Anomalous packing and dynamics of a polymer chain confined in a static porous environment

Zachary E. Dell and M. Muthukumar^{a)}

Department of Polymer Science and Engineering, University of Massachusetts—Amherst, Amherst, Massachusetts 01002, USA

(Received 11 June 2018; accepted 14 October 2018; published online 1 November 2018)

Polymers in confined porous environments are ubiquitous throughout biology, physics, materials science, and engineering. Several experiments have suggested that in some porous environments, chain dynamics can become extremely slow. While phenomenological explanations exist, the exact mechanisms for these slow dynamics have not been fully characterized. In this work, we initiate a joint simulation–theory study to investigate chain packing and dynamics in a static porous environment. The main theoretical concept is the free energy of the chain partitioning into several chambers of the porous environment. Both the theoretical results and Langevin dynamics simulations show that chain packing in each of the chambers is predominantly independent of chain length; it is determined by the maximal packing of segments in each chamber. Dynamically, short chains (compared to the chamber size) become trapped in a single chamber and dynamics become extremely slow, characteristic of an Ogston sieving-like behavior. For longer chains, on the other hand, a hierarchy of slow dynamics is observed due to entropic trapping, characterized by sub-diffusive behavior and a temporary plateau in the mean square displacement. Due to the slow nature of the dynamics, the inevitable long-time diffusive behavior of the chains is not captured by our simulations. Theoretically, the slow dynamics are understood in terms of a free energy barrier required to thread the chain from one chamber to the next. There is overall qualitative and quantitative agreement between simulations and theory. This work provides foundations for a better understanding of how chain dynamics are affected by porous environments. *Published by AIP Publishing.* <https://doi.org/10.1063/1.5043629>

I. INTRODUCTION

Polymers confined in porous environments are ubiquitous throughout engineering, materials science, and biology. In engineering and materials science, the conformational structure and dynamics of polymers embedded into porous environments can help guide the design of new materials^{1–7} and may shed light on existing mysteries such as reinforcement in elastomer composite systems.^{8,9} In biology, the inter- and intra-cellular environments are often composed of polymeric networks and gels^{10–12} through which other polymers must arrange and move.¹³ Additionally, the cellular environment is extremely crowded,¹⁴ which in a highly oversimplified fashion might be considered as porous. Finally, in gel electrophoresis, commonly employed to characterize biological macromolecules,^{15–20} understanding the role of dynamics in a porous environment is crucial.

Many previous theories attempt to explain the dynamics of a chain embedded in a porous system; however, most focus on limiting cases.^{2–4,16,19–32} Such limits include the small chain Ogston limit,^{27,28} a drift dominated regime relevant to electrophoresis, a reptation regime which is limited to tube-like confining environments,^{19,21,22,29,30,33,34} and a barrier dominated regime similar to translocation

phenomena.^{4,13,23–26,30,31,35} Recent experiments on the dynamics of polymers embedded in cross-linked hydro-gels³⁶ suggest that under certain conditions, a chain can localize at the center of mass (CM) level due to entropic, “topological” trapping. Additional experiments^{17,37–41} and simulations^{5,6,19,42} show evidence of slow dynamics and dynamic correlations in chains partitioned between the pores of a porous environment.

In this work, we formalize the entropic barrier ideas suggested by the recent experiments and develop a theory to understand the conformational packing and subsequent dynamics of a single chain embedded in multiple chambers of a porous environment (Fig. 1). In addition, we extend recent Langevin dynamics simulations⁴² to verify the theoretical predictions. While the simulated systems here are extremely similar to previously studied systems,⁴² here we investigate longer times and also study the local density fluctuations of the chain. For both the theory and simulations, we focus on a simplified system, where we model the porous environment as spherical cavities (chambers) connected by small cylindrical openings (pores) and ignore the influence of hydrodynamics, which should be largely screened in our system.

Theoretically, the free energy is associated with partitioning the chain into multiple compartments. This free energy is minimized to find the number of occupied compartments, which is determined by a balance between conformational entropy and enthalpy when different numbers of segments

^{a)}Electronic mail: muthu@polysci.umass.edu

FIG. 1. Schematic of the theoretical (a) and simulated (b) systems. In both cases, a polymer chain is confined into spherical chambers (radii R_s) connected by small cylindrical passageways (lengths L_c , radii R_c). The polymer chain occupies n_c chambers with m_i segments ($i = 1, 2, \dots, n_c$) in the respective chamber. Occupied chambers can be broadly characterized into two categories: tail chambers that contain the chain ends and tie chambers in which a central portion of the chain completely straddles the chamber. In the simulations, σ is the Lennard–Jones length scale.

occupy a given chamber. The theory predicts that segments will be evenly distributed among the occupied chambers, which is further verified by the simulations. To model the dynamics, we consider a transition state in which dynamics are completely localized at the chain end and calculate the associated barrier for the capture and threading of the chain end. This barrier yields a hierarchy of slow dynamics that depends on chain length. Our theoretical predictions are verified by simulations, for which the chain undergoes highly sub-diffusive motion; the center of mass (CM) and segmental (seg) mean square displacements (MSDs) are nearly constant. It should be noted that due to the slow nature of the dynamics, the inevitable diffusive regime is not observed in our simulations. The simulations also demonstrate that the chain relaxation occurs from the chain ends and propagates inward. This suggests that our theoretical approach is a valid starting point for predicting dynamics and can be improved in a perturbative manner by including the effects of additional chambers near the chain ends.

The remainder of the paper is organized as follows. Section II outlines our theoretical model and summarizes the equilibrium packing and dynamic predictions made by the theory. This is followed by Secs. III and IV which overview our simulation methods and results, respectively. We finish with discussion and conclusions in Sec. V.

II. THEORETICAL MODELS AND PREDICTIONS

Consider a system comprised of spherical chambers of radius R_s separated by cylindrical pores of radius R_c and length L_c (Fig. 1). For the cases studied here, a “1D” arrangement of chambers is employed; each spherical chamber is connected to exactly two neighboring spheres. A polymer chain comprised of N Kuhn segments, each with Kuhn length l_k , is imbedded in this geometry. The goal of this work is to understand the packing and dynamics of the chain under such confinement.

The foundation for both the equilibrium and dynamics theories is the conditional free energy for the chain confined in n_c chambers.

For the purposes of developing a theory, we consider a simplified geometry where the cylindrical pores are very thin, $R_c \approx l_k$, and the cylinder length is negligible, $L_c \rightarrow 0$. Thus the spherical chambers are directly connected by openings which are small enough to prevent the chain from back-tracking. Given this and that the spheres are arranged in a 1D manner, two independent portions of the chain cannot occupy a single chamber. Hence, each chamber can be treated independently. Assuming the chain partitions such that m_i Kuhn segments occupy chamber i , the conditional free energy $F(n_c, \{m_i\})$ can be expressed as

$$\beta F(n_c, \{m_i\}) = \sum_{i=1}^{n_c} \beta F_i(m_i),$$

with

$$N = \sum_{i=1}^{n_c} m_i. \quad (1)$$

Here, $\beta = (k_B T)^{-1}$ is the inverse thermal energy and $F_i(m_i)$ is the free energy for confining a chain of m_i segments into chamber i , subject to the appropriate boundary condition. The second line of Eq. (1) expresses the constraint that the total number of segments on the chain is N . For the purpose of this work, we mainly consider $n_c > 1$ and note that the $n_c = 1$ case has been previously studied in the context of capture and translocation.^{23,25,26,43,44}

For a general porous environment, each chamber can have a different free energy expression F_i which depends on the chamber shape, polymer–chamber interactions, and the positions of the openings to neighboring chambers. Here, we consider the special case for which the chambers are all identical spheres with openings to neighboring chambers that are either randomly oriented on the chamber surface [Fig. 1(a)] or are linearly oriented at the opposite poles of the sphere [Fig. 1(b)]. Under these conditions, by symmetry, the chamber free energy F_i will reduce to one of the two possibilities: (i) the tail free energy $F_{tail}(m_i)$ for $i = 1, n_c$ or (ii) the tie free energy $F_{tie}(m_i)$ for all other i [Fig. 1(a)].

