

PAPER

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Ring closure dynamics for a chemically active polymer

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The principles that underlie the motion of colloidal particles in concentration gradients and the propulsion of chemically-powered synthetic nanomotors are used to design active polymer chains. The active chains contain catalytic and noncatalytic monomers, or beads, at the ends or elsewhere along the polymer chain. A chemical reaction at the catalytic bead produces a self-generated concentration gradient and the noncatalytic bead responds to this gradient by a diffusiophoretic mechanism that causes these two beads to move towards each other. Because of this chemotactic response, the dynamical properties of these active polymer chains are very different from their inactive counterparts. In particular, we show that ring closure and loop formation are much more rapid than those for inactive chains, which rely primarily on diffusion to bring distant portions of the chain in close proximity. The mechanism presented in this paper can be extended to other chemical systems which rely on diffusion to bring reagents into contact for reactions to occur. This study suggests the possibility that synthetic systems could make use of chemically-powered active motion or chemotaxis to effectively carry out complex transport tasks in reaction dynamics, much like those that molecular motors perform in biological systems.

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1 Introduction

Active transport is a common mechanism employed by biological systems to carry out many functions in the cell and a large variety and number of molecular machines have evolved to perform specific tasks.¹ Now familiar examples include the family of kinesins and dyneins that move along microtubule filaments and actively transport vesicles, organelles and proteins in the cell, among the many other functions they perform. Other motors act as pumps or are involved in signalling processes in the networks of chemical reactions that control cell biochemistry. These few examples serve to indicate that cell biochemistry does not rely on simple diffusion alone to effect transport; evolution has led to the construction of molecular machines to overcome the indiscriminate nature of diffusion to achieve more effective function. The complex biochemical networks that underlie cellular functions produce, consume and transport large and small molecular and supermolecular entities in an inhomogeneous environment using both active and passive mechanisms.

Currently, a significant research effort is being devoted to the construction and study of synthetic nanoscale machines and motors.² One of the aims of this research is to imitate some of the desirable transport functions of biological machines. While

nature has designed molecular machines to assist in carrying out biochemical functions in the cell, much of condensed phase chemistry relies on simple diffusion to bring reagents into contact so that chemical reactions can proceed. This raises the question, can one design synthetic machines or implement active transport strategies to supplant simple diffusion and target reagents to encounter each other more effectively in order to produce desired products?

In this article we give a simple illustration of how active transport can be used to greatly reduce the time needed for ring closure or loop formation in polymeric systems. Loop formation in a polymer chain is a dynamic process by which two monomers along the chain approach each other within a small distance and possibly bind. We show how some of the ideas that underlie synthetic nanomotor propulsion can be used to design active polymer chains which contain the components of chemically-powered motors and undergo rapid ring closure.

Following the fabrication and study of small micron-scale bimetallic rod motors that use hydrogen peroxide fuel,^{3,4} different types of chemically-powered motors have been made and their potential applications have been explored.² One such motor is a sphere dimer motor comprising linked catalytic and noncatalytic spheres.^{5,6} Reactions at the catalytic sphere produce a concentration gradient that ultimately gives rise to directed motion of the motor. An active polymer is constructed by unlinking the catalytic and noncatalytic spherical particles, attaching them to different portions of a polymer chain, and allowing them to move in the concentration gradient generated by reactions at the catalytic sphere. Through such a mechanism

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we show that distant portions of the polymer chain can be targeted to encounter each other to form loops or rings.

In the next section we discuss the basic mechanism for diffusiophoretic motion in a concentration gradient. Section 3 presents the model for active polymers in detail and describes how the simulations of the dynamics are carried out. The results in Section 4 show that ring closure times can be greatly reduced for active polymer chains, when compared to those of their inactive counterparts. Other aspects of active polymer dynamics are also discussed in this section. The conclusions of the study are given in Section 5.

2 Diffusiophoretic particle motion

As an introduction to the mechanism that active polymers use to achieve rapid ring closure or loop formation, we briefly describe the simpler situation of the motion of a particle in a chemical gradient. It is well known that colloidal particles can move in response to chemical or other (electric field and temperature) gradients and the macroscopic theory that underlies these phoretic mechanisms is well established.^{7,8} Briefly, suppose there is an inhomogeneous distribution of solute B molecules in the vicinity of the colloidal particle. Interactions of the solute molecules with the surface of the colloid give rise to body forces, which, because of momentum conservation, lead to pressure and velocity gradients within a thin boundary layer around the particle within which the forces act. As a result, there is a fluid slip velocity, $\mathbf{v}_s$, on the outer edge of the boundary layer, which is given by the expression,

$$\mathbf{v}_s = -\frac{k_B T}{\eta} (\nabla_{\parallel} c_B(\mathcal{S})) \Lambda, \quad (1)$$

where $c_B(\mathcal{S})$ is the concentration of B molecules on the outer edge of the boundary layer, the gradient is taken along the surface of this layer, the viscosity of the solution is η and Λ is a parameter that gauges the strength of the interaction of the solute molecules with the surface of the particle. The velocity of the colloidal particle may then be expressed in terms of the average of this slip velocity over the surface $\mathcal{S}$ of the colloidal particle plus its boundary layer: $\mathbf{V} = -\langle \mathbf{v}_s \rangle_{\mathcal{S}}$.

