

11–9 In a subset of voltage-gated K^+ channels, the N-terminus of each subunit acts like a tethered ball that occludes the cytoplasmic end of the pore soon after it opens, thereby inactivating the channel. This “ball-and-chain” model for the rapid inactivation of voltage-gated K^+ channels has been elegantly supported for the *shaker* K^+ channel from *Drosophila melanogaster*. (The *shaker* K^+ channel in *Drosophila* is named after a mutant form that causes excitable behavior—even anesthetized flies keep twitching.) Deletion of the N-terminal amino acids from the normal *shaker* channel gives rise to a channel that opens in response to membrane depolarization, but stays open instead of rapidly closing as the normal channel does. A peptide (MAAVAGLYGLGEDRQHRKKQ) that corresponds to the deleted N-terminus can inactivate the open channel at $100\ \mu\text{M}$.

Is the concentration of free peptide ($100\ \mu\text{M}$) that is required to inactivate the defective K^+ channel anywhere near the local concentration of the tethered ball on a normal channel? Assume that the tethered ball can explore a hemisphere [volume = $(2/3)\pi r^3$] with a radius of $21.4\ \text{nm}$, which is the length of the polypeptide “chain” (**Figure Q11–2**). Calculate the concentration for one ball in this hemisphere. How does that value compare with the concentration of free peptide needed to inactivate the channel?

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CHAPTER 11 END-OF-CHAPTER PROBLEMS

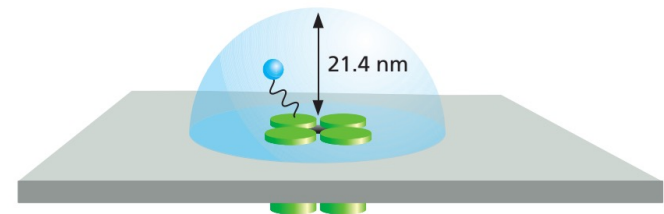


Figure Q11–2 A “ball” tethered by a “chain” to a voltage-gated K^+ channel (Problem 11–9).

Help design an experiment - 1

- Ion channel inactivation mechan

Is the concentration of free peptide (100 μM) that is required to inactivate the defective K^+ channel anywhere near the local concentration of the tethered ball on a normal channel? Assume that the tethered ball can explore a hemisphere [volume = $(2/3)\pi r^3$] with a radius of 21.4 nm, which is the length of the polypeptide “chain” (**Figure Q11-2**). Calculate the concentration for one ball in this hemisphere. How does that value compare with the concentration of free peptide needed to inactivate the channel?

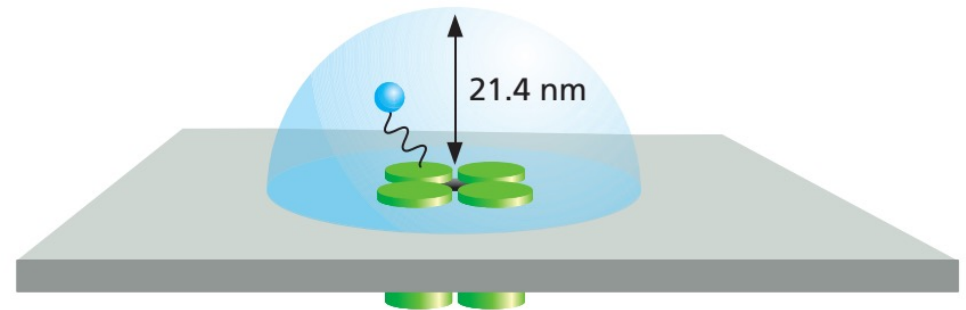


Figure Q11-2 A “ball” tethered by a “chain” to a voltage-gated K^+ channel (Problem 11-9).