In order to calculate the tie and tail free energies, we adopt our earlier work^{25,44,45} on self-consistent field theory for the free energy of a chain with excluded volume interactions under spherical confinement. In our case, one or both ends of the chain are fixed near the surface of the sphere; however, even when the chain ends are free to undergo translation inside the sphere, there have been conflicting views on the confinement free energy F_c of the chain.^{46,47} Basically, there have been three approaches to compute F_c :

- (i) Scaling argument: According to scaling arguments,⁴⁸ F_c of a chain of N segments inside a spherical cavity of radius R_s is given as

$$\beta F_c \sim \frac{N}{R_s^{1/\nu}}, \quad (2)$$

where ν is the size exponent for a single chain defined through the relation $R_g \sim N^\nu$ and R_g is the radius of gyration in infinitely dilute solution.

- (ii) Self-consistent field theory: Starting from the Edwards Hamiltonian for a confined chain,^{25,44,45} F_c is calculated self-consistently by accounting for the collective contributions from chain entropy and excluded volume interactions as a crossover function. In the asymptotic limit of high monomer concentration $\phi \sim N/R_s^3$, where the two-body repulsive excluded volume interactions dominate over the entropic contribution, F_c approaches the limit

$$\beta F_c \simeq \frac{wN^2}{R_s^3} \sim wN\phi, \quad (3)$$

where w is the two-body excluded volume parameter, which is related to the Flory–Huggins χ parameter via $w = (\frac{1}{2} - \chi)$.

- (iii) Thermodynamic theory: By drawing an analogy between a chain inside a cavity and a polymer solution, the confinement free energy is given by^{49,50}

$$\beta F_c = V \left[\frac{\phi}{N} \ln \phi + (1 - \phi) \ln(1 - \phi) + \chi \phi(1 - \phi) + v_3 \phi^3 \right] + \frac{1}{24\pi} \frac{V}{\xi^3}, \quad (4)$$

where V is the volume of the cavity ($V \sim R_s^3$). The terms inside the square brackets, defined as βF_0 , are the usual mean field contributions with various symbols defined above, and v_3 is the three-body interaction parameter. The final term on the right-hand side of Eq. (4) accounts for the concentration fluctuations; ξ is the correlation length for monomer concentration fluctuations. If the monomer concentration is under semidilute conditions⁴⁸ and not too high, then $\xi \sim \phi^{-3/4}$ and Eq. (4) becomes

$$\beta F_c = \beta F_0 + \frac{1}{24\pi} N \phi^{5/4}, \quad (5)$$

with some prefactors left out. If the monomer concentration is high,⁴⁸ the correlation length is Edwards' length^{48,51} given by $\xi \sim \phi^{-1/2}$ and

$$\beta F_c = \beta F_0 + \frac{1}{24\pi} N \phi^{1/2}. \quad (6)$$

For even higher packing fractions, the contribution from the fluctuation part is insignificant compared to the mean field part βF_0 , which is given from Eq. (4) as

$$\beta F_0 = V \left[\frac{\phi}{N} \ln \phi + (1 - \phi) \ln(1 - \phi) + \chi \phi(1 - \phi) + v_3 \phi^3 \right]. \quad (7)$$

Furthermore, the two- and three-body interactions dominate at these higher concentrations, so Eq. (4) reduces to

$$\beta F_c \simeq \beta F_0 \simeq N(w\phi + v_3\phi^2), \quad (8)$$

with a crossover for $\beta F_c/N$ from $\sim \phi$ to $\sim \phi^2$ behavior, as ϕ is increased.

In an attempt to clarify the utility of the above three different approaches, Cacciuto and Luijten⁴⁷ have computed the free energy of a chain confined inside a spherical cavity and argued

that $\beta F_c/N \sim \phi^{1.28}$ is in close agreement with the fluctuation part [the second term on the right-hand side of Eq. (5)]. The authors have labeled this behavior as the revised blob scaling prediction. However, a closer inspection of their simulation data shows a crossover from ϕ to ϕ^2 behavior as the monomer concentration is increased. This is actually in agreement with the expectation from the mean field contribution given by Eq. (8).

In view of the above discussion, it is ideally desirable to derive the free energy of tie and tail chains in confinement by explicitly accounting for chain entropy, two- and three-body excluded volume interactions, and fluctuations arising from correlations among entropy and enthalpy. In this paper, however, strong confinement results in high monomer concentrations and so the fluctuation term can be ignored. To leading order, the confinement free energy will be given by a Flory-type approach in which the entropic and excluded volume effects are assumed to be additive. Thus, the entropic contributions to the free energy can be calculated for an ideal Gaussian chain and added to the enthalpic contributions from the excluded volume interactions. This approach is further validated by both the quantitative and qualitative agreement with our simulations results, as discussed in Sec. IV. We note there is currently no study of how the fluctuations terms vary when one or both ends of the chain are tethered at a specific point. Thus our theoretical approach is at the cutting edge for this specific problem, and future work is necessary to further study the free energy fluctuations with tethering.

The derivation of the tie and tail free energies using the Flory-type argument is founded in previous theoretical work^{25,43,44} and for completeness, is given in Sec. S-I of the [supplementary material](#). Here, we overview the steps. For the entropic contributions, we start with the Green's function for a chain confined in a spherical chamber; the tail (tie) partition sum is constructed by considering one (both) end(s) of the chain to be tethered at a distance a away from the surface of the sphere. In our theory, $0 < a \lesssim l_k$ is necessary since by construction if the chain end is placed directly on the chamber surface, the Green's function will vanish. While a more proper numerical calculation would involve solving for the Green's function in the presence of a hole on the surface, no analytical solution exists. Additionally, this sort of approximate theory has been repeatedly used with success to describe the capture and absorption of polymer chains.^{25,52}

In calculating the partition sums, the degrees of freedom associated with free ends are integrated out. Additionally, we assume that the chambers are randomly oriented, allowing for angular averaging over the positions of any tether points. Finally we employ the ground state dominance (GSD) approximation to simplify the resulting sum in the partition function.^{23,25} The GSD approximation is valid for $m \gtrsim 10$. We have performed numerical tests of its validity and confirmed that it is appropriate for our calculations. Even for the cases with $m \lesssim 10$, the GSD provides a first approximation to the free energy and a full theoretical description is a simple numerical extension of our calculation.

Free energy expressions are constructed by taking the log of the corresponding partition sum. As discussed above,

we capture the role of excluded volume under a Flory-like approach; at first order, we assume that the chain conformational entropy with repulsions can be well approximated by the Gaussian result and simply add the enthalpic contributions due to the excluded volume interactions.⁵³ The tail and tie free energies are hence

$$\begin{aligned}\beta F_{\text{tail}}(m_i) &= -\log \left[\frac{2a}{R_s} \right] + \frac{\pi^2 l_k^2 m_i}{6R_s^2} + \frac{w m_i^2}{R_s^3}, \\ \beta F_{\text{tie}}(m_i) &= -\log \left[\frac{\pi a^2 l_k^3}{2R_s^5} \right] + \frac{\pi^2 l_k^2 m_i}{6R_s^2} + \frac{w m_i^2}{R_s^3},\end{aligned}\quad (9)$$

where $w = 2B_2$ is the excluded volume parameter and B_2 is the second virial coefficient for the polymer segments; the segment–segment interaction potential is $\beta U(r) = w\delta(\vec{r})$. The variable a is the distance away from the surface of the sphere that the chain is tethered. Note that the free energies are only weakly dependent on the tether distance.

