Polymer Chain with Stochastic Dipolar Active Forces: a Model for Spatial Organization of Chromatin

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A living cell is an active environment where the organization and dynamics of chromatin are affected by different forms of activity. Using a bead-spring polymer chain with stochastic dipolar active forces, we study how the subdiffusive motion of the loci leads to the large-scale coherent motion of the chromatin. In the presence of extensile (contractile) activity, the dynamics of loci grows faster (slower) and the spatial correlation length increases (decreases) compared to the case with no dipolar forces. Hence, both the dipolar active forces modify the elasticity of the chain. Interestingly, the dynamics and organization of such dipolar active chains largely differ from their thermal counterparts.

Active systems are inherently out of equilibrium [1]. It consumes energy perpetually from the environment which prevents relaxation into a thermal equilibrium state and exhibits a wide spectrum of novel steady-state behaviours such as the activity-driven phase separation [2] or large-scale collective motion [3]. Even inside the living cells, active systems have constituents that adapt in noisy environments and generate forces for uni-directional transport and spatial organization. Bio-polymers are an integral part of living cells, and their conformational and dynamical properties are significantly affected by the active processes [4,9]. For example, the microtubule and F-actin filaments of the cytoskeleton are driven forward by the myosin and kinesin families of motor proteins [10,11]. Another biopolymer inside the nucleus is chromosomal DNA [12-14] and it serves as a platform for number of biological processes such as Chromatin remodelling [15], transcription [16] and DNA repair [17]. Their spatial organization dramatically varies along with the different phases of the cell cycle, which seem to be driven by processes that consume ATP [18,19]. However, the exact procedure of energy consumption on the chromatin remains unclear and this is the primary interest of the present study.

Interphase chromatin are organized into transcriptionally active and inactive regions. Transcriptionally active regions, referred to as euchromatin, are loosely packed, whereas transcriptionally inactive regions, called heterochromatin, are tightly packed [20]. In a recent study, transcriptionally active regions are characterized by an effective temperature in which a Brownian-like random force is acting on chromosomes in addition to thermal noise [21,22]. Weber et.al. argued that random motions of chromatin loci are driven by the ATP-dependent fluctuations which behave like thermal fluctuations but with a greater magnitude and steeper temperature-dependence [23]. However, the active noises described in these models randomize the global structure of chromatin chain more efficiently as compared to the thermal noise and shorten the spatial correlation at a sufficiently large time [24]. On contrary, Zidovska et. al. demonstrated two types of chromatin motion experimentally: a fast local motion previously observed by tracking the motion of chromosomal loci and a slower large-scale motion in which collective motions of chromatin are seen to be coherent beyond the boundaries of chromosome territories, over micrometer-scale regions and seconds [25]. To explain the correlated motions of chromatin, Saintillan et. al. constructed a flexible polymer model with long-range hydrodynamic interactions that is driven by active force dipoles [26]. In their model, they obtained strong correlated motion for extensile activity, but not in the cases of passive and contractile activity [27]. In another study, Liu et. al. modelled the chromatin as active flexible polymer subjected to extensile and contractile monopoles [28]. They showed that both the extensile and contractile monopoles generate correlated motion without the hydrodynamic interactions and the contractile system exhibits larger displacements than the extensile one. Other theoretical models of active polymers have also been proposed in connection to chromosomal dynamics. Some of these models have focused on semiflexible [29] or flexible polymer [30] chains subject to correlated noise. Hence, the dynamics is superdiffusive in such models. However, superdiffusion has yet to be observed in the context of chromosomal dynamics.

To understand how the large-scale correlated chromatin dynamics emerges from the local subdiffusive motion, we construct a model for chromatin as a long semiflexible polymer with excluded volume interactions and stochastic dipolar extensile and contractile activities. We do not include hydrodynamic interactions in this study. We show that both the extensile and contractile active forces modify the elasticity of the chain, but leave...
We consider a bead-spring polymer chain composed of 1000 monomers of radius $\sigma$ and mass $m$ in a three-dimensional space. We simulate the following Langevin equation of all the monomers with the position $\mathbf{r}_n(t)$ at time $t$:

$$m \frac{d^2 \mathbf{r}_n(t)}{dt^2} = -\xi \frac{d\mathbf{r}_n}{dt} - \nabla_n V(\mathbf{r}_1, \mathbf{r}_2, \ldots) + \mathbf{f}_n(t) + \mathbf{F}_{a,n},$$

