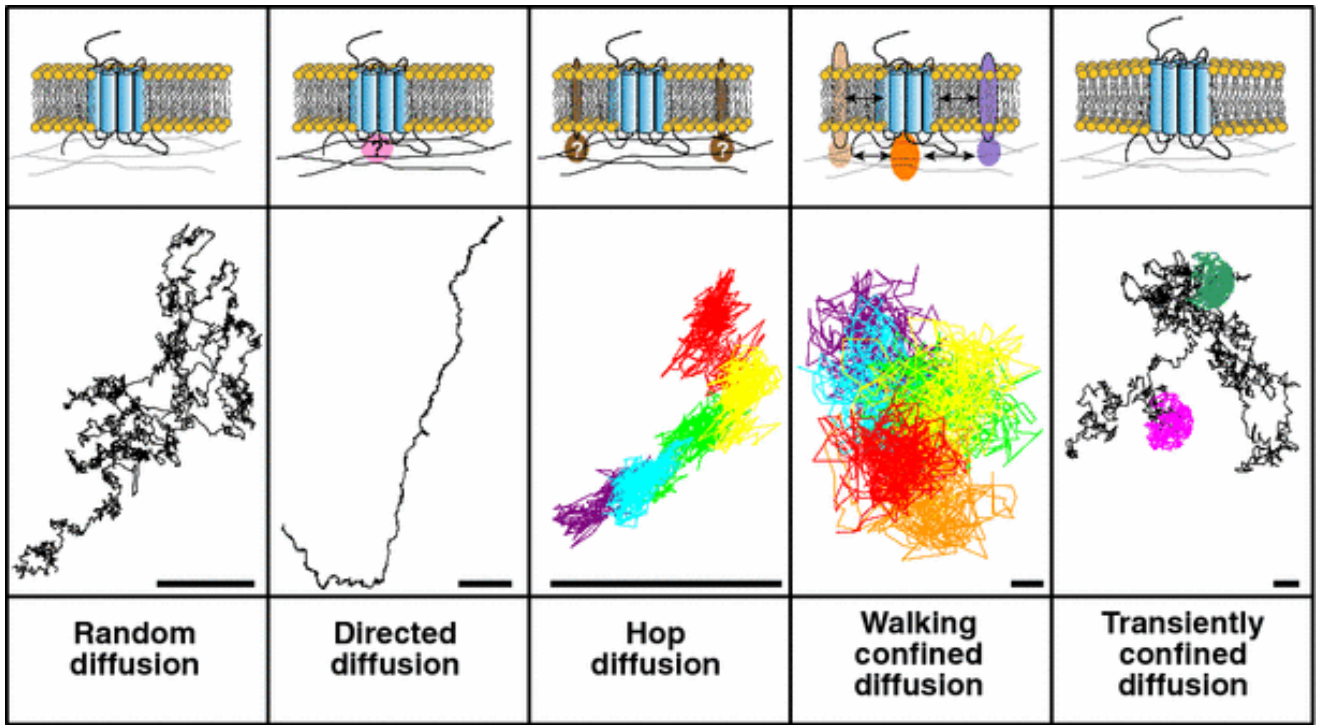
December 17, 2025

Review diffusion model

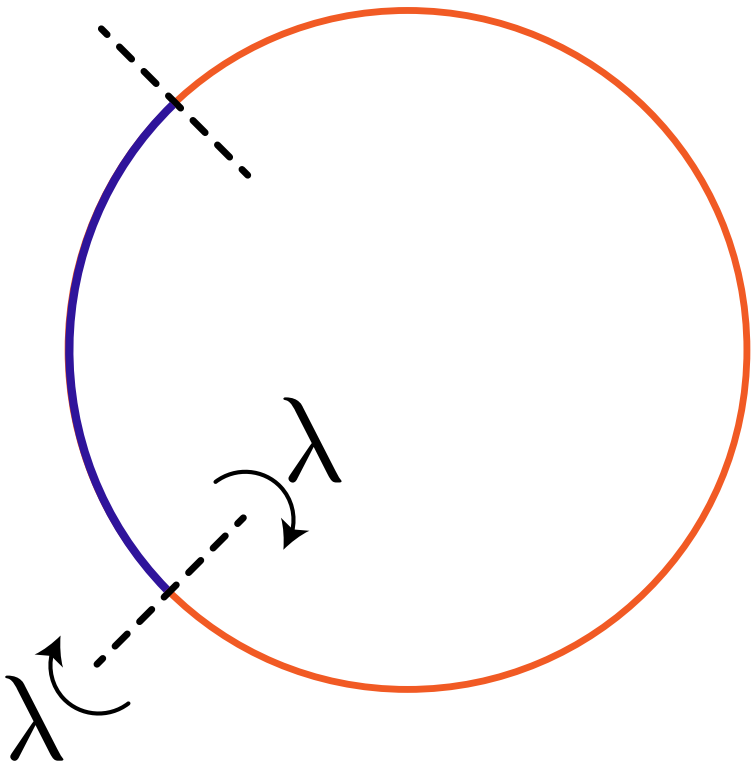
- Membrane skeleton (MS) confines the size of cholesterol- and sphingolipid-rich membrane mesodomains, "rafts"
- Idea: slower diffusion in these domains, combined with semi-permeable nature leads to apparent confinement which increase signalling, "hot-spots"