As a specific illustration of such motion that is relevant for the polymeric application discussed below, we suppose that we have two spherical particles in the solution (see Fig. 1, left

panel). One particle is catalytic (C) and catalyzes the reaction $A \rightarrow B$. The other particle is chemically inactive or noncatalytic (N) but interacts differently with the A and B species through potential functions V_A and V_B , respectively. The system is similar to that of a sphere-dimer nanomotor with linked catalytic and noncatalytic spheres.⁵ Self-diffusiophoresis, or other types of self-phoresis, provide the mechanism for directed motion.^{9,10} In the present case, where the C and N spheres are not linked, the A and B concentration field gradients cause the N sphere to chemotactically move towards the C sphere. We also note that the chemotactic response of synthetic nanomotors to chemical gradients has been observed experimentally.^{11,12}

The concentration fields of the A and B molecules can be found by solving the diffusion equation, $D\nabla^2 c_A(r) = 0$. This equation must be solved subject to the “radiation” boundary condition on its surface, $k_0 c_A(R_C, t) = k_D R_C \hat{\mathbf{r}} \cdot \nabla c_A(R_C, t)$, where R_C is the radius at which reaction takes place, and $c_A(r \rightarrow \infty) = c_0$, corresponding to a continual supply of fuel at the distant boundaries to establish a steady state. Here $C_A + C_B = C_0$, D is the diffusion coefficient of the solute species, $k_D = 4\pi R_C D$ is the Smoluchowski rate constant and k_0 is the intrinsic reaction rate constant. Solution of the diffusion equation yields the concentration field of B:

$$c_B(\mathbf{r}) = \frac{k_0 c_0}{k_0 + k_D} \frac{R_C}{r}, \quad (2)$$

with a similar expression for $C_A(r)$ that can be found from the conservation condition $C_A + C_B = C_0$ assuming the total density of the A and B species is locally conserved. The B particle concentration field is shown in Fig. 1 (left panel).

Suppose at some time instant t the N sphere is at a vector distance $\mathbf{R}(t)$ from the C sphere. To compute the velocity of N sphere we must average the gradient of the B concentration field over the outer edge of the surface of the boundary layer of the N sphere with radius R_N . Using eqn (2) in eqn (1) and evaluating the surface average to obtain the velocity of the N sphere projected along the direction of $\mathbf{R}(t)$, $V_z(t) = \hat{\mathbf{R}}(t) \cdot \mathbf{V}(t)$, we find,

$$V_z(t) = -\frac{2k_B T c_0 \Lambda}{3\eta} \frac{k_0}{k_0 + k_D} \frac{R_C}{R(t)^2} \equiv -\frac{\alpha}{R(t)^2}, \quad (3)$$

where Λ is given by

$$\Lambda = \int_0^\infty dr r \left(e^{-\beta V_B(r)} - e^{-\beta V_A(r)} \right), \quad (4)$$

with $\beta = 1/k_B T$. Note that if the A and B particles interact with the N sphere through repulsive potentials, and the B potential is less repulsive than that of A, the N sphere will move towards the C sphere (negative V_z). Since the time evolution of the separation between the spheres is given by $dR(t)/dt = V_z(t)$, we can integrate to find how the separation varies with time given an initial separation of R_0 : $R(t) = [R_0^3 - 3\alpha t]^{1/3}$. Thus the C sphere will encounter the N sphere (reach an encounter distance R_f) in a time,

$$\tau_c = \frac{(R_0^3 - R_f^3)}{3\alpha}. \quad (5)$$

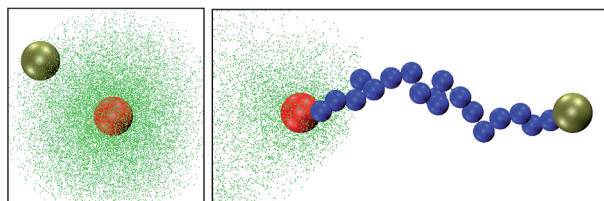


Fig. 1 Left: catalytic C (red) and noncatalytic N (green) spheres along with the B concentration field near the catalytic sphere. The initial separation between the C and N spheres is $R_0 = 10$. Right: an instantaneous configuration of a flexible active polymer with $N_b = 20$ beads. The B concentration field is also shown.

We now link the catalytic and noncatalytic particles by a polymer chain to make an active polymer chain (see Fig. 1, right panel). The diffusiophoretic mechanism will operate and drive the ends of the polymer chain together leading to ring closure. In this way one may expect that the dynamics and characteristic times of ring closure, or more generally loop formation, will be different from those of systems that rely solely on simple diffusion to achieve similar encounter distances. The remainder of the paper will examine such active dynamics in quantitative detail. However, since fluctuations are an important factor in the dynamics of these molecular systems, our investigations are carried out using mesoscopic particle-based simulations where the polymer chain is treated at coarse-grained level as a collection of beads and the solvent is evolved using multiparticle collision dynamics (MPCD), the details of which are given in the next section.