where $\xi$ is the friction coefficient which is related to the thermal Gaussian noise, $\mathbf{f}_n(t)$ through the fluctuation-dissipation theorem. The total potential energy, $V(\mathbf{r}_1, \mathbf{r}_2, \ldots)$ is composed of spring potential $V_{\text{FENE}}$, bending potential $V_{\text{BEND}}$, and excluded volume potential $V_{\text{WCA}}$. The term $\mathbf{F}_{a,n}$ denotes the stochastic dipolar active force on each bead that pushes simultaneously two neighbouring beads towards (contractile) or away (extensile) from each other along the unit bond vector for all the time with strength $F$ (Fig. 1 (A, B)).

This is where our model differs from the existing models where activity is introduced by putting the beads at a higher temperature [21, 22] (see supplementary Sec. I for more details).

To quantify the effect of dipolar extensile (DPE) and dipolar contractile (DPC) activities on the dynamics of the individual monomers, we first focus on the time-ensemble averaged mean squared displacement (MSD) of the tagged monomer, $\langle \Delta r_n^2(\tau) \rangle$ as a function of lag time $\tau$. For small DPE and DPC activities ($F = 4$), the dynamics of the tagged monomer is sub-diffusive (see supplementary Table S1) and we do not see any significant enhancement in $\langle \Delta r_n^2(\tau) \rangle$ as compared to the passive case ($F = 0$) as evident in Fig. 1C. But, for very high DPE and DPC activities ($F = 100$), we observe a clear difference in $\langle \Delta r_n^2(\tau) \rangle$, while the sub-diffusive dynamics of the monomer remains unaltered. In comparison to the passive case, the dynamics of the individual monomer is enhanced for high DPE force and suppressed for high DPC force respectively (Fig. 1D). However, the dipolar activity leaves the dynamical behavior of the center of mass (COM) unchanged (see supplementary Fig. S1), suggesting that the effective temperature as introduced in earlier studies of chromatin [21, 29], is not a good descriptor for dipolar activity.

Hence, the responses of the COM and individual monomer in the presence of dipolar activity suggest that the dipolar forces modify the stretching of the chain which essentially enhances or reduces the local space explored by the tagged monomer for the DPE or DPC forces respectively, but not the diffusive or sub-diffusive nature of the displacements.

To further quantify the effects of the DPE and DPC active forces on the loci mobilities, we investigate the probability distribution, $P(l_b)$ of the bond length, $l_b(= |\mathbf{r}_n - \mathbf{r}_{n-1}|)$ of the chain. Here $P(l_b)$s follow Gaussian distributions (Fig. 1D). For smaller DPC and DPE activities, $P(l_b)$s appear to be qualitatively similar to $P(l_b)$ of the passive system. But, $P(l_b)$s for high DPE and DPC forces show well-separated peaks (Fig. 1D). For large DPE force, the peak of $P(l_b)$ shifts towards a higher value of $l_b$ which accounts for the enhancement of stretching of the polymer chain. For large contractile force, $P(l_b)$ is sharply peaked at lower value of $l_b$ and the deviation of the peak value of $P(l_b)$ from the passive case is small as compared to the deviation for the DPE force. This small deviation for the contractile force is presumably due to the self-avoidance of the beads. The potential energy (PE) increases more for the DPC forces than for the DPE forces (see supplementary Fig. S2A) as the effect of self-avoidance translates to an increasing potential energy barrier for the contractile forces. On the other hand, the kinetic energy (KE) increases more for the DPE forces than for the DPC forces (see supplementary Fig. S2B) as the DPE forces show larger displacements than the DPC forces. Additionally, the probability distribution, $P(R_g)$ of the radius of gyration $R_g$ of the chain and the distribution, $P(N)$ of number of monomers, $N$ in a spherical probe volume indicate that DPE (or DPC) forces promote larger (or smaller) displacements of the system than the passive one (see...
Fig. 2. Spatial correlation functions $C(s, \tau)$ for the passive (A), DPE and DPC cases for $F = 4$ (B and C), $F = 100$ (D and E) respectively at different time lags, $\tau$. (F) Correlation lengths ($l_c$) as a function of $\tau$ for the passive, DPE and DPC activities.

supplementary Sec. III & IV and Fig. S3 & S4).