Review diffusion model

- Membrane skeleton (MS) confines the size of cholesterol- and sphingolipid-rich membrane mesodomains, "rafts"
- Idea: slower diffusion in these domains, combined with semi-permeable nature leads to apparent confinement which increase signalling, "hot-spots"

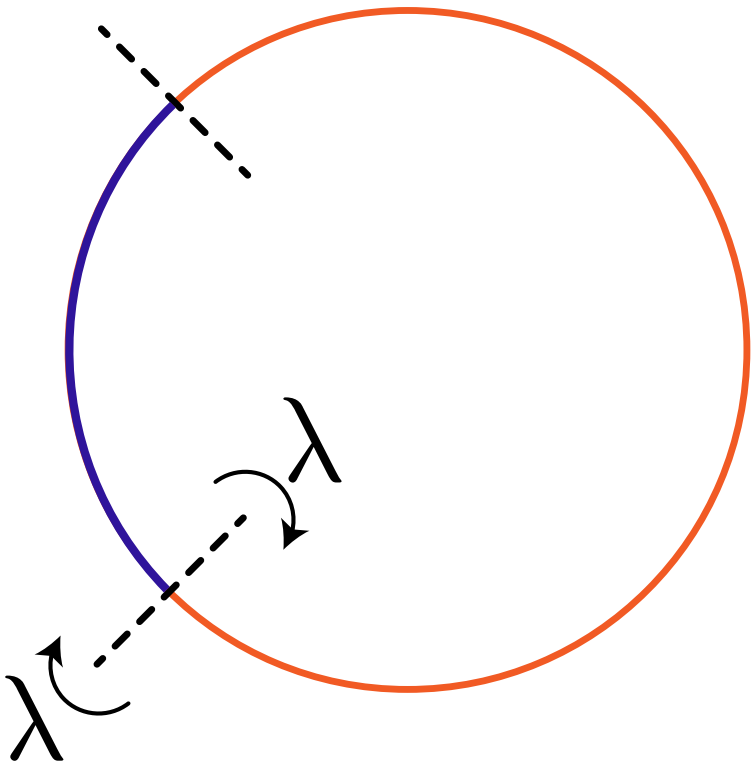


A simple first-approach



1. Random walk X_t occurs on $\mathbb{Z}$ mod N where N is the number of lattice sites and $t \in \mathbb{N}$
2. **Semi-permeable membranes** are inserted between lattice sites at positions $\{\mathcal{B}_i\}$

