Conformation and dynamics of model polymer in connected chamber-pore system

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Single polymer chains under spatially heterogeneous confinement are investigated through simulation of a chain in an infinite linear series of chambers and pores. Conformational properties studied include the number of occupied chambers and the radius of gyration along the chamber axis, both of which vary with chain length and chamber size according to simple scaling predictions. The probability distribution of chain spatial extent along the chamber axis is characterized by distinct peaks and troughs corresponding to favored and disfavored chain sizes. The large scale dynamics is characterized by the center-of-mass diffusion constant along the chamber axis, which exhibits an exponential dependence on chamber size with dramatically slower diffusion in larger chambers. Stepping time distributions change as the chamber size increases or chain length decreases from a symmetric form to a Poisson distribution. The evolution of the dynamics is suggestive of a substantial barrier, independent of chain length, that controls the large-scale motion for short-enough chains in large-enough chambers. Other known signatures of anomalous, nondiffusive dynamics are also observed. The onset of barrier-controlled or anomalous dynamics is conjectured to be the result of chains occupying only a small number of chambers simultaneously.

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I. INTRODUCTION

A. Translocation and dynamics in porous media

Translocation, the passage of a polymer chain through a narrow constriction, is a much-studied family of dynamical processes. Biological examples are passage of RNA through the nuclear membrane and injection of viral genetic material into a host, while technological applications include rapid sequencing of DNA by detecting and distinguishing the electrical signatures of each residue as it translocates through a pore. Many experiments,¹ theories,^{2–8} and simulations^{9–12} have been deployed to better understand translocation dynamics, but fundamental questions remain. A large number of system properties may affect the process, including chain parameters such as degree of polymerization and stiffness; pore characteristics such as width, shape, and chemistry; and features of the domains on either side of the pore, including differences in chemical and electric potential as well as confinement or obstacles.^{2–7} The consequences of variation in these parameters are complex and often interwoven, hindering development of a general, physical understanding of these systems.

Another broad and poorly understood form of dynamics is that of a polymer in a constrained or porous medium. This very general problem has been studied extensively in a variety of manifestations,^{13–34} and a diverse phenomenology is observed. Simulation studies^{14–17} found regimes of reptative, entropic barrier controlled, and Rouse-like motion. Experi-

mental studies of polymers driven through regions of varying confinement also detected reptative¹⁸ and entropic trapping behavior.^{18,19} A related issue is the partitioning of polymers in systems of variable confinement according to the competing constraints of excluded volume, confinement, and stretching penalties.^{20,21}

A particular application of porous media is in separation mechanisms designed to characterize polymers by molecular weight, charge, or radius of gyration according to their transport properties in a packed column, matrix of obstacles, or other tortuous media.^{22–25} Such mechanisms have been developed in many varieties and employ assorted combinations of obstacles, constant or varying electric fields, solvent flow, and transverse or asymmetric motion. The regimes of chain size, architecture, and chemistry over which these devices are applicable varies, and numerous phenomenologies are observed. In some cases^{26,27} these include a dilute-obstacle “sieving” regime,^{28,29} a strongly constrained reptation regime in which individual polymer chains interact with many obstacles simultaneously in an effective tube,^{14,18} and an intermediate regime in which chain dynamics, controlled by entropic trapping and escape, varies rapidly with molecular weight.³⁰ One consequence of this complexity is a variable dependence of the transport dynamics on chain length: in the same system, the mean velocity may increase or decrease with chain length depending on the driving force as well as the chain length itself.^{31,32} This behavior is termed band reversal, and knowledge of when and why it occurs is essential to control of separation mechanisms.

Despite the many studies of their behaviors under a variety of conditions, the fundamental physics of polymers in

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porous media are not well understood. In particular, the boundaries of the dynamical regimes, i.e., where the motion changes form and how it does so, are not established,³³ information that is essential to a fundamental understanding and control of these systems. The crossover between the entropic trapping and reptative regimes is thought to occur when the chain threads many obstacles or when the system becomes topologically correlated,¹⁷ but a better understanding is needed. Additionally, the nature of the entropic barriers is not yet established; some simulations of chains in random porous media¹⁷ and experimental studies of DNA in colloiddally templated media³³ observe barriers that increase with chain length, while experimental studies of DNA in variable-width channels²⁰ observe barriers that do not depend on chain length. The distinction between these two behaviors is important since the former situation, barriers scaling with chain length, suggests the entropic barrier is connected to the conformational peculiarities of polymers, while the latter chain-length-independent barrier behavior indicates the barrier is a property of the confining geometry.

Although both the translocation and porous medium motion of polymers are complex and highly system specific, on the most basic conceptual level they are similar. Both forms of dynamics consist of chain motion among regions of varying confinement. The goal of this study is to explore the conformational and dynamical consequences of spatially heterogeneous confinement on polymer chains via a simulation that mimics the most generic qualitative features of such systems. Our model, stripped of parameters invoking specific biological and materials applications, addresses translocation and porous medium phenomenology on the basic level at which they intersect. The underlying dynamics has characteristics of both reptation and entropic barrier hopping, with anomalous dynamics and apparent entropic barriers dominating for short chains and large chambers, and a more rapid form of dynamics suggestive of reptation dominating for long chains and small chambers.

B. Model system and simulation methodology

In this study, we simulate a single polymer chain under confinement in a continuous linear series of chambers and pores, as illustrated by the diagrams in Fig. 1. Such a system has many possible realizations. We consider models in which the pores separating chambers are narrow enough to prohibit hairpins, i.e., doublings over of the chain within a pore. There are two extremes of this geometry: chambers small relative to the unconstrained chain size, $R \ll R_g$, such that the chain occupies many chambers simultaneously and experiences many fluctuations of transverse diameter over its contour length [Fig. 1(a)]; and chambers large relative to the unconstrained chain size, $R \gg R_g$, such that the entire chain occupies only one chamber and rarely encounters its walls. An intermediate case may also be considered [Fig. 1(b)] in which the chain and chamber are of comparable size, $R \sim R_g$, and the chain occupies one or a small number of chambers, frequently sampling the intervening pores. These three regimes correspond, respectively, to the reptation, sieving, and entropic barrier regimes observed in porous media.

