

# Effect of epigenetics and extrusion on chromatin organization and dynamics

Surya K. Ghosh, Daniel Jost

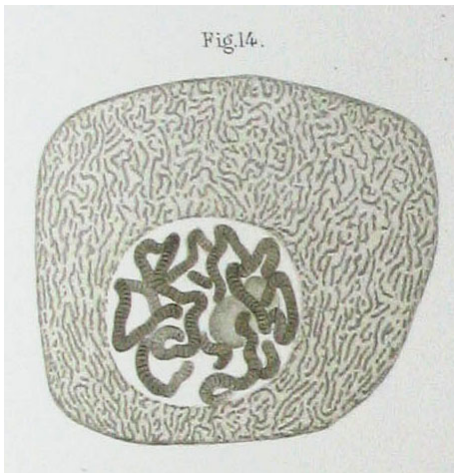
CNRS, University of Grenoble Alpes, Grenoble, France



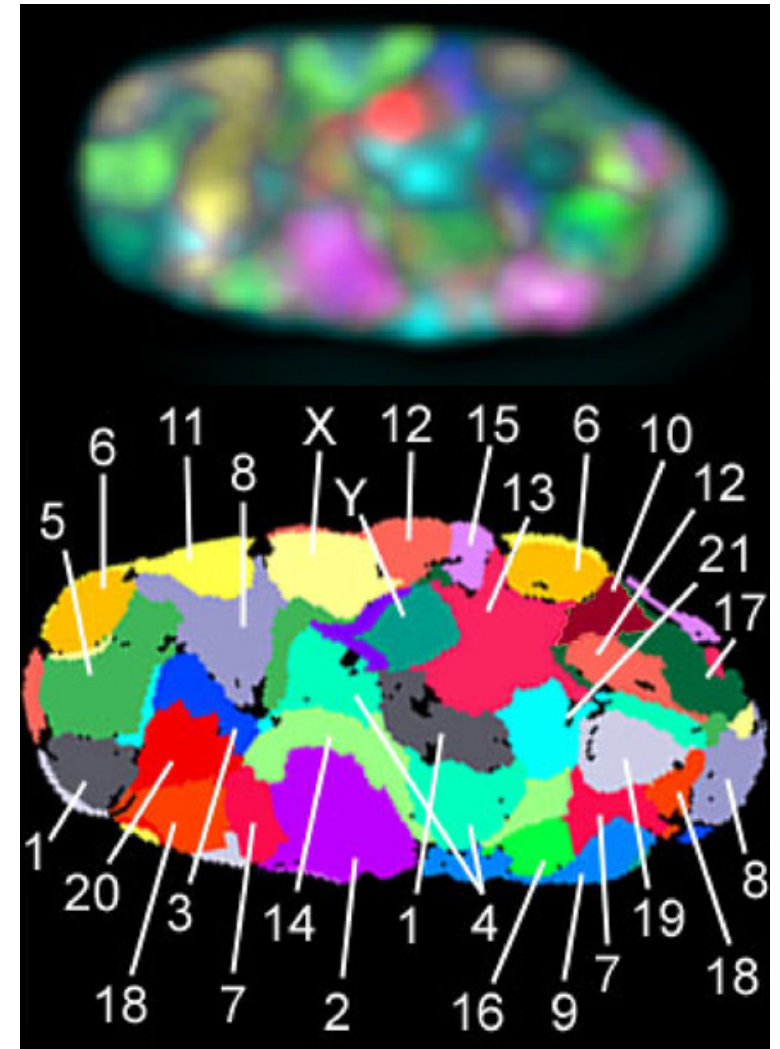
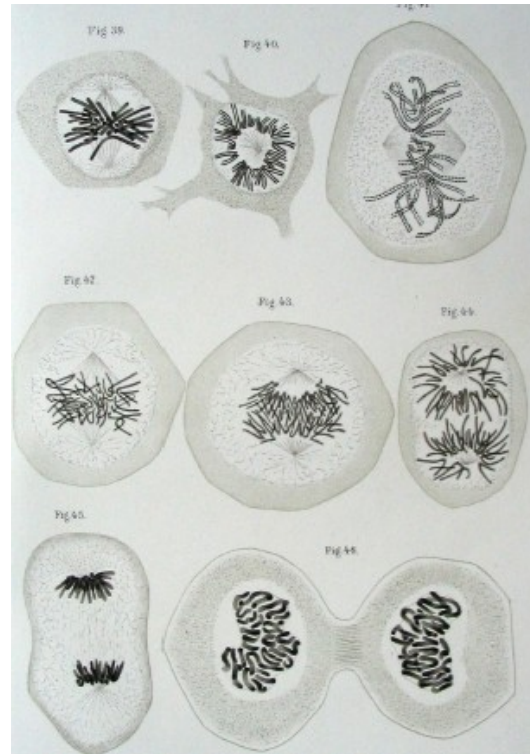
# Chromosome in 3D



Walther Flemming



Chromosomes : drawing by W. Fleming, 1885

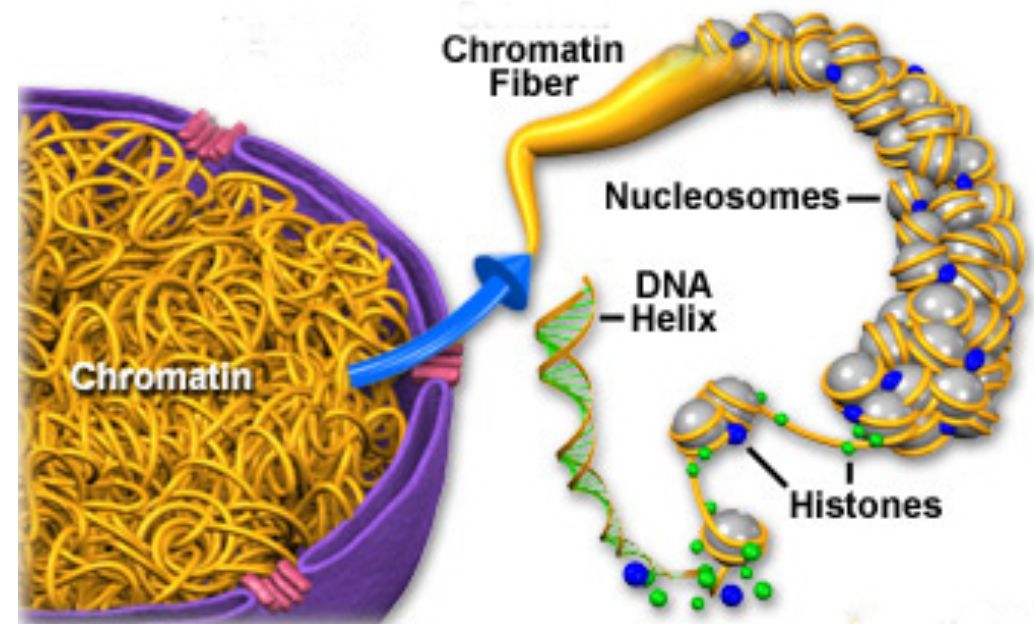


Chromosomes in 2005  
by Bolzer et al. PloS Bio

# The law code and executive power!

“Chromosomes are **law-code and executive power** - or, to use another simile, they are **architect's plan and builder's craft - in one.**”

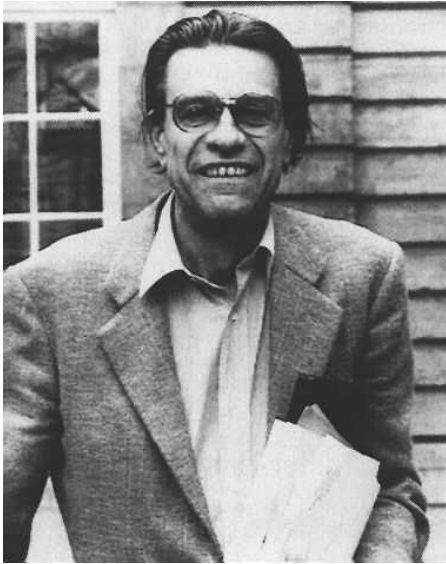
— Erwin Schrodinger, 1944,  
**What is Life?**



Chromosome large scale organization is a beautiful example of the  
**interplay between Physics and Biology!**

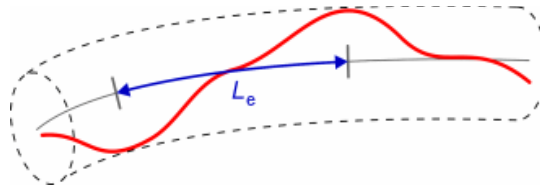


# Topologically Constrained System



de Gennes, 1975

- Entanglement Length( $L_e$ )
  - Density in Kuhn segment:  $\rho_k$
  - Kuhn Length:  $l_k$

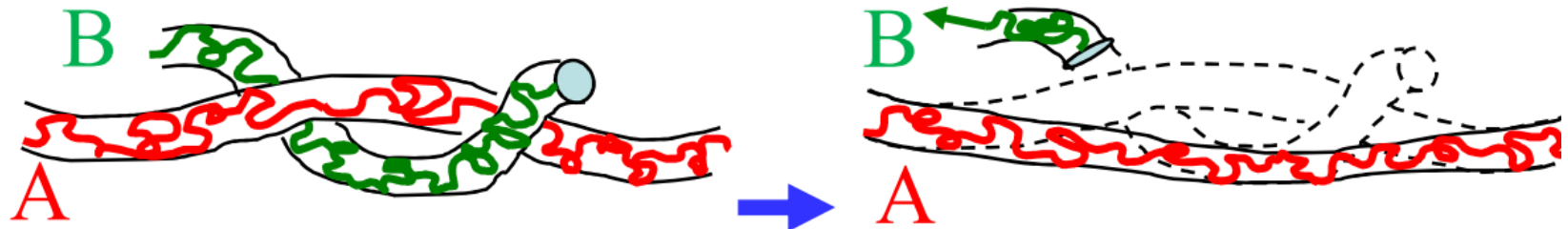


- Entanglement Length in nm:

$$L_e = l_k \left( \frac{c}{\rho_k l_k^3} \right)^2$$

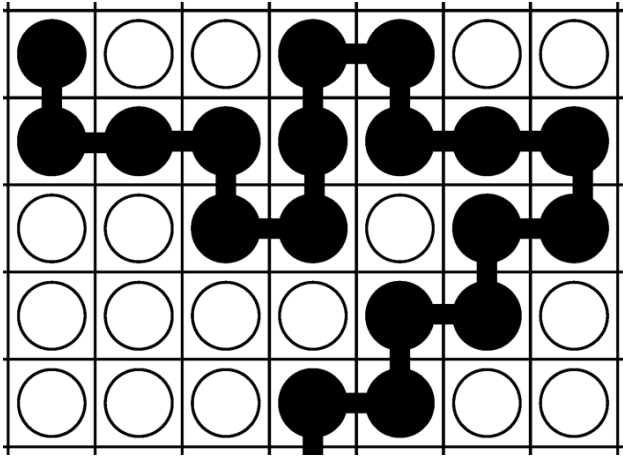
Ralf Everaers et. al. JCP, 2008, 128

- Reptation of Linear Chains

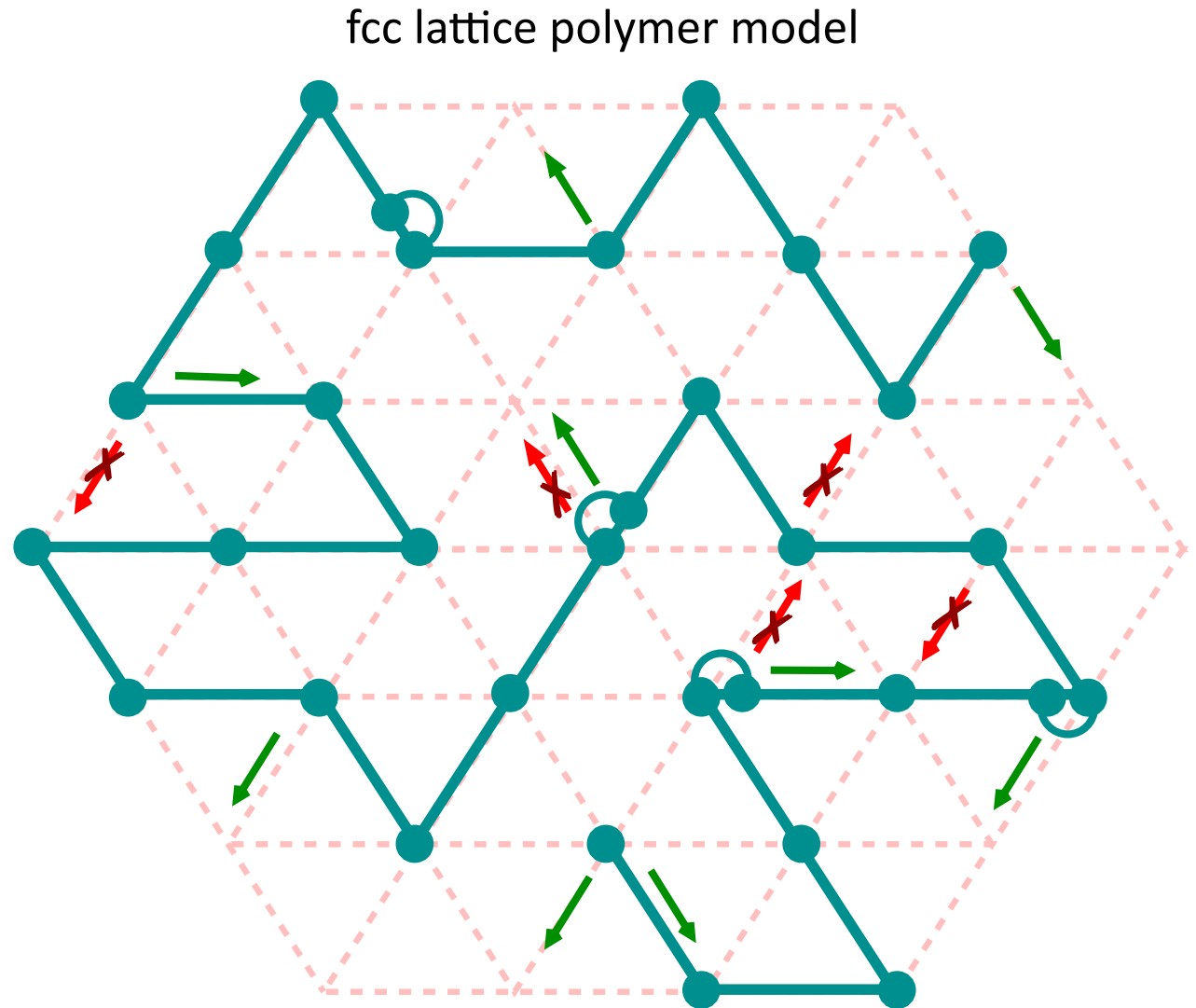




## Chromosome modeled as a lattice polymer



# lattice polymer model



Rubinstein, PRL, 1987; Barkema et al, JCP, 2018; Ghosh and Jost, Biorxiv 200584, 2017.