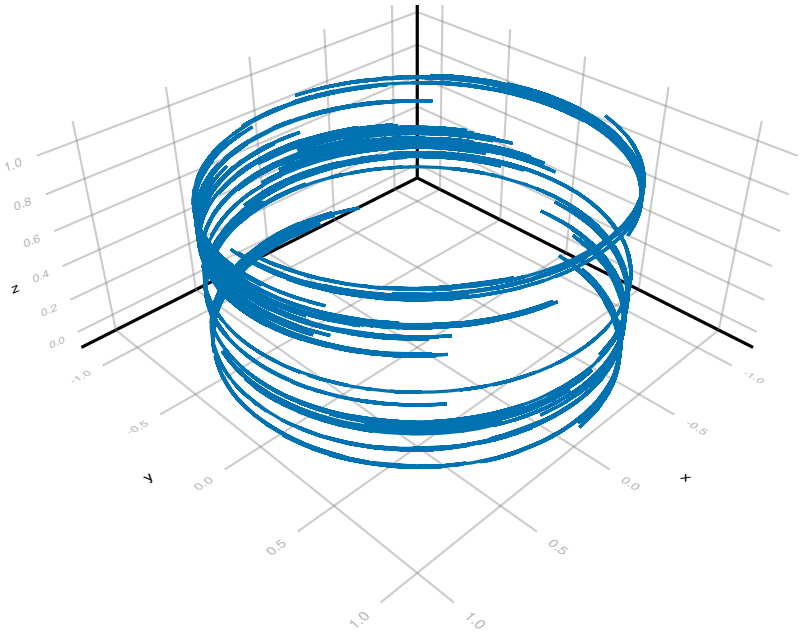
A simple first-approach

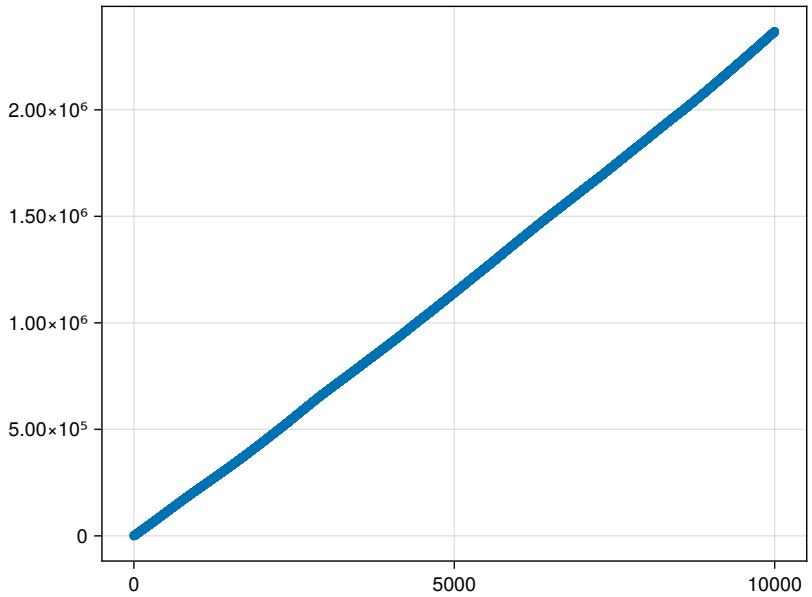


1. Random walk X_t occurs on $\mathbb{Z}$ mod N where N is the number of lattice sites and $t \in \mathbb{N}$
2. **Semi-permeable membranes** are inserted between lattice sites at positions $\{\mathcal{B}_i\}$
3. Propose a random hopping direction, $X_{t+1} = X_t \pm 1$
4. If this move would cross a membrane, $X_t < \mathcal{B}_i$ and $X_{t+1} > \mathcal{B}_i$ or vice versa, accept with probability $0 < \lambda < 1$, else reflect

Mean square displacement

- MSD quickly tapers off to a linear behaviour when integration is performed over a reasonable, 10^{-4}s, timescale





Occupation fraction

- The diffusion coefficient is defined by the fixed quantity $D = a_0^2/2\tau$ where a_0 is the lattice spacing and τ the step size
  - Fix $a_0 = 1$ nm and let the larger region have diffusivity $D_\mathrm{h} = 1\ \mu\mathrm{m}^2/\mathrm{s}$ so $\tau_\mathrm{h} = 0.5\ \mu\mathrm{s}$

Occupation fraction

- The diffusion coefficient is defined by the fixed quantity $D = a_0^2/2\tau$ where a_0 is the lattice spacing and τ the step size
  - Fix $a_0 = 1$ nm and let the larger region have diffusivity $D_\mathrm{h} = 1\ \mu\mathrm{m}^2/\mathrm{s}$ so $\tau_\mathrm{h} = 0.5\ \mu\mathrm{s}$