To study the spatio-temporal dynamics of our chromatin model, we calculate the spatial correlation function, $C(s, \tau)$ as a function of spatial distance between two loci for different values of the lag time $\tau$ [25]. The normalized spatial correlation between $i$-th and $j$-th loci over the time interval $\tau$ is evaluated as $C(s, \tau) = \frac{\sum_{i,j} \langle |\vec{r}_i(t+\tau) - \vec{r}_j(t)| \rangle_{\tau} \delta(s-|\vec{r}_i(t) - \vec{r}_j(t)|)}{\sum_{i,j} \langle |\vec{r}_i(t+\tau) - \vec{r}_j(t)| \rangle_{\tau}}$, where $\langle (\ldots)_{\tau} \rangle$ is an average over $t$ and over different ensembles. As $\tau$ increases, $C(s, \tau)$ shows slower spatial decay both in the case of with and without the active dipolar forces (Fig. 2). For passive and smaller DPC and DPE activities, $C(s, \tau)$ decays exponentially (Fig. 2 (A-C)). The corresponding correlaton lengths, $l_c$ increase monotonically with $\tau$ and eventually saturated at large $\tau$ (Fig. 2F). $C(s, \tau)$ shows similar exponentially decaying correlation with $\tau$ for higher DPE force (Fig. 2D). For large DPC force, we fit $C(s, \tau)$ with an bi-exponentially decaying function where $l_{c1}(\tau)$ and $l_{c2}(\tau)$ represent the correlation lengths for the initial faster and subsequent slower decay respectively (Fig. 2(E, F)). The correlation length $l_c$ of extensile active systems is greater than the same for the contractile active systems. This suggests that the motion of extensile active chain has long-ranged spatial coherence than the contractile active chain.

Other than $C(s, \tau)$, we look at the normalized distribution of local curvatures $P(\theta)$ to characterize the internal structure more quantitatively, where $\theta$ is the bond angle between the bond vectors. Fig. 3A shows that for small DPC and DPE activities, $P(\theta)$s are Gaussian and nicely collapse on $P(\theta)$ of the passive system. However, for large DPC and DPE systems, $P(\theta)$s display a clear difference from passive system. $P(\theta)$ for DPE chain with higher activity exhibits a peak at smaller bond angle and the width of $P(\theta)$ becomes narrower as compared to that of the DPC chain with higher activity (Fig. 3A). Fig. 3B is discussed in the latter part of the manuscript. Narrowed distribution of $P(\theta)$ with peak value at small bond angle for high DPE force implies effectively higher bending rigidity as compared to that of passive chain. This again confirms that extensile activity induces long-ranged spatial correlations compared to contractile activity.