# Physical quantities to measure

1. Mean Squared Displacement (MSD)
2. Physical Distance
3. Contact Probability

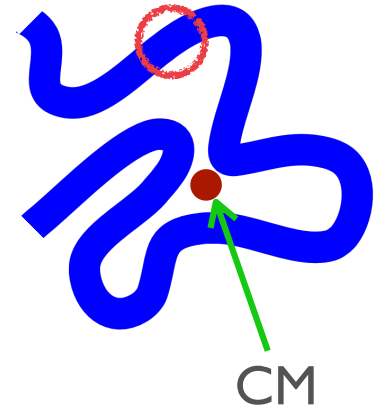


# Physical quantities to measure

## 1. Mean Squared Displacement (MSD)

1.1 MSD of each segment:  $g_{1i}(t) = \langle (\mathbf{r}_i(t) - \mathbf{r}_i(0))^2 \rangle$

1.2 MSD of the center of mass:  $g_3(t) = \langle (\mathbf{r}_{cm}(t) - \mathbf{r}_{cm}(0))^2 \rangle$



## 2. Physical Distance

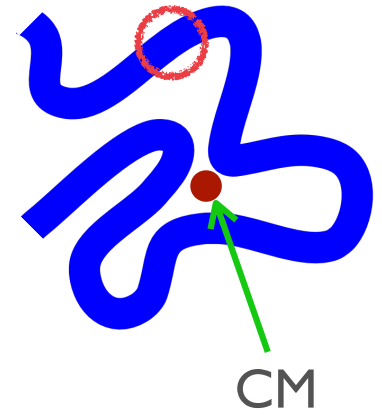
## 3. Contact Probability

# Physical quantities to measure

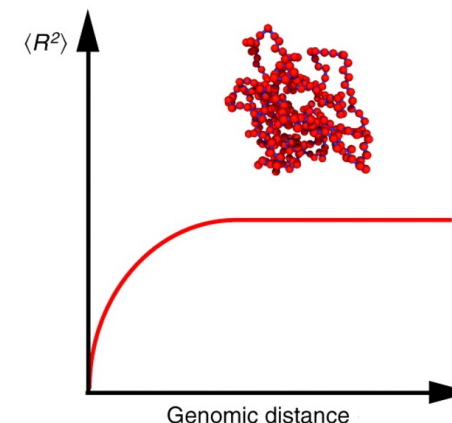
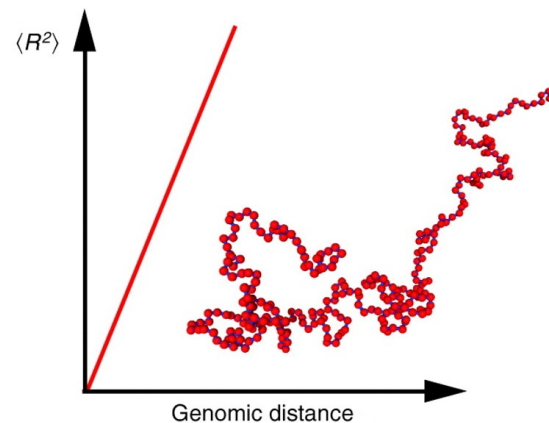
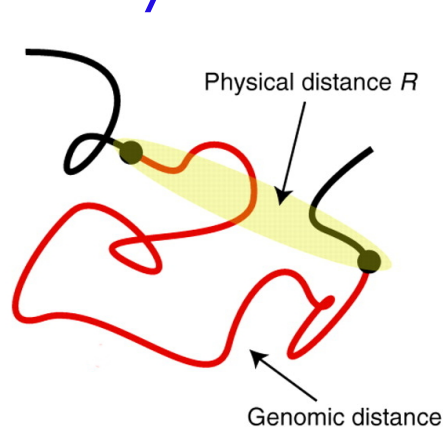
## 1. Mean Squared Displacement (MSD)

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## 2. Physical Distance



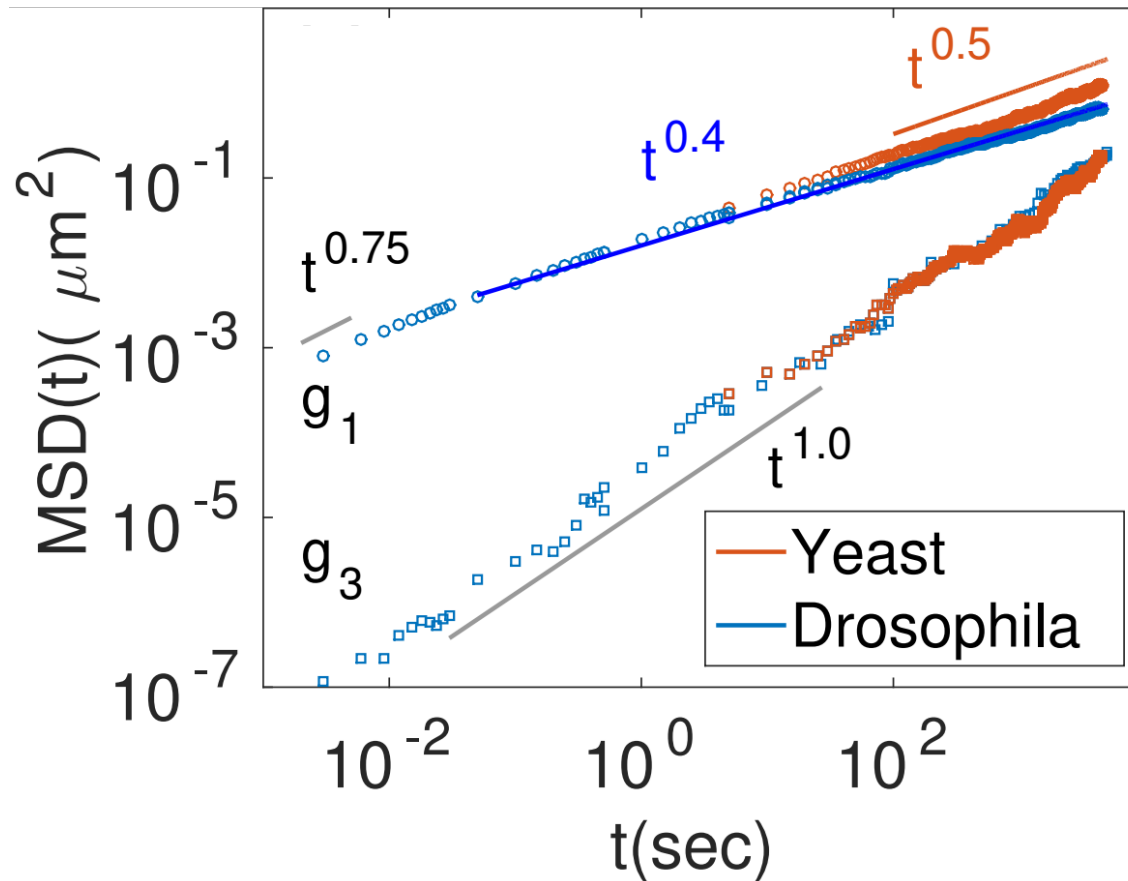
## 3. Contact Probability





# Time Mapping

- Mean Squared Displacement (MSD)
- Yeast and Drosophila Chromosome



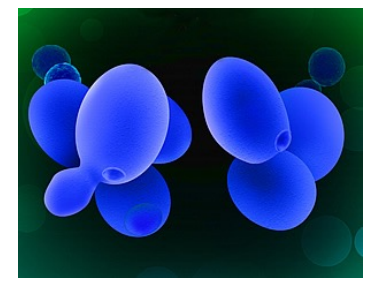
Ghosh and Jost, Biorxiv 200584, 2017.

- **Yeast**

$$L = 750 \text{ kbp}$$

$$\rho \approx 0.005 \text{ bp} / \text{nm}^3$$

$$L_e = 920 \text{ kbp}$$

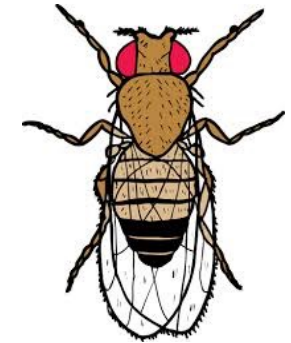


- **Drosophila**

$$L = 20 \text{ Mbp}$$

$$\rho \approx 0.009 \text{ bp} / \text{nm}^3$$

$$L_e = 285 \text{ kbp}$$



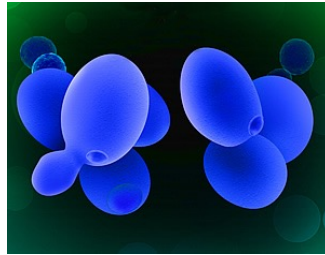
# Measured physical quantities

- Yeast

$$L = 750 \text{ kbp}$$

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$$L_e = 920 \text{ kbp}$$

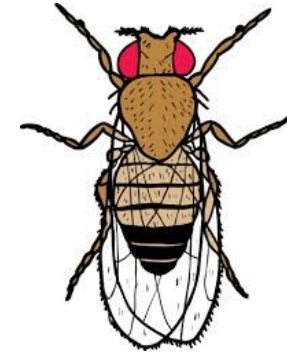


- Drosophila

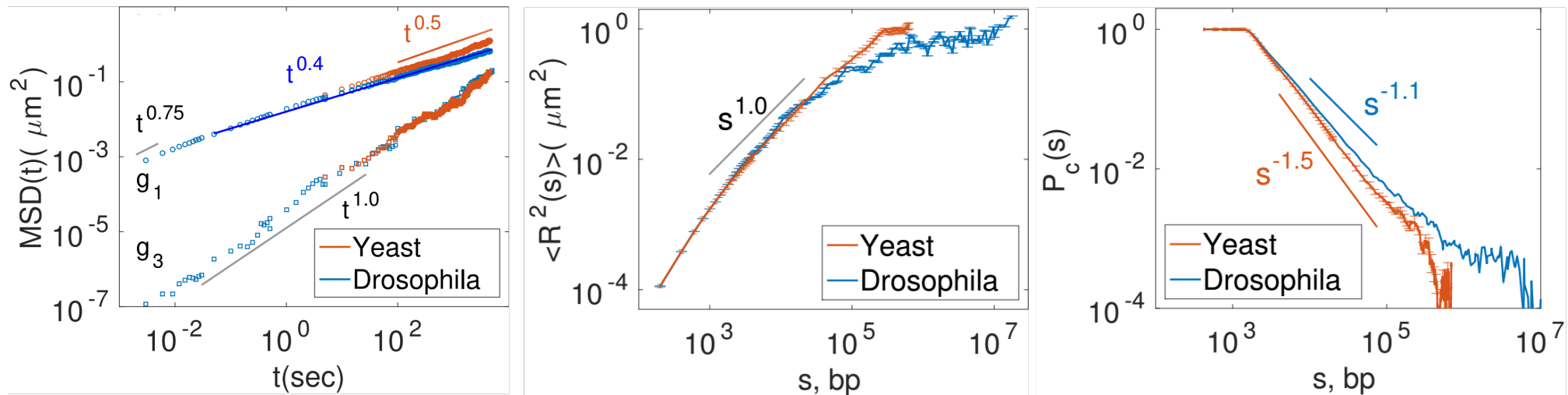
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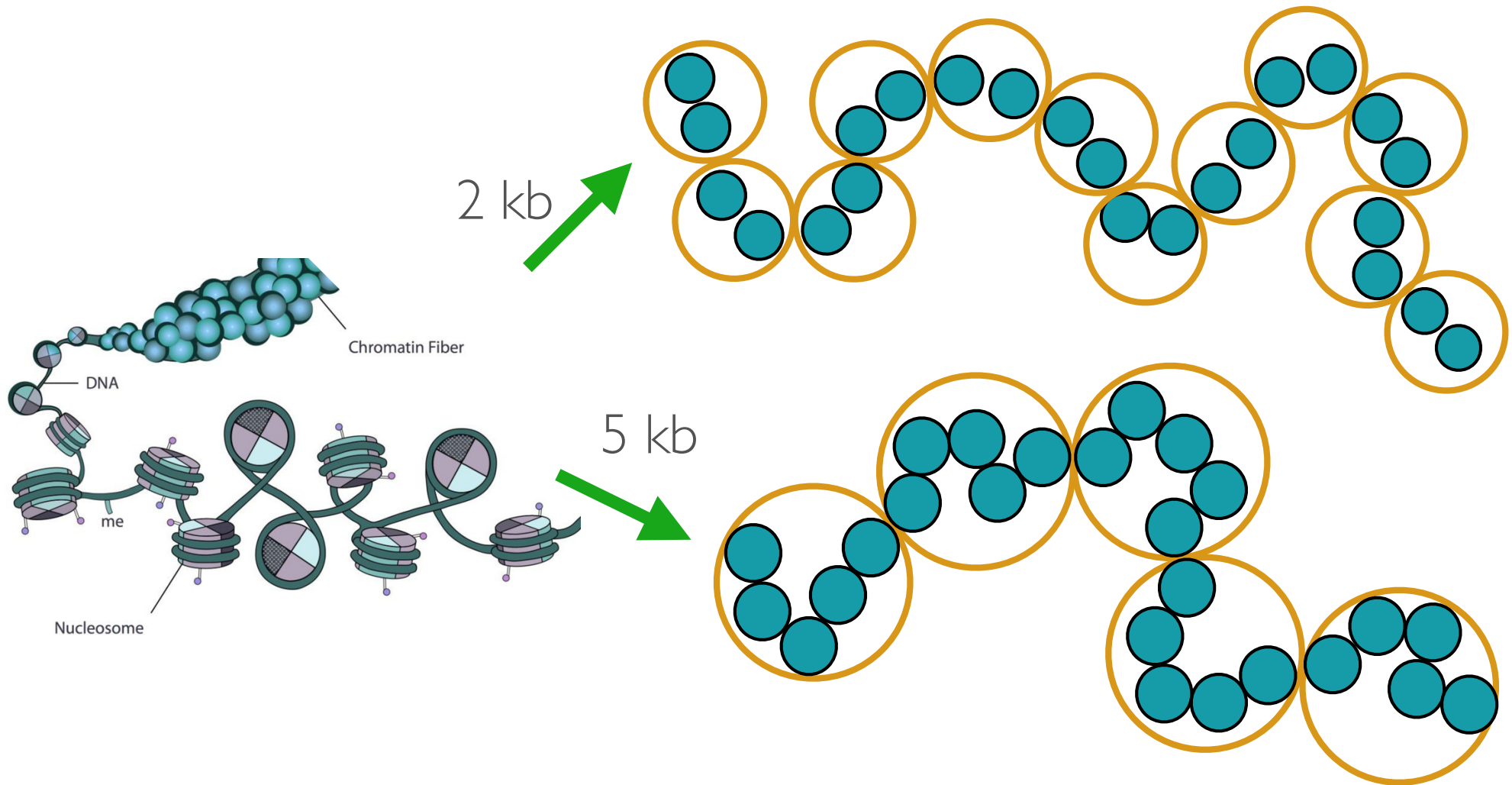
- Yeast, Drosophila Chromosome at nucleosome resolution



Ghosh and Jost, Biorxiv 200584, 2017.