FIG. 1. (a) Schematic of small-chamber system with chain threading many chambers. (b) Schematic of intermediate-chamber system with chain fully occupying one chamber. (c) Schematic of chamber-pore system, with chamber radius (R), bead diameter (σ), and chamber axis (x) marked.

In this study, we probe the intermediate and small-chamber regimes and the corresponding barrier-controlled and reptation dynamics and the crossover between them.

We model the polymer as a Kuhn chain of N segments connected by harmonic springs. Segments interact via a Lennard-Jones potential, $V(r) = 4\epsilon[(\sigma/r)^{12} - (\sigma/r)^6]$, with their diameter σ taken as the simulation unit of length and the strength of the segment-segment attraction ϵ taken as the simulation unit of energy. The chamber-pore system is composed of an infinite linear series of spherical chambers with radius R connected along the x -axis by cylindrical pores of diameter 1.8σ and length σ . Interactions between segments and the chamber walls are repulsive Lennard-Jones. The spherical/cylindrical geometry, a three-dimensional system with one-dimensional connectivity, was selected as the technically simplest choice. The pores were designed to be narrow enough to avoid doubling over of the chain within the pore (hairpins), and not so long as to add a large component of in-pore friction to the already slow dynamics. Study of the consequences of the pore size and shape is reserved for future work.

Our system variables are polymer chain length, N , and chamber radius, R ; all other parameters are taken as constants. We study the effects of N -variation in systems of size $R = 2\sigma$ ($N = 10 - 150$) and $R = 3\sigma$ ($N = 30 - 150$) and the effects of R -variation for chain lengths $N = 40$, $N = 75$ ($R = 1.75\sigma - 3\sigma$), and $N = 150$ ($R = 1\sigma - 3\sigma$). The degree of confinement is quantified by the ratio of the dilute solution (unconfined) chain radius of gyration to the chamber radius, R_g/R , which for the systems of our study ranges from 0.8 to 3.3. In this regime of modest confinement we are able to see multiple manifestations of two distinct dynamical behaviors.

To simulate the dynamics of the freely jointed chain, we numerically integrate the Langevin equation for each segment:

$$m \frac{d^2}{dt^2} \vec{r}_i = -\zeta \frac{d}{dt} \vec{r}_i + \vec{F}(\vec{r}_i; \{\vec{r}_j\}) + \delta \vec{f}_i. \quad (1)$$

Here $\vec{r}_i$ is the position of the i th segment, $F(\vec{r}_i; \{\vec{r}_j\})$ is the total force on the i th segment due to interactions with the

walls and other segments, and $\delta\vec{f}_i$ is the Gaussian thermal noise with magnitude

$$\langle \delta\vec{f}_i(t) \cdot \delta\vec{f}_j(0) \rangle = 6k_B T \zeta \delta_{ij} \delta(t), \quad (2)$$

where i and j are bead indices and Eq. (2) indicates that the random noise is directionally and temporally uncorrelated and is not correlated among the beads on the chain. The friction constant of a single bead in solvent, ζ , and the segment mass, m , are given values corresponding to a waterlike solvent and a generalized typical polymer segment, and the system is taken at room temperature. All quantities reported in this paper are given in simulation units of length, energy, mass, and time.

The Langevin equation is solved using a velocity Verlet algorithm with a stochastic force term. The polymer is equilibrated in two steps: a relaxation run, during which a mild contractile force is applied to the chain to relax it from an initial fully extended state, and an equilibration run, which is 100 times longer than the dilute solution equilibration time (the latter is 1–10 time units). Equilibration is followed by the production run, which is ten thousand to several tens of thousands of simulation units in duration (10^3 – 10^4 times the dilute solution equilibration time). Mean properties are calculated as the time average over the production run, or in some cases as the time- and ensemble-averages over multiple production runs with independent thermal noise.

Some of the quantities discussed in the following sections are compared with their values in dilute solution. Dilute solution results are obtained by conducting Langevin dynamics simulations for chains of length $N=30, 50, 75$, and 100 in the absence of confining walls, which mimics dynamics in solvent without hydrodynamics. Such chains (for $N \geq 50$) have conformations consistent with a self-avoiding walk, $R_g \sim N^{0.6}$, and undergo Rouse-like diffusion, $\tau_{\text{char}} \sim N^{2.2}$. Dilute solution results for other values of N , plotted for comparison in several figures throughout the paper, are extracted using these laws with prefactors obtained by fitting to the simulation results for $N=50, 75$, and 100.

In Sec. II of this paper, we present conformational results for a single chain in the chamber-pore system, and in Sec. III we discuss dynamical properties. A summary and concluding remarks are made in Sec. IV.

II. CONFORMATIONAL RESULTS

A. Theoretical prediction

A simple theoretical prediction of the equilibrium chain conformation under confinement may be made by invoking scaling or free energy arguments. We consider a chain of N segments occupying m chambers of radius R . Ignoring the monomers in the pores between chambers, which are expected to comprise only a small fraction of the chain, and assuming even distribution of segments, each chamber contains a number of segments $N_c \equiv N/m$. The radius of gyration of the chain along the chamber axis, $R_x \equiv \langle R_{g,x}^2 \rangle^{1/2}$, is similar to the end-to-end distance in the absence of hairpins and is roughly proportional to the number of occupied chambers.

1. Scaling predictions

Following de Gennes,³⁴ we liken the chamber-pore constraints to a smooth tube of radius R , ignoring transverse width fluctuations. The scaling formulation for the chain radius of gyration along the chamber axis is

$$R_x = R f_c(R_F/R), \quad (3)$$

where f_c is some confinement-induced dimensionless function of the Flory chain size $R_F \sim N^{\nu_d}$. We also expect that the chamber-axis radius of gyration scales linearly with N for a given chamber size, i.e., that N_c is a function only of R . Under these constraints the scaling treatment leads to

$$R_x \sim N R^{1-\nu_d^{-1}}. \quad (4)$$

We evaluate Eq. (4) in two cases, the three-dimensional limit and the one-dimensional limit, with different assumptions for the size exponent ν_d .