In our model of dipolar activity, DPE and DPC forces are working on every bead along the unit bond vector with constant magnitude, $F$. Another option is to introduce thermal extensile or contractile forces acting along the bond vector. The thermal extensile forces on the $n$th bead due to $(n-1)$th and $(n+1)$th beads become $\frac{F}{(\kappa_0)} (\vec{r}_n - \vec{r}_{n-1})$ and $\frac{F}{(\kappa_0)} (\vec{r}_n - \vec{r}_{n+1})$ respectively
where \( \langle l_b \rangle \) is the average bond length. The net force on nth bead, \( \frac{\partial}{\partial t} \left( 2\tau_n - \tau_{n+1} - \tau_{n-1} \right) \) becomes \( \frac{\partial}{\partial t} \langle \tau_n \rangle \) in the continuum limit. Thus, the effective spring constant \( k_{\text{eff}}^{\text{DPE}} \) is reduced by \( \left( k - \frac{F}{\langle l_b \rangle} \right) \) for the thermal extensile case. Similarly, for the thermal contractile case, \( k_{\text{eff}}^{\text{DPC}} \) is enhanced by \( \left( k + \frac{F}{\langle l_b \rangle} \right) \). We calculate \( \langle l_b \rangle \) from the distribution of \( P(l_b) \) (Fig. 1D) for both the extensile and contractile forces. Next, we simulate Eq. (2) with \( F_{a,n} = 0 \) and modified spring constants, \( k_{\text{eff}}^{\text{DPE}} = \left( k - \frac{F}{\langle l_b \rangle} \right) \) and \( k_{\text{eff}}^{\text{DPC}} = \left( k + \frac{F}{\langle l_b \rangle} \right) \) respectively. For \( F = 100 \), the spring constant, \( k = 30 \) of the thermal chain is modified to \( k_{\text{DPE}}^{\text{eff}} = 9.54 \) for extensile chain with \( \langle l_b \rangle = 4.88 \) and to \( k_{\text{DPC}}^{\text{eff}} = 80.56 \) for contractile chain with \( \langle l_b \rangle = 9.97 \). We compare the results, \( \langle \Delta r_2^2(\tau) \rangle \) (Fig. 4A, 5A), \( P(l_b) \) (Fig. 4B) and \( C(s, \tau) \) (Fig. 5) of our model of dipolar activity to thermal chain with these modified spring constants \( k_{\text{eff}}^{\text{DPE}} \) and \( k_{\text{eff}}^{\text{DPC}} \). We find that the thermal chain with \( k_{\text{eff}}^{\text{DPE}} = 9.54 \) is less stretched than the chain with active dipolar extensile force \( F = 100 \). Similarly, the thermal chain with \( k_{\text{eff}}^{\text{DPC}} = 80.56 \) is less compressed than the chain with active dipolar contractile force \( F = 100 \). In a semiflexible polymer, stretching and bending coefficients are not independent of each other \[29\]. Hence, if the stretching coefficient is modified, it also modifies the bending coefficient as evident in Fig. 3B. Large DPE (or DPC) activity strongly increases (or decreases) the probability of long straightened segments as compared to thermal chain with renormalized spring constants, \( k_{\text{eff}}^{\text{DPE}} \) and \( k_{\text{eff}}^{\text{DPC}} \). The behavior of steady state KE and PE (see supplementary Fig. S5), \( P(R_g) \) (see supplementary Fig. S6) and, \( P(N) \) (see supplementary Fig. S7) for both the dipolar activities and the thermal chain with \( k_{\text{eff}}^{\text{DPE}} \) and \( k_{\text{eff}}^{\text{DPC}} \) are given in the Supporting Material and we observe similar trends, DPE (or DPC) active forces promote larger (or smaller) displacements of the system than the thermal one with \( k_{\text{eff}}^{\text{DPE}} \) (or \( k_{\text{eff}}^{\text{DPC}} \)). The stretching (or compression) of the thermal chain with lower (or higher) spring constants as compared to the chain with large dipolar extensile (or contractile) activities arise because the magnitude of the dipolar active force is constant whereas the magnitude of the spring force is fluctuating. This leads us to propose that the extensile (or contractile) dipolar active system can not be mapped to a thermal system with larger (or lower) bending modulus and longer (or shorter) bond lengths.

Active forces inside a nucleus play an important role in both genome organization and dynamics. Experiments suggest that interphase chromatin is subjected to ATP-powered enzymes such as RNA polymerase [25]. Motivated by that, we implement the simplest two types of stochastic dipolar active forces, namely extensile and contractile on semiflexible, self-avoiding polymer chain. In our model, the COM motion is not enhanced in the presence of both the active forces. In that way, our model differs from typical active systems where one observes superdiffusion [3]. The MSD of a tagged monomer \( \langle \Delta r^2(\tau) \rangle \) for DPE system shows enhanced subdiffusion than the DPC one which is related to the shifting of peak values of distribution \( P(l_b) \) at large values of bond length \( l_b \) in the DPE case. In our model, spatial coherence emerges with or without dipolar activity. However, the correlation length increases or decreases for the DPE or DPC system as compared to the case with no dipolar forces. Hence, the dipolar activity modifies the elasticity (related to bending and stretching coefficients) of the chain. Interestingly, expansion or compaction of the polymer induced by active DPE or DPC forces are larger than the thermal DPE or DPC forces. Thus, chromatin models based on purely equilibrium forces arising from polymer elasticity and interactions [31] can not account for the active motorized systems.