3 Mesoscopic dynamics

3.1 Polymer model

The coarse-grained polymer consists of N_b beads with coordinates $\mathbf{r}_i$ interacting with each other through a potential given by

$$V_p(\mathbf{r}^{N_b}) = \sum_{i=1}^{N_b-1} V_s(b_i) + \sum_{i=1}^{N_b-2} V_B(\mathbf{b}_i, \mathbf{b}_{i+1}) + \frac{1}{2} \sum_{i,j=1}^{N_b} V_{LJ}(r_{ij}). \quad (6)$$

The two-body harmonic spring potential $V_s(\mathbf{b}_i) = \frac{1}{2} k(b_i - b_0)^2$ penalizes departures of the modulus, b_i , of the bond vector $\mathbf{b}_i = \mathbf{r}_i - \mathbf{r}_{i-1}$ from its equilibrium value of b_0 . For semi-flexible polymers there is a three-body bending potential $V_B(\mathbf{b}_i, \mathbf{b}_{i+1}) = \kappa(1 - \cos \phi_i)$ which penalizes departures of the angle ϕ_i between consecutive bond vectors from its equilibrium value of zero. The parameter $\kappa = 0$ for flexible polymers. There is also a repulsive Lennard-Jones (LJ) potential V_{LJ} acting between all pairs of beads. It has the form, $V_{LJ}(r) = 4\epsilon[(\sigma/r)^{12} - (\sigma/r)^6 + 1/4]$, $r \leq r_c$, where $r_c = 2^{1/6}\sigma$ is the cutoff distance and σ and ϵ take values that depend on the nature of the beads that are involved in the specific pair interaction. Two of the beads in the polymer are catalytic C and noncatalytic N, as discussed in the previous section. Usually these beads are chosen at the ends of the chain to study ring closure but other choices will be employed to study loop formation. The remainder of the beads that comprise the polymer chain are neutral and do not participate in the diffusiophoretic mechanism. Both of the end beads have same diameter $d_C = d_N = 4$, while all of the middle polymer beads have diameter $d_p = 2$. The system size and dynamical time scales are computationally convenient for our choice of bead diameters, but other choices could have been made. This will not affect the qualitative features of the phenomena considered in this paper.

The polymer is immersed in a fluid containing a large number N_s of A and B “molecules”. These solvent molecules interact with the beads in the polymer chain through repulsive LJ potentials with the same form as that given above but, again, the length and energy parameters depend on the specific pair interaction under consideration. Thus, the polymer bead–solvent potential takes the form,

$$V_{bs}(\mathbf{r}^{N_b}, \mathbf{r}^{N_s}) = \frac{1}{2} \sum_{i=1}^{N_b} \sum_{j=1}^{N_s} V_{LJ}(r_{ij}). \quad (7)$$

The interaction potentials for the A and B molecules with the C bead and neutral beads have same energy parameter ϵ , while these molecules have different energy parameters $\epsilon_A = \epsilon$ and ϵ_B , for their interaction with the N bead. There are no solvent–solvent intermolecular potentials. These interactions are embodied in multiparticle collisions discussed below. Thus, the potential energy of the entire system is $V(\mathbf{r}^{N_b}, \mathbf{r}^{N_s}) = V_p(\mathbf{r}^{N_b}) + V_{bs}(\mathbf{r}^{N_b}, \mathbf{r}^{N_s})$.

3.2 Dynamics

The time evolution of the system is carried out using a mesoscopic hybrid molecular dynamics-multiparticle collision dynamics (MD-MPCD) scheme.^{13,14} In this hybrid scheme, the evolution consists of a concatenation of streaming and multiparticle collision steps. In the streaming step, the dynamics is evolved by Newton's equations of motion governed by forces determined from the total potential energy $V(\mathbf{r}^{N_b}, \mathbf{r}^{N_s})$ of the system. In the collision steps, which occur at time intervals τ , the point-like solvent particles are sorted into cubic cells with cell size a_0 . The choice of cell size is such that the mean free path $\lambda < a_0$. Multiparticle collisions among the solvent molecules are performed independently in each cell, which results in the post collision velocity of solvent particle i in cell ξ being given by $\mathbf{v}'_i = \mathbf{V}_\xi + \hat{\omega}_\xi(\mathbf{v}_i - \mathbf{V}_\xi)$, where $\mathbf{V}_\xi$ is the center-of-mass velocity of particles in cell ξ and $\hat{\omega}_\xi$ is a rotation matrix. In order to ensure Galilean invariance for systems with small λ , a random grid shift is applied in each direction of the simulation box.^{15,16} The method described above conserves mass, momentum and energy and accounts for the hydrodynamic interactions and fluid flow fields,^{17,18} which are important for the dynamics of the active polymer chain.

A chemical reaction $A + C \rightarrow B + C$ takes place on the catalytic end of the polymer whenever A encounters C and leaves the boundary layer region. In this reaction the species identity is changed from A to B, but the position and velocity are not changed. The multiparticle collisions will change the magnitude and velocity of the particles so that the combination of species change and multiparticle collision may be regarded as a coarse-grained reactive event. Since the species change takes place just outside the boundary layer where interactions are zero, there are no discontinuous changes in the forces. In the absence of fluxes of chemical species, reactions on the C sphere would lead to the total conversion of A to B, and when this occurs the diffusiophoretic mechanism will cease to operate. In order to maintain the system in a nonequilibrium steady state, B molecules are converted back to A molecules when they diffuse sufficiently far from the catalytic sphere.