Combining Eqs. (1) and (9) with the constraint that the total chain length is fixed, $N = \sum_{i=1}^{n_c} m_i$ yields

$$\begin{aligned}\beta F(n_c, \{m_i\}) &= \sum_{i=1, n_c} \beta F_{\text{tail}}(m_i) + \sum_{i=2}^{n_c-1} \beta F_{\text{tie}}(m_i) \\ &= -2 \log \left[\frac{2a}{R_s} \right] - (n_c - 2) \log \left[\frac{\pi a^2 l_k^3}{2R_s^5} \right] + \frac{\pi^2 l_k^2 N}{6R_s^2} \\ &\quad + \frac{w}{R_s^3} \left[\sum_{i=1}^{n_c-1} m_i^2 + \left(N - \sum_{i=1}^{n_c-1} m_i \right)^2 \right].\end{aligned}\quad (10)$$

Equation (10) is the foundation for our equilibrium and dynamics theories.

A. Equilibrium properties

For the equilibrium properties, we are primarily interested in the number of chambers, n_c , that the chain will divide into and how the segments are distributed among these occupied chambers. In order to understand this, we minimize the conditional free energy of Eq. (10) with respect to the segment distribution $\{m_i\}$ and the number of occupied chambers n_c .

To minimize with respect to the segment distribution, one could calculate the derivative of the free energy for each m_i and simultaneously solve the resulting coupled equations. However by inspection of Eq. (10), it is clear that all of the m_i 's enter in the same manner. In other words, under the GSD, there is no difference in the free energy of tail and tie chambers up to constants. This symmetry allows one to immediately identify that the chain will equally partition into the occupied chambers; $m_i = m_j \equiv m_{eq}$, where $m_{eq} = N/n_c$. Under these conditions, the free energy becomes

$$\begin{aligned}\beta F_{\text{GSD}}(n_c) &= -2 \log \left[\frac{2a}{R_s} \right] - (n_c - 2) \log \left[\frac{\pi a^2 l_k^3}{2R_s^5} \right] \\ &\quad + \frac{\pi^2 l_k^2 N}{6R_s^2} + \frac{w}{R_s^3} \frac{N^2}{n_c}.\end{aligned}\quad (11)$$

To determine the number of chambers the chain will occupy, the free energy in Eq. (11) is minimized with respect to n_c . Solving $\partial \beta F_{\text{GSD}} / \partial n_c = 0$ yields

$$n_c = \left(\frac{w}{R_s^3} \right)^{1/2} \left(\log \left[\frac{2R_s^5}{\pi a^2 l_k^3} \right] \right)^{-1/2} N. \quad (12)$$

Equation (12) and $m_{eq} = N/n_c$ are the primary results of the equilibrium packing theory. The number of occupied chambers grows linearly with chain length. Additionally by either increasing the chamber size (via R_s) or weakening the chain repulsions (via w), we find that fewer chambers are occupied since more segments can pack into each chamber. These results capture maximal segmental packing in each chamber—given the ratio R_s^3/w is proportional to the ratio of the chamber volume to the “excluded” volume of a segment—with an additional logarithmic correction due to the entropic cost of creating ties. Finally note that when Eq. (12) predicts $n_c \leq 1$, the entire chain packs into a single chamber. In this case, the number of beads occupying that chamber is determined solely by the chain length, $m = N$.

As a final characterization of the equilibrium packing of the chain, we can estimate the chain radius of gyration R_g , defined via^{33,34}

$$R_g^2 = \frac{1}{2N^2} \sum_{\alpha, \gamma=1}^N \left\langle (\vec{R}_\alpha - \vec{R}_\gamma)^2 \right\rangle, \quad (13)$$

where $\vec{R}_\alpha$ is the position of the α th bead on the polymer chain. Rather than working this quantity out explicitly, which is extremely complex and cumbersome, a simple scaling argument can be made. Given the chain fully occupies n_c chambers, the size of the chain can be approximated by a self-avoiding walk of n_c steps with step length $2R_s$, the chamber diameter. Given this, the radius of gyration is

$$R_g \sim 2R_s n_c^\nu \sim 2R_s \left(\frac{w}{R_s^3} \right)^{\nu/2} \left(\log \left[\frac{2R_s^5}{\pi a^2 l_k^3} \right] \right)^{-\nu/2} N^\nu, \quad (14)$$

where in the second proportionality, Eq. (12) has been employed. The exponent ν is the size scaling for the desired chamber arrangement. For randomly oriented chambers, the self-avoiding walk value, $\nu = 0.6$, is required.³⁴ On the other hand, for a linear arrangement of chambers, the rigid rod value, $\nu = 1.0$, is appropriate. Hence the scaling dependence of the radius of gyration is influenced by the structure of the porous environment.

B. Chain dynamics

A full theoretical understanding of chain dynamics in porous environments is extremely complex and would involve solving the Rouse model with non-trivial boundary conditions due to the confinement potential. As in the models of entangled polymers and reptation,^{19,21,22,29,30,33,34} to make progress on this front, one must inject some physical intuition to the problem and consider a simplified approach motivated by physical assumptions. The test of any such theory will be comparison to existing experiments and simulations.

To understand dynamics in the proposed porous environment, we adopt an approach based on entropic barriers^{23–26}

and transition state theory.⁵⁴ In order for the chain to move to neighboring chambers, one end of the chain must be captured in the small pore and then the chain must thread from one set of chambers to the next. For the single chamber occupancy case, $n_c = 1$, the dynamics problem reduces to that previously studied in the context of translocation.^{23–26} For multi-chamber occupancy, this threading is very complex and will involve many chambers concurrently. For the sake of simplicity, in this work, we assume that the dynamics are localized to the chain end such that the threading of the chain into a new chamber only affects the occupancy of the tail chamber and all other chambers remain unaffected. While this assumption may be drastic, we have verified in the simulations that to first order, it is correct (see Sec. IV). Future work can relax this assumption, using a perturbative approach.

The capture of a chain end at a pore opening has an associated barrier due to the entropy loss of tethering one end of the chain to the surface of the spherical chamber. For single chamber occupancy, initially both ends of the chain are free, and when capture occurs, one end becomes tethered. For the multi-chamber case, only one end of the chain is initially free, and upon capture, the tail becomes a tie. In both cases, the difference in free energy between the initial and final states gives the capture barrier. Using the expressions for the free energies, Eq. (9), the capture barrier is hence given by

$$\beta\Delta F_{cap} = \log \left[\frac{4R_s^4}{\pi a l_k^3} \right]. \quad (15)$$

Note that the capture barrier is independent of whether the chain occupies a single chamber or many chambers, which is due to the ground state dominance approximation.

