

# 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

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

where  $\mathbf{r}_i$  is the position vector of the  $i$ th bead,  $\xi$  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[3, 1].

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

$$\langle \mathbf{F}_i^b \rangle = \mathbf{0}; \langle \mathbf{F}_i^b(t) \mathbf{F}_j^b(t') \rangle = 2k_B T_c \xi \delta_{ij} \delta(t - t') \quad (2)$$

$k_B$  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

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

where  $\lambda_i$  is strength of tension on the rod between  $i$ th 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

$$\mathbf{F}_i^{pseudo} = -\frac{\partial U_{met}}{\partial \mathbf{r}_i}; U_{met} = \frac{1}{2} k_B T_c \ln(\det G) \quad (4)$$

where  $G$  is the metric matrix of the bead-rod system[5].

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

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

where  $a$  is rod length.

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

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

$$T_{eff} = \frac{k_B T_c}{Fa} = \frac{k_B T_c}{\xi v a} \quad (6)$$

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, 7, 4]. 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.

## 1.2 Parameter estimation

Experimentalists defined the pair of loci of homologous are "associated" for distance between them less than  $0.35 \mu m$ [2]. So we assume the threshold of the chromosome been aligned is  $0.35 \mu m$ .

Then from what we have in our model, the distance between loci of different effective temperature follows Fig. 3b in the main text. Apparently the distance varies with position along the chromosome. But let us consider the midpoint of the loop which has the largest divergence, hence the largest drag force is needed. It turns out the corresponding effective temperature for the midpoint of a polymer loop with  $N = 500$  is  $T_{eff} \approx 1$  (The exact value is around 1.16). Actually  $N$  does not matter too much given such a low temperature region.

Substitute it into the definition of effective temperature Eq. 6, use the room temperature as characterizing temperature  $T_c = 300K$  and Kuhn length  $a = 100nm$ , we obtain an estimation of the strength of force field we need.

$$F = 3.57 \times 10^{-14} N \quad (7)$$

We can further estimate the needed moving speed based on the simplest Stroke's law and sphere model. Assume the force field is generated from the friction of the bead sphere. The Stroke's law gives  $F = 6\pi\mu Rv$ , where  $\mu$  is the viscosity of the nucleoplasm, which is 1000 folds of that of water.

$R$  is the radius of the bead sphere, which is hard to estimate given the complexity of real chromosome and the extremely simplified bead sphere model. Nevertheless, people who use this sort of bead chain model estimated the diameter of the abstracted bead is around  $30nm$ [6].

Use the above estimations of  $R$ , which would be a little bit underestimate, we obtain the moving velocity needed for the homologous to align is  $v = 1.41 \times 10^{-7} m/s$  which is close to the experimental observation  $v_{exp} = 4.17 \times 10^{-8} m/s$ . Another reasonable estimation  $R = 50nm$ , which is half of the Kuhn length, gives  $v = 4.24 \times 10^{-8}$ , which is very close to the experimental observation.

## References

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