In the three-dimensional limit, the chambers are sufficiently large that the polymer subchain in each chamber assumes a conformation largely unperturbed from the three-dimensional self-avoiding walk. The Flory chain size is then $R_F \sim N^{3/5}$ ($\nu_d=3/5$) and Eq. (4) becomes

$$R_{x,3D} \approx N/R^{2/3}. \quad (5)$$

In this case the number of occupied chambers is

$$m_{3D} \sim R_{x,3D}/R \sim N/R^{5/3}, \quad (6)$$

and the number of segments in each chamber is $N_{c,3D} \sim R^{5/3}$, consistent with the original assumption that the conformational scaling within each chamber is an undeformed three-dimensional self-avoiding walk.

In the one-dimensional limit, the chambers are small enough to force the chain to assume a quasi-one-dimensional conformation. In this limit, it is in the narrow pores that the chain approximates its limiting behavior, while the less restricted conformation in the chambers is the deviation. The corresponding Flory chain size is $R_F \sim N^1$ ($\nu_d=1$) and Eq. (4) becomes

$$R_{x,1D} \sim N. \quad (7)$$

In this limit, the number of chambers occupied is

$$m_{1D} \sim N/R \quad (8)$$

and the number of segments in each chamber is $N_{c,1D} \sim R$, consistent with the assumption of rodlike conformation.

2. Free energy treatment

We can also consider the chain's conformation in terms of its free energy. The primary effects of chamber-pore confinement are (a) stretching along the chamber axis and the consequent loss of conformational entropy and (b) enhanced segment density within chambers and the resulting increased excluded volume effect. The free energy for a chain occupying m chambers in the three-dimensional limit (again ignoring the segments within the pores, as well as chemical and other system-specific terms) is then

FIG. 2. Mean chamber occupation, $\langle m \rangle$, vs scaling predictions. Upper panel: $\langle m \rangle$ vs $NR^{5/3}$. Line is a fit to the scaling law: $\langle m \rangle \approx 0.21 \cdot N/R^{5/3}$. Lower panel: $\langle m \rangle$ vs N/R . Line is a fit to the scaling law: $\langle m \rangle \approx 0.13 \cdot N/R$. Statistical uncertainty in $\langle m \rangle$ is at most $\Delta m \sim 0.5$ (for long chains that occupy many chambers) and generally $\Delta m \sim 0.05$ or less.

$$F(m) \sim F_{\text{stretch}} + F_{\text{excl.vol.}} \sim \frac{(mR)^2}{N} + mR^3 \left(\frac{N/m}{R^3} \right)^2, \quad (9)$$

where mR is the chain length along the chamber axis, mR^3 is the chain volume, and N/mR^3 is the segment density in each chamber. Minimizing Eq. (9) as a function of m leads to the equilibrium number of occupied chambers $m^* \sim N/R^{5/3}$, consistent with the scaling result for three dimensions.

In the one-dimensional case, variations in the stretching term of the free energy are no longer important since the chain is assumed to be strongly stretched. A friction term arises due to the frequent contacts of the chain with the chamber walls, which occur in each chamber with probability proportional to the ratio of chamber wall area to volume,

$$F(m) \sim F_{\text{excl.vol.}} + F_{\text{friction}} \sim mR^3 \left(\frac{N/m}{R^3} \right)^2 + m \frac{R^2}{R^3}. \quad (10)$$

The resulting equilibrium chamber occupation, $m^* \sim N/R$, is consistent with the one-dimensional scaling result.

B. Mean chamber occupation number

The average number of occupied chambers is of interest as a measure of chain size as well as for (inexact) comparison to analytical treatments that consider only the most probable number of occupied chambers.³⁵ The simulation result for this quantity, $\langle m \rangle$, can be expressed in each of the limiting regimes as a linear function of a single parameter combining chain length and chamber size, as predicted in the previous subsection, and the accuracy of such linear predictions is shown in Fig. 2. In the top panel the three-dimensional fit, $\langle m \rangle \propto N/R^{5/3}$, is found to be effective up to $\langle m \rangle \sim 10$, which includes most of the systems of the study. However there is a clear deviation of the simulation results from the prediction for large chains in small chambers. The one-dimensional scaling is applied, $\langle m \rangle \propto N/R$, in the bottom panel of Fig. 2, and this fits the data except for the most extreme large- $\langle m \rangle$ point. Additionally, this scaling is reasonably effective (although less effective than the stronger

FIG. 3. Mean filling fraction. Top panel: Log-linear plot of $\langle \phi \rangle$ vs N for $R=2\sigma$ (red), 3σ (cyan). Also shown are domain volume fractions in dilute solution (crosses) and self-avoiding walk fit, $\langle R_{g,v} \rangle_{\text{dil}} \sim N^{0.6}$ (dashed line). Bottom panel: Log-linear plot of mean filling fraction vs R for $N=40$ (green), 75 (orange), and 150 (blue). Dashed lines are domain volume fractions in dilute solution from self avoiding walk fit for (from top) $N=40, 75, 150$.

R -dependence) in collapsing and fitting the data in the three-dimensional regime. The inability to fit the highest- $\langle m \rangle$ point may be due to the emerging importance of other factors, i.e., specifics of the chamber shape and information about the pores. The ambiguity in the optimal fit is due to a limited amount of data and range of study.