# Chromosome: Coarse Graining Long Polymers



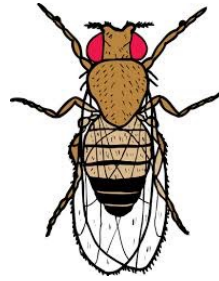
# Measured physical quantities

- **Drosophila**

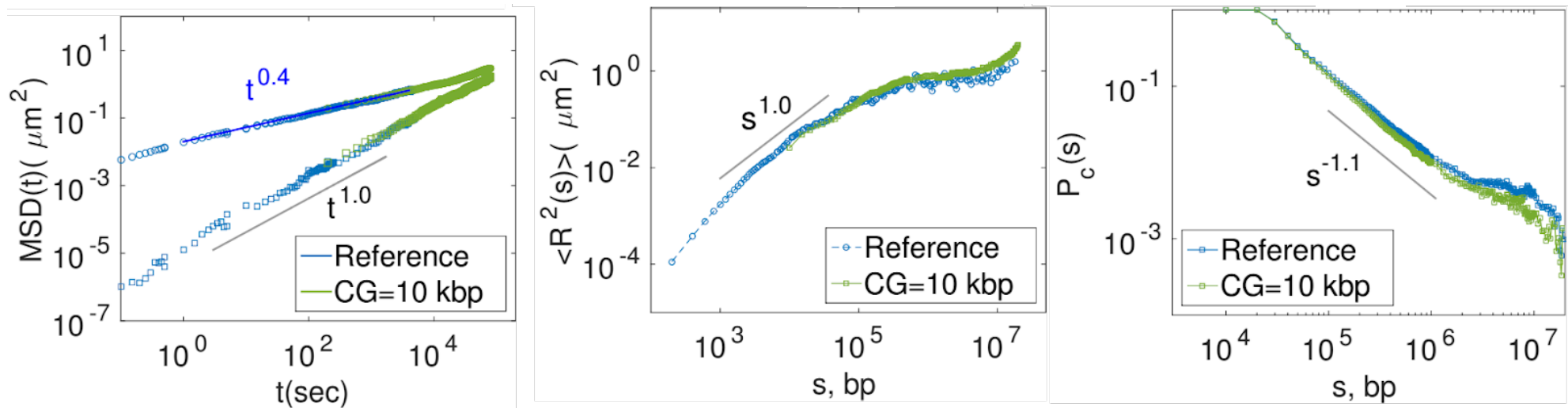
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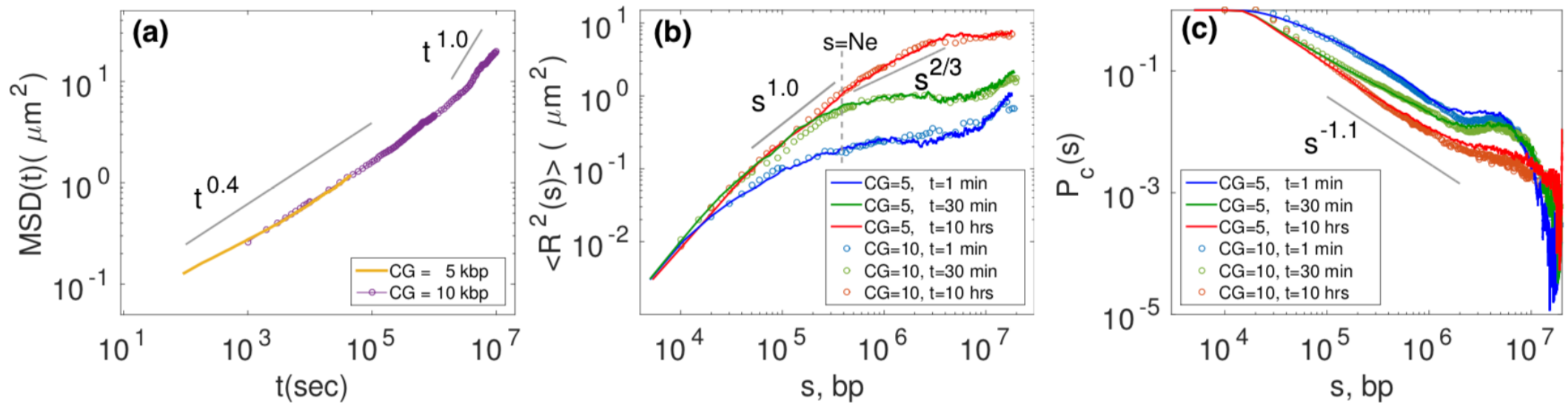
- Different Coarse Graining: **CG=0.2 kbp** vs. **CG=10 kbp**





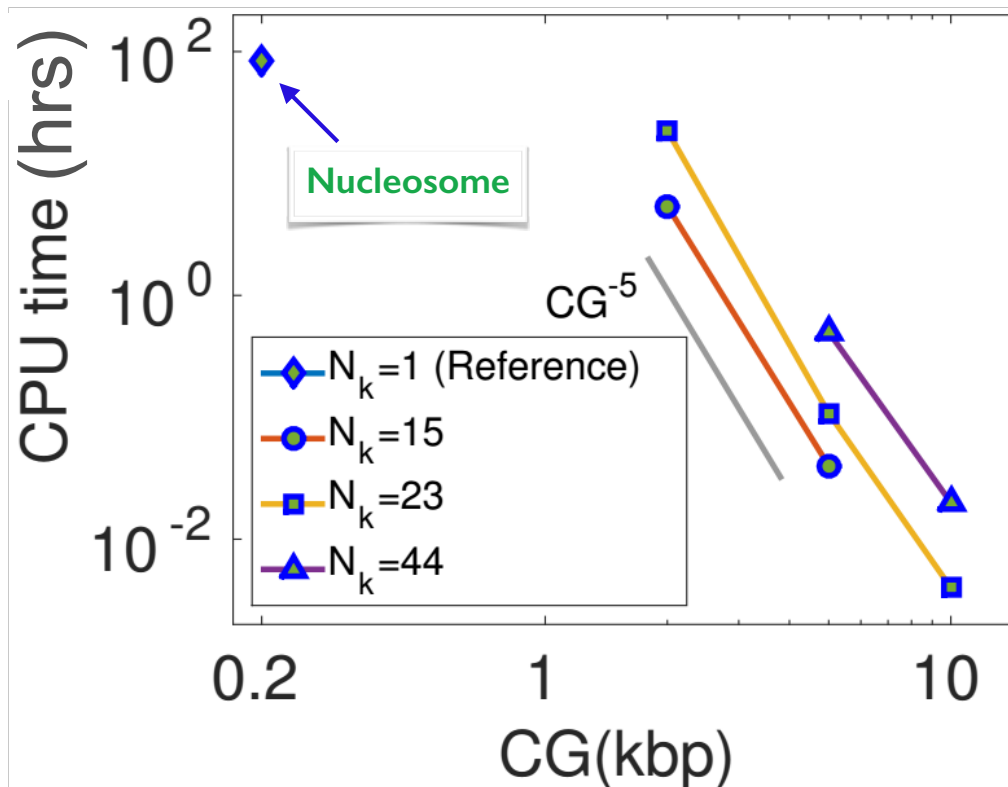
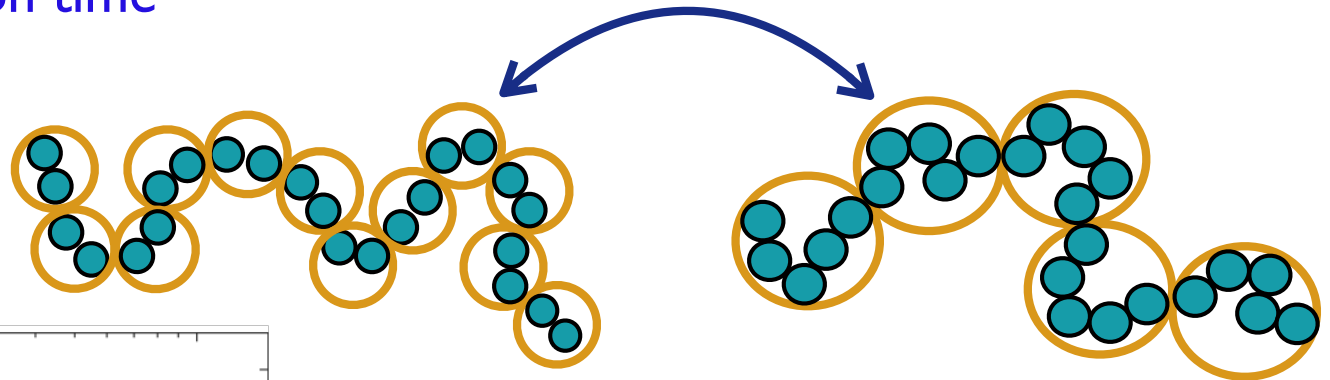
# Time evolution

- Different Coarse Graining: CG= 5 kbp vs. CG=10 kbp



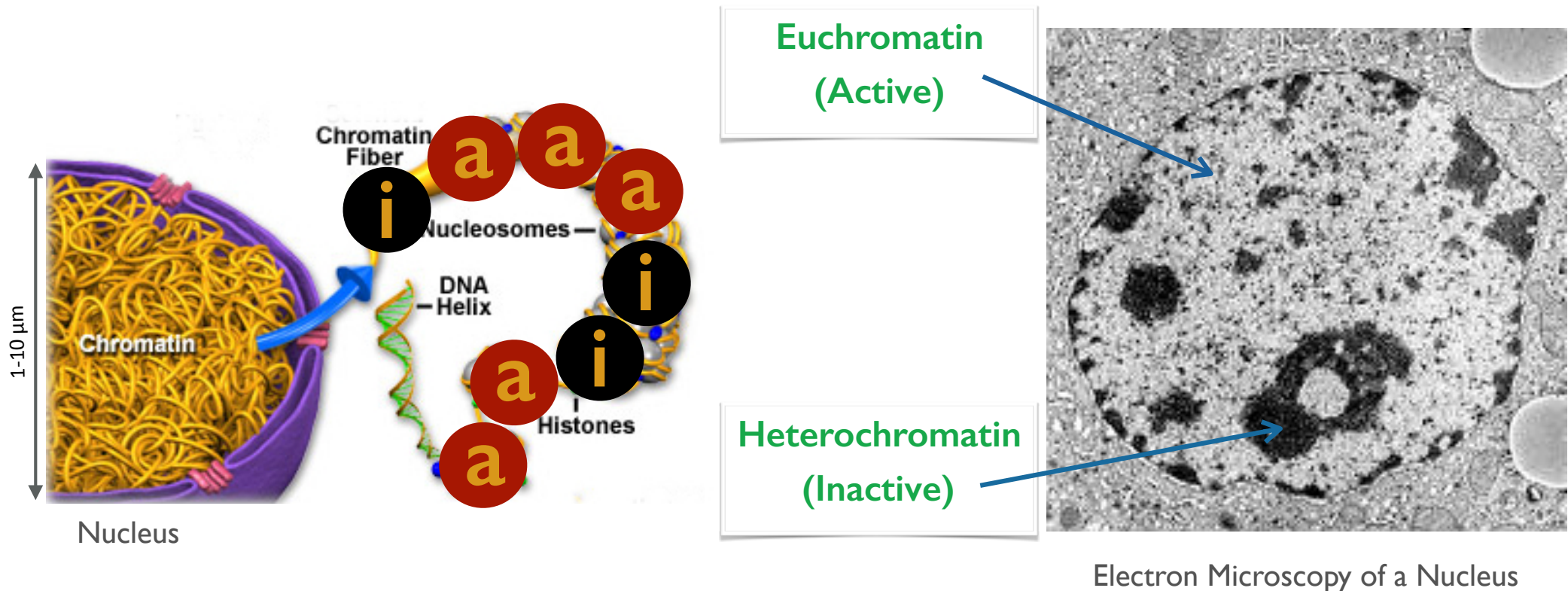
# Computation Time

- An efficient coarse grained polymer model
- Power law gain in computation time



# Physical Biology of Chromatin

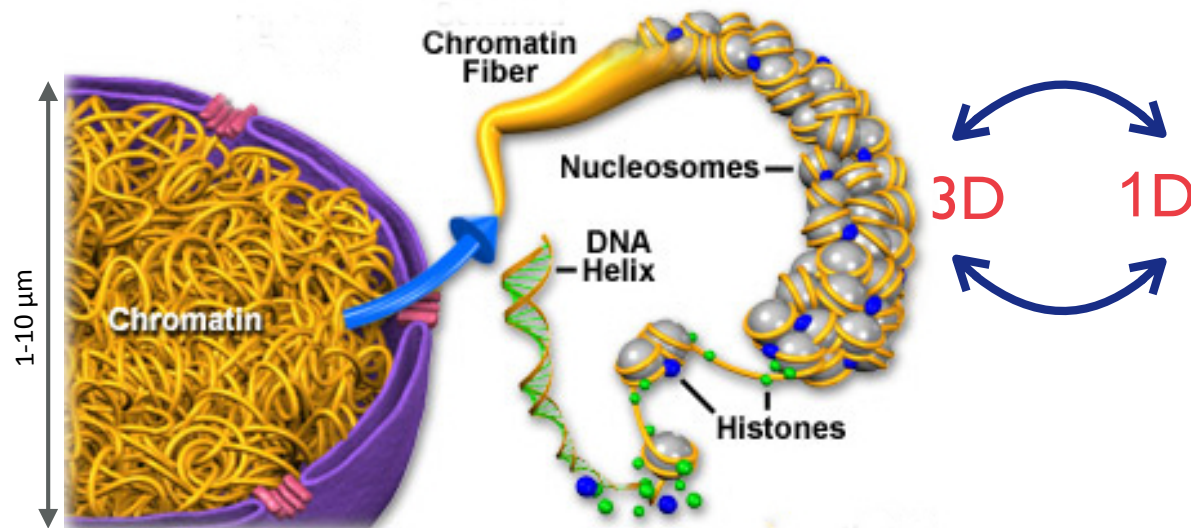
- Active and inactive genes occupy different areas of the nucleus
- Epigenetics modifies gene expression without altering genetic information