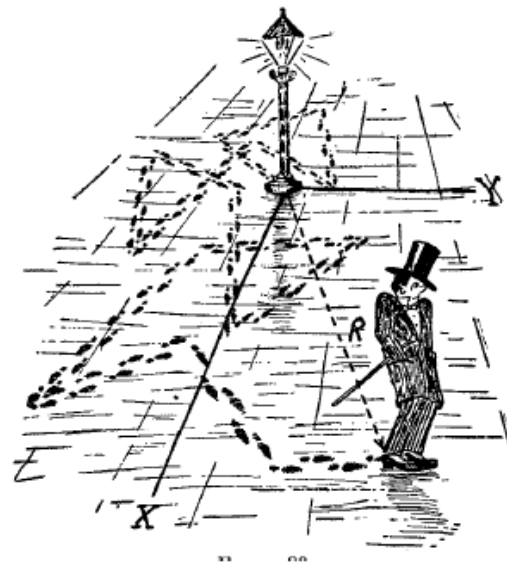
https://www.science.org/doi/10.1126/science.2122520?url_ver=Z39.88-2003&rfr_id=ori:rid:crossref.org&rfr_dat=cr_pub%20%20pubmed

Why single-celled organisms are small

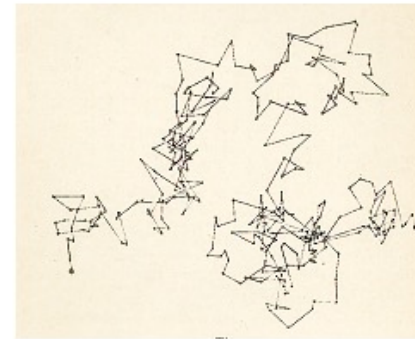
- Oxygen uptake increases with size – but a power of R
- Oxygen consumption (requirement) expected to increase as volume hence power of R^3
- For large R – cell would suffocate if its dependent on diffusion to get transport oxygen

MICROSCOPIC ORIGIN

- Understanding diffusion as random walk.
- Random??



Molecules move at 10^3 ms^{-1}
Collision rate : 10^{12} collisions per sec



Brown: 1828
Einstein: 1905
Perrin: 1913

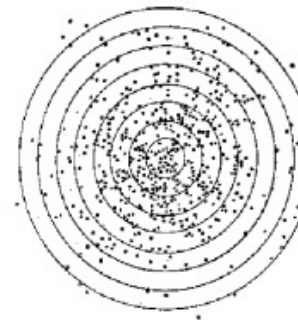
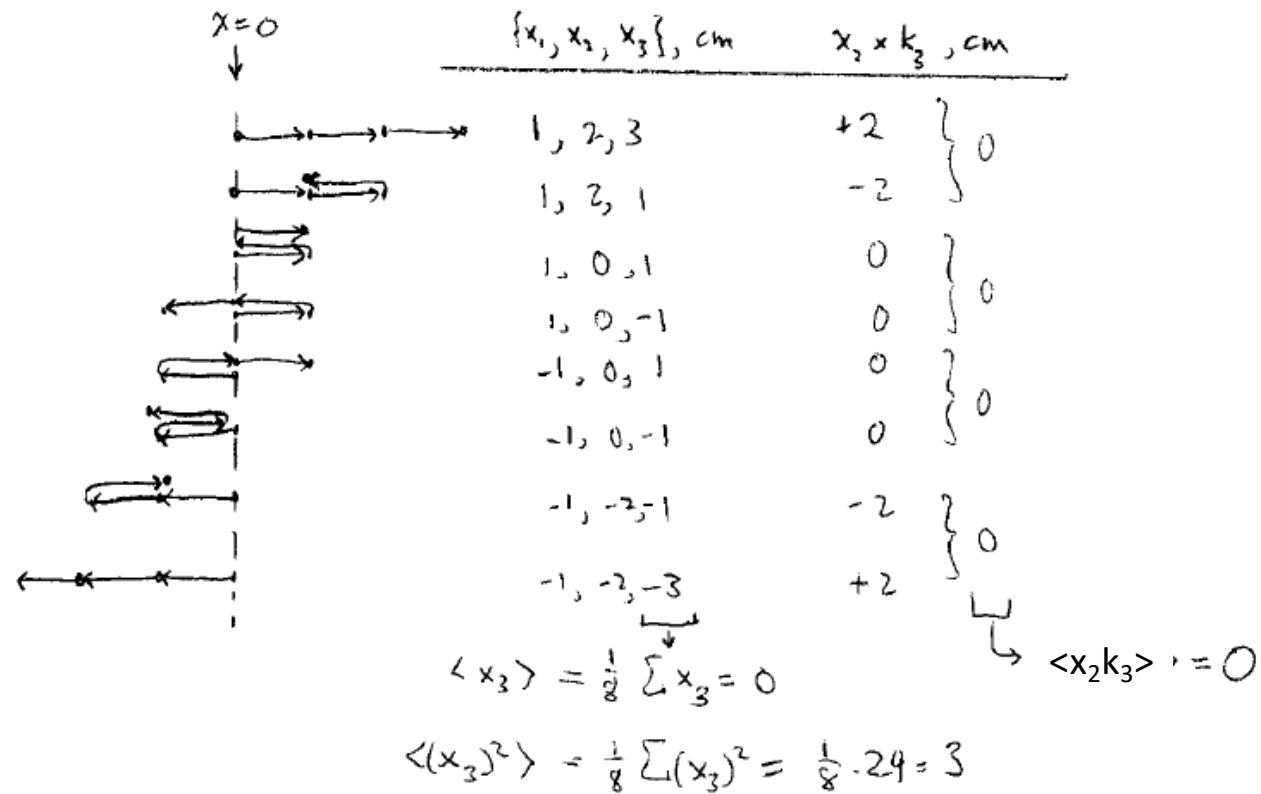


