Time scale of random sequential adsorption

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A simple multiscale approach to the diffusion-driven adsorption from a solution to a solid surface is presented. The model combines two important features of the adsorption process: (i) The kinetics of the chemical reaction between adsorbing molecules and the surface and (ii) geometrical constraints on the surface made by molecules which are already adsorbed. The process (i) is modeled in a diffusion-driven context, i.e., the conditional probability of adsorbing a molecule provided that the molecule hits the surface is related to the macroscopic surface reaction rate. The geometrical constraint (ii) is modeled using random sequential adsorption (RSA), which is the sequential addition of molecules at random positions on a surface; one attempt to attach a molecule is made per one RSA simulation time step. By coupling RSA with the diffusion of molecules in the solution above the surface the RSA simulation time step is related to the real physical time. The method is illustrated on a model of chemisorption of reactive polymers to a virus surface.

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Random sequential adsorption (RSA) is a classical model of irreversible adsorption (e.g., chemisorption) [1]. Given a sequence of times t_k, $k=1,2,3,\ldots$, an attempt is made to attach one object (e.g., a molecule) to the surface at each time point $t=t_k$. If the attempt is successful (i.e., if there is enough space on the surface to place the molecule), the object is irreversibly adsorbed. It cannot further move or leave the structure and it covers part of the surface, preventing other objects from adsorbing in its neighborhood (e.g., by steric shielding in the molecular context) [1,2].

In the simplest form, RSA processes are formulated as attempting to place one object per RSA time step, expressing the simulation time in units equal to the number of RSA time steps k rather than in real physical time t_k. Such an approach is useful to compute the maximal (jamming) coverage of the surface. To apply RSA models to dynamical problems, it is necessary to relate the time of the RSA simulation k and the real time t_k. This is a goal of this paper. We consider that the adsorbing objects are molecules which can covalently attach to the binding sites on the surface. We couple the RSA model with processes in the solution above the surface to study the irreversible adsorption of molecules in real time. The time (t_k-t_{k-1}) between the subsequent attempts to place a molecule is in general a nonconstant function of k which depends on the kinetics of the chemical reaction between the adsorbing molecules and the surface, and on the stochastic reaction-diffusion processes in the solution above the surface. We illustrate our method with an example of the chemisorption of reactive polymers to a virus surface [3,4]. Finally, we show that the stochastic simulation in the solution can be substituted by a suitable deterministic partial differential equation which decreases the computational intensity of the algorithm. We show that it is possible to get the values of t_k without doing extensive additional stochastic simulations.

We consider a three-dimensional cuboid domain $L_x\times L_x\times L_z$ in which molecules diffuse (see Fig. 1). The side $z=0$ of area $L_x\times L_x$ is assumed to be adsorbing, i.e., containing binding sites to which molecules can covalently attach. Our goal is to couple RSA on the side $z=0$ with stochastic reaction-diffusion processes in the solution above the adsorbing surface. Since those molecules which are far from the surface will have little influence on the adsorption process, it is a waste of resources to compute their trajectories. We will therefore carefully truncate our computational domain to that which is effectively influenced by the reactive boundary at $z=0$, which we denote by $z<L(t)$. Note that $L(t)$ is not fixed but a function of time—the formula for it will be derived later. Suppose that there are $N(t)$ diffusing molecules in the cuboid domain $L_x\times L_x\times L(t)$. Let us denote the z coordinate of the center of mass of the ith molecule by $z_i(t)$. Choosing a time step Δt, we compute $z_i(t+\Delta t)$ from $z_i(t)$, $i=1,\ldots,N(t)$, by

$$z_i(t+\Delta t)=z_i(t)+\sqrt{2D_i\Delta t}\xi_i, \tag{1}$$

where ξ_i is a normally distributed random variable with zero mean and unit variance and D_i is the diffusion constant of the ith molecule. Equation (1) states that the ith diffusing molecule can be viewed effectively as a point at position $z_i(t)$ above the surface; its three-dimensional structure will be taken into account later when we consider the adsorption of molecules to the surface. In principle, we should model the behavior of molecules as three-dimensional random walks in the cuboid domain $L_x\times L_x\times L(t)$, i.e., there should be equations analogous to Eq. (1) for the x and y coordinates, too. However, we can often assume that $L(t)\gg L_x$ in applications. Choosing the time step Δt large enough that a molecule travels over distances comparable to L_x during one time step, we