Q. What is the relation between epigenetics and chromatin organization?

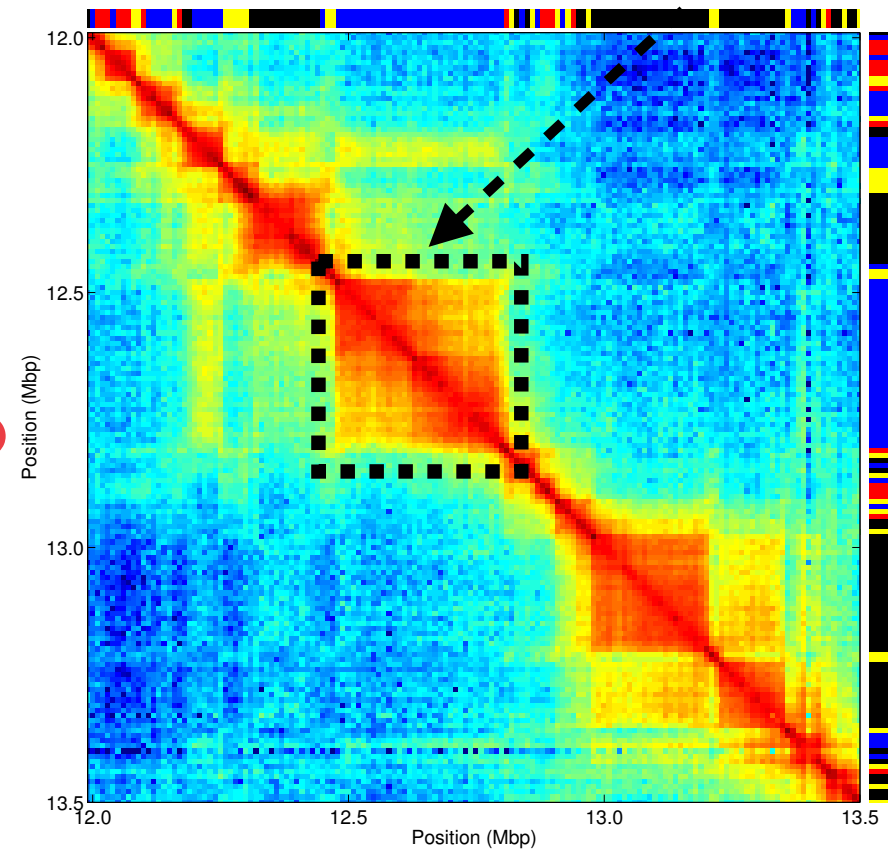
# Basics of Chromatin, Chromosome

- A hierarchal organized folding



- Genome: 1Mbp - 6Gbp (few mm to m)
- Base-Pair density: 0.001-0.1 bp/nm<sup>3</sup>

- Topologically Associated Domain (TAD)

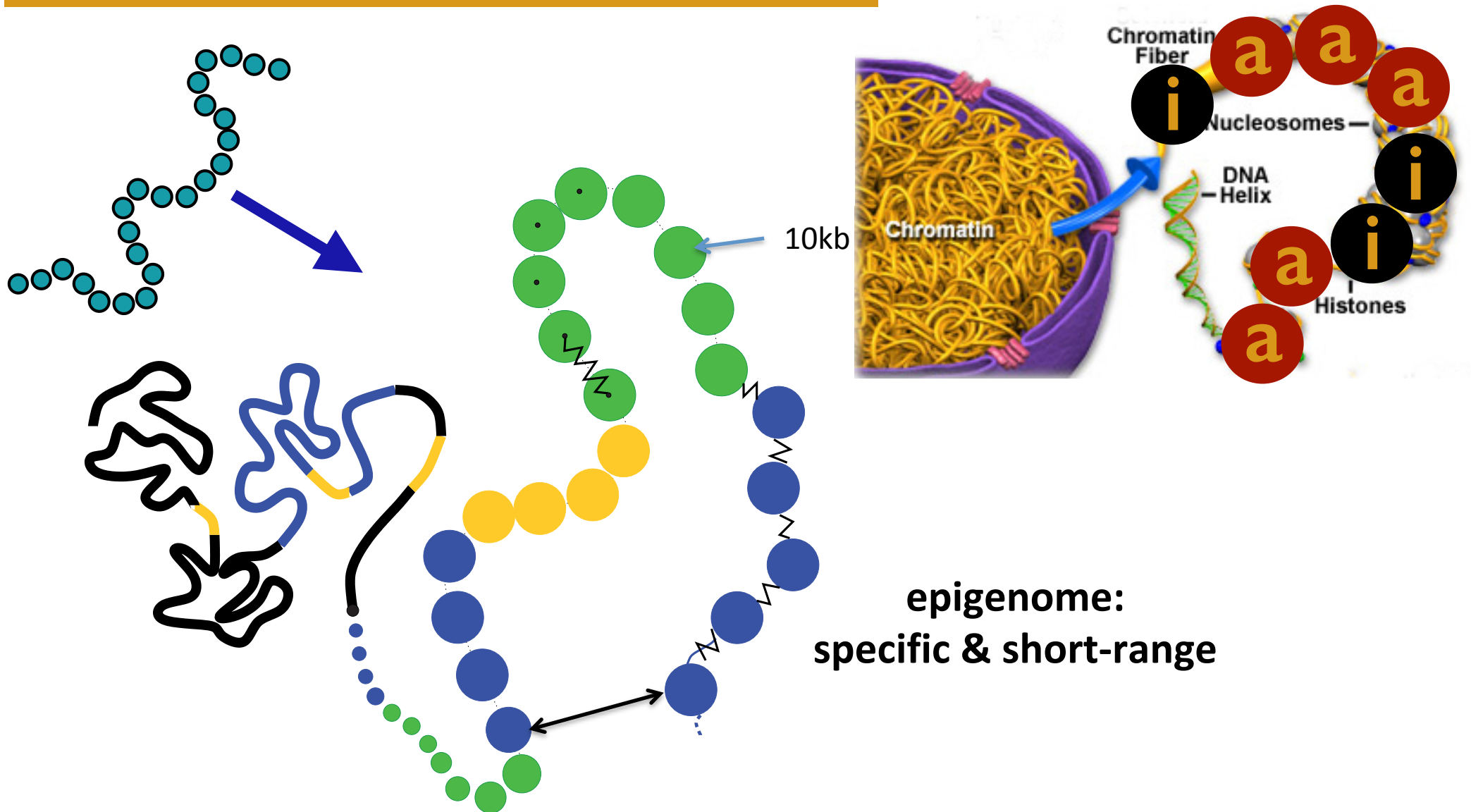


- HiC: Chromosomal Contact Map for Drosophila
- Whole genome is linearly partitioned

Sexton et. al. Cell, 2012, 148

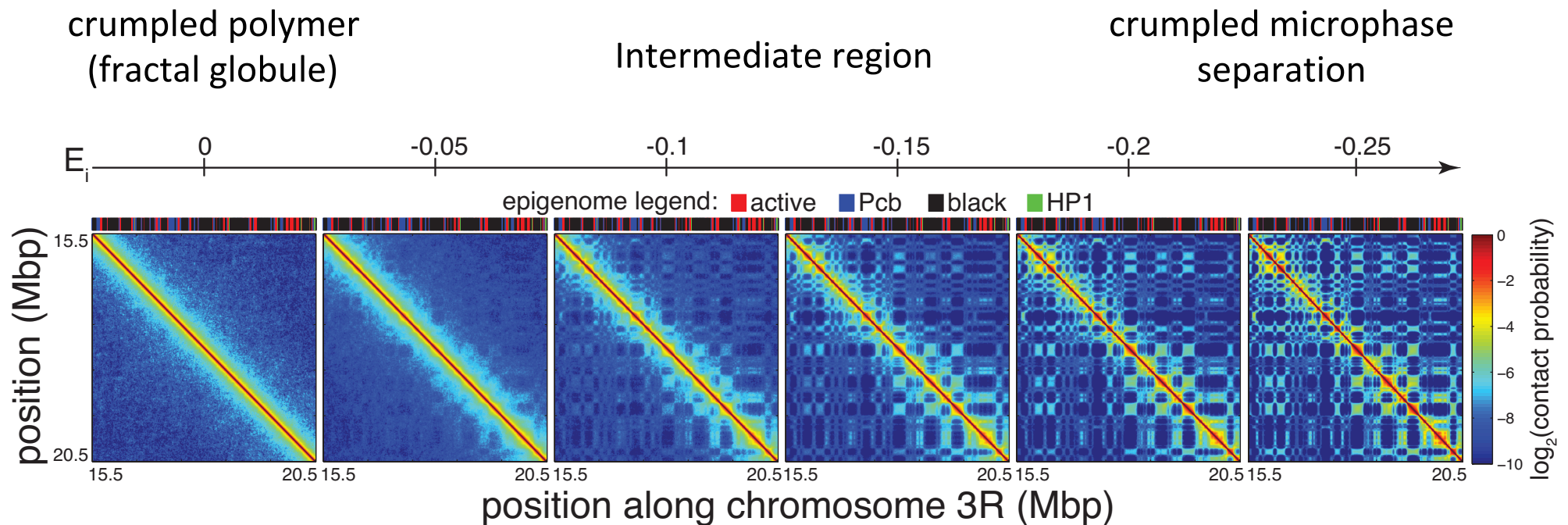


# Chromatin as a block copolymer



*How far can we go with this simple model?*

# Phase diagram of chromosome 3R

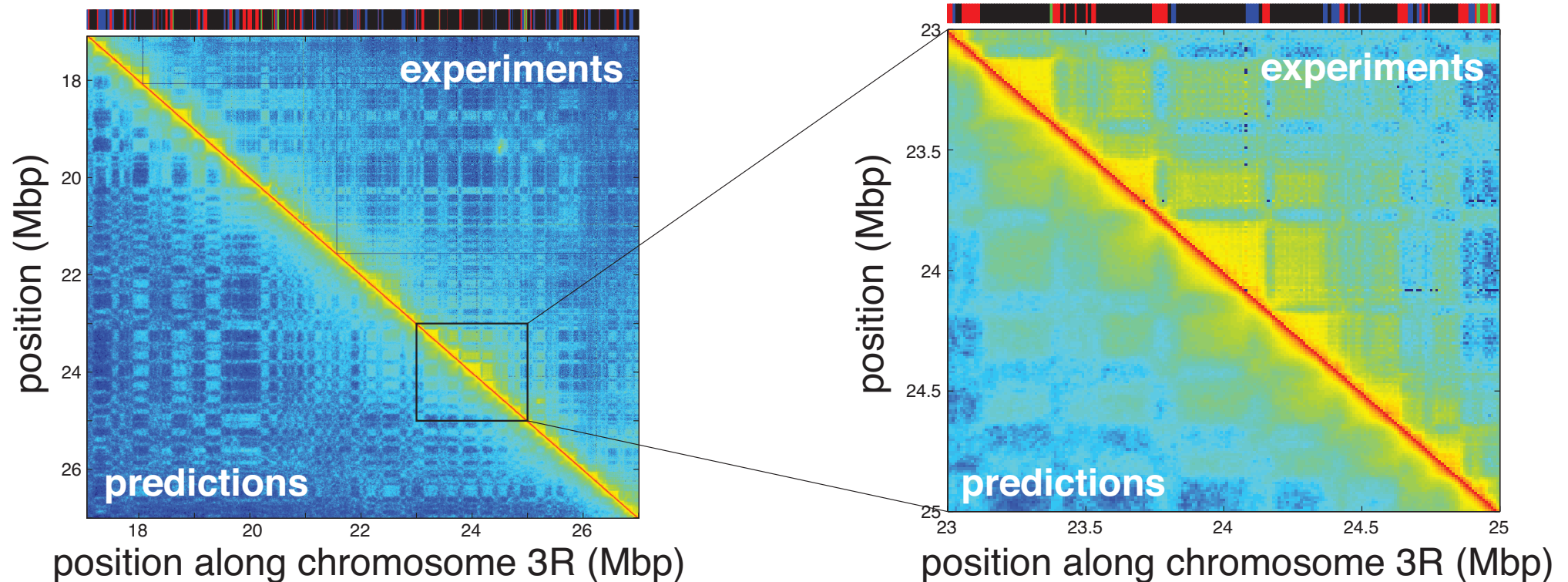


Ghosh et al. 2017

# Comparison with experiments

- Experiment: **intra-state** contact frequency about **1.5** more than **inter-state** contact frequency
- Corresponds to  $E_i = -0.1$ , ie in the **intermediate region**

Ghosh et al. 2017

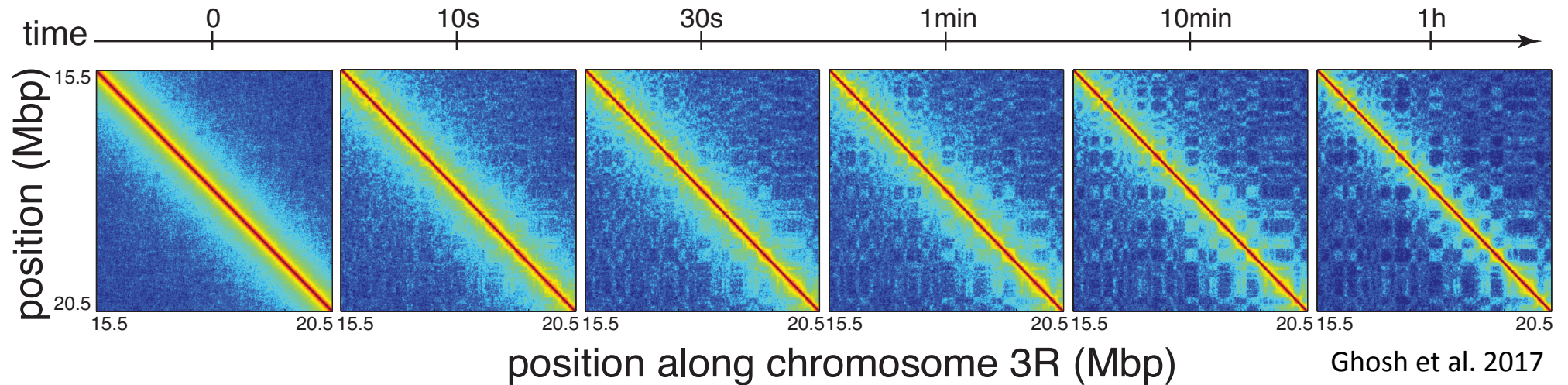


Same color legend!!



