Exercise 04

1. Diffusion and crowding

In this problem we extend the one-dimensional model of diffusion in the presence of crowding molecules to account for the difference in size between a tracer particle (considered to be present at low concentration) and the crowders. The tracer particles are assumed to be undergoing random-walk motion on the larger tracer lattice with lattice constant b, while the crowders are hopping between adjacent sites of smaller lattice, with lattice constant a (see Fig. 1). The two lattices are introduced to account for the difference in size between the two molecular species.

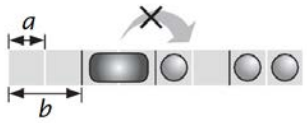

Figure 1: Lattice model of tracer particles of size b, diffusing in the presence of crowding molecules of size a. The tracer particle can hop to the neighbouring tracer site only if there are no crowding molecules present in the r = b/a adjacent crowding molecule sites. The fraction of sites occupied by crowding molecules is ϕ.

a) Calculate the diffusion coefficient by considering the possible trajectories of the tracer particles and their probabilities. Note that the tracer can hop to an adjacent site of the tracer lattice only if there are no crowders present. Express your answer in terms of the diffusion coefficient D_o of the tracer particles in the absence of crowders, the volume fraction of the crowders ϕ, and the ratio of the tracer and crowder sizes r = b/a.

b) Plot $\ln D/D_o$ as a function of th volume fraction for different values fo r. How well does this model explain the data shown in Figure 2? To make this comparison you will need to estimate the sizes of the molecules used in the experiment from their molecular masses and a typical protein density, which is 1.3 times that of water.

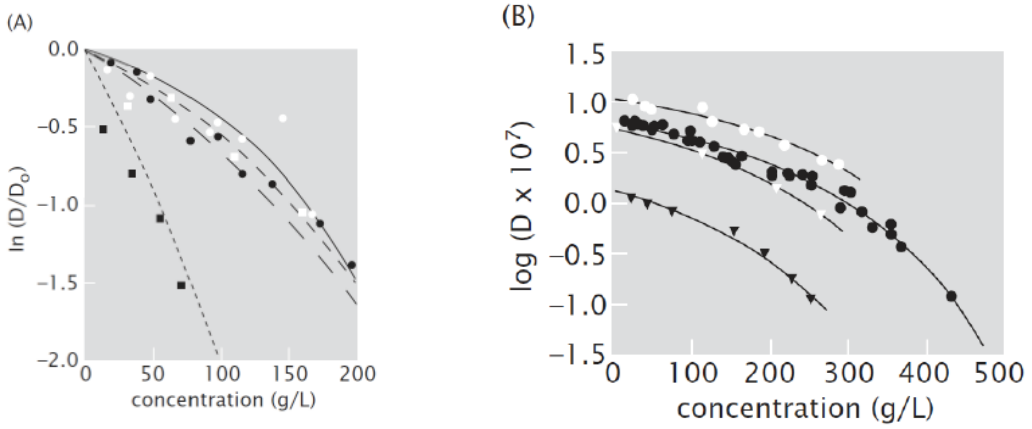

Figure 2: Diffusion and crowding. (A) Tracer diffusion as a function of protein concentration. FITC-aldolase diffusing in background of aldolase (open circles), BSA (filled circles), ovalbumin (open squares) and ribonuclease (filled squares). (B) Self-diffusion of globular proteins as a function of the protein concentration. Myoglobin (open circles), hemoglobin (filled circles), ovalbumin (open triangles), invertebrate hemoglobin (filled triangles). [Adapted from N. Muramatsu and A. P. Minton, PNAS, 1988; & S. B. Zimmerman and A. P. Minton, Ann. Rev. Bioph. Biomol. Struct, 1993]