

Supplementary information for Manuscript titled “*Reaction -Diffusion Systems in Intracellular Molecular Transport and Control*” by S. Soh, M. Byrska, K. Kandere-Grzybowska, and B.A. Grzybowski*

Section 1: Derivation of the average arrival time, τ_A , required for a particle to reach its target (to accompany Section 2.2 in the main text)

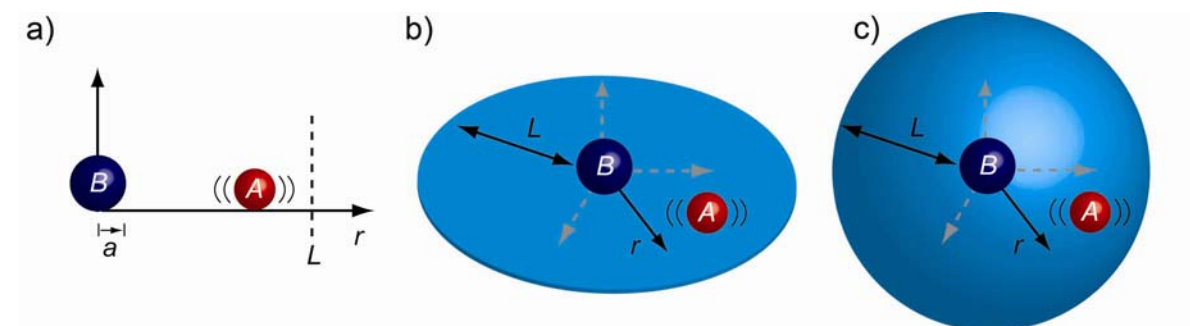


Figure S1. Scheme for the calculation of average time needed for a diffusing species, A to meet and react with an immobile species B in **a)** 1D, **b)** 2D and **c)** 3D domains.

1D diffusion

Particles of type A are diffusing on a bounded domain (e.g. a polymer chain of length, L) and react with immobile targets, type B , when they meet (see Fig. S1). For the simple, one-dimensional case, the diffusion space can be represented as a line (along r -axis in Fig. 1a), with B located at the origin, $r = 0$. B is assumed to occupy a radius of a . Initially ($t = 0$), A is uniformly distributed (with concentration c_0) at locations $r > a$. Subsequently, $t > 0$, reaction takes place between A and B with the concentration of A is kept at zero at $r = a$, where the two species react. Since the space is bounded, there is no flux of A out of the diffusion space at $r = L$. Together, these conditions can be expressed mathematically by the following RD equation:

$$\frac{\partial c}{\partial t} = D_1 \frac{\partial^2 c}{\partial r^2}, \quad (\text{S1})$$

Initial condition, $t = 0$: $c = c_0$, for $r > a$

Boundary condition: $c = 0$ at $r = a$ and $\partial c / \partial r = 0$ at $r = L$

where c denotes the concentration of A . The analytical solution to this problem is^[1]

$$c(r, t) = c_0 \sum_{n=0}^{\infty} \frac{4}{(2\pi + 1)\pi} \sin \frac{(2n+1)\pi(r-a)}{2L(1-k)} \exp \left(-\frac{D_1}{L^2} \left[\frac{(2n+1)\pi}{2(1-k)} \right]^2 t \right), \text{ where } k = a/L. \quad (\text{S2})$$

The average time needed by A to reach its target, B , has been defined by others^[2] as:

$$\tau_A = \int_0^{\infty} dt \cdot t \frac{d}{dt} \left\{ 1 - \frac{N(t)}{N(0)} \right\}, \quad (\text{S3})$$

where $N(t)$ is the total number of moles of A remaining in the diffusion space at time t . In

general, for a space of any dimension, $N(t) = \int_V dV \cdot c$, where V is the volume of the space. Note

that $N(0)$ is simply $c_0 V$. In a 1D space, $N(t)$ can be simplified to $N(t) = \int_V dV \cdot c = A_c \int_a^L dr \cdot c$,

where A_c is the cross-sectional area. This gives $\frac{N(t)}{N(0)} = \frac{\int_a^L dr \cdot c}{c_0(L-a)}$. Using this expression,

together with Eq. S2 and Eq. S3, the final expression for the average arrival time is

$$\tau_A = \frac{L^2 (1-k)^2}{D_1 3}, \text{ where } k = a/L \quad (\text{S4})$$

Since most of the biological processes we are concerned with involve a diffusion space of $L \gg a$

(or $k \ll 1$), the expression can be further simplified to:

$$\tau_A \approx \frac{L^2}{3D_1} \quad (\text{S5})$$

A comment is due regarding the definition of the average arrival time defined in (Eq. S3).

This formula can be justified by probabilistic arguments. To show this, we define the probability

density function of the rate of arrival of A at its destination, $r = a$, as $P(t)$. Once A arrives at $r = a$ and reacts with B , it is depleted from the $a < r < L$ domain. Therefore, the rate of arrival of A at its destination is equal to the rate of depletion: $-\frac{d}{dt}\{N(t)\}$, which can also be written as:

$$\frac{d}{dt}\{N(0) - N(t)\}. \text{ Normalizing this expression with } \int_0^\infty P(t) dt = 1 \text{ gives } P(t) = \frac{d}{dt} \left\{ 1 - \frac{N(t)}{N(0)} \right\}.$$

Therefore, the average time of arrival, or in the language of statistics, the “expected time of arrival” is $E(t) = \int_0^\infty dt \cdot tP(t)$. Replacing the previous expression for $P(t)$ gives

$$\tau_A = E(t) = \int_0^\infty dt \cdot t \frac{d}{dt} \left\{ 1 - \frac{N(t)}{N(0)} \right\}, \text{ which is Eq. S3.}$$

2D diffusion

For 2D systems, the diffusion space is now a disk (of radius, L), with the immobile species, B , at its origin. In this case, r is the radial coordinate and the RD equation is as follows:

$$\frac{\partial c}{\partial t} = \frac{D_2}{r} \left[\frac{\partial}{\partial r} \left(r \frac{\partial c}{\partial r} \right) \right] \quad (\text{S6})$$

Initial condition, $t = 0$: $c = c_0$, for $r > a$

Boundary condition: $c = 0$ at $r = a$ and $\partial c / \partial r = 0$ at $r = L$

Using this equation and following the general strategy outlined in the case of 1D, the approximate value of the arrival time is

$$\tau_A \approx \frac{L^2}{2D_2} \ln \left(\frac{L}{a} \right) \quad (\text{S7})$$

3D diffusion

Finally, for the 3D, the diffusion domain is a sphere of radius L , and the RD equation is:

$$\frac{\partial c}{\partial t} = \frac{D_2}{r^2} \left[\frac{\partial}{\partial r} \left(r^2 \frac{\partial c}{\partial r} \right) \right] \quad (\text{S8})$$

The initial and boundary conditions are the same as in the 1D and 2D cases, and the arrival time is approximately:

$$\tau_A \approx \frac{L^2}{3D_3} \left(\frac{L}{a} \right) \quad (\text{S9})$$

References:

- [1] H. S. Carslaw, J. C. Jaeger, *Conduction of Heat in Solids*, 2nd ed., Oxford University Press, Oxford, **1959**.
- [2] G. Adam, M. Delbrück, in *Structural Chemistry and Molecular Biology* (Eds.: A. Rich, N. Davidson), Freeman, San Francisco, **1968**.