To construct the free energy associated with threading, consider the case where m segments have already moved into the new chamber. For $n_c = 1$, the free energy is that associated with a chain having two tails of lengths m and $N - m$,

$$\beta F_{thread}(m, n_c = 1) = -2 \log \left[\frac{2a}{R_s} \right] + \frac{\pi^2 l_k^2 N}{6R_s^2} + \frac{w}{R_s^3} (m^2 + (N - m)^2). \quad (16)$$

For multiple chambers, the free energy is associated with a chain having a tail of length m , a tie of length $m_{eq} - m$, and $n_c - 1$ unaffected chambers,

$$\begin{aligned} \beta F_{thread}(m, n_c > 1) = & \beta F_0 - \log \left[\frac{2a}{R_s} \right] - \log \left[\frac{\pi a^2 l_k}{2R_s^5} \right] \\ & + \frac{\pi^2 l_k^2 m_{eq}}{6R_s^2} + \frac{w}{R_s^3} (m^2 + (m_{eq} - m)^2), \end{aligned} \quad (17)$$

where F_0 is the free energy associated with the remaining $n_c - 1$ chambers, which are unperturbed.

In both cases, Eqs. (16) and (17), the m dependence of the threading free energy is quadratic and symmetric around the minimum at the half way point of threading, $m = m_{eq}/2$. The barrier for threading will therefore be given by the difference

between this half way point and the fully threaded point, which is

$$\beta\Delta F_{thread} = \frac{w m_{eq}^2}{2R_s^3} = \frac{1}{2} \log \left[\frac{2R_s^5}{\pi a^2 l_k^3} \right]. \quad (18)$$

Given that $m_{eq} = N$ in the limit of single chamber occupancy, the expression in the first equality is general. In the second equality, the equilibrium result for the multi-chamber occupancy, Eq. (12), is employed. The complex interplay between the equilibrium packing and threading dynamics interestingly leads to a barrier which is solely associated with the entropic cost the chain must endure to form a tail. While the results of Eqs. (16)–(18) are dependent on the GSD assumption, we have verified that the qualitative form of the barrier does not vary by much in a more complete numerical treatment.

Given capture, Eq. (15), and the subsequent threading, Eq. (18), happen in series, the barriers can be added. Hence the net barrier for motion is $\beta F_{tot} = \beta\Delta F_{cap} + \beta\Delta F_{thread}$. From the associated equations, it is clear that the net barrier will increase with the sphere radius as there is a higher entropic penalty for both capturing and maintaining an extra tie. This is consistent with the intuition that larger chambers will act as entropic traps for the chain. Employing numbers relevant to the simulations (determined from the equilibrium results; see Sec. IV A), we find that this barrier is in the range $F_{tot} = 10\text{--}20 k_B T$. Such a large barrier is consistent with our simulation results for $R_s \geq 2\sigma$, where σ is the Lennard–Jones (LJ) length scale for our simulated beads. Note that in the small chamber limit, the above analysis must break down, as only a few segments occupy each chamber. In this limit, further theoretical analysis must be considered, which is left to future work.

III. SIMULATION METHODS

In addition to developing a theoretical understanding of a chain confined to this simplified porous environment, we also performed Langevin dynamics simulations as verification of the theoretical ideas. For our system of interest, hydrodynamics will largely be screened; both polymer–polymer and polymer–wall screening effects will come into play at the high concentrations of interest, and thus hydrodynamic interactions should not play a major role. In turn, we ignore hydrodynamic forces (apart from drag) in all of the following simulations. Future simulations can be done to verify this approximation and study the screening effects more completely.

To model the polymer chain in the simulations, we adopt the standard bead-spring model of Kremer and Grest.^{55,56} In this model, the intra-molecular bonding potential is given by the finite extensible nonlinear elastic (FENE) potential^{55,56}

$$U_{FENE}(r) = -\frac{kR_{max}^2}{2} \log \left[1 - (r/R_{max})^2 \right], \quad (19)$$

where k is the spring constant and R_{max} is the maximum bond length. For small separations $r \ll R_{max}$, Eq. (19) reduces to a harmonic bond $U_{FENE} \approx kr^2/2$ and the effective Kuhn length can be estimated as $l_k \approx (3k_B T/k)^{1/2}$.

In addition to the bonding potential, each bead repels every other bead with the truncated Lennard–Jones (LJ) or Weeks–Chandler–Anderson (WCA) potential,^{57,58}

$$U_{WCA}(r) = \begin{cases} 4\epsilon \left[\left(\frac{\sigma}{r} \right)^{12} - \left(\frac{\sigma}{r} \right)^6 + \frac{1}{4} \right], & r < 2^{1/6}\sigma, \\ 0, & r \geq 2^{1/6}\sigma, \end{cases} \quad (20)$$

where ϵ and σ are the Lennard–Jones energy and length scales, respectively. Finally, a thermal (random) force and the corresponding friction force (Γ is the friction constant) were applied to each bead. The simulations were performed in reduced units—lengths in units of σ , energies in units of ϵ , and times in units of $\tau \equiv \sigma(m/\epsilon)^{1/2}$, where m is the mass of a single bead. Under these units, the standard Kremer–Grest parameter selection was employed:^{55,56} $k_B T = \epsilon$, $R_{max} = 1.5\sigma$, $k = 30\epsilon/\sigma^2$, and $\Gamma = 0.5m/\tau$. This chain model has been widely characterized in simulations and has been shown to mimic real, uncrossable chains.

In addition to the chain, we model the confinement geometry as consisting of linearly arranged spherical chambers of radii (R_s) connected by short, narrow cylindrical passages, $R_c = L_c = \sigma$. The linear arrangement of the sphere allows the system to be quasi-infinite along the chamber axis (z -direction). Rather than explicitly employing beads for the boundary which would drastically slow down the simulation, or employing a reflection rule which might not properly capture the physics for stochastic motion, we adopt a simplified boundary condition. For each bead, we find the point on the boundary which is the closest and implement a WCA repulsion between the bead and that point, Eq. (20). This boundary condition physically captures the proper confining nature of the chamber walls; however under very tight confinement, it may overestimate the strength of such confining forces. We expect no qualitative difference in our simulation and one with a more explicit boundary. Furthermore, we have verified that the results for single bead motion in such a confined environment agree with expectations.

To solve for the motion of the polymer, we employ a second order Langevin integrator for each bead^{59–61} (see Sec. S-II of the [supplementary material](#) for details). This method is the generalization of the velocity Verlet integration scheme to a stochastic equation of motion. We employ a time step $\Delta t = 0.01\tau$. The chain is initialized in a linear configuration along the chamber axis, with velocities drawn at random from a Maxwell–Boltzmann distribution.⁶² The chains are then allowed to equilibrate for 10^7 time steps, until $t = 10^5\tau$. In each case, equilibration is ensured by verifying that the chain radius of gyration R_g in the z -direction (along the chamber axis) has plateaued. The final time step of these simulations was analyzed to characterize the equilibrium properties of the system. To study dynamics, a second set of simulations was performed with the equilibrated states as input. These simulations were performed for additional 10^7 time steps.

We performed simulations to study both the chamber size dependence and the chain length dependence on packing and dynamics. For the former, we fixed the chain to $N = 50$ beads and investigated chamber radii in the range $R_s = 1.0\sigma$ – 5.0σ . Note that in the case $R_s = 1.0\sigma$, the confinement geometry

is purely cylindrical since $R_s = R_c$. To study the chain length dependence, we considered two chamber sizes $R_s = 2.0\sigma$ and 5.0σ and varied the number of beads on the chain N from 10 to 200. In all cases, 120 independent simulations were run and averaged over for the analysis.