An alternative method for examining the chamber occupation results is to define a mean chamber filling fraction directly from the mean chamber occupation,

$$\langle \phi \rangle \equiv \frac{N(\sigma/2)^3}{\langle m \rangle R^3}. \quad (11)$$

By definition this quantity (shown in Fig. 3) ignores the effect of pores and is therefore slightly inaccurate, particularly for small chambers ($R \leq 1.5\sigma$), but it is useful as a simple approximation for larger chambers. For comparison, a dilute solution volume fraction may be estimated as

$$\langle \phi_{\text{dil}} \rangle \equiv \frac{N(\sigma/2)^3}{\langle R_{g,\text{dil}}^2 \rangle^{3/2}} \sim N^{-4/5}, \quad (12)$$

where the scaling $N^{-4/5}$ is obtained from excluded volume assumptions. The resulting $\langle \phi_{\text{dil}} \rangle$ is an overestimate relative to $\langle \phi \rangle$ since the radius of gyration is less than the actual domain encompassed by the chain; however, the two results should scale similarly, and adjusting Eq. (13) to reflect spatial domain is a correction of only $\sim 10\%$ for $N=50, 100$. Equation (13) thus provides a useful dilute solution analog to Eq. (12).

As shown in the top panel of Fig. 3, the chamber filling fraction of Eq. (12) increases with chain length for short chains but rapidly approaches an R -dependent plateau value, consistent with the linear N -dependence of the chamber occupation. The dilute solution volume fraction, in contrast, decreases markedly with increasing N and for long chains is substantially smaller than $\langle \phi \rangle$, illustrating the monomer density is strongly increased due to confinement in the cham-

bers. As the chamber radius increases (bottom panel of Fig. 3), the confinement is relieved, and short ($N=40$) chains approach their dilute solution volume fraction. A broad range of chamber filling fractions is accessible by moderate adjustments of chamber size. The plateau in the N -dependence is reflected by the approximate collapse in R -dependence, consistent with the assumption that the chain scaling in each chamber depends much more strongly on R than on N .

C. Radius of gyration

A second measure of chain size is the mean square radius of gyration,

$$\langle R_g^2 \rangle = N^{-1} \langle \sum |\vec{r}_i - \vec{r}_{\text{com}}|^2 \rangle, \quad (13)$$

where $\vec{r}_{\text{com}}$ is the chain center-of-mass position and the sum is over all beads in the chain. The corresponding radius of gyration along the chamber axis is

$$\langle R_{g,x}^2 \rangle = N^{-1} \langle \sum (x_i - x_{\text{com}})^2 \rangle. \quad (14)$$

In an isotropic system, the radius of gyration along each axis would be identical, $\langle R_{g,x}^2 \rangle \equiv \langle R_{g,y}^2 \rangle \equiv \langle R_{g,z}^2 \rangle \equiv \frac{1}{3} \langle R_g^2 \rangle$. In our radially confined system, the chain size along the y and z axes is restricted by the chamber walls, while the radius of gyration on the x axis varies freely according to the chain length and degree of confinement.

The radius of gyration along the chain axis is roughly proportional to the mean chamber occupation number but can be compared directly to its unconfined (dilute solution) analog. Since the chain in dilute solution is expected to be prolate along a freely rotating axis, we consider the dilute solution radius of gyration on the instantaneous long axis of the chain. Existing simulation studies of self-avoiding walks provide shape measurements³⁶ that lead to the result

$$\langle R_{g,\text{long}}^2 \rangle \approx 0.775 \langle R_g^2 \rangle. \quad (15)$$

The prefactor in Eq. (15) is only very slightly N -dependent; the numerical value in Eq. (15) corresponds to the result for $N=100$ and is used throughout this study. Self-avoiding walk fits to our dilute solution simulation results are used as input to Eq. (15).

The N -dependence of the chamber-axis radius of gyration under confinement is linear (Fig. 4), similar to the mean chamber occupation: $\langle R_{g,x}^2 \rangle^{1/2} \sim N$. This is a stronger variation than the dilute solution scaling, $\langle R_{g,\text{long}}^2 \rangle^{1/2} \sim N^{3/5}$; however the numerical size of the chains is not necessarily larger. Long confined chains are stretched relative to their dilute solution conformation, while short confined chains are contracted. For $R=2\sigma$, the crossover from contraction to stretching occurs at $N \sim 40$, while for $R=3\sigma$ chains are contracted relative to dilute solution chains for $N < 150$. The chamber-axis radius of gyration also decreases with increasing chain size as more transverse volume becomes available to the chain. With increasing R , the chain transitions from stretched to contracted relative to dilute solution when the chamber diameter is on the order of the dilute solution size. As the chamber size increases further, the chain is increasingly contracted.

FIG. 4. Root mean square radius of gyration along chamber axis, $R_{g,x} \equiv \langle R_{g,x}^2 \rangle^{1/2}$, vs chain length for $R=2\sigma$ (red), 3σ (cyan) with linear fits: $R_{g,x} \approx 0.086N$ ($R=2\sigma$); $R_{g,x} \approx 0.050N$ ($R=3\sigma$). Dashed line is dilute solution result.

The simulation results for radius of gyration along the chamber axis demonstrate competition between two effects of confinement in the chamber-pore system: (a) enhanced excluded volume among monomers in a chamber, dominant for long chains and small chambers, which promotes stretching into additional chambers, and (b) the entropic penalty for threading pores, dominant for large chambers in which the contrast between chamber and pore is greatest, which promotes contraction along the chamber axis. This competition is capable of producing deformation of the chain size in either direction depending on the system parameters.

The transverse radius of gyration of the chain is the average of the statistically identical radii of gyration on the y and z axes. This quantity is closely tied to the chamber size:

$$\langle R_{g,\text{trans}}^2 \rangle^{1/2} = \sqrt{\frac{1}{2} (\langle R_g^2 \rangle - \langle R_{g,x}^2 \rangle)} \approx cR. \quad (16)$$

The multiplicative factor c has a mean value of 0.34 and a range of 0.3–0.4 for all the systems of our study. This indicates the mean chain size in the transverse direction is controlled not by the segment density (which varies strongly with R) or by connectivity and stretching effects (as it might be if the chain were very strongly stretched with only a few beads in each chamber) but by the entropic and excluded volume incentives for exploring the chamber volume and the excluded volume penalty of interacting with the chamber walls.

