

Migration and Separation of Polymers in Nonuniform Active Baths

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Polymerlike structures are ubiquitous in nature and synthetic materials. Their configurational and migration properties are often affected by crowded environments leading to nonthermal fluctuations. Here, we study an ideal Rouse chain in contact with a nonhomogeneous active bath, characterized by the presence of active self-propelled agents which exert time-correlated forces on the chain. By means of a coarse-graining procedure, we derive an effective evolution for the center of mass of the chain and show its tendency to migrate toward and preferentially localize in regions of high and low bath activity depending on the model parameters. In particular, we demonstrate that an active bath with nonuniform activity can be used to separate efficiently polymeric species with different lengths and/or connectivity.

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Living systems continuously exchange information and energy with the surrounding environment and their biological function unavoidably relies on mechanisms that are only allowed out of equilibrium [1]. This inherent nonequilibrium state, exemplified by the hallmark feature of self-propulsion, gives rise to a diversity of collective behaviors shared by biological systems across various scales, ranging from molecular motor assemblies [2–4] to swarming bacteria [5] and flocking birds [6–8]. While a comprehensive theory that encompasses the diverse properties of living matter is still elusive due to the astonishing complexity of the biological world, significant efforts have been directed toward constructing a theoretical framework for *active matter* [9–13]. Prominent examples from biology include flagellated bacteria [14], algae [15,16] and other motile microorganisms [17], molecular motors on cytoskeletal filaments [18], active worms [19,20], and many others. Active colloidal molecules are also experimentally synthesized in the lab [17,21,22] using techniques such as self-diffusiophoresis via catalytic reactions [23–25], light-induced self-thermophoresis [26], nonreciprocal deformation cycles [27,28], and the integration of biological components with synthetic structures in biohybrid systems [29].

Numerous active biological systems, including some of the examples mentioned above, appear as filamentous or polymerlike structures. It is well-established that several polymeric molecules in the interior of a cell rely on a variety of active reactions to regulate their biological functions. For example, DNA is continuously processed by enzymes such as DNA polymerase and helicase to ensure its successful replication [30], ribosomes slide along

RNA strands to synthesize proteins [30], and the chromosomal loci dynamics is strongly affected by ATP-dependent nonthermal fluctuations [31]. For this reason, the field of *active polymers* [32,33] has gained a growing level of attention in recent years, yielding insights into the impact of nonequilibrium fluctuations and activity on structural and dynamic properties of both isolated chains and suspensions of polymers [32–48]. In this Letter, we focus on the effect of a nonequilibrium bath featuring a spatially nonuniform degree of activity on a polymeric molecule described as an ideal Rouse chain. While recent attention has been devoted to the impact of inhomogeneous activity [49–61], there exists a notable gap in our understanding regarding its influence on polymerlike structures. We reveal a previously unexplored effect in these systems: nonhomogeneous active baths induce qualitatively different spatial distributions in Rouse polymers depending on their contour length and connectivity. More precisely, short polymers preferentially accumulate in regions of low bath activity, whereas long ones in regions of high bath activity. Moreover, we demonstrate that highly connected structures typically display a tendency to localize where the activity is lower. Our Letter does not refer to a specific biological or synthetic system, rather it is inspired by the ubiquity of polymeric structures in nature.

The model—We study a minimal stochastic d -dimensional model of an ideal Rouse polymer composed by N units, subjected to exponentially correlated noises, which account for the interaction with an active bath. The chain connectivity is encoded in the matrix M_{ij} [62], which determines all the pairs of interacting monomers. See Fig. 1 for a sketch of a