In the simulations described below, all quantities are reported in dimensionless units based on energy ϵ_A , mass m_A and distance σ_A . In these units the masses of both A and B species are $m = 1$ and the masses of the C and N spheres and polymer beads, m_C , m_N and m_p , respectively, were adjusted

according to their diameters to ensure density matching with the solvent. Periodic boundary conditions were applied on the cubic simulation box with sides $L = 50$. We chose the average number of particles per cell to be $n_0 \approx 10$ in all simulations. The rotation operator for MPC dynamics is taken to correspond to rotation about a randomly chosen axis by an angle of $\pi/2$. The system temperature was fixed at $T = 0.2$. For integrating the Newton's equation of motion with the velocity Verlet algorithm, the MD time step is taken as $\Delta t = 0.01$, and the MPC time is $\tau = 0.5$. Unless specified the repulsive LJ potential has $\epsilon_A = 1.0$ and $\epsilon_B = 0.1$ for interactions with the N sphere.

4 Polymer ring closure and loop formation

Ring closure and loop formation in polymers are dynamical processes with broad applications. For example, often loop formation is induced in DNA by a protein or protein complex that binds to two different sites of DNA simultaneously. The resulting loop formation may regulate aspects of DNA metabolism.^{19,20} In addition to loop formation in biopolymers, studies of ring closure and loop formation in other polymeric systems, as well as in carbon nanotubes, have been carried out.^{21–24} The presence of long-range interactions can influence chain closure dynamics and it has been suggested that such long-range interactions may play a role in protein folding rates.²⁵ In other studies related to long-range interactions, it was shown that the presence of a viscoelastic fluid around the polymer changes the manner in which the polymer relaxes and this influences loop formation dynamics.²⁶ The presence of hydrodynamic interactions and denaturants in the solution also modifies the mean first passage time of the polymer that characterizes the ring closure rate.^{27,28} Other factors which affect the cyclization dynamics are the polymer structure, the “goodness” of the solvent and solvent viscosity.^{29–31}

The average end-to-end ring closure time, $\bar{\tau}_c$, scales with the number of polymer beads, N_b as $\bar{\tau}_c \sim N_b^\gamma$, and the details of the scaling structure depend on the factors governing the motion of the chain ends, the connectivity of the chains and solvent effects. A very simple model for polymer cyclization is the free particle model of Brereton and Rusli,³² where the motion of the chain was treated as that of independent particles which, at equilibrium, satisfy the same Gaussian distance distribution that they would obey if they were connected by a chain with N_b segments. This model predicted the value $\gamma = 3/2$ for a polymer in a θ solvent and $\gamma = 9/5$ for a good solvent. Wilemski and Fixman (WF)³¹ showed that $\gamma = 2$ for a free-draining Rouse chain, which is different from the prediction of Szabo, Schulten and Schulten (SSS)²¹ who found $\gamma = 3/2$ for this type of chain. Later, it was pointed out by Portman³³ that the SSS theory gives a lower bound to the chain closing time while the WF theory gives an upper bound; the discrepancy between two models can be resolved by a proper choice of the effective diffusion coefficient in the SSS theory to yield a $\gamma = 2$ dependence.³⁴ Another theoretical study³⁵ probing the effect of hydrodynamics on ring closure using renormalization group calculations predicted

$\gamma = 3/2$ for a θ solvent, which is in good agreement with the result obtained for a Zimm chain in θ solvent conditions treated within the WF framework.²⁷

Experimentally, a value of $\gamma = 1.62 \pm 0.10$ was found for polystyrene in cyclohexane²⁹ at 34.5 °C, the θ condition for the polymer, which matches very well with the predictions made in theoretical models. Another study of the cyclization of polystyrene in toluene³⁶ in a good solvent found $\gamma = 1.35$, a value that is smaller than that predicted by models for cyclization dynamics under similar conditions; the discrepancy was attributed to the polydispersity of the polymer samples. In a study of the cyclization of polypeptides of the alanine-glycine-glutamine trimer, the closure time scaling exponent was found to be $\gamma = 3/2$ for peptides having lengths more than 15 residues.³⁷ All of these results indicate that the exponent γ is anticipated to fall in the range $1.5 \leq \gamma \leq 2.0$, and that its precise value depends on the nature and length of the polymer chain, its interactions and the solvent.

4.1 Chemically-inactive polymer chains

The flexible polymer chains considered in this study exist in extended conformations under equilibrium conditions. The ring closure time for a polymer chain was computed from our MD-MPCD simulations as follows: Initial polymer configurations were selected from an equilibrium distribution of chain conformations with a given number N_b of beads; thus, each initial conformation of the chain has a different value of the end-to-end distance R_0 . Such initial conditions are possibly more easily realized in the laboratory than those corresponding to chains with a fixed end-to-end length. The probability distribution of R_0 values obtained from this sampling procedure is shown in Fig. 2 for chains of several lengths. The solid lines are fits of the data with Gaussian distributions whose mean, $\bar{R}_0$, increases with N_b (Table 1).