IV. SIMULATION RESULTS

A. Equilibrium properties

We focus on three equilibrium properties: (i) the number of beads in (occupancy of) the tail and tie chambers, (ii) the average number of chambers occupied, and (iii) the average radius of gyration along the axis of the chambers. The former two properties are calculated from the final time step of the equilibration simulation, with statistics averaged over 120 independent simulations. The radius of gyration as a function of time is averaged over the 120 simulations, and it is verified that proper equilibration has occurred. The equilibrium R_g is then calculated as a time averaged value over the equilibrated plateau region of these results.

In all simulations, histograms of the average occupancy of the tail and tie chambers were generated (characteristic examples are shown in Fig. S1 of the [supplementary material](#)). In all cases, the occupancy shows strong Gaussian behavior, and the average tail occupancy is equal to the average tie occupancy within a standard deviation. This implies that the chain equally partitions between occupied chambers, which is consistent with the theoretical predictions of Sec. II A.

Given the equipartitioning of the chain, the equilibrium chamber statistics are fully determined by the number of occupied chambers n_c (corresponding to an occupancy $m_{eq} = N/n_c$). The main frame of Fig. 2 shows the number of occupied chambers, n_c , as a function of the number of beads on the chain, N . Two chamber radii are shown $R_s = 2.0\sigma$ (purple squares) and 5.0σ (orange circles). Additionally error bars showing the standard deviations are shown and are smaller than the point

FIG. 2. Equilibrium results for simulation (points) and theory (dashed lines). Main: The number of occupied chambers n_c of the polymer chain as a function of chain length N . The purple squares (orange circles) show the simulation results for chamber radius $R_s = 2.0\sigma$ (5.0σ). The dashed curves show the theoretical predictions of Eq. (12) with $a = 0.1\sigma$, $l_k = 10^{-1/2}\sigma$, and $w = 1.4\sigma^3$. Inset: The radius of gyration R_g in units of Lennard–Jones length scale σ for the same systems with theoretical predictions given by Eq. (14) with $\nu = 1.0$.

size. For both chamber sizes, the number of occupied chambers increases linearly with N . This is consistent with the theoretical result of Eq. (12). Quantitative theoretical comparisons can be made by employing the Kuhn length determined from the simulated bonding potential, $l_k = 10^{-1/2}\sigma$, a tethering distance of $a = 0.1\sigma$, and by fitting Eq. (12) to the simulation results via the excluded volume parameter w . The fits with $w = 1.4\sigma^3$ are shown by the corresponding dashed lines in Fig. 3. The simulated and theoretical results show excellent agreement, and the predicted excluded volume parameter is reasonable for a WCA-like repulsive chain.

Additionally, we note that these fits are only weakly dependent on the specific value of the tether distance a employed in the theory. As previously stated, the tethering distance is theoretically necessary since the pores are not explicitly included in the calculation of the entropic terms and also should satisfy $a \lesssim l_k$. The predicted free energies and equilibrium results are only logarithmically dependent on the choice of a , as shown in Eqs. (10) and (12). Furthermore, the fits shown in Fig. 3 are independent of the choice of the tethering parameter for $a \leq 0.1\sigma$. More surprisingly, if a large value of the tethering parameter is chosen, $a = \sigma$, the fits in Fig. 3 can be reproduced with only a minimal change in the excluded volume parameter to $w = 1.2\sigma^3$. This robustness to the tethering distance shows that our theory is predictive, given an accurate measure of the Kuhn length and excluded volume of the chain.

In addition to the number of occupied chambers, the radius of gyration R_g along the axis of the chambers is shown in the inset of Fig. 2 as a function of N for the same systems. For both chamber sizes, R_g increases linearly with N for chains that occupy multiple chambers (all N for $R_s = 2.0\sigma$ and $N > 50$ for $R_s = 5.0\sigma$). This linearly scaling distinctly differs from the scaling of the unconfined chain and is strongly dependent on the chamber arrangement. A more quantitative theoretical comparison is calculated via Eq. (14) with $\nu = 1.0$ and the same parameters as used for n_c . Our simulation results show excellent agreement with the theoretical results,

FIG. 3. Equilibrium results for simulation (points) and theory (dashed lines) at constant chain length $N = 50$ as a function of sphere size R_s relative to the Lennard-Jones length scale σ . Main: The number of occupied chambers n_c . The dashed curve shows the theoretical predictions of Eq. (12) with $a = 0.1\sigma$, $l_k = 10^{-1/2}\sigma$, and $w = 1.4\sigma^3$. Inset: The radius of gyration R_g in units of Lennard-Jones length scale σ for the same systems with theoretical predictions given by Eq. (14) with $\nu = 1.0$. For $R_s \leq 1.2\sigma$, the radius of gyration is given by the rigid rod value $R_g = N\sigma/\sqrt{12}$.

which further confirms the free energy expression derived in Sec. II A.

To investigate the role of the chamber size on the equilibrium properties, we also performed simulations of chains with a constant number of beads, $N = 50$, in various confined environments. For these simulations, we focus on small chamber sizes $R_s = 1.0$ – 5.0σ . Note that when $R_s = R_c = \sigma$, the confinement is purely cylindrical (no chambers) and the chain behaves as a rigid rod. As R_s is increased, the chambers slowly grow in and chain-like behavior is slowly recovered.

Figure 3 shows the equilibrium results of these simulations. The main frame shows the number of occupied chambers as a function of the chamber radius. No result is shown for $R_s = \sigma$ (pure cylinder) since there are no chambers. As the chamber size increases, the simulations (purple squares) show a rapid decrease in the number of occupied chambers. This decrease is accurately captured by the theoretical prediction of Eq. (12), with the same parameters as employed above. The inset of Fig. 3 shows the radius of gyration along the chamber axis for the same simulations. The $R_s = 5.0\sigma$ result is not shown, as the chain occupies a single chamber and R_g is equivalent to that of an unconfined chain. For $R_s = 1.5$ – 2.0σ , the chain occupies many chambers and the theoretical expression from Eq. (14) ($\nu = 1.0$, dashed curve) roughly agrees with the results. When $R_s \leq 1.25\sigma$, the chambers do not provide enough space for the chain to explore, and so the chain behaves more like a rigid rod with $R_g = N\sigma/\sqrt{12}$. This prediction is shown by the plateau of the dashed curve. The primary reason for the differences between the theoretical and simulation results is that Eq. (14) is a quasi-scaling argument for the radius of gyration and cannot properly capture the crossover to the rod scaling behavior.

Overall the simulation results for the N and R_s dependence of the equilibrium properties of the confined chain (Figs. 2 and 3) show excellent qualitative and quantitative agreement with the predictions from the free energy expression in Eq. (10). This confirms the theoretical ideas at the equilibrium level. Furthermore, this provides foundations for studying the dynamics of the confined chains in both the simulation and theoretical frameworks.