# Dynamics of TAD formation

Predicted HiC-map on synchronized cells

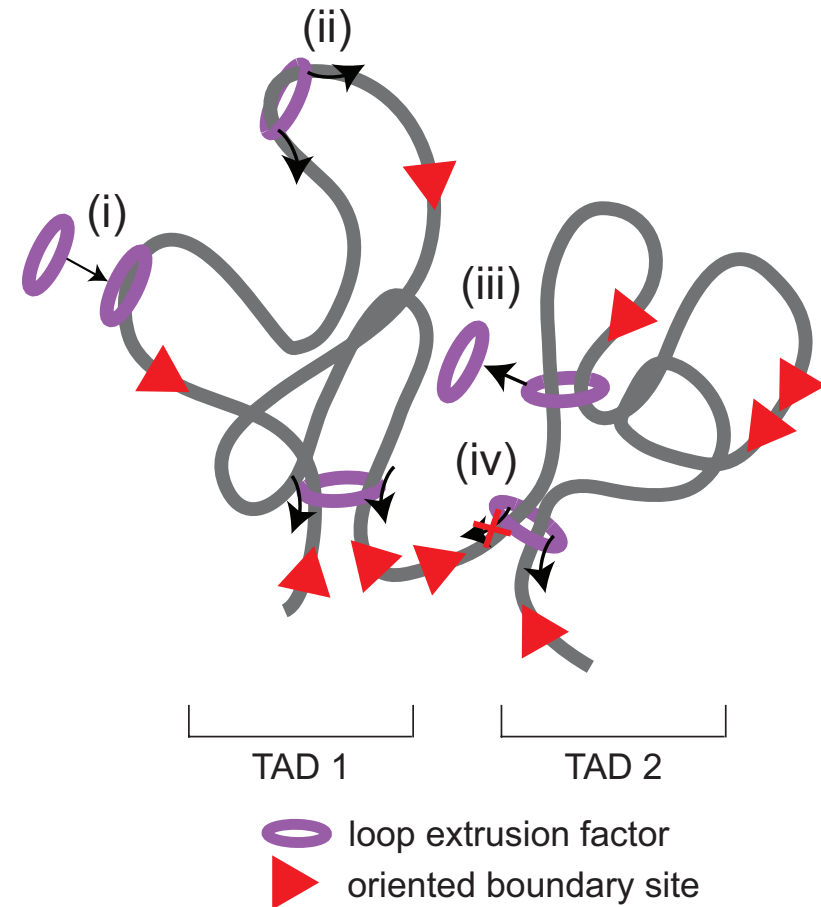


- TADs quickly form: 1-10 minutes
- Long-range inter-TAD interactions more slow >1h
- Consistent with HiC on synchronized – mammalian – cells (Naumova et al, Nature 2012)

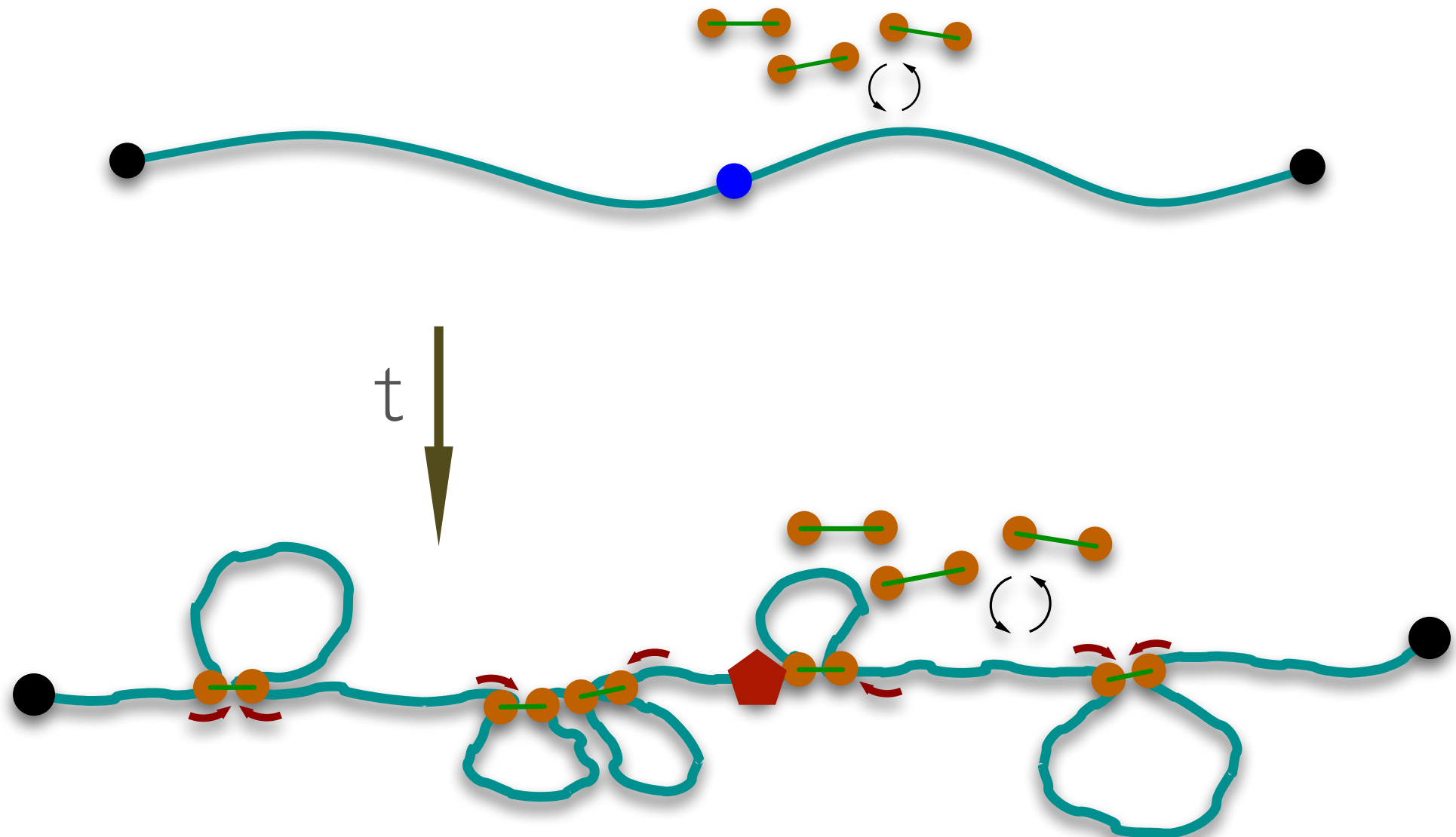


# Perspective

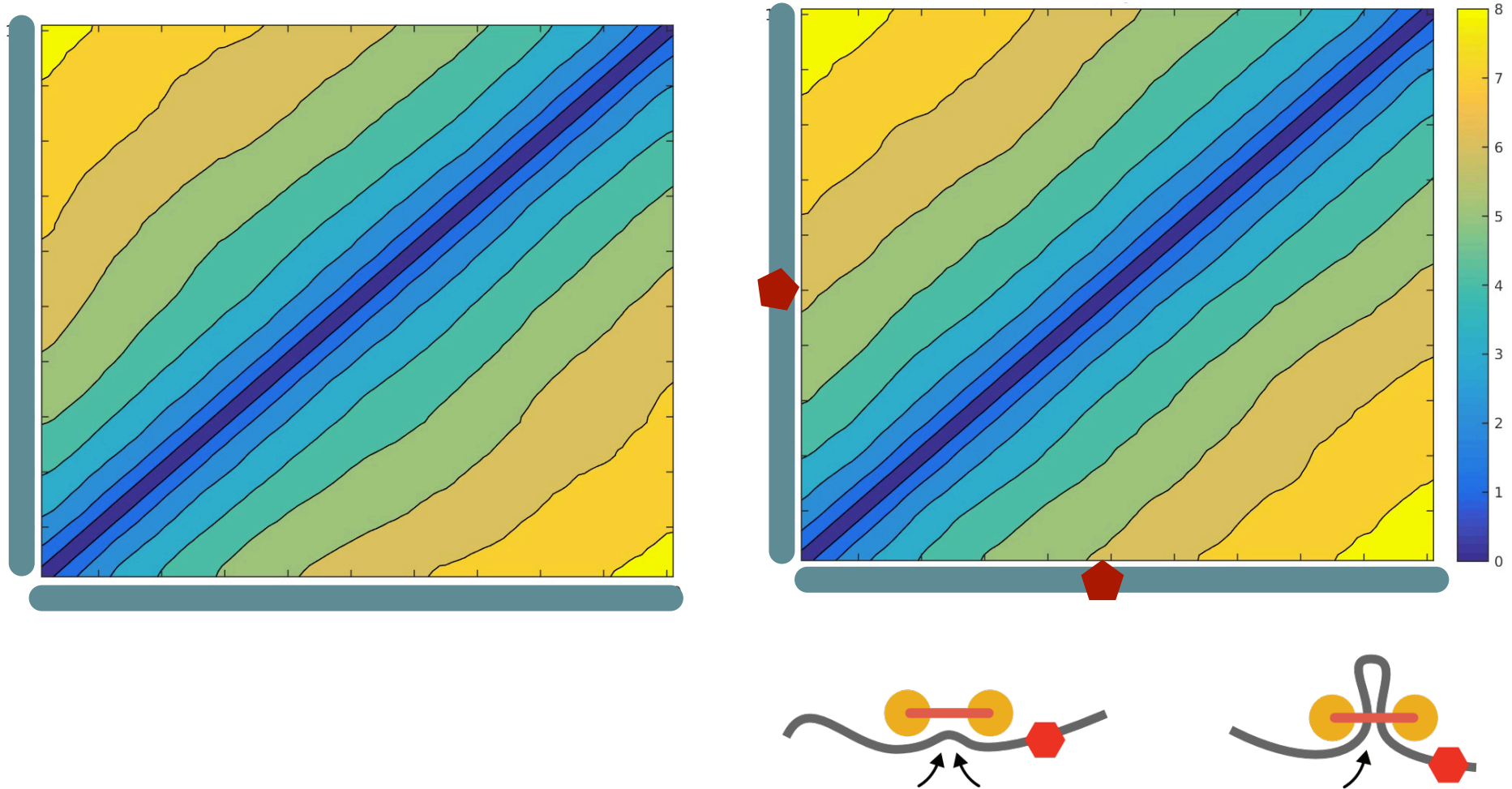
- Effect of extrusion on chromosome folding.
- Interaction with membrane



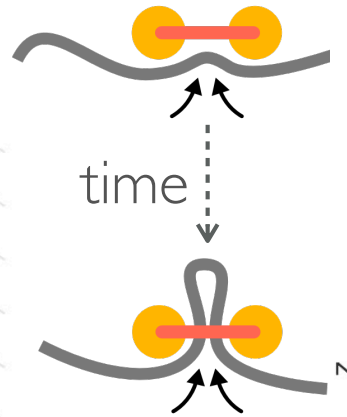
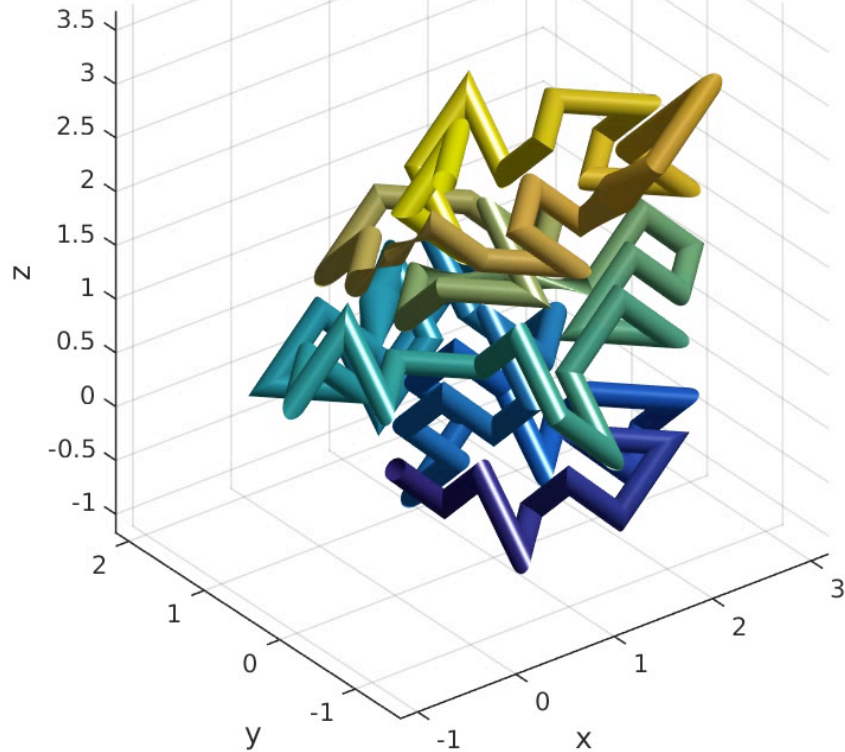
# Extrusion



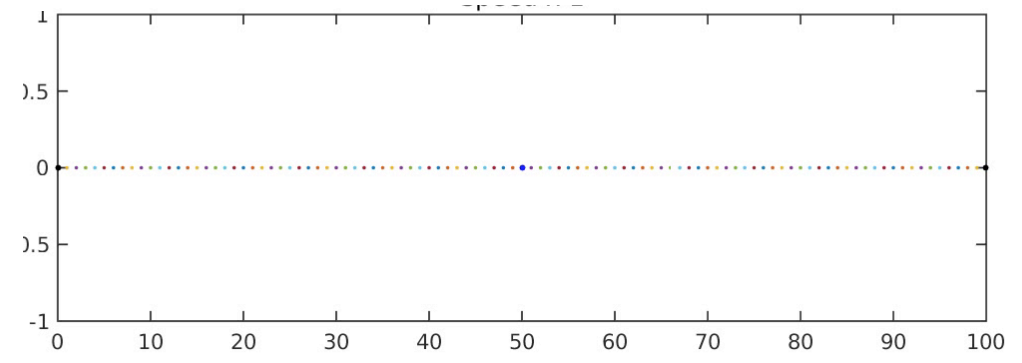
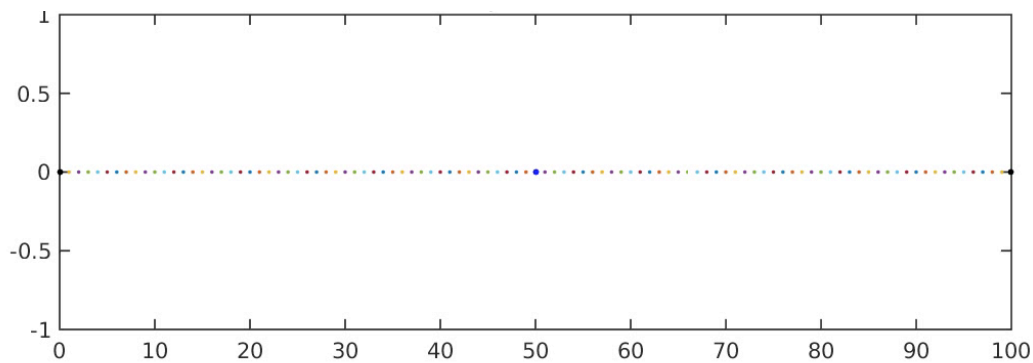
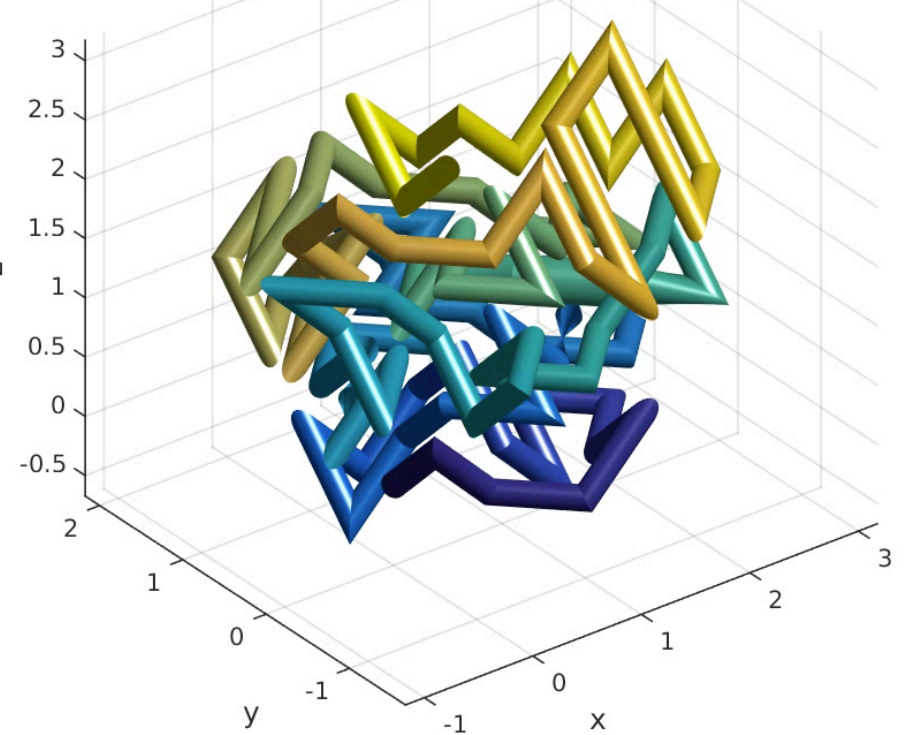
# Effect of Boundary