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SUPPLEMENTAL MATERIAL

I. Model and Simulation Details

We consider a bead-spring polymer chain composed of 1000 monomers of radius $\sigma$ in a three-dimensional space. We implement the following Langevin equation to simulate the dynamics of all the monomers of our system with mass $m$ with the position $r_i(t)$ at time $t$:

$$m \frac{d^2\vec{r}_i(t)}{dt^2} = -\xi \frac{d\vec{r}_i}{dt} - \nabla_i V(\vec{r}_1, \vec{r}_2, \ldots) + \vec{f}_i(t) + \vec{F}_{\text{a,n}},$$

where $\xi$ is the friction coefficient which is related to the thermal Gaussian noise through

$$\langle \vec{f}_i(t) \rangle = 0, \quad \langle \vec{f}_i(t') \cdot \vec{f}_j(t'') \rangle = 6\xi k_B T \delta(t' - t'').$$

(2)

The total potential energy, $V(\vec{r}_1, \vec{r}_2, \ldots) = V_{\text{angle}} + V_{\text{WCA}} + V_{\text{bond}}$ is composed of a bond contribution between neighbouring beads

$$V_{\text{bond}} = \frac{k}{2} (|\vec{r}_{i,i+1}| - r_0)^2,$$

(4)
a bending energy

$$V_{\text{angle}} (\theta_i) = k_a (1 - \cos \theta_i),$$

(5)

and an excluded volume interaction modelled with Weeks-Chandler-Andersen (WCA) potential [32]:

$$V_{\text{WCA}}(r) = \begin{cases} 4\epsilon \left( \left( \frac{\sigma}{r} \right)^{12} - \left( \frac{\sigma}{r} \right)^6 \right) + \epsilon, & \text{if } r < 2^{1/6}\sigma \\ 0, & \text{otherwise,} \end{cases}$$

(6)

where $\vec{r}_{i,i+1} = \vec{r}_i - \vec{r}_{i+1}$ is the vector between the position of the beads $i$ and $i + 1$, $k$ is the force constant, $r_0$ is the equilibrium bond distance, $\cos \theta_i = \frac{\vec{r}_{i,i+1}(t) \cdot \vec{r}_{i,i+2}(t)}{\left| \vec{r}_{i,i+1}(t) \right| \left| \vec{r}_{i,i+2}(t) \right|}$, $k_a$ is the bending modulus, $r$ is the separation between a pair of monomers in the medium, $\epsilon$ is the strength of the interaction, and $\sigma$ determines the effective interaction diameter. In our simulation, we consider $\epsilon$, $k_B T$ and $\tau_0 = \sqrt{\frac{m \sigma^2}{k_B T}}$ as the unit of length, energy and time scales.

The term $\vec{F}_{\text{a,n}}$ denotes the stochastic dipolar active force that pushes simultaneously two neighbouring beads towards (dipolar contractile (DPC)) or away (dipolar extensile (DPE)) from each other. Here, for all the time, the dipolar active force is acting on every bead along the unit bond vector with strength $F$. All the simulations are performed using Langevin thermostat and equation of motion integrated using the velocity Verlet algorithm in each time step. The parameters used for the simulation are $k = 30\epsilon/\sigma^2$, $r_0 = 2\sigma$, $k_a = 2\epsilon$, $m = 10^{-3}$. All the production simulations are carried out for $10^7$ steps where the integration time step is considered to be $\delta t = 10^{-5}r_0$. The simulations are carried out using LAMMPS [33], a freely available open-source molecular dynamics package. For a given set of parameters, we generate 10 independent trajectories of the polymer.

II. Mean Square Displacement

The most straightforward tool for understanding the properties of motion from the trajectories is the mean square displacement (MSD). The time-averaged MSD is defined as $\Delta r^2(\tau) = \frac{1}{N} \int_0^\tau \int_0^\tau \left( \vec{r}_i(t_0 + \tau) - \vec{r}_i(t_0) \right)^2 dt_0$ from the time series $\vec{r}_i(t)$ where $T$ is the total run time and $\tau$ is the lag time. The ensemble-averaged MSD during time $\tau$ is defined in terms of the distance from their initial position $\vec{r}_i(0)$ as MSD $= \sum_{i=1}^{N'} \left[ \vec{r}_i(\tau) - \vec{r}_i(0) \right]^2$ where $N'$ is the number of independent trajectories. Finally, the time- and ensemble-averaged MSD is obtained by performing both types of averaging: $\langle \Delta r^2(\tau) \rangle = \frac{1}{N} \sum_{i=1}^{N'} \Delta r^2_i(\tau)$. The MSD $\langle \Delta r^2(\tau) \rangle$ of the center of mass (COM) diffuses freely at all times in the presence or absence of extensile and contractile activity (Fig. S1). In addition, all the active and passive $\langle \Delta r^2(\tau) \rangle$ are merging with each other (Fig. S1).