B. Chain dynamics

In order to study the dynamical properties of the chain, further simulations starting from the equilibrated states were performed. From these simulations, the center of mass (CM) and segmental (seg) mean square displacements (MSDs) along the chamber axis ($\hat{z}$) were calculated via⁵⁴

$$\begin{aligned} \mu_{CM}(t) &\equiv \langle (z_{CM}(t_0 + t) - z_{CM}(t_0))^2 \rangle_{t_0}, \\ \mu_{seg}(t) &\equiv \frac{1}{N} \sum_{i=1}^N \langle (z_i(t_0 + t) - z_i(t_0))^2 \rangle_{t_0}, \end{aligned} \quad (21)$$

where $z_{CM}(t)$ and $z_i(t)$ are the positions of the center of mass and the i th bead in the $\hat{z}$ direction at time t , respectively. The square brackets $\langle \dots \rangle_{t_0}$ denote both an average over the initial time t_0 and over the 120 independent simulations. For the segmental MSD, a further average over all of the beads along the chain was also performed—shown explicitly by the sum

FIG. 4. The center of mass [CM, (a)] and segmental [seg, (b)] dynamics for polymer chains with chamber radius $R_s = 5\sigma$. Main: The mean square displacements (MSDs, μ) in units of the Lennard-Jones length scale σ as a function of time in simulation units t/τ . The curves for chain lengths $N \leq 40$ all roughly overlap. For $N \geq 50$, at $t = 10^5 \tau$, the successively larger MSD curves correspond to higher N . The dashed lines show various power laws mentioned in the main text. Inset: The numerical derivative α , capturing the effective power law behavior for the MSD; $\mu \sim t^\alpha$.

in Eq. (21). To further analyze the dynamics, the time dependence of the MSDs was characterized by an effective power law behavior, $\mu \sim t^\alpha$, where the power α is calculated from the numerical derivative,

$$\alpha = \frac{d \log \mu}{d \log t}. \quad (22)$$

We emphasize that the manner in which α is defined does not indicate true power law behavior, as in many cases, the effective power law does not extend over a decade. Rather, α is a numerical derivative that captures the local dynamical details of the MSD and in certain limits, can extract the true power law behavior. The MSD results for the dynamics of various confined chains are shown in Figs. 4 and 5 and in Fig. S2 of the [supplementary material](#).

Figure 4 shows the CM (a) and segmental (b) dynamics (along the chamber axis) for chains of various lengths ($N = 10$ –200) in chambers with sphere radius $R_s = 5\sigma$. The main frames show the MSDs, and the insets show the effective powers α . Frame (a) shows the center of mass MSD normalized by σ^2/N , and several clear regimes of dynamics occur. At short times $t \lesssim 10\tau$, all curves collapse to the expected ballistic behavior, $\mu_{CM} \sim t^2$ (black dotted curve). At $t = 10\tau$, a crossover occurs to one of the two behaviors: for small chain lengths $N \lesssim 40$, the CM MSD immediately plateaus, while for $N > 50$, the CM MSD first relaxes diffusively ($\mu_{CM} \sim t$, red dotted curve) before eventually plateauing. Due to very slow dynamics, the terminal relaxation regime was not observed on

the simulation time scales for any of these simulations. The effective power law behavior, α (inset), confirms this analysis. Note that in all plots of the effective power law, the data get very noisy near the end of simulation runs since there are fewer statistics for the MSD and is further exacerbated by taking the numerical derivatives.

The segmental dynamics for the same simulations show similar behavior. The primary difference being that the ballistic behavior ($\mu \sim t^2$, black dotted line) is much shorter and is followed by super-diffusive, non-ballistic behavior ($\mu \sim t^{1.8}$, blue dotted line). Beyond $t = \tau$, the super-diffusive behavior crosses over to a plateau either immediately ($N \lesssim 40$) or after a brief sub-diffusive regime ($N > 50$, $\mu \sim t^{0.5}$, green dotted line). Again these regimes are supported by the effective power laws shown in the inset.

The two distinct behaviors in the intermediate time regime ($\tau \lesssim t < 10^5$) can be physically understood by noting that for $R_s = 5\sigma$, the crossover from single chamber to multi-chamber occupancy occurs at $N \approx 50$, the chain length where the dynamic behavior transitions. Hence for $N < 50$, when the chain occupies a single chamber, the dynamic plateau comes almost solely from the capture barrier. Additionally, no intermediate Rouse-like regime^{33,34} is observed as the chain very quickly equilibrates for such short chain lengths. On the other hand when the chain occupies many chambers, an extended sub-diffusive (segmental) or diffusive regime emerges. This regime can be interpreted as the relaxation of the Rouse modes^{33,34} in the confined environment. This conclusion is

FIG. 5. The same as Fig. 4 but for constant chain length $N = 50$ for various chamber radii R_s/σ . For frame (a), at $t/\tau = 10^4$, the curves with smaller MSDs represent larger chamber size R_s . For frame (b), the same is true, except for $R_s = 5\sigma$, which is the curve with the larger plateau at $t/\tau = 10^4$. The dashed curves represent various power laws discussed in the main text.

primarily confirmed by the effective power α for segmental dynamics [Fig. 4(b), inset]. Focusing on the longest chain, $N = 200$ (pink curve), for $t > 10\tau$, the effective power drops to $\alpha \approx 0.25$ and then slowly recovers to $\alpha \approx 0.5$ over the next few decades in time. These powers are indicative of Rouse-like motion in a confining tube and are predicted and observed in entangled polymer melts.^{21,22,29,33,34} In summary, when the chain is confined in many chambers, the Rouse modes of the chain fully relax before the emergence of a dynamic plateau due to the entropic barriers associated with capture and further motion.

This interpretation of the chain dynamics in the context of a confined Rouse chain is further confirmed by studying the dynamics of chains with various lengths in chambers with radii $R_s = 2\sigma$ (Fig. S2 of the [supplementary material](#)). In this case, all of the studied chains occupy multiple chambers, and hence, the confined Rouse behavior is expected for all chains. The results shown in Fig. S1 confirm this behavior, with all chains passing through a confined Rouse-like regime, before the MSD plateaus.

To investigate the role of the confining chamber size, R_s , on the dynamics, we studied chains of $N = 50$ beads under various confining geometries $R_s = 1.0\text{--}5.0\sigma$. The MSDs for these simulations are shown in Fig. 5. For $R_s = \sigma$, the confinement is purely cylindrical and the chain behaves as a rigid rod. In this case, the CM and segmental MSDs show only two regimes, ballistic ($t \lesssim \tau$, $\mu \sim t^2$, black dotted lines) and 1D long time diffusion ($t \gtrsim \tau$, $\mu \sim t$, purple dotted lines), as expected. As the chamber size is increased, $\sigma < R_s \leq 1.5\sigma$, chain-like behavior is recovered and an intermediate Rouse regime is captured between the ballistic and diffusive regimes. This regime is characterized by additional power laws: $\mu_{CM} \sim t^{0.75}$ [teal dotted line in Fig. 5(a)] and $\mu_{seg} \sim t^{0.5}$ [teal dotted line in Fig. 5(b)]. Given the chamber size is small for $\sigma < R_s \leq 1.5\sigma$, the entropic barrier for capture and threading is low since only a few segments occupy each chamber. Hence, in these cases, the terminal diffusive regime is observed. For chamber sizes $R_s \geq 1.75\sigma$, the entropic barrier is large enough to temporarily localize the chain. In the case $R_s = 1.75\sigma$ (green curves), both localization and terminal relaxation are captured; however for larger chambers, the terminal relaxation regime is not observed since the entropic barrier is large and dynamics are extremely slow.

Finally we note that for large chambers, the segmental dynamics undergo a super-diffusive but non-ballistic regime at

intermediate times ($10^{-1}\tau < t \lesssim 5\tau$); however as the chamber size is reduced, this regime crosses over to a diffusive-like regime (pink dotted line). From this, we believe that this super-diffusive regime is tied to ballistic motion of the chain under the confined environment; however, an exact mechanism still eludes the authors.