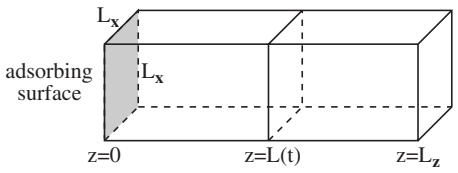

FIG. 1. Three-dimensional cuboid domain.

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FIG. 2. A schematic diagram of RSA.

can assume that the molecules are effectively well-mixed in the x and y directions on this time scale. Consequently, the x and y coordinates of molecules do not have to be simulated. If the original adsorbing surface is large, one often models by RSA only a representative part of it, i.e., a square $L_x \times L_x$ which contains a relatively large number of binding sites, but still satisfies $L_x \ll L(t)$. The diffusion of molecules (1) is coupled with other processes in the solution and on the surface as follows.

CHEMICAL REACTIONS IN THE SOLUTION

Our illustrative example is the polymer coating of viruses [3,4]. In this case, the polymer molecules have reactive groups which can covalently bind to the surface. The reactive groups also hydrolyze in solution. Assuming that there is one reactive group per polymer molecule (such a polymer is called semitelechelic), we have effectively one chemical reaction in the solution—a removal of the reactive polymers from the solution with rate λ [5]. Assuming that $\lambda \Delta t \ll 1$, the stochastic modeling of the process in the solution is straightforward. At each time step, the ith molecule moves according to Eq. (1). We then generate a random number r_i uniformly distributed in the interval [0, 1]. If $r_i < \lambda \Delta t$, we remove the molecule from the system. More complicated reaction mechanisms in the solution can be treated using stochastic simulation algorithms which have been proposed for reaction-diffusion processes in the literature [6–8]. In our case, we treat diffusion using the discretized version of the Langevin (Smoluchowski) equation (1). Consequently, we can follow Andrews and Bray [6] to introduce higher-order reactions to the system.

ADSORPTION TO THE SURFACE

The surface $L_x \times L_x$ at $z=0$ is assumed to be adsorbing. We use a simple version of the RSA model from [4] which postulates that the binding sites on the surface lie on a rectangular lattice—see Fig. 2. We assume that the polymer radius is of the same order as the distance between neighboring binding sites h, i.e., a "wiggling tail" of a polymer which is bound to a lattice site prevents the binding of another polymer to the neighboring lattice sites through steric shielding. In this paper, we consider a solution of polymers which adsorb as "crosses" [4]—see Fig. 2. Binding a polymer to a lattice site prevents the binding of another polymer to this lattice site and to its four nearest neighbors. We assume that the "wiggling tails" can overlap. Therefore, our illustrative model of adsorption is the classical RSA with nearest neighbor exclusion [1]. Such a RSA model can be simulated on its own as shown in [4]. In this paper, we simulate it together with the z variables of molecules in the solution (1) to get the RSA evolution in real physical time. Whenever a molecule hits the boundary $z=0$, it is adsorbed with some probability, and reflected otherwise. This partially adsorbing boundary condition is implemented in the RSA context using the following two steps (a) and (b).

(a) If $z_i(t+\Delta t)$ computed by Eq. (1) is negative then, with probability $P\sqrt{\Delta t}$, we attempt one step of the RSA algorithm with the ith molecule. If the ith molecule is adsorbed, we remove it from the solution. Otherwise, we put $z_i(t+\Delta t) = -z_i(t) - \sqrt{2D_i \Delta t}\xi_i$.

