Supplementary Material for "Free energy analysis of binding of functionalized nanoparticles to membrane surface reveals the importance of membrane entropy and nanoparticle entropy in adhesion of flexible nanoparticles"

S. Farokhirad[1], R.P. Bradley[2], and R. Radhakrishnan[2,3,*]
[1] *Department of Mechanical and Industrial Engineering, New Jersey Institute of Technology, Newark, NJ, 07102*
[2] *Department of Chemical and Biomolecular Engineering, University of Pennsylvania, Philadelphia, PA, 19104, USA*
[3] *Department of Bioengineering, University of Pennsylvania, Philadelphia, PA, 19104, USA*
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Details of the Monte Carlo Techniques for Nanoparticles-Membrane Simulations

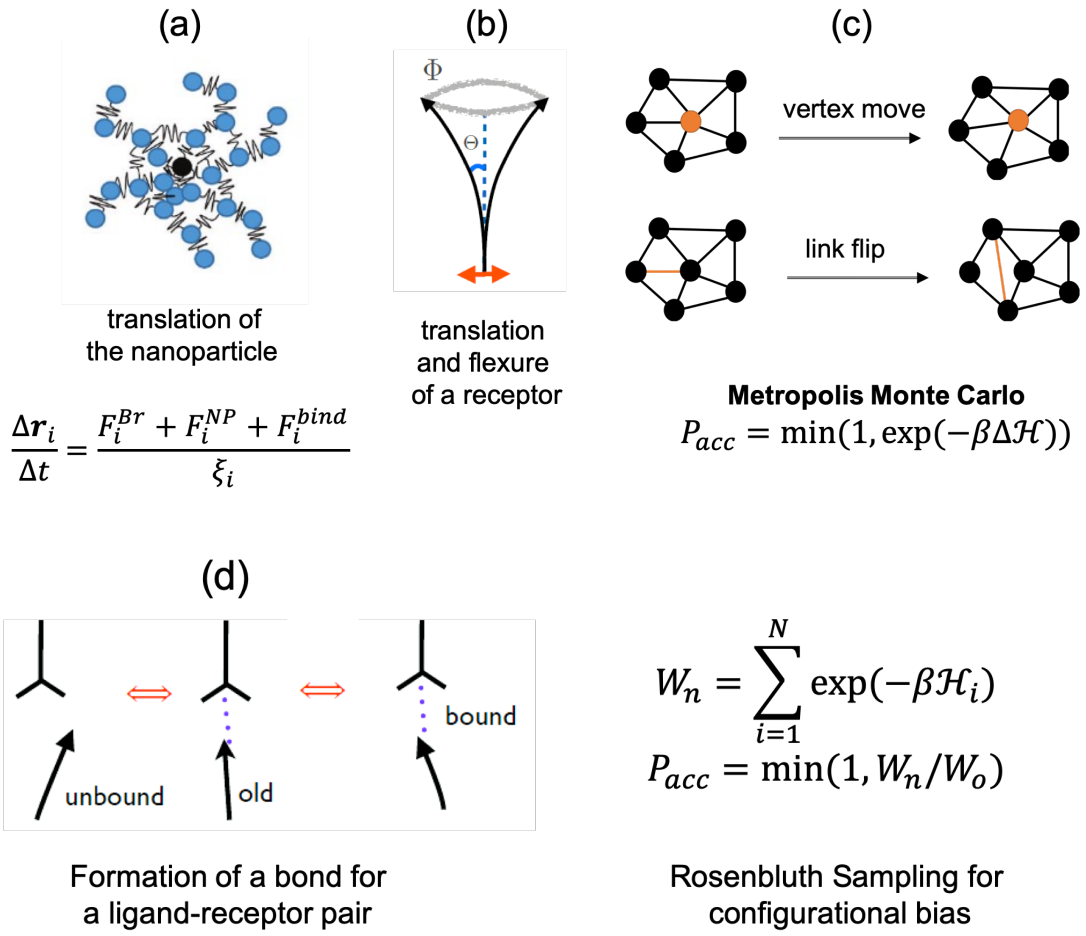

FIG. 1: A schematic of the Monte Carlo moves to evolve the equilibrium state of the membrane-NP system. (a) translational moves of the NP, (b) diffusion and flexure of the receptors, (c) dynamically triangulated Monte Carlo moves for the membrane, and (d) Rosenbluth sampling based configurational bias for formation and breakage of receptor-ligand bonds.