The average segmental and CM MSDs characterize the global dynamics of the chain. In order to investigate dynamics at a more local level, we track the average occupancy of each chamber as a function of time. This occupancy number is directly related to the density of beads in each chamber, and hence this analysis is related to recent experimental investigations on density fluctuations of DNA in chambered environments.^{37–39} In order to align the chamber numbers in various simulations, we assign chamber 0 to the chamber which initially contains the center of mass of the chain. The chamber numbers increase sequentially in the $+z$ and $-z$ directions (along the chamber axis). After such alignment, the average number (over 120 simulations) of beads in each chamber, its occupancy $\langle m \rangle$, is investigated as a function of time.

Figure 6 shows the results for the average occupancy for chain length $N = 50$ and chamber radius $R_s = 1.50\sigma$. Figures S3 and S4 of the [supplementary material](#) show the results from several other cases. This case was specifically chosen since the chain reaches its terminal diffusion regime. Frame (a) shows the chambers to one side of the center of mass, while frame (b) shows the same chamber numbers (same color) on the opposite side of the center of mass. Note that dynamics are roughly symmetric on the two sides as expected. The small differences on the two sides can be attributed to statistical error and to the fact that the occupancy of a chamber includes the cylindrical pores attached toward the positive $\hat{z}$ -direction, which creates a small asymmetry in the analysis.

For the case shown in Fig. 6, initially the chain fully occupies the 13 chambers between -6 and $+6$. The ± 7 chambers are partially occupied, which arises due to fluctuations about the mean occupancy of the chain; simulations initially occupy either 14 or 15 chambers. As time proceeds, it is clear that beads leave chambers ± 6 and begin to enter chambers ± 7 and ± 8 , which are initially partially occupied and empty, respectively. As a specific example, consider a chain moving in the $+\hat{z}$ direction. As time progresses, the occupancy of chamber $+8$ will increase as the occupancy of chamber -6 decreases. This is clearly observed in the displayed results. Additionally these results show that the chain dynamics are mainly

FIG. 6. The average occupancy $\langle m \rangle$ as a function of time, in simulation units t/τ , for chambers in the (a) $-\hat{z}$ and (b) $+\hat{z}$ directions (along the axis of chambers). Chamber numbers are indicated in the legends, with chamber 0 corresponding to the chamber which contains the center of mass and positive chamber numbers corresponding to the $+\hat{z}$ direction. Here, the chain has $N = 50$ beads and the chamber radius is $R_s = 1.50\sigma$.

localized to the chain ends; chain motion requires density fluctuations in the tail chamber and possibly one neighboring chamber.

All in all, our dynamics simulations show evidence to support the theoretical picture outlined in Sec. II B. We observe that for large chamber sizes (when the GSD is most appropriate), dynamics display a hierarchy of sub-diffusive behavior tied to the relaxation of the Rouse modes and entropic trapping of chains, suggesting the presence of a barrier to motion. The terminal relaxation regime is not observed in all of the present simulations, preventing any direct evidence for the scaling behavior of the barrier. That being said, the picture of capture and threading cannot be far from the true nature of chain dynamics. Additionally, by investigating the dynamic occupancies of the simulations, we have confirmed that dynamics primarily occur at the chain ends, buttressing the theoretical assumption that only the tail chamber is affected when the chain moves. While the theoretical barriers of $10\text{--}20\ k_B T$ —yielding terminal relaxation time scales $\tau_t \sim \tau \exp(\beta \Delta F) \sim 10^4\text{--}10^8 \tau$ —seem reasonable for simulations with $R_s \geq 1.75\sigma$, the barrier cannot be this large for small chamber sizes. This breakdown of the theory is because for small chambers, only a few beads occupy each chamber, and hence the polymer based techniques employed are not valid. In future work, we plan to run longer simulations, allowing us to access the terminal relaxation regime, for which diffusion is ultimately expected, and more fully test the theoretical conclusions.

V. DISCUSSION AND CONCLUSIONS

In this work, we have developed a theoretical approach and performed Langevin dynamics simulations to study the equilibrium packing and subsequent dynamics of a polymer chain confined in a static porous environment. Theoretically, we calculate the free energy of a chain confined to many chambers under the assumption that only one portion of the chain is in each chamber; there are no loops. The equilibrium occupancy of the chain was determined by minimizing this free energy. For chain dynamics, the entropic barriers associated with capture and threading using the same free energy were calculated. In the simulations, the equilibrium and dynamic occupancies were analyzed as well as the center of mass and segmental mean square displacements.

For the equilibrium statistics of the chain, the theoretical predictions and the simulations agree both qualitatively and quantitatively. The chain equally partitions itself among occupied chambers, regardless of whether the chain ends or chain center are considered. Additionally, the occupancy number is primarily determined by optimal packing of the polymer segments, with a logarithmic entropic correction. The radius of gyration observed in the simulations also agrees well with a simple scaling argument and is highly dependent on the chamber structure.

For the dynamics, we observe multiple regimes including standard ballistic and Rouse regimes and a hierarchy of slow regimes due to entropic trapping of the chain. The slow regimes are characterized by a plateau in the mean square displacements, which is seen irrespective of the chain length for

large chamber sizes. Additionally investigations of the dynamics of the chamber occupancy indicate that motion is primarily initiated at the chain ends, having little effect on the center of the chain. This observation buttresses our theoretical assumption that only the tail chamber is modified when the chain moves. At small chamber sizes, $R_s < 1.75\sigma$, we know that this assumption must break down due to the small occupancy number in each chamber. In this regime, the theory can be easily extended in a perturbative manner to include further chambers.

Overall, our dynamic observations are similar to reptation in entangled systems,^{21,22,29,33,34} being initiated at the chain ends. However, the physical origin of confinement in the two cases is quite different, and hence the long time dynamics will depend on different system properties. In the future, we wish to extend the simulation time scales to probe the long time dynamics and more properly compare to the theoretical predictions. Additionally, the simulations can be extended to analyze the density correlations as in the recent experimental work.^{37–39} Theoretically, we will analyze the chain dynamics more completely in the presence of entropic traps. This work provides a foundation for more fully understanding chain dynamics in confined porous environments.

SUPPLEMENTARY MATERIAL

In [supplementary material](#), we include theoretical derivations and additional simulations results. Section S-I contains a complete derivation of the theoretical free energy employed in the main text. Section S-II outlines the derivation of the second order integration scheme employed for updating the Langevin equation in our simulations. Finally, Sec. S-III contains some additional simulation results. These include the equilibrium occupancy histograms (Fig. S1), the MSDs for systems with $R_s = 2\sigma$ (Fig. S2), and the dynamic occupancy number for other parameter values (Figs. S3 and S4).

ACKNOWLEDGMENTS

The authors of this paper acknowledge Di Jia and Sabin Adhikari for useful discussion of the theoretical approach and simulation results. This work was supported by the National Science Foundation (Grant No. DMR-1713696), the Air Force Office of Scientific Research (Grant No. FA9550-17-1-0160), and the National Institute of Health (Grant No. R01HG002776-15).

¹L. Durlfösky and J. F. Brady, *Phys. Fluids* **30**, 3329 (1987).

²J. D. Honeycutt and D. Thirumalai, *J. Chem. Phys.* **90**, 4542 (1989).

³J. Honeycutt, D. Thirumalai, and D. Klimov, *J. Phys. A: Math. Gen.* **22**, L169 (1989).

⁴A. Rahalkar and M. Muthukumar, *Macromolecules* **50**, 8158 (2017).

⁵D. Sean and G. W. Slater, *Electrophoresis* **38**, 653 (2017).

⁶G. W. Slater, C. Holm, M. V. Chubynsky, H. W. de Haan, A. Dubé, K. Grass, O. A. Hickey, C. Kingsbury, D. Sean, T. N. Shendruk, and L. Zhan, *Electrophoresis* **30**, 792 (2009).