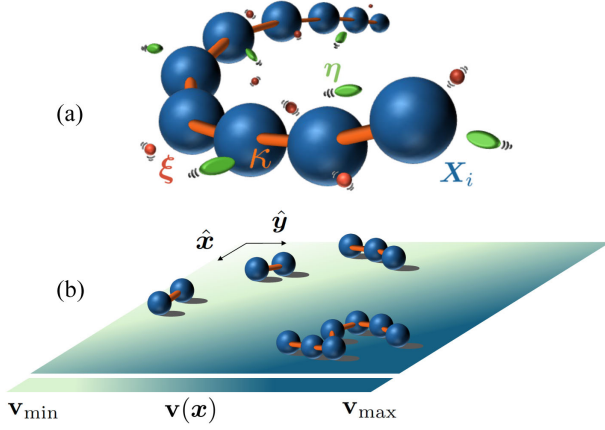


FIG. 1. (a) Sketch of a linear polymer immersed in an active bath. The blue monomers, connected by orange bonds with stiffness κ , interact with the red passive molecules (thermal bath) and are subjected to additional time-correlated forces due to the collision with the green active agents suspended in the surrounding fluid. (b) Spontaneous separation of polymer species with different lengths dispersed in a medium characterized by a nonuniform activity field $v(\mathbf{x})$.

polymer with linear connectivity. The polymer is characterized by a quadratic Hamiltonian,

$$\mathcal{H} = \frac{\kappa}{2} \sum_{i=0}^{N-1} \sum_{j=0}^{N-1} M_{ij} \mathbf{X}_i \cdot \mathbf{X}_j, \quad (1)$$

with $\mathbf{X}_i$ the position of the i th monomer and κ the coupling strength of interacting monomers. We neglect inertial effects compared to viscous forces and assume that the polymer's motion follows the overdamped Langevin equation

$$\dot{\mathbf{X}}_i(t) = -\mu \nabla_{\mathbf{X}_i} \mathcal{H} + \mu \mathbf{f}_a(\mathbf{X}_i) \boldsymbol{\eta}_i + \boldsymbol{\xi}_i(t). \quad (2)$$

Here, μ denotes the mobility of the monomers and $\{\boldsymbol{\xi}_i(t)\}$ are zero-mean Gaussian white noises with correlation $\langle \boldsymbol{\xi}_{i\alpha}(t) \boldsymbol{\xi}_{j\beta}(s) \rangle = 2D \delta_{ij} \delta_{\alpha\beta} \delta(t-s)$, describing thermal fluctuations. The thermal diffusivity is related to the mobility via the Einstein's relation $D = \mu T$, with the Boltzmann constant set to $k_B = 1$ throughout the Letter. As a result of the collisions with the active agents dispersed in the bath, the polymer experiences additional nonthermal fluctuations that violate the detailed balance condition and drive it out of equilibrium. This effect is modeled by the active forces $\mathbf{f}_a(\mathbf{X}_i) \boldsymbol{\eta}_i$ in Eq. (2), characterized by a typical magnitude that varies nonhomogeneously in space according to the function $\mathbf{f}_a(\mathbf{x})$. These active forces are aligned with the orientation vectors $\boldsymbol{\eta}_i$, which evolve as the Ornstein-Uhlenbeck processes $\tau \dot{\boldsymbol{\eta}}_i = -\boldsymbol{\eta}_i + \boldsymbol{\zeta}_i(t)$. Here, $\{\boldsymbol{\zeta}_i(t)\}$ are N independent zero-mean Gaussian white noises with correlations $\langle \boldsymbol{\zeta}_{i\alpha}(t) \boldsymbol{\zeta}_{j\beta}(s) \rangle = 2\tau d^{-1} \delta_{ij} \delta_{\alpha\beta} \delta(t-s)$, and τ is the characteristic relaxation time of the Ornstein-Uhlenbeck processes that sets the persistence time of the active forces.

The time-translation-invariant correlation function of the orientation vectors reads $\langle \eta_{i\alpha}(t) \eta_{j\beta}(s) \rangle = \delta_{ij} \delta_{\alpha\beta} \mathcal{C}_\eta(t-s)$, with $\mathcal{C}_\eta(t-s) = d^{-1} \exp(-|t-s|/\tau)$. The variance of $\zeta_{i\alpha}$ has been chosen such that $\langle \|\boldsymbol{\eta}_i\|^2 \rangle = \langle \sum_\alpha \eta_{i\alpha}^2 \rangle = 1$ for all d and i . Note that the model can alternatively be used to describe a chain of active particles, each endowed with its own polarity, which use energetic resources distributed in the bath according to the activity $\mathbf{f}_a(\mathbf{x})$ to self-propel.