(b) If $z_i(t+\Delta t)$ computed by Eq. (1) is positive then, with probability $\exp[-z_i(t)z_i(t+\Delta t)/(D_i \Delta t)]P\sqrt{\Delta t}$, we attempt one step of the RSA algorithm with the ith molecule. If the ith molecule is adsorbed, we remove it from the solution.

Here, P is a positive constant which can be related to the rate constant of the chemical reaction between the binding sites on the virus surface and the reactive groups on the polymer [9]. This relation depends on the stochastic model of diffusion and for Eq. (1) is given later—see formula (6). Conditions (a) and (b) state that only the fraction $P\sqrt{\Delta t}$ of molecules which hit the boundary have a chance to create a chemical bond (provided that there is no steric shielding). Obviously, if $z_i(t+\Delta t)$ computed by Eq. (1) is negative, a molecule has hit the boundary. This case is incorporated in (a). However, Andrews and Bray [6] argue that there is a chance that a molecule hit the boundary during the finite time step Δt even if $z_i(t+\Delta t)$ computed by Eq. (1) is positive; that is, during the time interval $[t, t+\Delta t]$ the molecule might have crossed to z_i negative and then crossed back to z_i positive again. They found that the probability that the molecule hit the boundary $z=0$ at least once during the time step Δt is $\exp[-z_i(t)z_i(t+\Delta t)/(D_i \Delta t)]$ for $z_i(t) \geq 0$, $z_i(t+\Delta t) \geq 0$. This formula is used in (b).

NUMERICAL RESULTS

It is important to note that the boundary conditions (a) and (b) can be used for any RSA algorithm and for any set of reactions in the solution. To apply it to the virus coating problem, we have to specify some details of the model. First of all, it can be estimated that the average distance between the binding sites is about 1 nm [3], i.e., we put $h=1$ nm. We choose $L_x=100$ nm. Therefore, there are about 10 000 binding sites on the adsorbing side $z=0$. We use RSA on a 100×100 lattice with the nearest neighbor exclusion, which is a special case of the model from [4]. We consider a monodisperse solution of semitelechelic 50 kDa polymers, i.e., $D_i \equiv D$, where $D=5 \times 10^{-5}$ mm^2 s^{-1} [10]. The rate of hydrolysis of the reactive groups on polymers can be estimated from data in [5] as $\lambda = 1.3 \times 10^{-4}$ s^{-1}. We choose $P=1$ s$^{-1/2}$. Since we simulate the behavior of polymer molecules in solution only along the z direction, we express the concentration of polymer $c(z,t)$ in numbers of polymer molecules per volume $L_x \times L_x \times [1 \text{ mm}]$ where $L_x = 10^{-4}$ mm is fixed. A typical experiment starts with a uniform concentration of reactive polymers. Considering that the initial concentration of 50 kDa polymer is 0.1 g/l, we obtain the initial condition $c_0 = 1.2 \times 10^4$ molecules per mm of the height above the sur-

face (let us note that the units of the "one-dimensional" concentration $c(z,t)$ are molecules/mm because L_x is considered fixed). Next, we have to specify $L(t)$ (see Fig. 1), i.e., we want to find the region of the space which is effectively influenced by the boundary condition at $z=0$. To that end, we note that the concentration $c(z,t)$ satisfies the partial differential equation

$$\frac{\partial c}{\partial t} = D\frac{\partial^2 c}{\partial z^2} - \lambda c. \tag{2}$$

Now any partially reacting boundary will have less impact on the spatial profile of $c(z,t)$ than perfect adsorption at $z=0$. Thus we may find an upper bound for the region of influence of the boundary by solving Eq. (2) subject to

$$c(0,t) = 0, \quad \lim_{z\to\infty} c(z,t) = c_0 \exp[-\lambda t], \tag{3}$$

for $t \in [0,\infty)$, and the initial condition $c(z,0)=c_0$, for $z \in [0,\infty)$. The solution of Eqs. (2) and (3) is

$$c(z,t) = c_0 \exp[-\lambda t]\mathrm{erf}\left(\frac{z}{2\sqrt{Dt}}\right), \tag{4}$$