For the flexible nanoparticles (NPs) we model the polymer microstructure as a fixed number of strands attached to a core, which mimics the experimentally inferred architecture for this material, where each strand is modeled by beads connected through four Kuhn springs in series, as shown in Fig. 1(a). The core radius is set to $a = 6.8$ nm following the experimental estimates of [1, 2]. We set the size of each bead in the arms to be the same as that of the core, i.e., $a = 6.8$ nm. The initial microstructure is a unit star polymer with 25 arms attached to a core, with each

arm modeled by beads connected through four links in series; that is, each link connecting two adjacent beads in an arm is modeled as a Kuhn spring. The model is identical and is adopted from the work of Sarkar *et. al.* [3], where the stiffness of each link and the equilibrium distance is determined using a freely jointed chain model. The molecular weight of a dextran monomer is 162 Da and for a typical molecular weight of 70 kDa of the dextran polymer used to synthesize the NP, the number of monomers per arm is $\frac{70{,}000}{162}$, and the number of monomers per bead is $N = \frac{70{,}000}{4\times 162}$. If the number of Kuhn's segments per bead is N_k and size of each Kuhn's segment is b_k, we impose $N_k b_k = Nb$, where b is the size of each monomer. For dextran, b_k is 0.44 nm and the size of the monomer (b) is 1.5 nm using which we calculate the stiffness (k_s) of the links between beads as derived from the freely jointed chain (FJC) model, i.e., $k_s = \frac{3k_BT}{N_k b_k^2}$. We also model the stiffness of the coarse-grained crosslinks to be identical to the stiffness of each link. We mimic the experimental protocol to obtain a relaxed structure of the polymer assembly; details are available in [3]. For each NP stiffness we model $3-4$ configurations (replicas) and then carry out Monte Carlo simulations as described below in each of the replicas. The error bars of the reported quantities are determined through the standard deviations of the four replicas.

Fig. 1 shows the six different Monte Carlo moves to evolve microstates of the nanoparticle (NP)-membrane system:

(1) Vertex move: A random chosen vertex on the triangulated surface of the membrane is displaced to a new position (as shown in Fig. 1 (c)) holding the triangulation fixed [4, 5].

(2) NP translation: An attempt to translate the NP to a new position within a time step through the use of equations of motion using Brownian Dynamics to evolve the beads of NP, as demonstrated in Fig. 1 (a). The value of time step is chosen (and also modified during runtime) such that nearly 50% of the attempted moves are accepted.

(3) Link flip: A link shared by two neighboring faces of the triangulated surface is removed and reconnected to the two initially unconnected nodes as illustrated in Fig. 1(c), [4, 5].

(4) Translation of receptors: An attempt to randomly displace a receptor molecule to a new position on the membrane surface [6, 7].

(5) Flexure of receptors: An attempt to change the flexure angles of the receptor from $\theta, \Phi \rightarrow \theta + \Delta\theta, \Phi + \Delta\Phi$, where $\Delta\theta$ is drawn from a distribution $\sin^{-1}([-1.0, 1.0])$ and $\Delta\Phi$ is drawn from an uniform distribution in the interval $[0, 2\pi]$ [6, 7].

Moves (1)-(5) fall under the class of canonical Monte Carlo and hence are accepted according to a standard Metropolis scheme [8] in the canonical ensemble such that $P_{acc} = min(1, \exp(-\beta\Delta\mathcal{H}))$.

(6) Formation and breakage of receptor-ligand bonds: The formation of a receptor-ligand bonds is very sensitive to the conformations of the membrane and position of the NP and hence can be treated as a rare event compared to moves (1)-(5). In order to carefully sample the bonded states of the system, we use the Rosenbluth sampling technique [9] to sample bond formation and breakage moves. The attempted move is accepted according to $P_{acc} = min(1, W_n/W_o)$ [10], where $W_n = \sum_{j=1}^{N} \exp(-\beta\mathcal{H}_i)$ is the weight factor to generate N independent configurations with energy $\mathcal{H}_i$ and $W_o = \exp(-\beta\mathcal{H}_*) + \sum_{j=2}^{N} \exp(-\beta\mathcal{H}_i)$ is the weight factor to generate $N-1$ independent configurations starting with the initial configuration whose energy is given by $\mathcal{H}_*$. **Half of the MC moves are distributed equally between moves (1-4) and the rest half are distributed between moves (5) and (6) in the ratio of 2:5.**

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