Effective dynamics—The stochastic dynamics in Eq. (2) can be rewritten within the Rouse domain [63] for the Rouse modes $\boldsymbol{\chi}_i = \sum_j \varphi_{ij} \mathbf{X}_j$, where the matrix φ_{ij} is chosen in such a way to diagonalize the symmetric connectivity matrix M_{ij} and with the rows normalized to unity. The modes evolve as

$$\dot{\boldsymbol{\chi}}_i = -\gamma_i \boldsymbol{\chi}_i + \sum_j \varphi_{ij} v(\mathbf{X}_j) \boldsymbol{\eta}_j + \tilde{\boldsymbol{\xi}}_i(t), \quad (3)$$

where the Gaussian white noise $\tilde{\boldsymbol{\xi}}_i(t)$ has the same statistics as $\boldsymbol{\xi}_i(t)$, and the monomer position $\mathbf{X}_j$ can be rewritten in terms of the Rouse modes using the inverse transformation φ^{-1} . The typical swim speed of the monomers due to activity is $v(\mathbf{x}) \equiv \mu \mathbf{f}_a(\mathbf{x})$, which we will refer to as the activity field. The relaxation rates $\{\gamma_i\}$ of the Rouse modes in the absence of activity are proportional to the eigenvalues $\{\lambda_i\}$ of the connectivity matrix, i.e., $\gamma_i = \gamma \lambda_i$, where $\gamma = \mu \kappa$. Unlike the case of a Rouse polymer in a thermal bath at equilibrium, the Rouse modes are now coupled via the activity field $v(\mathbf{X}_i)$, which makes the analytical treatment of the problem more challenging. We denote with $\mathcal{P}(\{\boldsymbol{\chi}\}, \{\boldsymbol{\eta}\}, t)$ the joint probability density that the Rouse modes and the orientation vectors assume the values $\{\boldsymbol{\chi}\}$ and $\{\boldsymbol{\eta}\}$ at time t , respectively. Being the underlying dynamics of the system Markovian, the time evolution of $\mathcal{P}(\{\boldsymbol{\chi}\}, \{\boldsymbol{\eta}\}, t)$ follows the Fokker-Planck equation [64,65]

$$\partial_t \mathcal{P} = (\mathcal{L}_0 + \mathcal{L}_a + \mathcal{L}_\eta) \mathcal{P}, \quad (4)$$

with the set of operators $\{\mathcal{L}_0, \mathcal{L}_a, \mathcal{L}_\eta\}$ defined as

$$\begin{aligned} \mathcal{L}_0 &\equiv \sum_{i=0}^{N-1} \nabla_i \cdot [\gamma_i \boldsymbol{\chi}_i + D \nabla_i], \\ \mathcal{L}_a &\equiv \sum_{i=0}^{N-1} \nabla_i \cdot \left[-\sum_j \varphi_{ij} v(\mathbf{X}_j) \boldsymbol{\eta}_j \right], \\ \mathcal{L}_\eta &\equiv \sum_{i=0}^{N-1} (d\tau)^{-1} \left[\tilde{\nabla}_i^2 + d \tilde{\nabla}_i \cdot \boldsymbol{\eta}_i \right]. \end{aligned} \quad (5)$$

Here, we used the shorthand notation $\nabla_i \equiv \nabla_{\boldsymbol{\chi}_i}$ and $\tilde{\nabla}_i \equiv \nabla_{\boldsymbol{\eta}_i}$. The operator $\mathcal{L}_0$ corresponds to the Fokker-Planck operator of a free Rouse chain in contact with an

equilibrium thermal bath, while the effect of the activity is brought in by $\mathcal{L}_a$ and $\mathcal{L}_\eta$.