D. Spatial extent

The spatial extent of the polymer chain is the distance along the x -axis between the rightmost and leftmost beads:

$$s_x = x_{\text{right}} - x_{\text{left}}. \quad (17)$$

These extrema are not in general the end beads of the polymer, but s_x scales as the end-to-end distance due to the restriction on hairpins. Figure 5 shows the spatial extent distribution for various chain sizes and $R=2\sigma$. Each curve represents the probability distribution of the spatial extent for a chain of a given length N , obtained by histogramming the spatial extent over the course of the production run. The distributions exhibit one ($N=10$) or more ($N > 10$) peaks of

FIG. 5. Spatial extent distribution for $R=2\sigma$; $N=10$ (red), 20 (orange), 30 (green), 60 (blue), 75 (cyan), and 100 (purple).

avored spatial extent separated by substantial troughs; these features correspond not to specific positions within the chamber system but to the total span of the chain along the chamber axis.

In addition to having larger spatial extents, i.e., distributions with peaks at higher s_x , long chains generally have a broader range of acceptable spatial extents, i.e., larger number of peaks. The distributions are qualitatively different for each chain length studied, indicating that chambers of radius 2σ are capable of conformational partitioning of chains of length $N \leq 150$ with good resolution. In larger chambers, $R=3\sigma$, the spatial extent distributions retain the gross features of peaks and troughs, but the specificity is drastically reduced as even the longest chains studied do not have a significant probability of occupying more than two chambers. In these larger chambers, the distributions associated with different chain lengths are much harder to distinguish; for significantly longer chains, however, we expect the partitioning ability would be recovered.

III. DYNAMICAL RESULTS

A. Center of mass motion

Our study of the dynamics of the confined chain focuses on the motion of the chain center of mass along the chamber axis. The center of mass trajectory is shown for various chain and chamber sizes in Fig. 6. The motion is analyzed by calculating the mean square center of mass displacement,

$$\langle x_{\text{com}}^2(\Delta t) \rangle_t = \langle (x_{\text{com}}(t + \Delta t) - x_{\text{com}}(t))^2 \rangle_t. \quad (18)$$

This is a time average over the simulation run, and the longest lag times Δt are subject to greatest statistical noise because the run contains fewer independent time intervals over which to perform the average. Figure 7 shows the mean square center-of-mass displacement for various systems.

In small chambers ($R=2\sigma$, top panel of Figs. 6 and 7), chains are fairly mobile and there is no qualitative difference between the center-of-mass trajectories for the two different chain lengths. Although the chamber period imprints the small-scale dynamics, over long timescales the chains diffuse through numerous chambers and the dynamics do not show a strong signature of the confinement. The mean square center-

FIG. 6. Center of mass trajectories in chambers of size $R=2\sigma$ (upper panel) and $R=3\sigma$ (lower panel) for $N=40$ (green) and $N=75$ (orange). Scales of both axes differ between upper and lower panels.

of-mass displacements in Fig. 7 vary almost identically for the two chain lengths. The mean square displacements are diffusive, $\langle \Delta x_{\text{com}}^2(\Delta t) \rangle \propto \Delta t^1$, for times $\Delta t > 1$, with a slight subdiffusive plateau at shorter times (see Sec. III D 1).

In large chambers ($R=3\sigma$, bottom panels of Figs. 6 and 7), the dynamics are slower and differ qualitatively from the dynamics in small chambers. The center of mass trajectories are much slower, even on the compressed timescale of the bottom panel of Fig. 6, and individual steps between chambers, separated by long periods of near stationarity, are clearly perceptible. The $N=75$ chain is also noticeably slower than the $N=40$ chain, exhibiting fewer steps with less center-of-mass confinement (greater conformational entropy) between steps. The mean square center of mass displacements, although diffusive at long times, exhibit much more pronounced subdiffusive plateaus in the $R=3\sigma$ chamber. Moreover, the plateaus for the two chain lengths have different shapes; the $N=40$ plateau is lower (due to prediffusive trapping on the smaller single-chamber length scale) and ends at a shorter lag time than the $N=75$ plateau, and in contrast with the upper panel the curves are not parallel for intermediate times. The $N=40$ dynamics become diffusive at

FIG. 7. Mean square center-of-mass displacement in chambers of size $R=2\sigma$ (upper panel) and $R=3\sigma$ (lower panel) for $N=40$ (green) and $N=75$ (orange). Line segments with slope 1 indicate diffusive behavior.

FIG. 8. Chamber-to-chamber stepping time distributions for $R=2$, $N=15$ (red) and $N=75$ (blue) with fits: Poisson fit for $N=15$ with $\bar{\tau}=5.0$ (solid line); log-normal fit for $N=75$ with $\bar{\tau}=17.3$, $\omega^2=1$ (dashed line).

$\Delta t \sim 10$; the $N=75$ dynamics, however, remains subdiffusive until much longer times ($\Delta t \sim 10^3$). This indicates diffusion requires navigation of a substantial regime of anomalous dynamics, possibly characterized by processes of varying time and length scales or substantial and/or multiple entropic barriers.

B. Chamber-to-chamber stepping time

To address dynamics on the chamber length scale, we employ a generalized definition of a chamber-to-chamber step as the process by which the chain center of mass moves a single chamber-pore period along the x -axis. The chamber-to-chamber stepping time is the time interval between the chain center of mass crossing one chamber center and crossing the adjacent chamber center in either direction, regardless of how many chambers the chain itself occupies. For large chains the stepping time involves center-of-mass motion on a length scale substantially smaller than the chain size.

The probability distribution of stepping times is of interest as a qualitative probe of the dynamics on the chamber length scale. Most of the systems addressed in this study exhibit a log-normal distribution of the stepping time,

$$P(\tau_{\text{step}}) \sim \tau_{\text{step}}^{-1} \exp[-(\ln \tau_{\text{step}} - \ln \bar{\tau})^2 / 2\omega^2], \quad (19)$$

where ω^2 is a measure of the breadth of the distribution and $\bar{\tau}$ is a characteristic time roughly equal to the mean. In the log-normal distribution, the logarithm of the stepping time has a Gaussian distribution; such distributions arise frequently in biological systems and indicate the events are a multiplicative combination of uncorrelated components.³⁷

Systems with large chambers or short chains exhibit a Poisson distribution of stepping times,

$$P(\tau_{\text{step}}) \sim \tau_{\text{step}} e^{-\tau_{\text{step}}/\bar{\tau}}, \quad (20)$$

where $\bar{\tau}$ is a characteristic timescale roughly twice the mean stepping time. The Poisson distribution corresponds to uncorrelated identical events.