The dynamics of each realization of the polymer chain was then followed until its end beads reached a predetermined final separation distance $R_f = 5$, and the time τ_c for this “closure” event was recorded. The ring closure time $\bar{\tau}_c$ was then taken to

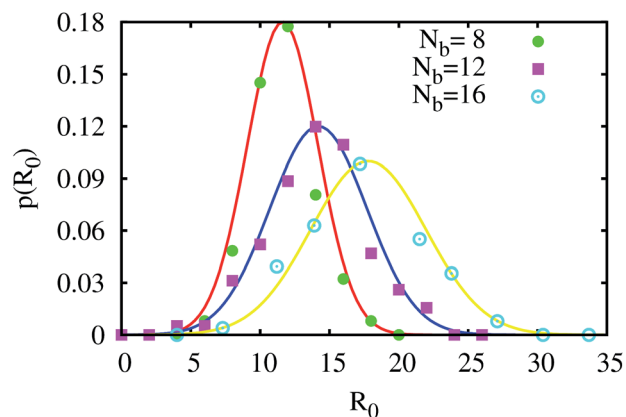


Fig. 2 The distribution of the end-to-end distance R_0 for flexible polymer chains having $N_b = 8, 12$ and 16 beads. Each distribution was determined from 100 initial conformations.

Table 1 The initial value of the mean end-to-end distance $\bar{R}_0$ for polymer chains having N_b monomers

N_b	6	8	10	12	14	16	20
$\bar{R}_0$	8.8	11.6	12.0	14.2	16.1	17.8	21.2

be the average value of these τ_c times. From its definition, we see that the average over realizations used to obtain $\bar{\tau}_c$ includes an average over a distribution of initial end-to-end separations R_0 with mean $\bar{R}_0$. The results of our simulations for flexible polymer chains show that $\bar{\tau}_c \sim N_b^{3/2}$ (Fig. 3).

4.2 Chemically-active polymer chains

A chemically-active flexible polymer chain with catalytic and noncatalytic end groups displays considerably different ring closure dynamics. The chemical gradient generated at the catalytic C end induces a chemotactic response at the non-catalytic N end of the chain, which tends to drive the polymer to the closed ring conformation by the diffusiophoretic mechanism discussed in Section 2. Examples of initial (left) and final (right) configurations of a flexible polymer chain, along with the concentration field of the B product molecules that plays an essential role in the mechanism, are shown in Fig. 4.

One signature of a chemotactic response is the existence of a non-zero value of the average velocity of the N end bead projected on the instantaneous unit vector distance from the C to N beads, $V_z = \hat{\mathbf{R}} \cdot \mathbf{V}$. From eqn (3) for independent C and N spheres, we expect that this velocity will depend on the instantaneous end-to-end distance $R(t)$ in the polymer chain.

We first consider a simpler and more global measure of the response by computing the probability distribution, $p(V_z)$, determined from a time average over the entire history of the evolution, from the initial to final values of $R(t)$, for each trajectory in an ensemble of trajectories. This distribution will have a non-zero mean for chemotactic motion, and the mean

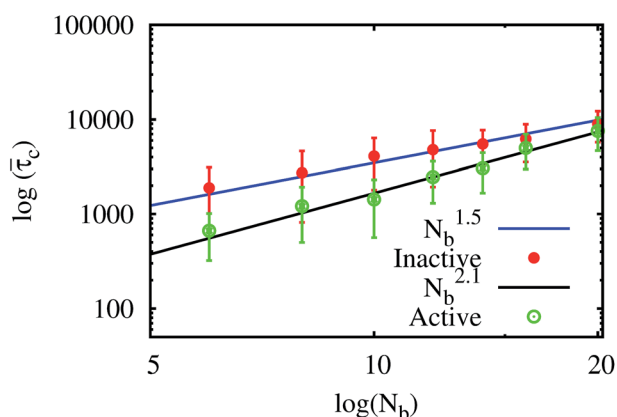


Fig. 3 log–log plot of the ring closure time $\bar{\tau}_c$ vs. N_b for flexible chemically inactive (red) and active (green) polymers. The values of the parameters are $\varepsilon_A = \varepsilon_B = 1.0$ for the inactive polymer and $\varepsilon_A = 1.0$, $\varepsilon_B = 0.1$ for the active polymer. Each value of $\bar{\tau}_c$ in the plot is the result of an average over 100 realizations.