Fig 3. Brownian motion, after Jean Perrin [12]: An example of a trajectory (above) and statistical distribution of displacements (below, the circles correspond to fractions and multiples of the square root of the mean square displacement $\langle x^2 \rangle$)

MICROSCOPIC ORIGIN



$$\langle (x_N)^2 \rangle = \langle (x_{N-1} + k_N L)^2 \rangle = \langle (x_{N-1})^2 \rangle + 2L \langle x_{N-1} k_N \rangle + L^2 \langle (k_N)^2 \rangle.$$

Position after Nth step

$$\langle (x_N)^2 \rangle = NL^2.$$

$$N = t/\Delta t \quad D = L^2/2\Delta t. \quad \longrightarrow \quad \langle (x_N)^2 \rangle = 2Dt$$

One dimensional random walk

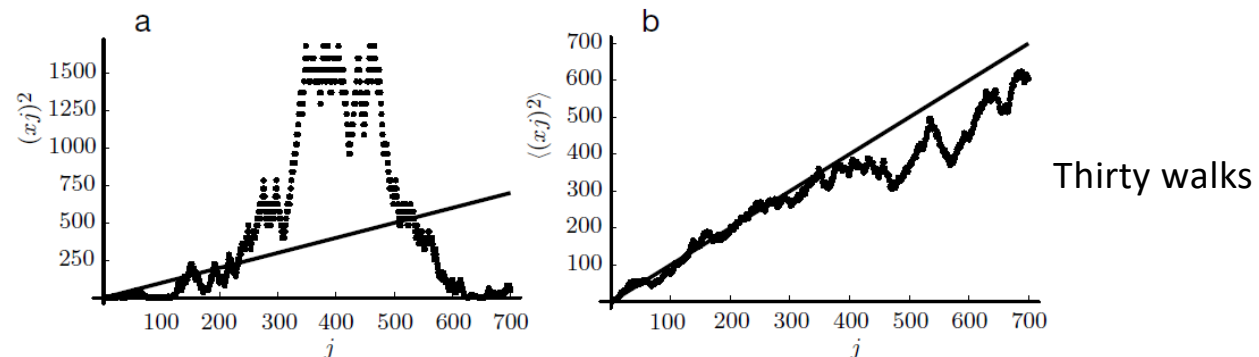


Figure 4.5: (Mathematical functions.) (a) Squared deviation $(x_j)^2$ for a single, one-dimensional random walk of 700 steps. Each step is one unit long. The solid line shows j itself; the graph shows that $(x_j)^2$ is not at all the same as j . (b) As (a), but this time the dots represent the *average* $\langle (x_j)^2 \rangle$ over thirty such walks. Again the solid line shows j . This time $\langle (x_j)^2 \rangle$ does resemble the idealized diffusion law (Equation 4.4).

From: Nelson

Discuss how do we get information out of SINGLE walk?