Figure 8 shows stepping time distributions for $N=15$ and $N=75$ chains in small chambers ($R=2\sigma$). The $N=15$ stepping time has a Poisson distribution and the $N=75$ stepping

time has a log-normal distribution; the shape of the distribution shifts continuously as N increases from 15 to 30 (for $R=3\sigma$ the crossover occurs similarly, with a fully Poisson distribution arising for all chains smaller than $N=60$). A transition between distributions can also be seen for decreasing chamber size at constant chain length. For $N=40$ chains, the crossover from log-normal to Poisson distribution occurs as R decreases below 2σ . For this crossover chain size, the distribution is fit by a log-normal distribution on its short-time branch and by a Poisson distribution on its long-time branch. For $N=75$ the crossover occurs between $R=2.5$ (log-normal) and $R=2.75$ (Poisson). These trends suggest Poisson distributions are associated with $\langle m \rangle < 2$, i.e., chains that do not on average fully occupy two chambers.

Our findings are qualitatively similar to recent experimental results. Studies of DNA in a regular array of templated cavities³³ find Poisson statistics for jumps between chambers by chains that occupy only one chamber at a time, for which $\langle R_g^2 \rangle^{1/2}/R \sim 0.3-1.1$. The largest of these chains has roughly the same ratio of chain to chamber size as our $N=20$, $R=2$ system, which exhibits Poisson statistics for the stepping time. The experimental study also examines a longer chain, $\langle R_g^2 \rangle^{1/2}/R \sim 1.6$, for which the most common occupation number is two. In this system the observed dynamics suggest an emerging crossover to reptation.³³ This corresponds to our $N=40$, $R=2.25\sigma$ or $R=2.5\sigma$ system, and our simulation results from these systems are in a crossover regime from Poisson to log-normal dynamics. The majority of the systems we study have longer chains than the experimental study and the dynamics we observe, while carrying signatures of entropic barrier effects, are controlled primarily by the faster log-normal process.

C. Transport coefficients

1. Scaling treatment

To describe the long-time dynamics of the chain in the chamber-pore system, we consider the characteristic relaxation time. This quantity differs from the chamber-to-chamber stepping time in that its length scale is N -dependent and for long chains it quantifies relaxation over several chambers. A scaling treatment may be developed by considering that the limiting behavior of the system will resemble reptation dynamics, $\tau_{\text{char}} \sim R_x^2/D \sim N^3$ (assuming the one-dimensional Fickian diffusion constant $D \sim N^{-1}$). The scaling formula for the characteristic relaxation time (for relaxation along the chamber axis) is

$$\tau_{\text{char}} = \tau_F f_c(R_F/R), \quad (21)$$

where τ_F is the relaxation time in the Flory limit, $\tau_F \sim R_F^2/D \sim N^{2\nu_d+1}$. The scaling result follows from these considerations as

$$\tau_{\text{char}} \sim N^3 R^{2-2/\nu_d}. \quad (22)$$

FIG. 9. Center-of-mass diffusion constant, D , vs N for $R=2$ (upper panel) and $R=3$ (lower panel). Lines are fit to N^{-1} : $D \sim 41/N$ (upper panel); $D \sim 1.7/N$ (lower panel).

In the three-dimensional limit, Eq. (22) becomes $\tau_{\text{char},3D} \sim N^3/R^{4/3}$, while in the one-dimensional limit the scaling result is $\tau_{\text{char},1D} \sim N^3$ with no dependence on chamber size.

2. Simulation results

The long time center-of-mass diffusion constant, D , is defined by

$$\lim_{\Delta t \rightarrow \infty} \langle x_{\text{com}}^2(\Delta t) \rangle_t = 2D\Delta t. \quad (23)$$

The diffusion constant is calculated by fitting a line to the long-time regime of the mean square displacement and extracting its slope. This method is somewhat subjective since there is generally a small range of acceptable linear fits, but it is robust in its ability to extract reasonable results from limited data.

Figure 9 shows the N -dependence of the diffusion constant for two different chamber sizes, $R=2\sigma$ and $R=3\sigma$. Although the data exhibit substantial scatter, particularly for $R=3\sigma$ and small values of N (for which diffusion is slower and therefore requires more computer time to sample thoroughly), the simulation results are consistent with the scaling prediction of Eq. (25) for chains that are not too small ($N \geq 40$). The N^{-1} scaling is also observed for simulations in dilute solution (with much less scatter); confinement suppresses the diffusion constant by one order of magnitude for $R=2\sigma$ and three orders of magnitude for $R=3\sigma$.

For both chamber sizes, the shortest chains have a smaller diffusion constant than predicted by the N^{-1} fit. This is likely a consequence of the onset of a regime of slower dynamics, as manifested in the previous section through the crossover to a Poisson stepping time distribution. It may also indicate the onset of band reversal. In fact band reversal is seen for $R=3\sigma$; the diffusion constant is apparently non-monotonic with a maximum at $N=40$, however the non-monotonicity comprises only one data point and better long-time results for this system as well as simulations of other short chains are called for.