## Slow Movement



## Fast Movement





# Open Questions and Challenges

Q. How can small proteins control large genome organization?

consecutive loops



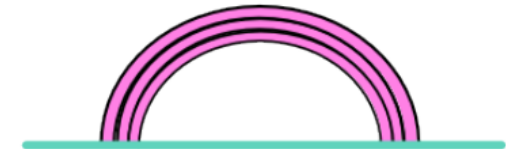
Q. How 3D contributes to 1D establishment and maintenance?

nested loops



- Dramatic change in chromosome configurations when cell progress through cell cycle
- The mechanism of active loop extrusion hold a great promise for explaining chromosome folding

stacked loops



# Acknowledgements

## Computational and Physical Biology:

### **TIMC-IMAG, Grenoble:**

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Paul Terzian

### **ENS Lyon:**

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Ralf Everaers

## Experimental Biology:

### **IGH, Montpellier:**

Giacomo Cavalli

### **University of Bern:**

Peter Meister

### **IAB, Grenoble:**

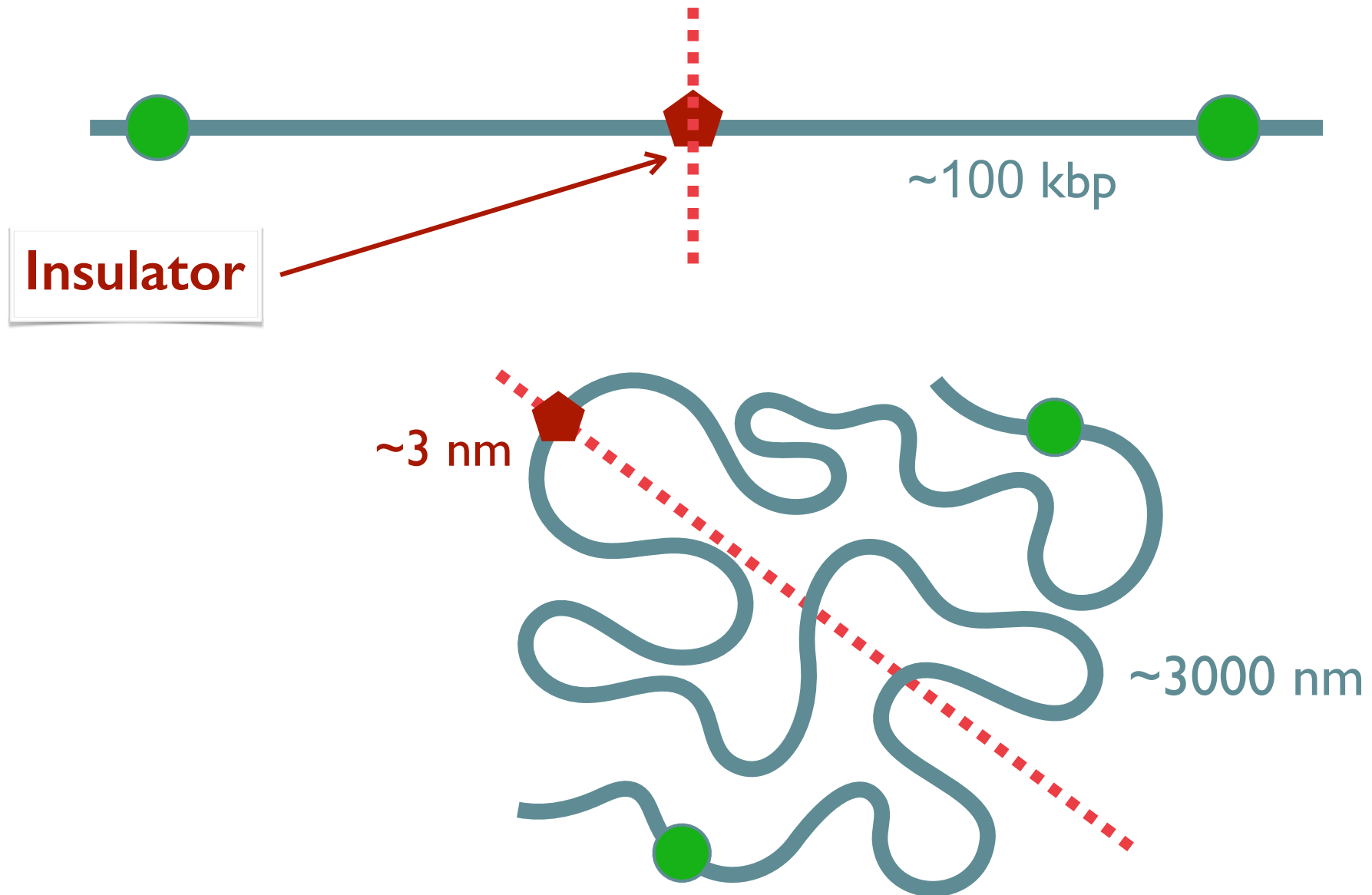
Saadi Khochbin  
Elisabeth Brambilla





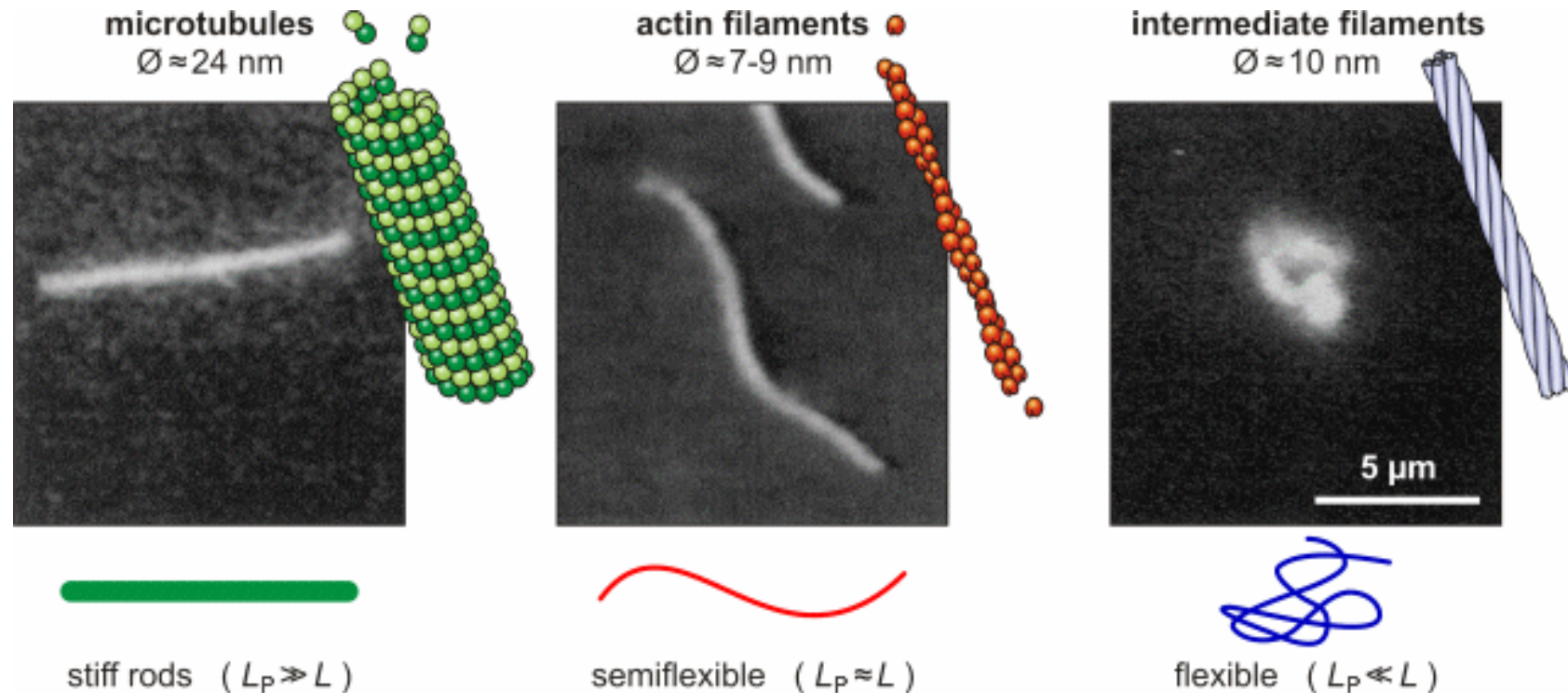
## Future Plan

Q. How can small proteins control large genome organization?





# Polymers in biology



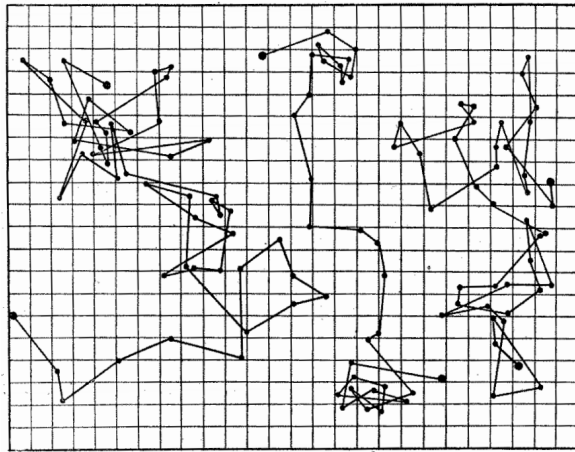
- Three different component of cytoskeleton
- They are differ in stiffness
- Characterized by the persistent length  $L_p$

# Polymer models

- Flexible Polymer: Random Walk
- Semi flexible polymer: Worm Like chain (WLC)

# Polymer models

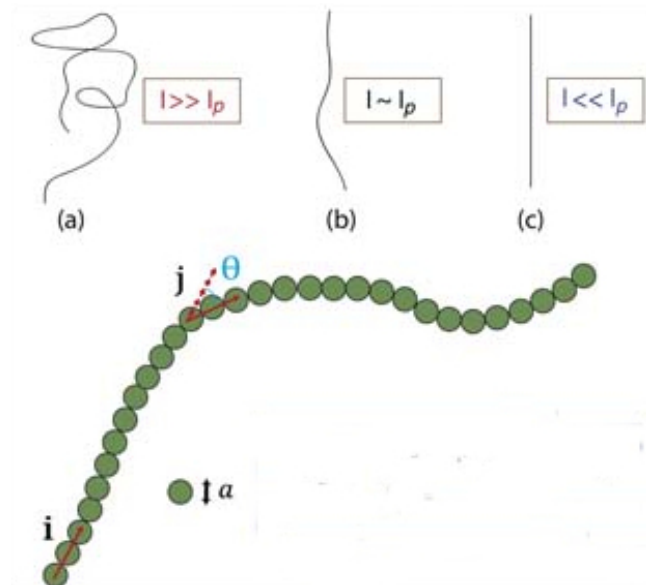
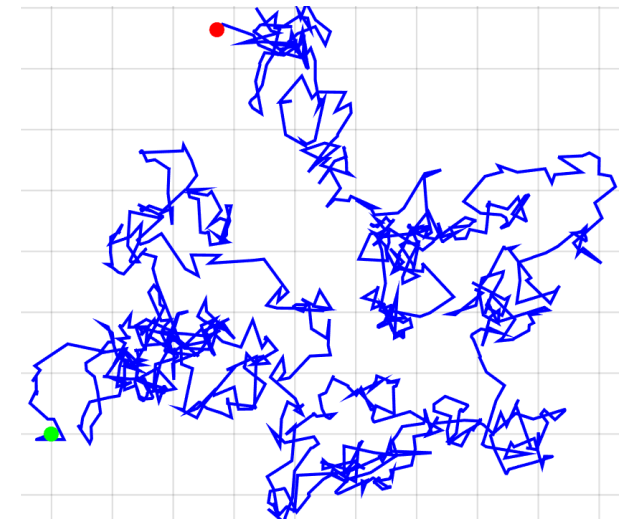
- Flexible Polymer: Random Walk



| Perrin, Comptes Rendus (Paris) 146 (1908) 967

- Semi flexible polymer: Worm Like chain (WLC)

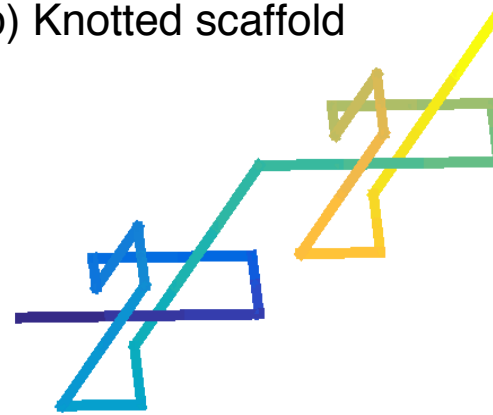
$$\frac{H}{k_B T} = \frac{L_p}{2} \int_{s=0}^L \kappa^2(s) ds$$