III. Distribution Functions of the Radius of Gyration

To further quantify the effects of the contractile and extensile active forces on the loci mobilities, we analyze the probability distribution, $P(R_g)$ of the radius of gyration $R_g$ of the chain where $R_g = \sqrt{\frac{1}{N} \sum_{i=1}^{N} (\vec{r}_i - \vec{r}_c)^2}$. For smaller DPC and DPE activities, $P(R_g)$ is Gaussian and appear to be qualitatively similar to $P(R_g)$ of passive system. But, $P(R_g)$ for high DPE and DPC forces show well-separated peaks (Fig. S3). For large DPC force, $P(R_g)$ is Gaussian and sharply peaked at lower values of $R_g$. The broader distribution of $P(R_g)$ with peak at higher value of $R_g$ deviates from the Gaussian for large DPE force which accounts for the enhancement of stretching of the polymer chain. For the high DPC force, the deviation of the peak value of $P(R_g)$ from the passive case is small as compared to the deviation for the DPE force. This small deviation for the DPC force is most probably due to the self-avoidance of the beads. To test the effect of self-avoidance as an energetic barrier, we compute the potential energy and kinetic energy (KE) of the polymer chain at each instant of time in the steady state. PE increases more for the DPC forces than for the DPE forces (Fig. S2A) as the effect of self-avoidance translates to an increasing potential energy barrier for the DPC forces. On the other hand, KE increases more for the DPE forces than for the contractile forces (Fig. S2B) as the DPE forces show larger displacements than the DPC forces.
Fig. S1. Log-Log plot of MSDs \( \langle \Delta r_2^2(\tau) \rangle \) as a function of lag time \( \tau \) at different DPE and DPC active forces for the COM of polymer chain.

IV. Number Fluctuations

To gain a deeper understanding of the underlying complex movement of the monomers, we investigate the number fluctuations. To compute the number fluctuations, we randomly select a number of small spherical probes of radius \( 4\sigma \) at different locations within the system. We then construct a histogram over different spherical probes and independent trajectories from which probabilities \( (P(N)) \) are computed. In equilibrium, the statistics of fluctuations in \( N \) inside a small spherical probe volume follows Gaussian distribution. For small values of DPE and DPC forces, we find that the the probability distributions \( P(N) \) are indeed Gaussian (Fig. S4). For large DPC force, \( P(N) \) also exhibits the Gaussian distribution. For large DPC force, the peak of \( P(N) \) shifts towards a higher value of \( N \) and the width of \( P(N) \) becomes narrower than the passive one (Fig. S4). Hence, large DPC force generates high density regions, leading to decrease in mobility. On contrary, for large DPE force, \( P(N) \) decays exponentially with \( N \), indicating that DPE forces promote larger displacements of the system than the passive one.

| \( F \) | \( \alpha \) | \( \beta \) |
|---|---|---|
| 0 | 0.88 | 0.77 |
| 4 (DPE) | 0.88 | 0.65 |
| 4 (DPC) | 0.89 | 0.63 |
| 100 (DPE) | 0.93 | 0.68 |
| 100 (DPC) | 0.74 | 0.67 |

TABLE S1. The exponents, \( \alpha \) and \( \beta \) of \( \langle \Delta r_2^2(\tau) \rangle \) at short and long times for the passive and different dipolar activities.

Fig. S2. Steady state PE (A) and KE (B) as a function of time \( t \) at different DPE and DPC active forces for polymer chain.

Fig. S3. The probability distribution function \( (P(R_g)) \) of the radius of gyration \( (R_g) \) in the presence of at different DPE and DPC active forces.

Fig. S4. Number density fluctuations \( (P(N)) \) at different DPE and DPC activities.

Fig. S5. Steady state PE (A) and KE (B) as a function of time \( t \) for the thermal chain with effective spring constants \( k_{DPE}^{eff} \) and \( k_{DPC}^{eff} \) and large DPE and DPC dipolar active forces.
Fig. S6. The probability distribution function \((P(R_g))\) of the radius of gyration \((R_g)\) for the thermal chain with effective spring constants \(k_{DPE}^{\text{eff}}\) and \(k_{DPC}^{\text{eff}}\) and large DPE and DPC dipolar active forces.

Fig. S7. Number density fluctuations \((P(N))\) for the thermal chain with effective spring constants \(k_{DPE}^{\text{eff}}\) and \(k_{DPC}^{\text{eff}}\) and large DPE and DPC dipolar active forces.
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