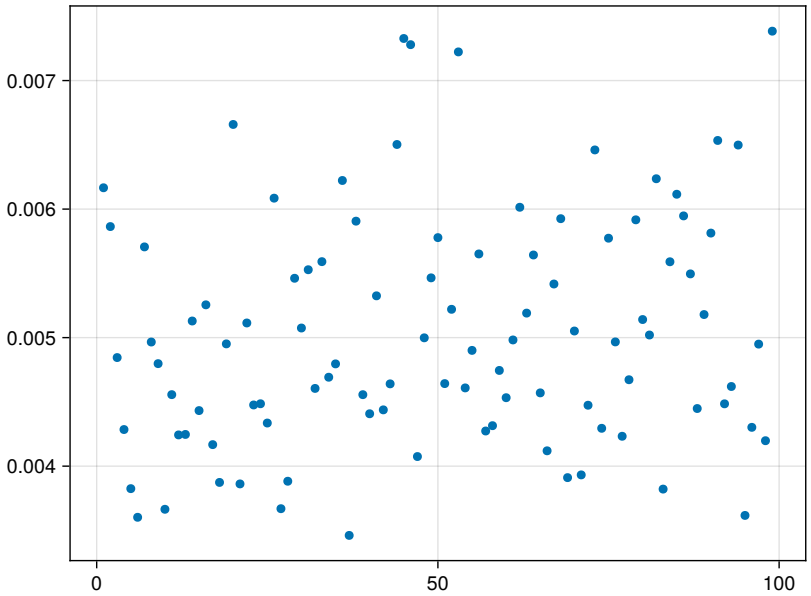


Figure: Occupation fraction versus $\lambda \times 10^2$ for $D_\mathrm{l} = 10\ \mu\mathrm{m}^2/\mathrm{s}$.

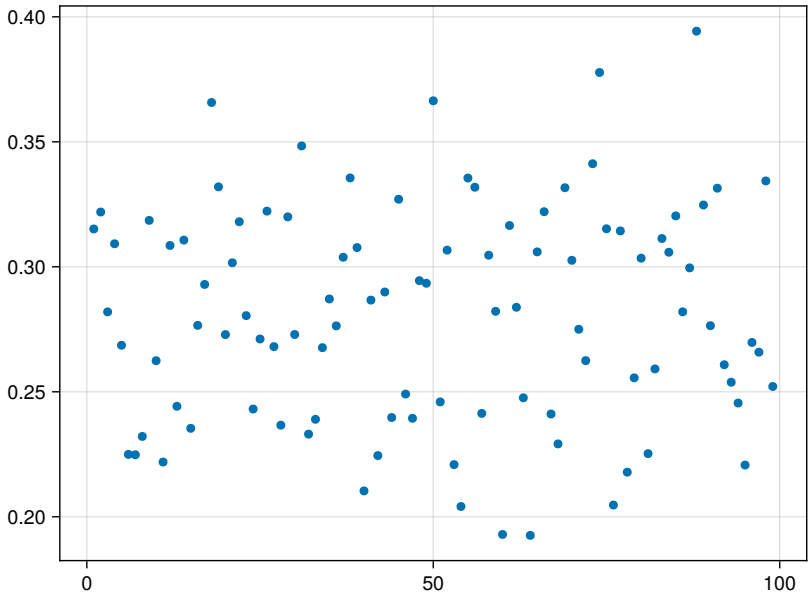


Figure: Occupation fraction versus $\lambda \times 10^2$ for $D_\mathrm{l} = 0.1\ \mu\mathrm{m}^2/\mathrm{s}$.

But what about anomalous diffusion?

- A critical feature of our model is that the ensemble average MSD must have an apparent anomalous behaviour
- How can we recover this?
  1. Heavy-tailed domain sizes/ diffusivities (quenched radius model[1])

But what about anomalous diffusion?

- A critical feature of our model is that the ensemble average MSD must have an apparent anomalous behaviour
- How can we recover this?
  1. Heavy-tailed domain sizes/ diffusivities (quenched radius model[1])
  2. Heavy-tailed barrier heights (random barrier model[2])

But what about anomalous diffusion?

- A critical feature of our model is that the ensemble average MSD must have an apparent anomalous behaviour
- How can we recover this?
  1. Heavy-tailed domain sizes/ diffusivities (quenched radius model[1])
  2. Heavy-tailed barrier heights (random barrier model[2])
- A combination of both might make the most sense: if it is harder for the proteins and raft components to escape a given membrane partition (higher barrier height), then we may also expect higher local diffusivity

References

[1] P. Massignan, C. Manzo, J. A. Torreno-Pina, M. F. García-Parajo, M. Lewenstein, and G. J. Lapeyre, Phys. Rev. Lett. **112**, 150603 (2014).

[2] A. Milchev, J. Brankov, and V. D. Pereyra, Phys. Rev. E **58**, 4299 (1998).