(a) Hedgehog scaffold



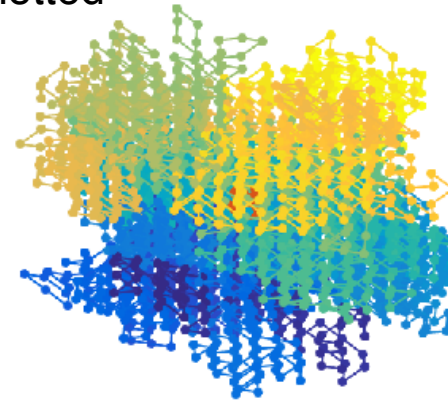
(b) Knotted scaffold



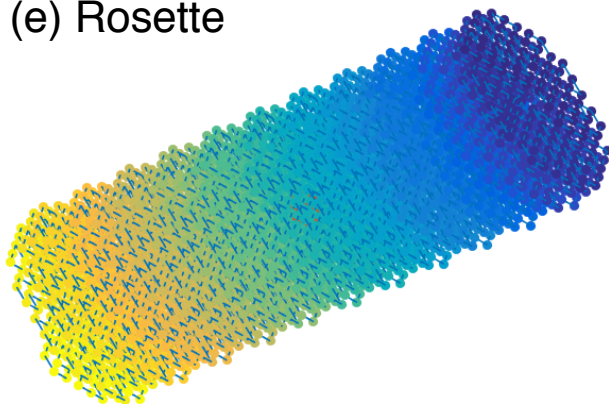
(c) Hedgehog



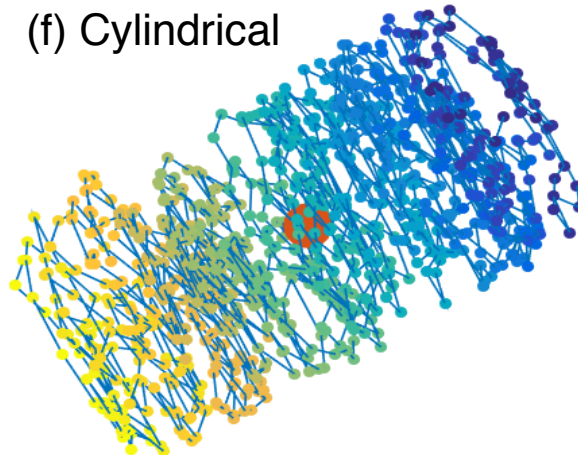
(d) Knotted



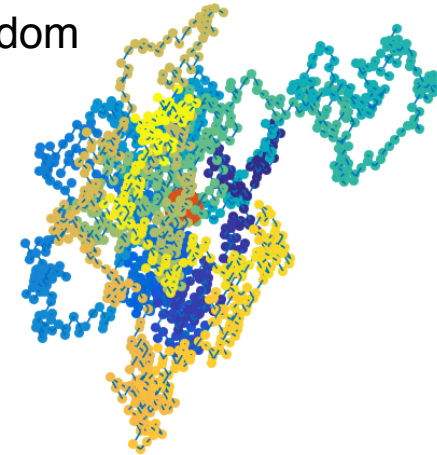
(e) Rosette



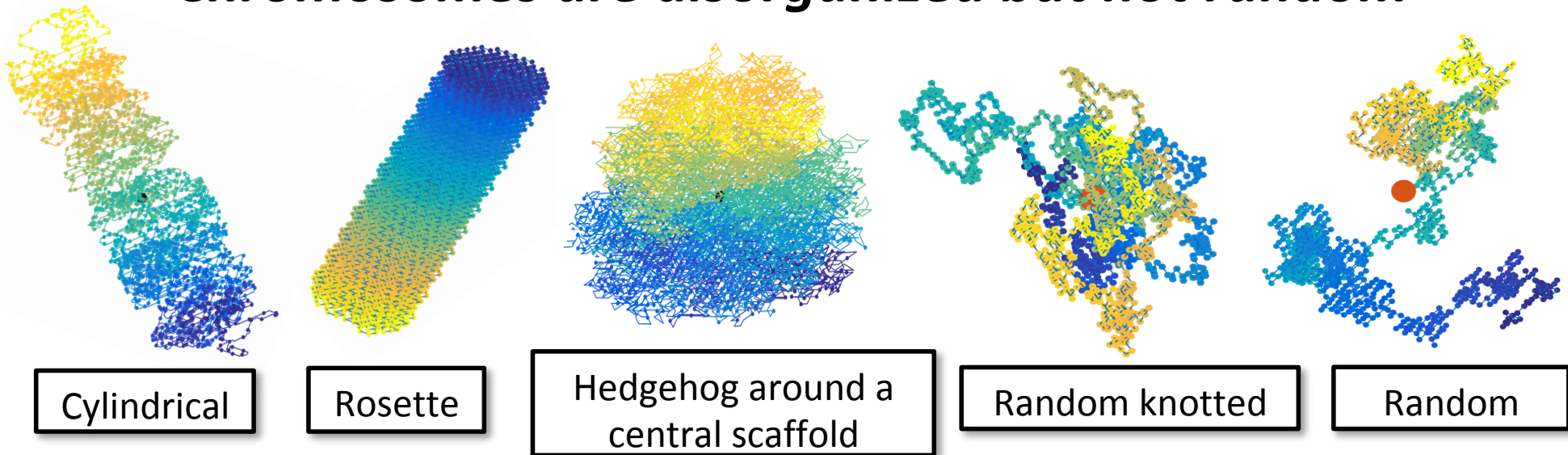
(f) Cylindrical



(g) Random



# Chromosomes are disorganized but not random

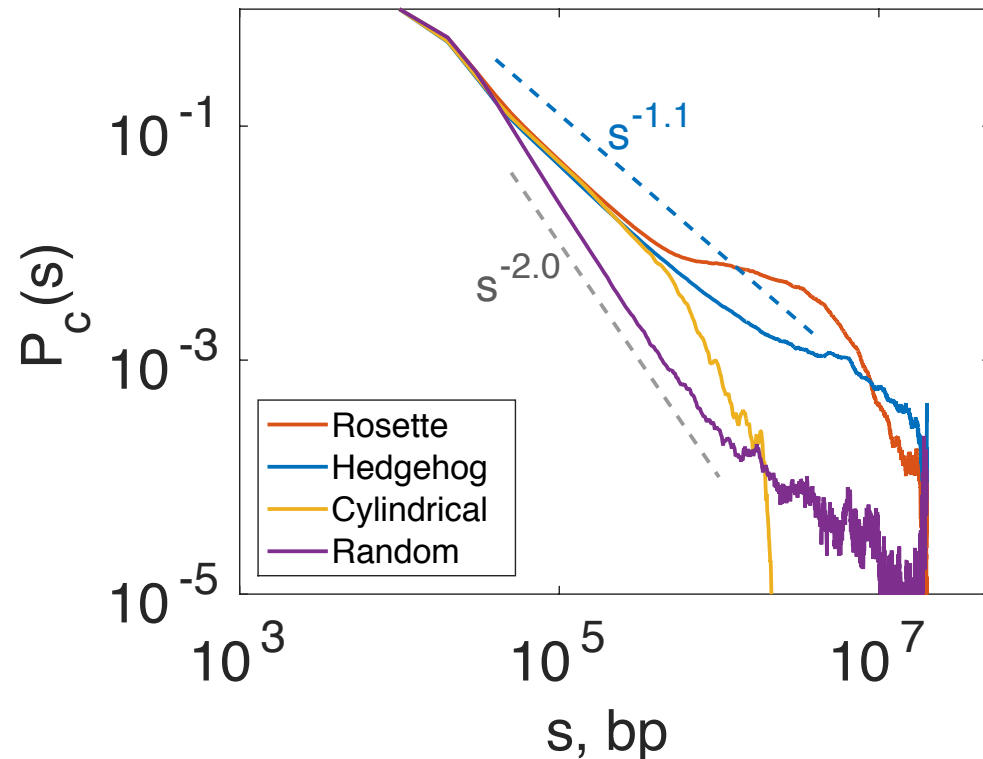


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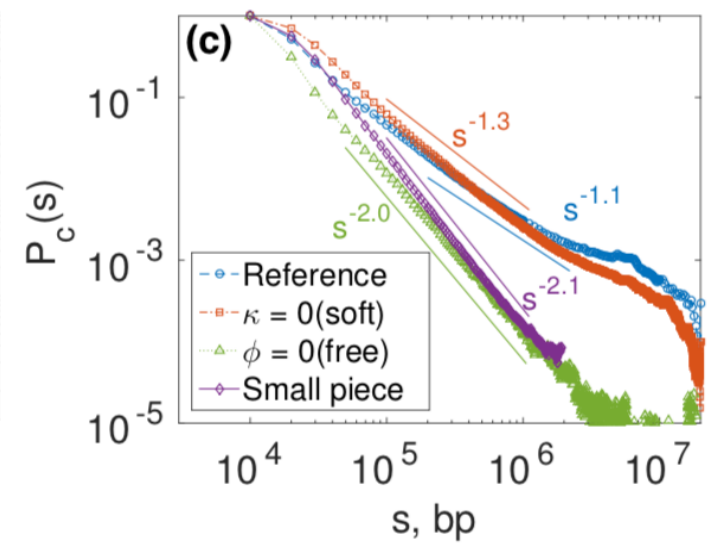
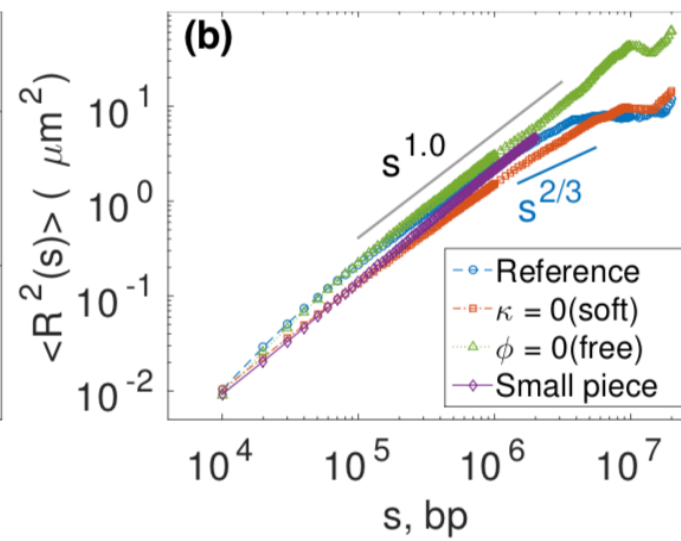
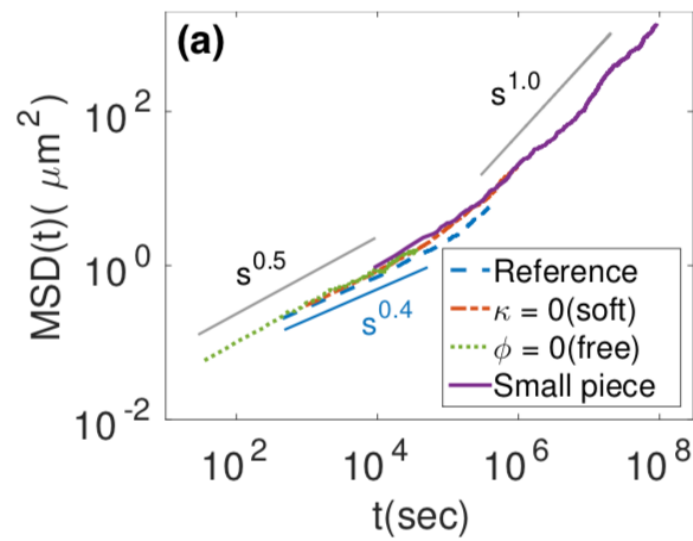
- Ghosh et al, 2017 in submission
- Naumova N. et al. 2013 Science
- Earnshaw W.C. and U.K. Laemmli. 1983. J. Cell Biol

