

BB 101: Physical Biology

TUTORIAL 2: Solutions

1. Balancing the drag forces for the downward movement of paddle gives

$$\begin{aligned} -\gamma_1 u &= \gamma_2 (u - v) \\ u &= \frac{\gamma_2 v}{\gamma_1 + \gamma_2} \end{aligned} \quad (1)$$

Similarly, drag forces for the upward movement of paddle gives

$$u' = \frac{\gamma_2 v'}{\gamma_1 + \gamma_2} \quad (2)$$

Displacement Δx of the microorganism due to downward movement of paddle

$$\Delta x = tu$$

Since motion of paddle is geometrically reciprocal, therefore distance travelled by paddle during both upward and downward movement must be identical

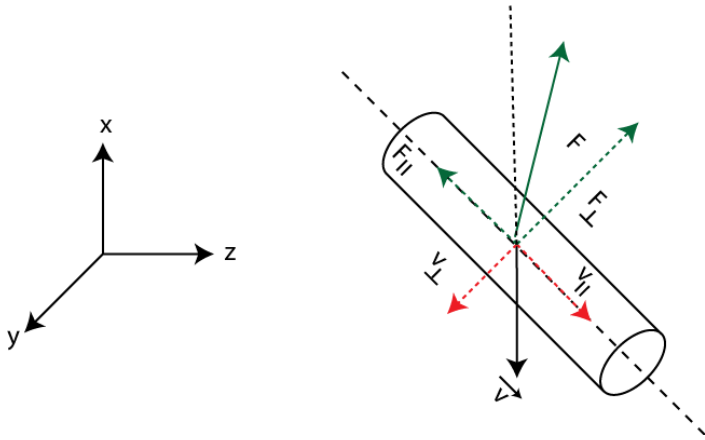
$$tv = t'v' \quad (3)$$

Now, displacement $\Delta x'$ of the microorganism due to upward movement of paddle

$$\begin{aligned} \Delta x' &= -t'u' \\ &= -\left(\frac{tv}{v'}\right) \left(\frac{\gamma_2 v'}{\gamma_1 + \gamma_2}\right) \text{ using (2) and (3)} \\ &= -\left(\frac{tv}{v'}\right) \left(\frac{\gamma_2 v'}{\gamma_1 + \gamma_2}\right) \\ &= -t \left(\frac{\gamma_2 v}{\gamma_1 + \gamma_2}\right) \\ &= -tu = -\Delta x \text{ using (1)} \end{aligned}$$

Since $\Delta x' = -\Delta x$, There will not be any net displacement

2.



As shown in above figure, if the cylinder is moving with velocity v downward due to cranking of the helix then net drag force F on the cylinder will not be in a direction exactly opposite to v . The direction of the net drag force F will be tilted in the forward direction. This happens since drag force in perpendicular direction is higher drag force in parallel direction when cylinder moves.

One can think of a helix to be consisting of many such cylinders. Components of the drag force of these cylinders in x-y plane will be cancelled for the helix and only z-component survives. Thus, if a bacterial is placed to the right of the helix then it will be propelled due to these non-vanishing z-components of F .

3. (i) Amount of ATP produced = $1008/12 = 84$ moles/day

(ii) Weight of ATP produced = $84 \times 0.5 = 42$ Kg

4. (i)

$$\frac{P_B}{P_A} = e^{-4.14/4.14} = e^{-1} \approx 0.37$$

(ii)

$$\frac{P_B}{P_A} = e^{-0.414/4.14} = e^{-1/10} \approx 0.90$$

(iii) At $T = 0$, $\frac{P_B}{P_A} = 1$

This means that at $T \rightarrow \infty$ there is a lot of thermal energy available from surrounding and biomolecule can easily switch from one state to other. Therefore, probability of finding the systems in both states is identical.