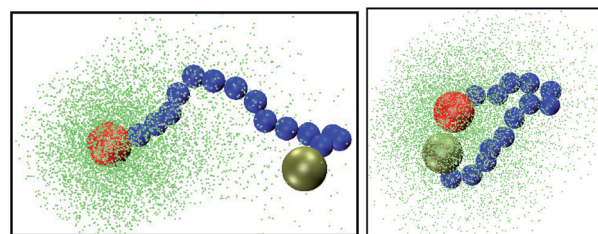


Fig. 4 Instantaneous configurations of a polymer chain in the extended initial (left) and closed final (right) states. The figure also shows the B particle concentration field due to the A $\rightarrow$ B reaction at the catalytic (red) bead.

velocity, $\bar{V}_z$, will be the average of the velocity over the different histories in the ensemble. This probability distribution is plotted in Fig. 5, which presents results for both chemically active and inactive flexible polymer chains. For the inactive polymer the velocity distribution has an equilibrium Maxwell–Boltzmann form with width, $\sqrt{k_B T/m_N}$, and zero mean. By contrast, the active polymer chain has a distribution of the same form with the same width but with a non-zero mean of $\bar{V}_z = 0.012$ for $N_b = 8$ and $\bar{V}_z = 0.005$ for $N_b = 16$.

The dynamics of the end bead can be probed further by considering the time evolution of the end-to-end distance averaged over realizations, $\bar{R}(t)$, which is plotted in Fig. 6, bottom panel.

For independent freely-moving C and N spheres, we showed in Section 2 that $R(t)^3$ should vary linearly with time. Consequently, for the active polymer we have chosen to plot $\bar{R}_0^3 - \bar{R}(t)^3$ versus time for several values of $\bar{R}_0$ (N_b). In the simulations, $\bar{R}(t)$ was determined from an average over an ensemble of trajectories; when a trajectory reached the closure separation R_f it continued to carry this value for subsequent times. Thus, using this definition, for sufficiently long times the average $\bar{R}(t)$ will take the value R_f . For comparison with the polymer data, in top panel of the figure, we show time evolution of $\bar{R}_0^3 - \bar{R}(t)^3$ for independent C and N spheres, again for several values of $\bar{R}_0$ (in this case the initial condition can be chosen to be $\bar{R}_0$ for each

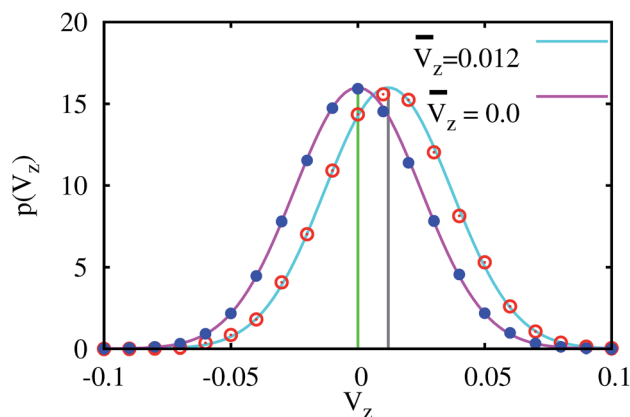


Fig. 5 Velocity probability distribution $p(V_z)$ versus V_z for flexible chemically inactive (filled circles) and active (open circles) polymers with $N_b = 8$.

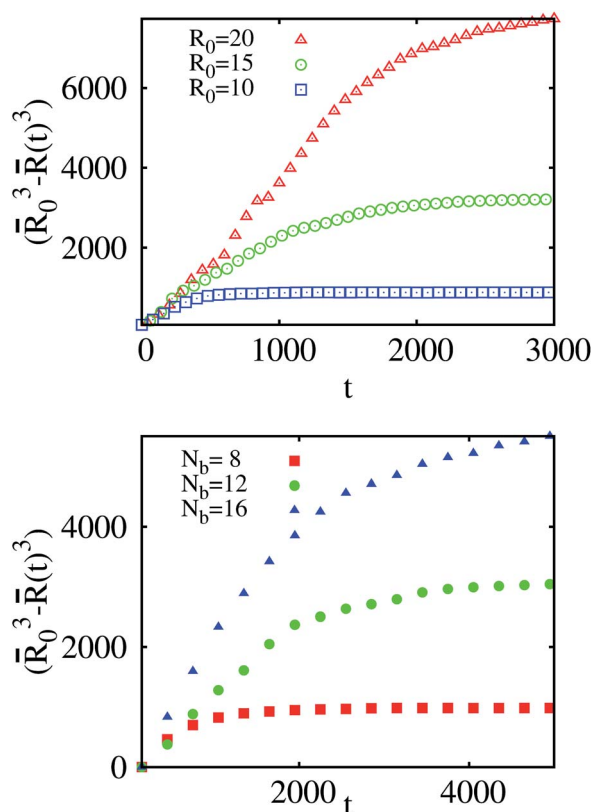


Fig. 6 Top: plots of $\bar{R}_0^3 - \bar{R}(t)^3$ versus time for independent C and N spheres for various values of $\bar{R}_0$. Bottom: plots of the same quantity for a flexible active polymer having $N_b = 8$ (red squares), $N_b = 12$ (green circles) and $N_b = 16$ (blue triangles) beads.

realization). The results show a linear variation with time at short times, before the plateau leading to the final $\bar{R}_0^3 - R_f^3$ value is reached. The initial slopes are independent of $\bar{R}_0$ as predicted by the deterministic theory. Table 2 shows the comparison of $\bar{\tau}_c$ obtained from simulations and deterministic theory for both independent C and N spheres and flexible polymers. In the deterministic theory, the $\bar{\tau}_c$ values were taken to be the times at which the extrapolated linear region of $\bar{R}_0^3 - \bar{R}(t)^3$ reaches the value $\bar{R}_0^3 - R_f^3$.