The chamber size dependence of the long-time diffusion constant is shown in Fig. 10. The variation over the range of chamber sizes studied is substantially stronger than the varia-

FIG. 10. Log-linear plot of center-of-mass diffusion constant, D , vs R for $N=40$ (green), $N=75$ (orange), and $N=150$ (blue). Line is exponential fit, $D \sim \exp[-3.9R]$.

tion with chain length, and a single exponential fit provides a reasonable approximation over most of the range of R for all values of N , $D \propto \exp[-4R]$. The full simulation result for the diffusion constant is then

$$D \sim N^{-1} \exp[-4R]. \quad (24)$$

This leads to a prediction for the characteristic relaxation time that differs from the scaling result by an exponential factor,

$$\tau_{\text{char},3D} \sim N^3 R^{-4/3} \exp[4R], \quad (25)$$

$$\tau_{\text{char},1D} \sim N^3 \exp[4R].$$

The form of Eq. (25) suggests an entropic barrier-hopping mechanism in which the barrier is proportional to chamber size (as well as presumably depending on other geometric characteristics of the system) but is independent of chain length. The exponential dependence is purely empirical, however, and may be an artifact of the limited range of data. The ability of the reptation-based scaling to describe the N -dependence even for rather short chains and its failure to describe the R -dependence over any part of the regime studied indicate that the nonreptative behavior arises primarily not from the chains being too short to thread sufficient numbers of chambers but from the degree of variation in transverse diameter along the axis of our system, i.e., the mere existence of chambers separated by narrow pores.

D. Non-Gaussian behavior

1. Subdiffusive exponent

The mean square displacement associated with motion in a given system, in this instance the time-averaged motion of the chain center of mass, can be characterized as a power law in the elapsed time,

$$\langle (\Delta x_{\text{com}}(\Delta t))^2 \rangle \propto (\Delta t)^\alpha. \quad (26)$$

The exponent α is the characteristic dynamic exponent; in general it is a function of elapsed time. For diffusive processes, $\alpha=1$, and this behavior is observed in chamber-pore motion at long times (Fig. 7). At shorter times, however, the

FIG. 11. Moving average of time-dependent subdiffusive exponent $\alpha(t)$ vs time for $N=75$ chains in chambers of size $R=2\sigma$ (red), 3σ (cyan). Dashed line is $\alpha=1/2$.

dynamics are subdiffusive, $\alpha < 1$. The subdiffusive exponent quantifies the anomalous component of the dynamics and is bounded below by zero, which corresponds to total dynamic arrest. Subdiffusive behavior is observed for the translocation coordinate in studies of single translocations^{6,9} and for the mean square particle displacement in glassy dynamics,³⁸ as well as for polymer chains undergoing Rouse (exponent 0.5) or reptation (exponent 0.25) dynamics.

The time-dependent subdiffusive exponent is shown (as a moving average, to reduce the effect of noise) for two systems of our study in Fig. 11. The upper curve ($N=75$, $R=2\sigma$) exhibits slight diffusivity at short times, deepening slightly at intermediate times before recovering diffusive motion at roughly the time of the chamber-to-chamber stepping event. This qualitative behavior is typical for chains in $R=2\sigma$ chambers. At all times accessible to our study, the subdiffusive exponent is greater than the Rouse relaxation value of 0.5. However the dilute-solution relaxation time is ~ 0.3 and therefore at least the first order of magnitude in time shown in the figure is expected to involve the relaxation of Rouse modes. This suggests an interaction between the Rouse modes and the confinement leading to a longer period (up to $t \sim 10$ rather than up to $t \sim 0.3$) of less pronounced ($\alpha > 0.5$) subdiffusivity.

The lower curve in Fig. 11 ($N=75$, $R=3\sigma$) demonstrates substantial subdiffusivity at short times, releasing to a local maximum at intermediate times before decreasing substantially to a deep minimum. Finally, at very long times, the subdiffusive exponent increases and eventually diffusion is recovered. This behavior is significantly more anomalous than that of chains in smaller chambers and suggests at least a partial separation of timescales, with much of the Rouse relaxation occurring at $t \lesssim 0.1$ and much of the confinement relaxation occurring, with stronger subdiffusivity, at $t > 1$. The subdiffusivity profile bears qualitative similarities to that of the reptation model, which predicts a short-time subdiffusivity of 0.5 (due to Rouse relaxation on length scales below the tube diameter) evolving to a minimum of 0.25 at intermediate times (corresponding to Rouse relaxation in the tube) and then increasing to 1 as first the Rouse modes and

then the tube constraints are relaxed. However, the motion of chains in large chambers is not expected to mimic reptation and the precise physical origins of the observed behavior are unclear. Chains of other lengths in $R=3\sigma$ chambers exhibit similar behavior or other strongly subdiffusive variations.

In a general sense, the depth and persistence of subdiffusivity are a measure of anomalous dynamics. Our results suggest dynamics in small chambers are nonanomalous or only mildly anomalous, while dynamics in large chambers exhibit strongly anomalous behavior. This conclusion is supported by the minimum value of the subdiffusive exponent which decreases steadily with decreasing N and increasing R . This value and its associated timescale describe the strength and nature of the constraints leading to subdiffusivity and the dynamics of recovering diffusive behavior, but detailed analysis is curtailed by the statistical limits of our data. However, a deeper study of such properties could serve as a tool to compare a variety of superficially different anomalous systems.

2. Non-Gaussian parameter

The non-Gaussian parameter, α_2 , is a time-dependent quantification of the breadth of the relaxation process, and is commonly studied for systems exhibiting glassy dynamics.^{39–41} It is derived from the first correction to the Gaussian approximation of the incoherent dynamic structure factor,

$$F(q, t) \equiv \langle e^{-i\vec{q} \cdot \vec{r}(t)} \rangle \approx e^{-q^2 \langle r^2(t) \rangle / 6} \left\{ 1 + \frac{1}{2} \alpha_2(t) [q^2 \langle r^2(t) \rangle / 6]^2 + \dots \right\}. \quad (27)$$

Thus the non-Gaussian parameter is an important measure of the dynamic heterogeneity or non-Fickian behavior of a system. It is calculated from the distribution of particle displacements:

$$\alpha_2(t) \equiv \frac{3}{5} \frac{\langle r^4(t) \rangle}{\langle r^2(t) \rangle^2} - 1. \quad (28)$$

When the distribution is Gaussian, the non-Gaussian parameter is zero, and when the distribution is broader than Gaussian the parameter is greater than zero. Typically the non-Gaussian parameter peaks at an intermediate time and decays at long times as the relaxation is completed and diffusive dynamics becomes dominant. In this study, the ensemble averages are replaced by time averages of the center-of-mass displacement distributions,

$$\alpha_2(\Delta t) = \frac{1}{3} \frac{\langle [x_{\text{com}}(t + \Delta t) - x_{\text{com}}(t)]^4 \rangle_t}{\langle [x_{\text{com}}(t + \Delta t) - x_{\text{com}}(t)]^2 \rangle_t^2} - 1, \quad (29)$$

where the numerical coefficient is adjusted to reflect the one-dimensional nature of the motion.