where $\mathrm{erf}(\cdot)$ denotes the error function. Defining $\omega=\mathrm{erf}^{-1}(0.99) \doteq 1.821$ we set

$$L(t) \equiv 2\omega\sqrt{Dt}. \tag{5}$$

Then $c(L(t),t)=0.99c_0 \exp[-\lambda t]$, so that the concentration of the reactive polymer at point $z=L(t)$ at time t is equal to 99% of the polymer concentration at points which are "infinitely far" from the adsorbing boundary. In particular, we can assume that the adsorbing boundary effectively influences the polymer concentration only at heights $z \in [0,L(t)]$ above the boundary and we can approximate $c(z,t) \sim c_0 \exp[-\lambda t]$ for $z > L(t)$. Formula (5) specifies the computational domain as $L_x \times L_x \times L(t)$ at each time (see Fig. 1).

The results of the stochastic simulation of the solution above the surface are shown in Fig. 3 as gray histograms. To simulate the behavior of $N(t)$ reactive polymers, we consider only their z positions. We use $\Delta t = 10^{-2}$ s and we update the z positions of molecules during one time step according to Eq. (1). At each time step, we also generate a uniformly distributed random number r_i and we remove the ith molecule from the system if $r_i < \lambda \Delta t$. We work in the one-dimensional domain $[0,L(t)]$ where $L(t)$ is given by Eq. (5). The RSA boundary condition at $z=0$ is implemented using (a) and (b) described above. The right boundary increases during one time step by $\Delta L(t)=L(t+\Delta t)-L(t)$. During each time step, we have to put on average $m(t)=c_0 \exp[-\lambda t]\Delta L(t)$ molecules into the interval $[L(t),L(t+\Delta t)]$. This is done as follows. We put $\lfloor m(t) \rfloor$ molecules at random positions in the interval $[L(t),L(t+\Delta t)]$, where $\lfloor \cdot \rfloor$ denotes the integer part. Moreover, we generate random number $r_{\Delta t}$ uniformly distributed in $[0,1]$ and we add one molecule at a random position in the interval $[L(t),L(t+\Delta t)]$ if $r_{\Delta t} < m(t) - \lfloor m(t) \rfloor$. This will ensure that we put on average $m(t)$ molecules to the interval $[L(t),L(t+\Delta t)]$ during one time step.

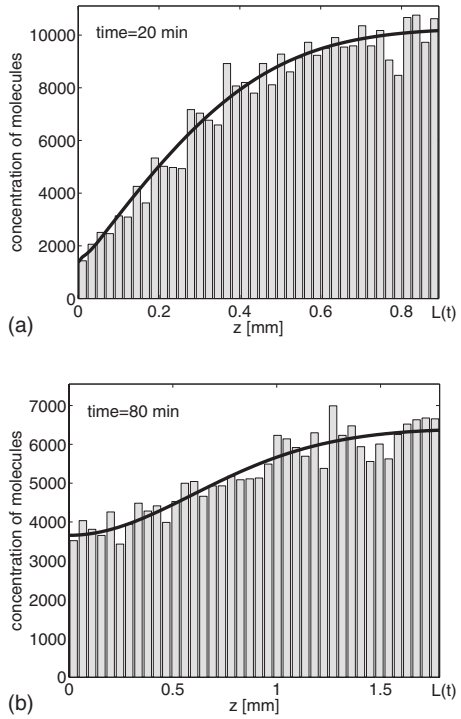

FIG. 3. Concentration of polymer molecules in the solution above the adsorbing surface $z=0$ at times 20 and 80 min.

Introducing the moving boundary decreases the computational intensity of the model. Initially we simulate a relatively small region with a high concentration of reactive polymers. The simulated region increases with time but the concentration of reactive molecules decreases with rate λ. Using Eq. (4), it can be computed that the maximal number of simulated polymers in solution is achieved at time $t_m=(2\lambda)^{-1} \doteq 64$ min (and is about 8×10^3 molecules for our parameter values).