⁷W. Zhang, Z. Tu, J. Qian, S. Choudhury, L. A. Archer, and Y. Lu, *Small* **14**, 1703001 (2018).

⁸M. R. Kessler, *Poly. Rev.* **52**, 229 (2012).

⁹Q. T. H. Shubhra, A. K. M. M. Alam, and M. A. Quaiyyum, *J. Thermoplast. Compos. Mater.* **26**, 362 (2013).

¹⁰P. Panorchan, D. Wirtz, and Y. Tseng, *Phys. Rev. E* **70**, 041906 (2004).

- ¹¹S. Hvidt and K. Heller, in *Physical Networks: Polymers and Gels*, edited by W. Burchard and S. Ross-Murphy (Elsevier, London, 1990), pp. 195–208.
- ¹²M. A. Meyers, P.-Y. Chen, A. Y.-M. Lin, and Y. Seki, *Prog. Mater. Sci.* **53**, 1 (2008).
- ¹³P. Park and W. Sung, *Int. J. Bifurcation Chaos* **8**, 927 (1998).
- ¹⁴R. J. Ellis, *Trends Biochem. Sci.* **26**, 597 (2001).
- ¹⁵S. A. Allison, H. Pei, and Y. Xin, *Biopolymers* **87**, 102 (2007).
- ¹⁶E. M. Johnson, D. A. Berk, R. K. Jain, and W. M. Deen, *Biophys. J.* **70**, 1017 (1996).
- ¹⁷N. Fatin-Rouge, K. J. Wilkinson, and J. Buffle, *J. Phys. Chem. B* **110**, 20133 (2006).
- ¹⁸G. B. Salieb-Beugelaar, K. D. Dorfman, A. van den Berg, and J. C. T. Eijkel, *Lab Chip* **9**, 2508 (2009).
- ¹⁹G. W. Slater, J. Rousseau, and J. Noolandi, *Biopolymers* **26**, 863 (1987).
- ²⁰B. H. Zimm and O. Lumpkin, *Macromolecules* **26**, 226 (1993).
- ²¹P. G. de Gennes, *J. Chem. Phys.* **55**, 572 (1971).
- ²²M. Doi, *J. Poly. Sci.: Poly. Phys. Ed.* **21**, 667 (1983).
- ²³M. Muthukumar, *Polymer Translocation* (CRC Press, Taylor & Francis Group, Boca Raton, FL, USA, 2011).
- ²⁴M. Muthukumar, *J. Non-Cryst. Solids* **131-133**, 654 (1991).
- ²⁵M. Muthukumar, *Adv. Chem. Phys.* **149**, 129 (2012).
- ²⁶M. Muthukumar and A. Baumgärtner, *Macromolecules* **22**, 1937 (1989).
- ²⁷D. Rodbard and A. Chrambach, *Proc. Natl. Acad. Sci. U. S. A.* **65**, 970 (1970).
- ²⁸A. G. Ogston, B. N. Preston, and J. D. Wells, *Proc. R. Soc. A: Math., Phys. Eng. Sci.* **333**, 297 (1973).
- ²⁹M. Rubinstein, *Phys. Rev. Lett.* **59**, 1946 (1987).
- ³⁰G. W. Slater and S. Yan Wu, *Phys. Rev. Lett.* **75**, 164 (1995).
- ³¹R. Zwanzig, *J. Phys. Chem.* **96**, 3926 (1992).
- ³²A. P. Thompson and E. D. Glandt, *Macromolecules* **29**, 4314 (1996).
- ³³M. Doi and S. F. Edwards, *The Theory of Polymer Dynamics* (Clarendon, Oxford, UK, 1986).
- ³⁴M. C. Rubinstein and R. H. Colby, *Polymer Physics* (Oxford University Press, Oxford, UK, 2003).
- ³⁵D. K. Lubensky and D. R. Nelson, *Biophys. J.* **77**, 1824 (1999).
- ³⁶D. Jia and M. Muthukumar, *Nat. Commun.* **9**, 2248 (2018).
- ³⁷A. R. Klotz, H. W. De Haan, and W. W. Reisner, *Phys. Rev. E* **94**, 042603 (2016).
- ³⁸A. R. Klotz, M. Mamaev, L. Duong, H. W. De Haan, and W. W. Reisner, *Macromolecules* **48**, 4742 (2015).
- ³⁹A. R. Klotz, L. Duong, M. Mamaev, H. W. De Haan, J. Z. Chen, and W. W. Reisner, *Macromolecules* **48**, 5028 (2015).
- ⁴⁰N. Easwar, *Macromolecules* **22**, 3492 (1989).
- ⁴¹P. A. Gurnev, C. B. Stanley, M. A. Aksoyoglu, K. Hong, V. A. Parsegian, and S. M. Bezrukov, *Macromolecules* **50**, 2477 (2017).
- ⁴²E. J. Saltzman and M. Muthukumar, *J. Chem. Phys.* **131**, 214903 (2009).
- ⁴³M. Muthukumar, *J. Chem. Phys.* **118**, 5174 (2003).
- ⁴⁴C. Kong and M. Muthukumar, *J. Chem. Phys.* **120**, 3460 (2004).
- ⁴⁵R. Kumar and M. Muthukumar, *J. Chem. Phys.* **131**, 194903 (2009).
- ⁴⁶M. Muthukumar, *Phys. Rev. Lett.* **86**, 3188 (2001).
- ⁴⁷A. Cacciuto and E. Luijten, *Nano Lett.* **6**, 901 (2006).
- ⁴⁸P. G. de Gennes, *Scaling Concepts in Polymer Physics* (Cornell University Press, Ithaca, NY, USA, 1979).
- ⁴⁹M. Muthukumar and S. Edwards, *J. Chem. Phys.* **76**, 2720 (1982).
- ⁵⁰M. Muthukumar, *J. Chem. Phys.* **85**, 4722 (1986).
- ⁵¹S. Edwards, *Proc. Phys. Soc.* **88**, 265 (1966).
- ⁵²E. Eisenriegler, *Polymers Near Surfaces* (World Scientific Publishing, River Edge, NJ, USA, 1993).
- ⁵³P. J. Flory, *Statistical Mechanics of Chain Molecules* (Hanser Publishers, Cincinnati, OH, USA, 1989).
- ⁵⁴R. Zwanzig, *Nonequilibrium Statistical Mechanics* (Oxford University Press, USA, 2001).
- ⁵⁵K. Kremer and G. S. Grest, *J. Chem. Phys.* **92**, 5057 (1990).
- ⁵⁶R. Auhl, R. Everaers, G. S. Grest, K. Kremer, and S. J. Plimpton, *J. Chem. Phys.* **119**, 12718 (2003).
- ⁵⁷J. P. McDonald and I. R. Hansen, *Theory of Simple Liquids* (Elsevier, USA, 2006).
- ⁵⁸J. D. Weeks, D. Chandler, and H. C. Andersen, *J. Chem. Phys.* **54**, 5237 (1971).
- ⁵⁹E. Vanden-Eijnden and G. Ciccotti, *Chem. Phys. Lett.* **429**, 310 (2006).
- ⁶⁰A. Greiner, W. Strittmatter, and J. Honerkamp, *J. Stat. Phys.* **51**, 95 (1988).
- ⁶¹G. Milstein, *Numerical Integration of Stochastic Differential Equations* (Springer, Netherlands, 1995).
- ⁶²D. Chandler, *Introduction to Modern Statistical Mechanics* (Oxford University Press, Oxford, UK, 1987).