Figure 12 shows the non-Gaussian parameter for chains of two different lengths ($N=40, 75$) in large and small chambers. For both chamber sizes, the non-Gaussian parameter has a smaller maximum value and peaks at longer times for the longer chain, indicating that while the anomalous behavior is less pronounced its dissipation is slower. The effect of chain size is much less, however, than that of chamber size.

FIG. 12. Log-log plot of non-Gaussian parameter for $R=2\sigma$; $N=40$ (red), 75 (orange); $R=3\sigma$; 40 (green), 75 (blue).

The non-Gaussian parameter is significantly greater in magnitude and peaks at longer times with increasing chamber size, indicating that the anomalous behavior is more pronounced and dissipates more slowly in larger chambers. For sufficiently long chains in sufficiently small chambers, the non-Gaussian parameter becomes inconsequential, corresponding to the recovery of reptationlike dynamics.

The trends demonstrated by the four systems in the figure are, with a few discrepancies, general. Unlike other properties we studied, for the non-Gaussian parameter decreasing chain length and increasing chamber size do not have the same qualitative effect; while both increase the magnitude of the non-Gaussian parameter, they have opposite consequences for its characteristic time. Non-Gaussian behavior such as observed here indicates a broad distribution of displacements over the ensemble of times. This suggests a non-Fickian relaxation mechanism and is often indicative of barriers requiring rare thermal excitations to surmount. However the result may correspond to some other mechanism, and further studies of the microscopic, monomer-level aspect of the motion are necessary to gain a better understanding of the cause and nature of the non-Gaussian behavior.

IV. CONCLUSIONS

In this paper we discussed conformational and dynamical properties extracted from our simulation study of a single polymer chain in a linear series of chambers and pores. We found that the chain conformation in most systems is well described by scaling treatments that ignore the heterogeneity of confinement and penalties for pore threading, incorporating the effects of chain and chamber size into a single parameter that depends on the assumptions of the scaling treatment. Spatial extent distributions show that chains have preferred and excluded spans which vary with chain size, and that the ability of the system to differentiate between chain lengths through this property is dependent on chamber size. Dynamics are quantified through the diffusion constant, which is inversely proportional to chain length and decreases exponentially with chamber size; the strong chamber-size dependence is not predicted by the scaling treatment. The dis-

tribution of characteristic times for motion on the chamber scale evolves from log normal to Poisson with decreasing chain length and increasing chamber size. Non-Gaussian behavior, including subdiffusivity of the mean square displacement and an intermediate-time non-Gaussian parameter, is also observed.

The results of this study indicate a smooth variation in conformation with chain and chamber size, which spans a crossover between two distinct dynamical regimes. Long chains in small chambers exhibit a comparatively rapid dynamics with log-normal distribution of stepping times and an insubstantial non-Gaussian parameter, while small chains in large chambers have a much slower dynamics with a Poisson distribution of stepping times and significant non-Gaussian parameter. This suggests the slow regime is controlled by entropic barriers to passing through pores; in the fast regime, where the conformational entropy surrendered on entering the pore is less and the chain consistently threads multiple chambers, the dynamics are suggestive of reptation in the absence of a significant barrier.

The dependence of simulation properties, particularly the dynamics, on chain length is complex. The apparent barrier that appears in the diffusion constant is N -independent, but chain length has clear consequences for the non-Gaussian parameter and stepping time distribution. One relevant experimental study probes DNA traveling through a series of constricted and comparatively open regions under an electric field.¹⁸ The DNA is found to encounter an entropic barrier at the entrance to each constriction that depends on the comparative confinement but not on chain length. Longer chains surmount the barrier more rapidly because they experience a larger driving force.¹⁸ Our study differs from the experiment in that no external force is applied, and the dynamics do not accelerate with increasing chain length. However, long chains still have more degrees of freedom both locally (more monomers experiencing thermal fluctuations) and on the scale of chamber occupation numbers (a larger number of chambers are occupied in the most probable state) and this may allow surmounting of geometric barriers with less deviation from Gaussian diffusive motion.

Some evidence of band reversal similar to that observed in separation experiments is suggested by the results of our study, but further simulation of shorter chains and larger chamber diameters is necessary to verify and understand the phenomenon. In addition, the N -dependence of the diffusion constant in the simulation is similar to that seen in free diffusion and opposite that seen in force-driven electrophoresis,³¹ suggesting the existence of a crossover force magnitude (or range of force magnitudes) for which the N -dependence is flat or nonmonotonic. Related simulations⁴² of chains in the chamber-pore system under an applied force further address this issue.

Many interesting properties of the chamber-pore system have not been considered in this study. Our goal has been to explore primarily long-time, chain-level properties such as mean conformation and center-of-mass diffusion. However, short time and segment-level properties likely carry much additional information. Quantities of interest include the velocity autocorrelation functions for the center of mass and

segment motions, the segment diffusion constant, and variations in conformation and instantaneous dynamics with differing location in the chamber-pore system. The chamber-to-chamber steps could also be analyzed more closely by exploring differences between failed and successful attempts at passing between chambers as well as the degree of rearrangement and decorrelation experienced by chains between steps.

Alternative systems of polymers under spatially heterogeneous confinement may be imagined in which the confinement itself depends on chain length. For example, in randomly packed media^{9,17} regions of all sizes coexist and shorter chains are better able to explore the detailed geometry of the system. In semientangled semidilute solutions the physical nature of the system depends on the length of the chains of which it is composed. In these systems, where penalties for moving between regions and possibly the nature of those regions depend on the size and stiffness of the chain, it seems likely entropic barriers—for the regimes in which they exist—are chain length dependent.

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