The number of polymers adsorbed to the RSA surface at $z=0$ as a function of real physical time is shown in Fig. 4. Since the polymer solution is assumed to be monodisperse, we can run the RSA algorithm first and record the times $k_1,k_2,k_3,\ldots$ (expressed in numbers of the RSA time steps) of successful attempts to place the polymer on the RSA lattice. Then the stochastic simulation of the reaction-diffusion processes in the solution can use $k_1,k_2,k_3,\ldots$ as its input. We

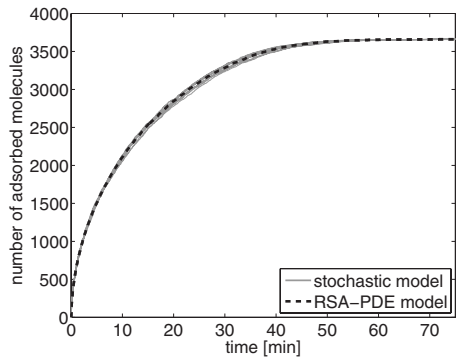

FIG. 4. Number of polymer molecules adsorbed to the RSA lattice as a function of the real physical time.

will shortly consider another approach to the problem, replacing the stochastic simulation of the solution by the continuum limit (2) with a suitable Robin boundary condition. To enable a direct comparison of the two approaches, we use the same sequence $k_1, k_2, k_3, \ldots$ in ten realizations of the full stochastic model of adsorption; the results are shown as gray solid lines in Fig. 4.

RSA-PDE APPROACH

Moving the right boundary $L(t)$ is one way to decrease the computational intensity of the problem. Another possibility is to use the deterministic equation (2) together with a Robin boundary condition

$$\frac{\partial c}{\partial z}(0,t) = \alpha_{\mathrm{RSA}}(t)\frac{2P}{\sqrt{D\pi}}c(0,t) \tag{6}$$

at the adsorbing boundary $z=0$. Here, the fraction $2P/\sqrt{D\pi}$ corresponds to the rate of the chemical reaction between the adsorbing boundary and the diffusing molecules in the solution—see [9] for the derivation of this formula and further discussion. Factor $\alpha_{\mathrm{RSA}}(t) \in \{0,1\}$ provides the coupling between the RSA model and Eq. (2). To find the value of $\alpha_{\mathrm{RSA}}(t)$, we estimate the number of attempts to place the polymer on the RSA lattice by

$$\kappa(t) = \left\lfloor \int_0^t \frac{2P\sqrt{D}}{\sqrt{\pi}} c(0,t)dt \right\rfloor, \tag{7}$$

where $\lfloor \cdot \rfloor$ denotes the integer part [9]. We start with $\alpha_{\mathrm{RSA}}(t)=1$ and we solve Eqs. (2) and (6) numerically. Whenever $\kappa(t)$ increases by 1, we attempt one step of the RSA. If the attempt is successful, we put $\alpha_{\mathrm{RSA}}(t)=1$. If the attempt to place the molecule is not successful, we put $\alpha_{\mathrm{RSA}}(t)=0$. Thus $\alpha_{\mathrm{RSA}}(t)$ has only two values, 0 and 1, and changes at computed time points depending on the output of the RSA simulation. We call this procedure the RSA-PDE approach. It also leads to the sequence of real physical times $t_{k_1}, t_{k_2}, t_{k_3}, \ldots$, of successful attempts to place the polymer on the RSA lattice. The numerical solution of Eq. (2) with the Robin boundary condition (6) at $z=0$ is presented in Fig. 3 as the solid line for comparison. We also plot the number of adsorbed polymers as a function of the real time as the dashed line in Fig. 4. To enable the direct comparison, we run the RSA algorithm first and we record the times of successful attempts to place the polymer on the lattice. We obtain the sequence $k_1, k_2, k_3, \ldots$ of times expressed in number of RSA time steps. This sequence is used in both the stochastic model (10 realizations plotted in Fig. 4 as gray solid lines) and the RSA-PDE approach (dashed line in Fig. 4). The comparison of the results obtained by the full stochastic model and by the RSA-PDE model is excellent.