To investigate how the spatial localization of the polymer correlates with the bath activity, we look for a description that includes the center of mass of the polymer $\mathbf{X}_{\text{com}} = \boldsymbol{\chi}_0/\sqrt{N}$ as the only relevant variable. Accordingly, we perform a coarse-graining procedure based on a moment expansion and a small-gradient approximation, as detailed in the Supplemental Material (SM) [66]. In particular, we assume that the activity field v has small spatial variations on the length scales of $\ell_b = \sqrt{dT/k}$ and $\ell_p = v\tau$, which correspond to the bond length and the persistence length of an active particle, respectively. As a consequence, the marginal density $\rho_0(\boldsymbol{\chi}_0, t)$ of the zeroth Rouse mode and its associated probability flux $\mathcal{J}_0$ will also exhibit small gradients on the same length scales. This simplifying assumption makes the gradient expansion (see, e.g., Refs. [50,61,67]) a suitable approach to derive an effective equation for ρ_0 . In particular, by neglecting contributions of order $\mathcal{O}(\nabla_0^2)$ and higher in $\mathcal{J}_0$, thus truncating the expansion to the drift and diffusion order (see SM for details), we obtain that $\rho_0(\boldsymbol{\chi}_0, t)$ evolves according to

$$\partial_t \rho_0 = -\nabla_0 \cdot [\mathbf{V} \rho_0 - \nabla_0 (\mathcal{D} \rho_0)], \quad (6)$$

where we introduced the effective drift $\mathbf{V}(\boldsymbol{\chi}_0)$ and diffusivity $\mathcal{D}(\boldsymbol{\chi}_0)$ given by

$$\mathcal{D}(\boldsymbol{\chi}_0) = D + \frac{\tau}{d} v^2 \left(\frac{\boldsymbol{\chi}_0}{\sqrt{N}} \right), \quad (7)$$

$$\mathbf{V}(\boldsymbol{\chi}_0) = (1 - \epsilon/2) \nabla_0 \mathcal{D}(\boldsymbol{\chi}_0). \quad (8)$$

Equation (7) shows that the effective diffusivity $\mathcal{D}$ consists of the term D , due to thermal fluctuations, and of the enhancement induced by nonequilibrium fluctuations caused by the active forces. Moreover, the spatial variations of the activity field induce the effective drift $\mathbf{V}$ in Eq. (8), which is always aligned with the activity gradient. The entity of this drift depends on the parameter ϵ , which is related to the polymer architecture and to the persistence time τ of the active forces by the following expression:

$$\epsilon = 1 - \sum_{i=1}^{N-1} \frac{1}{1 + \tau \gamma_i}. \quad (9)$$

We recall here that the relaxation rates $\{\gamma_i\}$ carry information on the polymer connectivity, being proportional to the eigenvalues $\{\lambda_i\}$ of the connectivity matrix. In particular, for a linear chain, $\lambda_j = 4\sin^2(j\pi/2N)$. Furthermore, it should be noted that Eq. (9) gives $\epsilon < 1$ for any choice of the model parameters, implying that the effective drift $\mathbf{V}$

always points in the direction of greatest increase of the activity field. This might lead to the wrong conclusion that all polymeric structures tend to accumulate in regions of high bath activity, driven by $\mathbf{V}$. However, high activity regions are also characterized by a larger effective diffusivity $\mathcal{D}$, whose effect is to reduce the typical residence time of the polymer in those areas, thus counteracting the effective drift. The competition between these two effects is governed by ϵ : depending on their degree of polymerization and connectivity, different chains will preferentially localize in different regions of space.

Stationary distributions—In fact, by solving Eq. (6) at steady state with zero flux condition, and introducing $\rho(\mathbf{X}_{\text{com}}) \equiv \rho_0(\sqrt{N}\mathbf{X}_{\text{com}})$, we get

$$\rho(\mathbf{X}_{\text{com}}) = \mathcal{N} \left[1 + \frac{\tau v^2(\mathbf{X}_{\text{com}})}{dD} \right]^{-\epsilon/2}, \quad (10)$$

with $\mathcal{N}$ a normalization constant. Equation (10) implies that all chains with $\epsilon > 0$ will typically spend more time in regions of low bath activity, whereas those with $\epsilon < 0$ will preferentially accumulate in high activity areas.