5. (i) Partition function

$$\begin{aligned} Z &= e^{-\frac{\epsilon_1}{k_B T}} + e^{-\frac{\epsilon_2}{k_B T}} + e^{-\frac{\epsilon_3}{k_B T}} \\ &= e^{-\frac{0}{4.14}} + e^{-\frac{4.14}{4.14}} + e^{-\frac{8.28}{4.14}} \\ &= e^{-0} + e^{-1} + e^{-2} \\ &= 1 + 0.368 + 0.135 \\ &= 1.503 \end{aligned}$$

(ii) Average separation $\langle l \rangle$ is given by

$$\langle l \rangle = \sum_{i=1}^3 p_i l_i$$

Now,

$$p_1 = \frac{e^{-\frac{\epsilon_1}{k_B T}}}{Z} = \frac{e^{-0}}{Z} = \frac{1}{1.503} = 0.665$$

$$p_2 = \frac{e^{-\frac{\epsilon_2}{k_B T}}}{Z} = \frac{e^{-1}}{Z} = \frac{0.368}{1.503} = 0.249$$

$$p_3 = \frac{e^{-\frac{\epsilon_3}{k_B T}}}{Z} = \frac{e^{-2}}{Z} = \frac{0.135}{1.503} = 0.090$$

Therefore,

$$\begin{aligned} \langle l \rangle &= 0.665 \times 1 + 0.249 \times 1.5 + 0.090 \times 2.0 \\ &= 0.665 + 0.374 + 0.180 \\ &= 1.219 \text{ \AA} \end{aligned}$$

(ii) Average energy of the loop $\langle \epsilon \rangle$ is given by

$$\langle \epsilon \rangle = \sum_{i=1}^3 p_i \epsilon_i$$

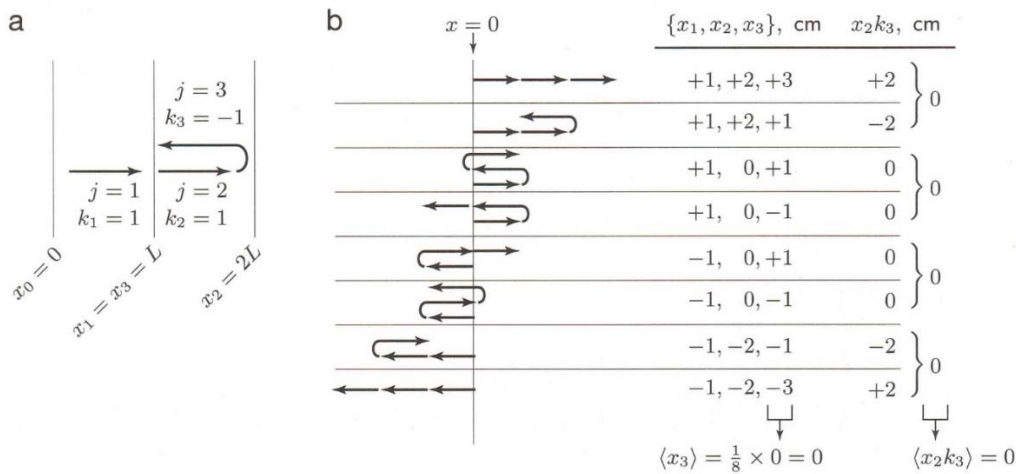
,

$$\begin{aligned} &= 0.665 \times 0 + 0.249 \times 4.14 + 0.090 \times 8.28 \\ &= 0 + 1.031 + 0.745 \\ &= 1.776 \text{ pN nm} \end{aligned}$$

6. Each step is of length L . Thus the displacement of step j is $k_j L$, where k_j is equally likely to be ± 1 . Call the position after j steps x_j ; the initial position is $x_0 = 0$ (see Figure)

Then $x_1 = k_1 L$, and similarly the position after j steps is $x_j = x_{j-1} + k_j L$

We can't say anything about x_j because each walk is random. We can, however, make definite statements about the average of x_j over many different configurations: For example, Figure below shows that $\langle x_3 \rangle = 0$. The diagram makes it clear why we got this result: In the average over all possible configurations, those with net displacement to the left will cancel the contributions of their equally likely analogs with net displacement to the right.



Please note that

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

In the above expression, the final term just equals L^2 , because $(\pm 1)^2 = 1$. For the middle term, note that we can group all 2^N possible walks into pairs (see the last column of Figure above). Each pair consists of two equally probable walks with the same x_{N-1} , differing only in their last step, so each pair contributes zero to the average of $x_{N-1} k_N$.

$$\text{Therefore, } \langle (x_N)^2 \rangle = \langle (x_{N-1})^2 \rangle + L^2$$

Thus, above Equation says that a walk of N steps has mean-square displacement bigger by L^2 than a walk of $N-1$ steps, which in turn is L^2 bigger than a walk of $N-2$ steps, and so on. Carrying this logic to its end, we find

$$\langle (x_N)^2 \rangle = N L^2$$