1 Supplement Materials

1.1 Simulation

To control the number of free parameters, we choose the ideal bead-rod polymer model to describe the dynamics of chromosomes in nucleus, without considering the exclusive volume effect. As we will see later that the system can be reduced to a one free parameter model, i.e. T_{eff}.

The simulation of model bead connected with rigid rod utilize the technique of Brownian Dynamics[1]. The dynamical equation of beads representing chromosome loci is

$$\dot{\mathbf{r}_i} = \frac{1}{\xi}(\mathbf{F}_i^b + \mathbf{F}_i^c + \mathbf{F}_i^e + \mathbf{F}_i^{pseudo}) \tag{1}$$

where $\mathbf{r}_i$ is the position vector of the ith bead, ξ is friction coefficient, $\mathbf{F}_i^b$ is random force, $\mathbf{F}_i^c$ is constraint force caused by rigid rod constraints, $\mathbf{F}_i^e$ is external force and $\mathbf{F}_i^{pseudo}$ is pseudo force added to mimic the statistics of bead-spring. Notice that the statistics of bead-rod is not exactly same as bead-spring. Subtle differences are caused by the intrinsic "rigid" of rods[2, 1].

The random force, which characterize the fluctuation origin of beads dynamics, is a typical Brownian force satisfies the following conditions

$$< \mathbf{F}_i^b >= \mathbf{0}; < \mathbf{F}_i^b(t)\mathbf{F}_j^b(t') >= 2k_BT_c\xi\delta_{ij}\delta(t-t') \tag{2}$$

k_B is Boltzmann constant and T_c is *characterizing temperature* characterize the level of randomness arise from the thermal motion of solvent molecules and some sorts of interactions between chromosome and proteins.

The constraint force for a specific bead in a bead-rod ring writes

$$\mathbf{F}_i^c = \lambda_i\mathbf{u}_i - \lambda_{i-1}\mathbf{u}_{i-1} \tag{3}$$

where λ_i is strength of tension on the rod between ith and $(i+1)$th bead, $\mathbf{u}_i$ is the unit vector along this rod and $i = N$ ends to $i = 0$.

In case of constant force field, the external force is constant $\mathbf{F}_i^e = -\xi\mathbf{v}$ acting on every bead except the pinned one representing SPB.

The pseudo force is calculated using

$$\mathbf{F}_i^{pseudo} = -\frac{\partial U_{met}}{\partial \mathbf{r}_i}; U_{met} = \frac{1}{2}k_BT_c ln(detG) \tag{4}$$

where G is the metric matrix of the bead-rod system[4].

Since the rods present in our model are rigid rods, additional constrained equations are needed to keep the rod length unchangeable

$$(\mathbf{r}_{i+1} - \mathbf{r}_i)^2 - a^2 = 0 \tag{5}$$

where a is rod length.

Parameters above can be eliminated and dimensionless term of the dynamical equations can be obtained by the scaling $\mathbf{r}' \to \mathbf{r}/a$; $t' \to t/(\xi a^2/k_BT_c)$;

$\mathbf{F}' \to \mathbf{F}/(k_B T_c/a)$. Our only free parameter *effective temperature* which is also dimensionless is defined as

$$T_{eff} = \frac{Fa}{k_B T_c} = \frac{\xi v a}{k_B T_c} \tag{6}$$

Numerical scheme employed to solved the set of constrained differential equations (1) and (5) is predictor-corrector algorithm used widely in bead-rod simulation[1, 5, 3]. Basic steps include calculating a prediction of $\mathbf{r}_i(t + \delta t)$ without considering the constraint force followed by a correction step, i.e. solving the algebra constraint equations to get constraint forces and re-plugin to the original equations for the corrected $\mathbf{r}_i(t + \delta t)$. The differential equations are solved using Euler iterative method with a time step $dt = 10^{-4}$. Statistical results are all obtained based on the ensemble of 10^{10} steps after equilibrium.

References

[1] C. Cruz, F. Chinesta, and G. Régnier. Review on the Brownian Dynamics Simulation of Bead-Rod-Spring Models Encountered in Computational Rheology. *Archives of Computational Methods in Engineering*, 19(2):227–259, May 2012.

[2] EJ Hinch. Brownian motion with stiff bonds and rigid constraints. *Journal of Fluid Mechanics*, pages 219–234, 1994.

[3] Tony W. Liu. Flexible polymer chain dynamics and rheological properties in steady flows. *The Journal of Chemical Physics*, 90(10):5826, 1989.

[4] Matteo Pasquali, David C Morse, and Brownian Dynamics. An efficient algorithm for metric correction forces in simulations of linear polymers with constrained bond lengths. 116(5), 2002.

[5] Madan Somasi, Bamin Khomami, Nathanael J. Woo, Joe S. Hur, and Eric S.G. Shaqfeh. Brownian dynamics simulations of bead-rod and bead-spring chains: numerical algorithms and coarse-graining issues. *Journal of Non-Newtonian Fluid Mechanics*, 108(1-3):227–255, December 2002.