At fixed bath conditions, i.e., fixed timescale ratio $\alpha \equiv \tau\gamma = \tau\kappa\mu$, there are only two ways to vary ϵ . The first one is to change the degree of polymerization N of the chain by adding or removing monomeric units. The left panel of Fig. 2 shows the steady state density of the center of mass for the case of linear chains of various lengths. Theoretical predictions [Eq. (10), solid lines] and numerical simulations (symbols) are compared in $d = 2$, for polymers in a box with size L endowed with periodic boundary conditions, and a sinusoidal activity field $v(x) = (v_0/2)[1 + \cos(2\pi x/L)]$ along the x axis and uniform along the remaining, orthogonal axis. The plot shows that short chains (e.g., dimers) preferentially localize in low activity regions, whereas the density of longer chains increasingly peaks around regions of high activity as the number of monomers increases. The minimum number of monomers above which linear chains localize in regions of high activity depends on the persistence time τ of the active forces and on the stiffness κ of the interaction between interconnected monomers. The separation between localization in high or low activity regions is evident in the diagram of Fig. 2 (right panel), which identifies the domains of the parameter space (N, α) corresponding to these two cases. An immediate conclusion drawn from the diagram is that for single particles and dimers, the effective diffusivity always prevails over the drift contribution, leading to localization in regions of low activity for any value of α . In fact, for $\alpha \rightarrow 0$, the coefficient $\epsilon \simeq 2 - N$, implying that only chains with $N > 2$ localize in regions of high activity. For finite α , the dominant contribution to the coefficient ϵ comes from Rouse modes that relax slower than the correlation time τ of the active bath. This corresponds to the observation that with increasing τ , linear