The polymer results for $\bar{R}_0^3 - \bar{R}(t)^3$ in Fig. 6 (bottom) also display a roughly linear behavior at short times; however, in this case the slopes are no longer equal. Evidence for the cubic

Table 2 Comparison of $\bar{\tau}_c$ obtained from simulation and deterministic theory for independent C and N sphere capture and active flexible polymer chains

Independent C and N spheres			
$\bar{R}_0$	10	15	20
$\bar{\tau}_c$ (simulation)	442	1449	2089
$\bar{\tau}_c$ (theory)	340	1200	2100
Flexible active polymers			
N_b	8	12	16
$\bar{\tau}_c$ (simulation)	891	2352	3812
$\bar{\tau}_c$ (theory)	898	2587	2720

dependence on $\bar{R}(t)$ can be seen in spite of now averaging over a Gaussian distribution of initial R_0 values. Since intermediate polymer chains with differing numbers of beads link the C and N end beads, the evolution of the end-to-end distance will depend on the characteristics of the intermediate chain. This feature can lead to $\bar{R}_0^3 - \bar{R}(t)^3$ curves with different slopes for different values of N_b .

4.2.1 Scaling of ring closure time with N_b . Active polymers undergo ring closure much more rapidly than their inactive counterparts. As shown in Fig. 3, the small active polymer chains considered in this paper scale with the chain length as $\bar{\tau}_c \sim N^{2.1}$, in contrast to the $\bar{\tau}_c \sim N^{3/2}$ scaling found for our inactive chains. Since, according to eqn (2), the B concentration field decays as the reciprocal of the distance from the catalytic end bead, there is an effective attractive long-range interaction between the end beads. In this connection it is interesting to note that the theoretical description³⁸ of ring closure dynamics for polymers with nonlocal interactions in theta solvent conditions yielded a ring closure time exponent of 2.09, similar to that for our active polymers. The probability distribution of closing times, $p(\tau_c)$, provides more detailed information on the ring closure dynamics. Fig. 7 plots histograms of $p(\tau_c)$ for flexible polymers with lengths of $N_b = 8$ and 16. For both polymer chains one can observe distributions of τ_c values with long tails, especially for the polymer with a longer chain length. The spread in initial R_0 values in realizations of the dynamics, in conjunction with the fact that the velocity $V_z(t)$ depends on the instantaneous separation as $R(t)^{-2}$, will give rise to a wide dispersion ring closure times: realizations with shorter R_0 values will be strongly chemotactically driven to close while those with larger R_0 will only be driven very weakly. This feature is supported by the fact that $p(\tau_c)$ for independent C and N spheres with a fixed initial R_0 separation does not display a very long tail.

Eqn (5) showed that the capture time for independent C and N spheres scaled as R_0^3 . Even though the flexible polymer initial conditions include sampling over a distribution of R_0 values with mean $\bar{R}_0$, this scaling persists. Fig. 8 plots the $\bar{\tau}_c$ as a function of $\bar{R}_0$ on a log-log scale and shows that $\bar{\tau}_c \sim \bar{R}_0^3$. This further

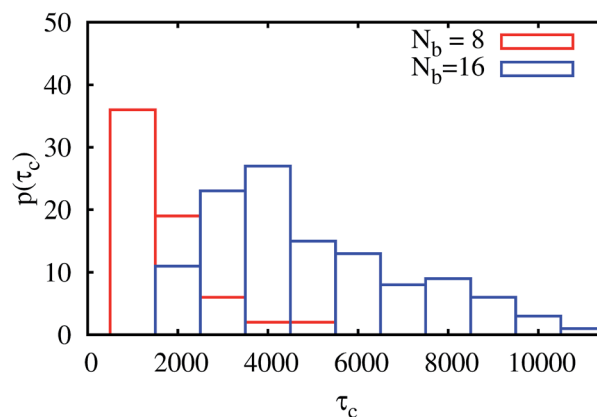


Fig. 7 The distribution $p(\tau_c)$ of capture times τ_c for flexible active polymers having $N_b = 8$ and $N_b = 16$ beads determined from 100 realizations of the dynamics. The energy parameters are $\varepsilon_a = 1.0$, $\varepsilon_b = 0.1$.

confirms the operation of the diffusiophoretic mechanism for end-to-end capture and its effect on the structure of $p(\tau_c)$.

The scaling behavior changes for the semiflexible polymers. Fig. 8 also shows $\bar{\tau}_c$ versus $\bar{R}_0$ for a semiflexible polymer with $\kappa = 0.5$. Semiflexibility makes the closure dynamics slower and we find $\bar{\tau}_c \sim \bar{R}_0^{2.5}$. Stiffness hinders closure, especially for smaller polymer chains. Increasing κ further makes it more difficult for the polymer to close and, while it takes more time to close, the overall the scaling remains the same. While a thorough study of scaling would require more extensive simulations for polymers with larger N_b , the main result of our study, more rapid ring closure for active chains, is demonstrated by our simulations.