Formulas (6) and (7) can also be used to estimate the characteristic time scale T of the RSA algorithm (in the real physical time). Let K be the average number of RSA time steps which are needed for adsorption of one half of the final (jamming) number of polymers to the surface. Then K is the characteristic time scale of the RSA algorithm expressed in the number of RSA time steps. The number K is proportional to the total number of lattice sites L_x^2/h^2. It can be estimated from the kinetic properties of the particular RSA algorithm [11]. In our case, we have $K \approx L_x^2/(3h^2)$. Knowing K, we can estimate T as follows. Using formula (6), we see that $c(0,t)$ is of the order $(c_0/2P)\sqrt{\pi/T}$ provided that we approximate α as 1. Consequently, formula (7) implies that

$$K \approx \frac{2P\sqrt{D}}{\sqrt{\pi}} \int_0^T c(0,t)dt \approx c_0\sqrt{DT}.$$

Solving for T, we obtain that the time scale of the RSA can be approximated as

$$T \approx \frac{K^2}{Dc_0^2} \approx \frac{L_x^4}{9Dc_0^2h^4}.$$

Using our parameter values $D=5\times10^{-5}$ mm^2 s^{-1}, $c_0=1.2\times10^4$ molecules per mm, $L_x=10^{-4}$ mm, and $h=10^{-6}$ mm, we compute $T\approx26$ min. Comparing with Fig. 4, we see that we obtained a reasonable estimate of the RSA time scale. The computed number T is larger than the time when half of the final number of polymers is adsorbed because we approximated α as 1 during the computation of this time scale. If we want to get the precise relation between the RSA time and the physical time, we have to follow the stochastic algorithm described above, or the less computationally intensive RSA-PDE approach.

CONCLUSION

We have presented a method to perform RSA simulation in real physical time. The key part of the method is the boundary conditions (a) and (b) which can be coupled with any reaction-diffusion model in the solution and any RSA algorithm. We illustrated this fact on a simple model of the polymer coating of viruses. Moreover, we showed that the RSA algorithm can be coupled with Eq. (2) using the Robin boundary condition (6) to get comparable results. The Robin boundary condition (6) is also not restricted to our illustrative example. It can be used for the coupling of any RSA model with the PDE model of the reaction-diffusion processes in the solution above the adsorbing surface.

ACKNOWLEDGMENTS

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[1] J. Evans, Rev. Mod. Phys. **65**, 1281 (1993).
[2] J. Talbot, G. Tarjus, P. Van Tassel, and P. Viot, Colloids Surf., A **165**, 287 (2000).
[3] R. Erban, S. J. Chapman, K. Fisher, I. Kevrekidis, and L. Seymour, e-print arxiv.org/physics/0602001, Math. Models Meth. Appl. Sci. (to be published).
[4] R. Erban and S. J. Chapman, e-print arxiv.org/physics/0609029, J. Stat. Phys. (to be published).
[5] V. Šubr, Č. Koňák, R. Laga, and K. Ulbrich, Biomacromolecules **7**, 122 (2006).
[6] S. Andrews and D. Bray, Phys. Biol. **1**, 137 (2004).
[7] J. Hattne, D. Fange, and J. Elf, Bioinformatics **21**, 2923 (2005).
[8] S. Isaacson and C. Peskin, SIAM J. Sci. Comput. (USA) **28**, 47 (2006).
[9] R. Erban and S. J. Chapman, Phys. Biol. **4**, 16 (2007).
[10] Š. Prokopová-Kubinová, L. Vargová, L. Tao, K. Ulbrich, V. Šubr, E. Syková, and C. Nicholson, Biophys. J. **80**, 542 (2001).
[11] V. Privman, J. S. Wang, and P. Nielaba, Phys. Rev. B **43**, 3366 (1991).