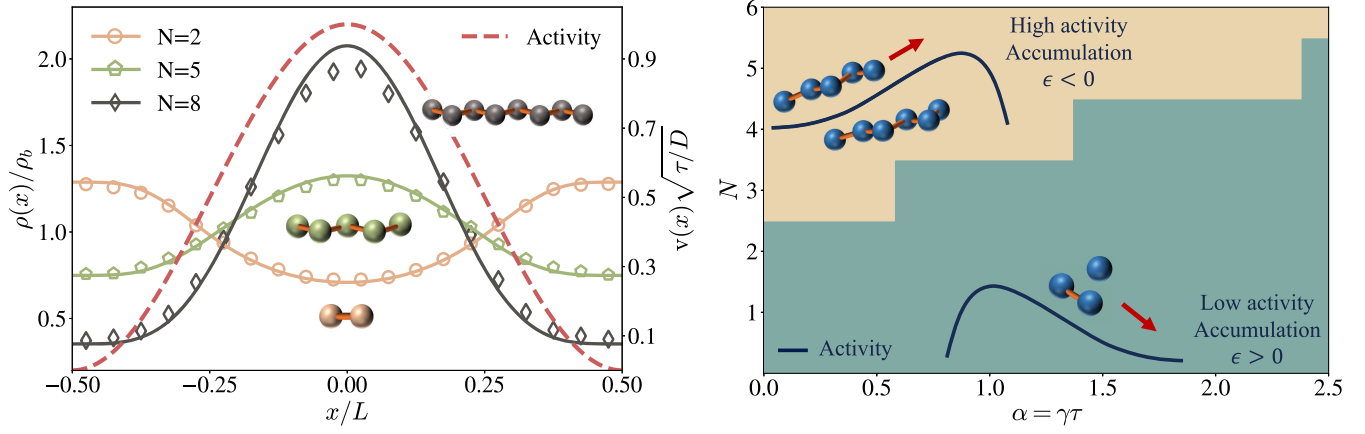


FIG. 2. Left panel: comparison between the analytical expression of the steady state density ρ of the polymer's center of mass (Eq. (10), solid lines, left axis) and numerical simulations (symbols). The red dashed line shows the activity profile (right axis) and ρ is reported in units of $\rho_b = 1/L$. The parameters of the simulation are $T = 0.1$, $\kappa = 1.0$, $\mu = 1.0$, $\tau = 1.0$, $v_0 = 1.0$, $L = 10$, and the integration time step $\Delta t = 0.001$. Right panel: region of preferential accumulation (corresponding to the sign of ϵ) of linear chains as a function of the time scale ratio $\alpha = \gamma\tau$ and the number of monomers N . For the purpose of visualization, the boundaries between the different signs of ϵ are drawn at half-integer values of N .

chains require a higher degree of polymerization to preferentially localize where the activity is larger (Fig. 2).

The second way to change the sign of ϵ is to vary the connectivity matrix M_{ij} of the chain by keeping fixed the number N of monomers. In order to demonstrate this, we determined the stationary density $\rho(\mathbf{X}_{\text{com}})$ for different structures, e.g., linear, ring, and star polymer as well as fully connected network. Figure 3 shows the resulting ρ , obtained with the same activity field as in Fig. 2. It turns out that, for a fixed degree N of polymerization ($N = 6$ in Fig. 3), the most constrained structure from the point of view of internal interactions, i.e., the fully connected

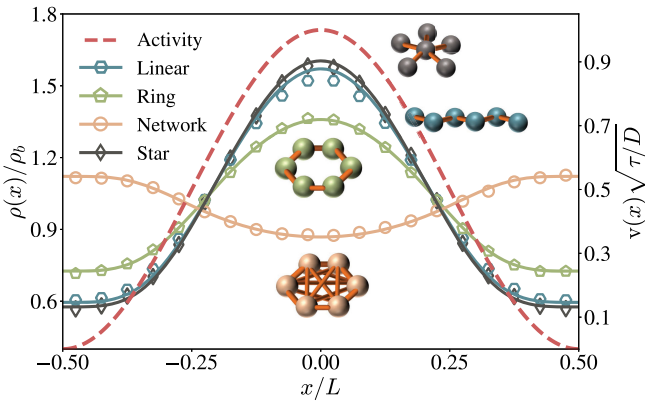


FIG. 3. Stationary probability density ρ of the center of mass of polymers with $N = 6$ monomers and different connectivity matrix: linear (blue), ring (green), star (gray), and fully connected (light orange) polymer. We compare analytical predictions [Eq. (10), solid lines] and simulations results in $d = 2$ dimensions (symbols). The activity field is represented by the red dashed line (right axis). The parameters of the simulation are the same as in Fig. 2.

network, is unable to localize in the region of high activity, whereas the structures with a lower degree of connectivity typically spend more time where the activity is higher. Moreover, as can be seen in Fig. 3, the localization is more effective for those chains characterized by the fewest number of bonds.

To understand heuristically the possible preferential localization of the polymers in regions with high activity, we note from Eq. (9) that negative values of ϵ primarily arise from modes k that are much slower than the correlation time τ of the active forces, i.e., which have $\tau\gamma_k \ll 1$. Accordingly, one can estimate $|\epsilon - 1| \gtrsim K$, where K denotes the number of these slow modes, which do not relax during the persistence time τ of the active forces, thus pinning the polymer motion. In turn, these slow modes effectively play the role of passive cargos for the remaining active modes, which turn out [59,61] to drift preferentially toward the region in space with higher activity.