4.2.2 End-to-end versus internal-to-end loops. Studies of polymer cyclization have focused primarily on the formation of “external” or end-to-end loops; however, for biopolymers the appearance of “internal” loops where two interior points on the chain make contact, is perhaps a more relevant process. For example, in DNA internal loops play a key role in various aspects of gene expression.³⁹ The formation of an internal-to-end loop is another possibility. Studies related to internal chain looping are limited.^{40,41} In general, one expects that loop formation involving internal sites will be slower than that for end-to-end loops of equal contour length due to the restricted conformational freedom of the internal polymer groups.

Fig. 9 shows the loop length dependence of the loop formation time for a flexible active polymer. To study internal-to-end loop formation, we consider the polymer having $N_b = 12$ beads and make one of the internal beads the noncatalytic sphere. The average time it takes to form an internal-to-end loop of length j is denoted by $\bar{\tau}_{0j}(N_b)$, while the time it takes to form an end-to-end loop in a polymer of the same length j is $\bar{\tau}_{0j}(j)$. The time $\bar{\tau}_{0j}(N_b)$ is always longer than $\bar{\tau}_{0j}(j)$ for a loop of the same length j because of the restricted conformational freedom of the interior noncatalytic sphere, as noted above. Greater

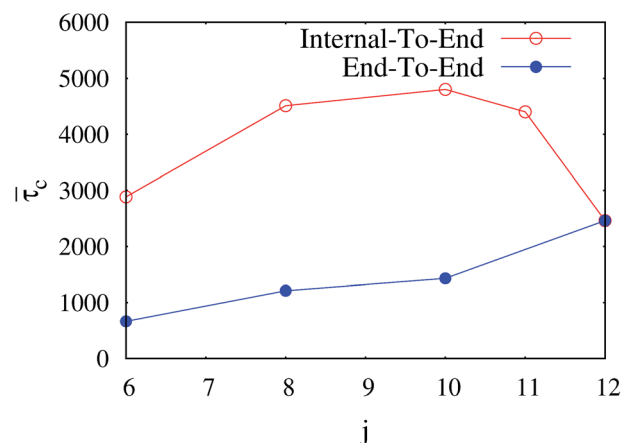


Fig. 9 Loop length dependence of the loop formation time. Filled circles are for end-to-end loop formation while unfilled circles are for internal-to-end loop formation for flexible active polymers with $N_b = 12$.

values of the internal-to-end loop formation time compared to end-to-end loop formation of same length has been observed in recent experiments.⁴¹

5 Conclusions

The results presented in this paper demonstrated that chemically-active polymers which undergo ring closure or loop formation more rapidly than inactive polymer chains can be constructed. Our studies of ring closure showed how the long-range nature of the chemical concentration gradients, self-generated by the presence of a catalytic bead on which a chemical reaction $A \rightarrow B$ occurs, could cause a distant bead which responds to this gradient to chemotactically move toward the source of the gradient. Thus, the chemical gradient serves both to guide the beads to encounter each other and provides the source of the directed motion.

Apart from presenting detailed documentation on the nature and magnitude of ring closure dynamics for active polymer chains, our study addresses the broader issue of how phoretic mechanisms that synthetic self-propelled nanomotors use to execute directed motion can be exploited to design systems where chemical reagents are targeted to find each other in order to carry out specific chemical reactions. In this context, the polymer ring closure problem is simply an example designed to illustrate potential applications to other types of reactive systems. One can imagine situations where this mechanism could be used to enhance reaction rates. The motor components could be attached to different molecules or macromolecules in order to bring them into contact so that they could react, and, subsequent to the reaction, the active groups could be removed by other means. Possibly through investigations of this type insight may be gained into how active motion could be used to more efficiently carry out reactive process that normally rely on simple diffusion-influenced kinetics.

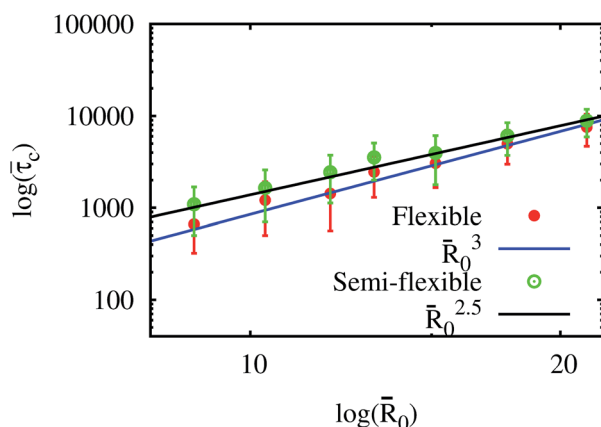


Fig. 8 Plot of $\bar{\tau}_c$ vs. the average initial distance between the end beads $\bar{R}_0$ for flexible (red) and semiflexible (green) chemically active polymers. The values of the parameters are $\varepsilon_a = 1.0$, $\varepsilon_b = 0.1$. Each $\bar{\tau}_c$ time is the result of an average over 100 realizations. Each $\bar{R}_0$ corresponds to certain number of beads of polymer which is given in Table 1.

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