The fact that polymer chains localize in regions of high or low activity depending on their degree of polymerization and connectivity can lead to the spontaneous spatial separation of different polymer species, when these are immersed in a nonuniform active bath. This can be observed, for example, in molecular dynamics simulations of a mixture of linear chains of various lengths in a sinusoidal activity field, as shown in Fig. 4. After an initial phase in which all chains are prepared in a mixed phase localized around the center of the box, different species begin to migrate to different regions of space according to their length. In particular, the chains with $N = 20$ and 25 localize where the activity is higher, while the shorter chains spend more time in the region of low activity. To better appreciate the separation along the x axis, where the activity is nonuniform, a harmonic confining potential

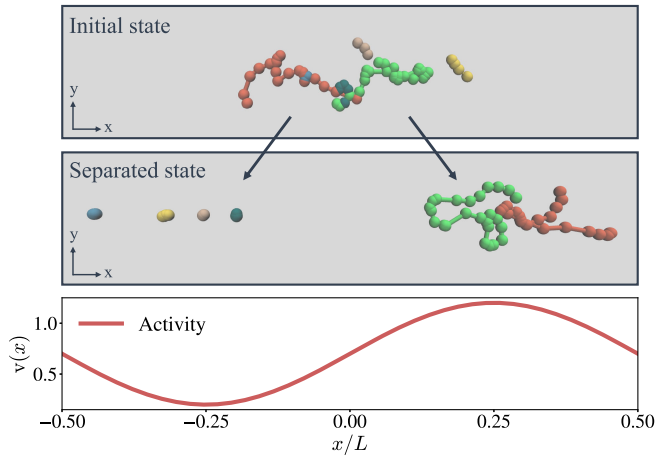


FIG. 4. Molecular dynamics simulations proving the spontaneous separation of linear polymer chains with various lengths in a sinusoidal activity field $v(x) = 0.2 + 0.5[1 + \sin(2\pi x/L)]$ (bottom panel) and in $d=2$. Polymers with $N \in \{2, 3, 4, 5, 20, 25\}$ are initially localized and mixed at the center of the box (top snapshot). Over time, different species migrate to different regions in space, based on their polymerization degree (middle snapshot). Simulation parameters: $T = 0.01$, $\kappa = 3.0$, $\mu = 1.0$, $\tau = 3.0$, $L = 20$. Integration time step: $\Delta t = 0.001$.

along the y axis (see Fig. 4) has been introduced. A similar spontaneous separation, will occur even in the presence of steric hindrance (see the SM for details) and interchain interactions (neglected here), at least for dilute polymer mixtures, and possibly with different timescales, as the initial mixed state will take longer to untangle. Note that the spontaneous separation described above occurs only in nonequilibrium conditions. In fact, it would be absent if the equation of motion of the polymer obeys detailed balance, i.e., if the energy injections introduced by the time-correlated forces are compensated by an additional dissipation modeled by a friction with an appropriate memory kernel.

Perspectives—The ability to segregate and sort biomolecules or synthetic polymerlike structures at micro or nanometer scale is of paramount importance in a variety of applications, spanning from diagnostics and biomedicine to biological analyses and chemical processing [74]. Nonequilibrium conditions have already proved useful in length-selective accumulation of oligonucleotides subjected to thermal gradients [75] and elasticity-based polymer sorting in active fluids [76]. The mechanism investigated here has potential to be employed in active sorting techniques to separate polymers based on both their length and structural connectivity. In a more realistic setting, the relaxation timescales of the chain will be influenced by additional interactions (e.g., bending rigidity, steric hindrance, and hydrodynamics) and the active bath may also exhibit more than one timescale. Our theoretical predictions might be experimentally tested with synthetic chains assembled from magnetic colloidal beads [77,78]

immersed in a bath with photokinetic bacteria, the swimming speed of which depends on the incident light intensity [79,80]. Our theoretical predictions could also be relevant in cells where naturally occurring activity gradients in the actin cytoskeleton influence mechanics. For instance, in mouse oocytes, activity gradients facilitate the central positioning of the nucleus through active diffusion [81–83]. In such cells, the transport behavior of polymerlike structures, whether externally introduced or assembled locally, would depend on their length and topology, as predicted by our theory, rather than merely diffusing down the activity gradient. Whether such activity gradient-driven processes are at work in real cells, contributing to the precise localization and transport of biomolecules remains an intriguing possibility that deserves further investigation.

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