- Contact probability

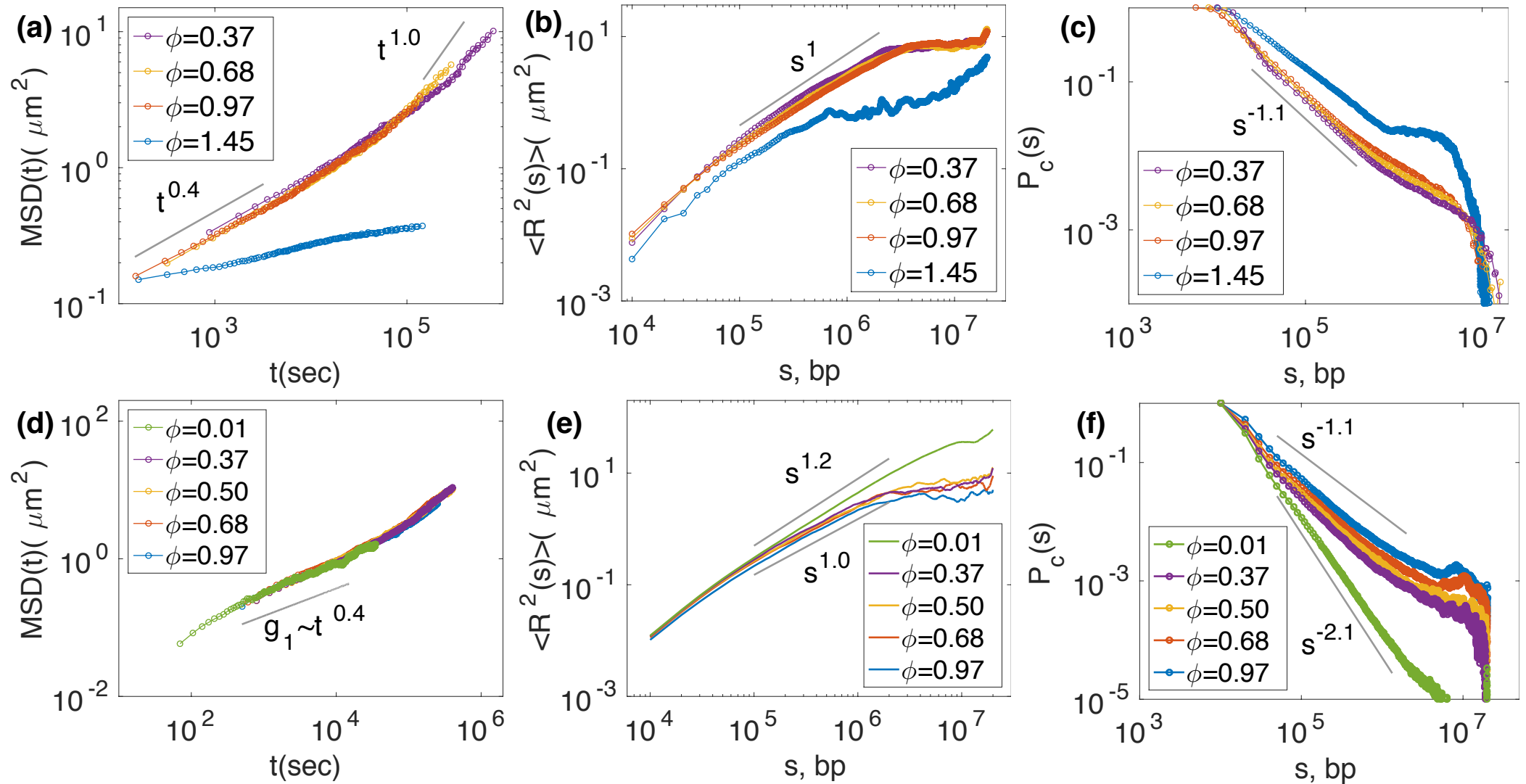
$$P_c(s) \approx s^{-1}$$



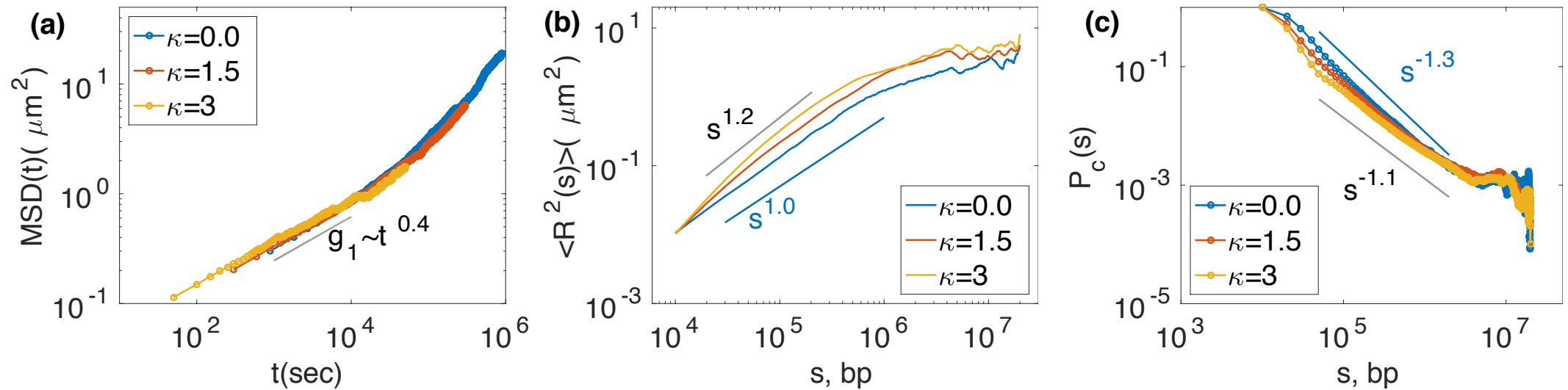




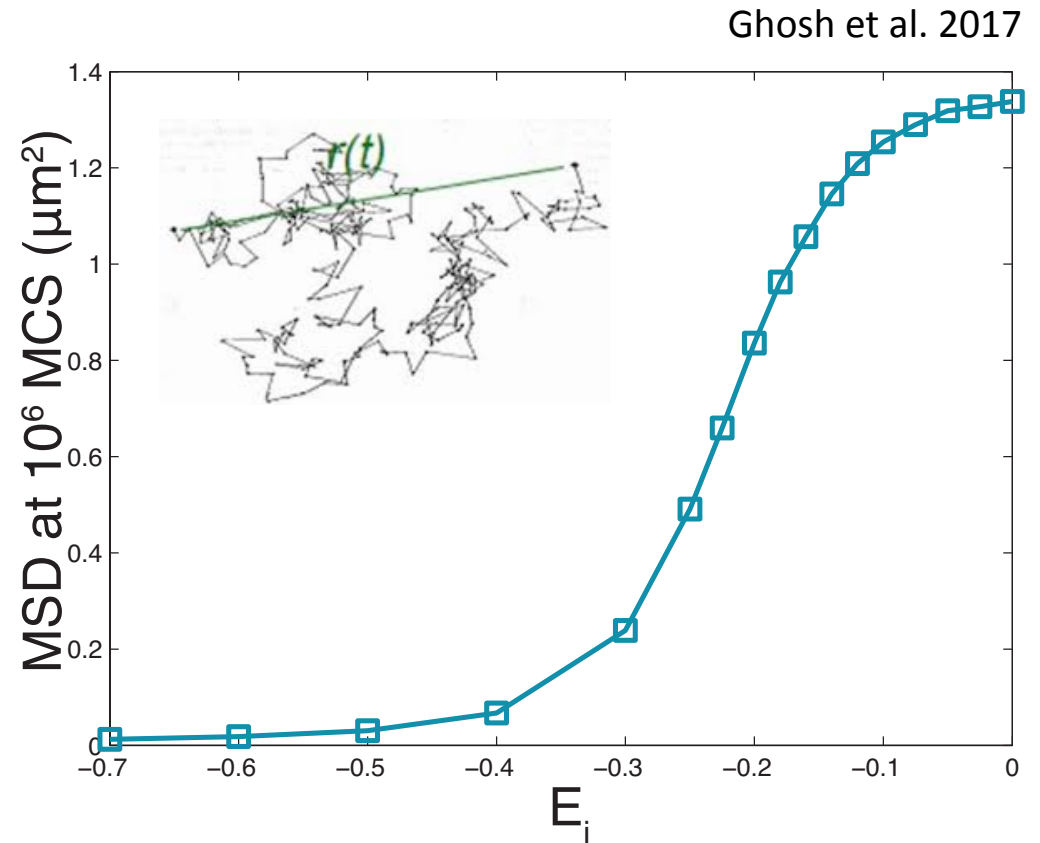
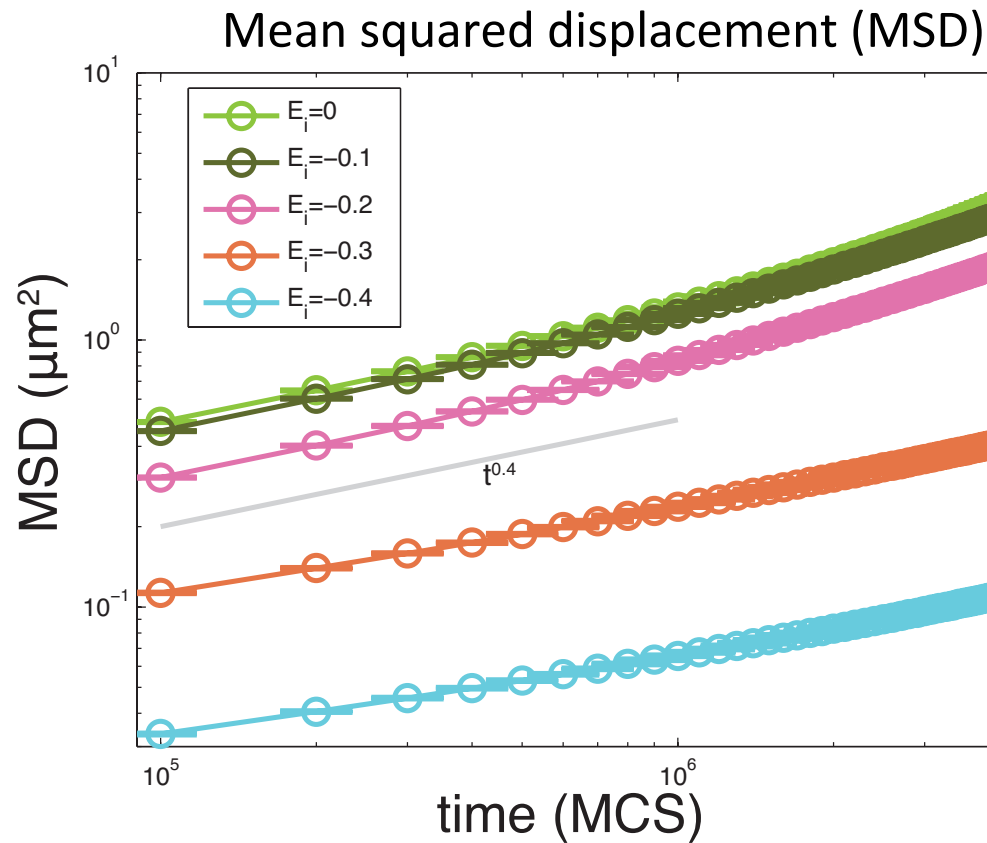
# Vary Lattice Density



# Vary Stiffness



# Phase diagram of chromosome 3R

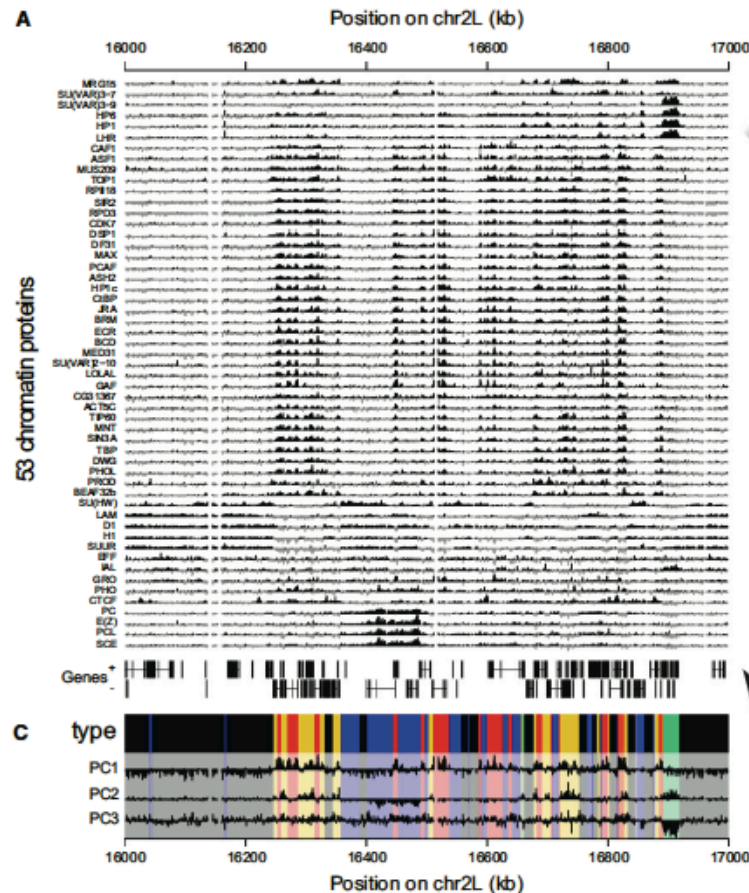


- $\text{MSD} \sim t^{0.4}$ , typical of crumpled polymers (Tamm et al, PRL 2015)
- Critical slowing-down at high interaction strength values: glass-like dynamic transition

• Time mapping:  $\text{MSD}_{\text{exp}}(\mu\text{m}^2) \approx 0.01 t^{0.5 \pm 0.1}$  (t in sec.) 1 MCS = 0.04 sec

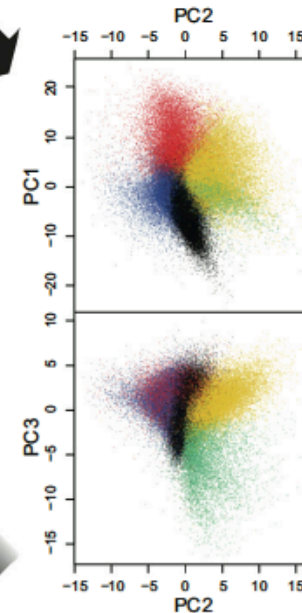
# From many chromatin tags to few chromatin states

- Genome-wide characterization of epigenome (drosophila, human, mouse, plants, yeast, etc.)



**B**

Principal component analysis



*Drosophila*  
(Filion et al., 2010)

Hidden Markov model

inactive (I)

épigénome:

A

actif

Polycomb

HP-1

ultra-répressive

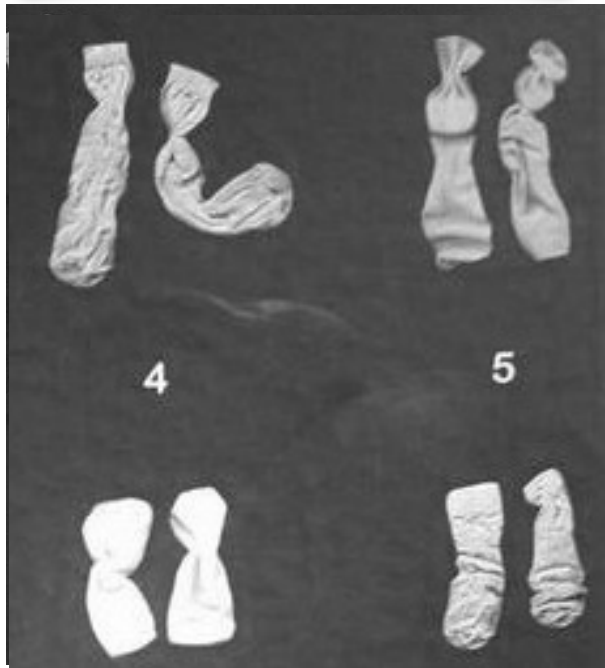


chromatin domains

position (Mbp)



# Drosophila :



For 2 kbp : 10001 , Ne = 285.25 kbp

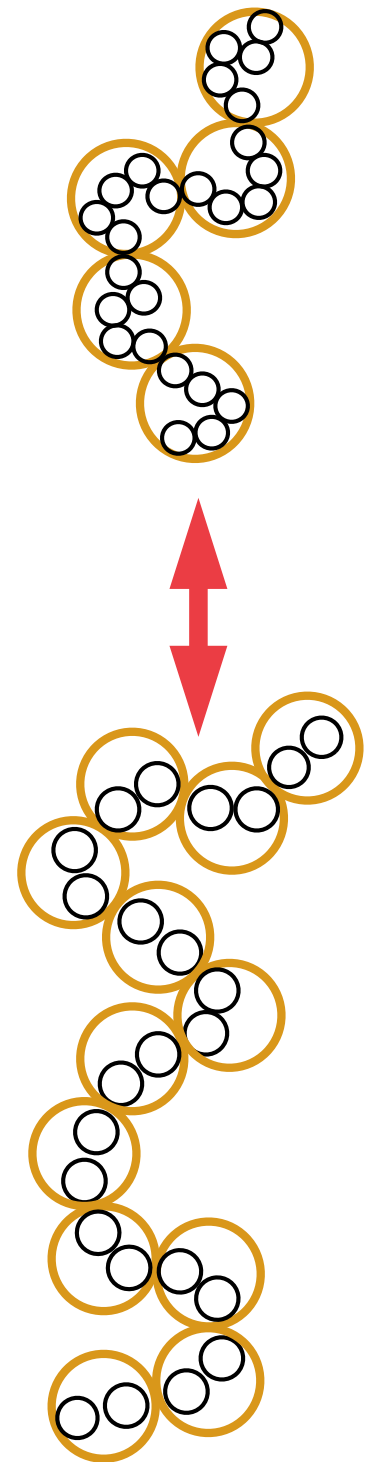
L	Phi	k	Nk (kbp)	1 MCS ( $10^{-3}$ )
45	0.0274	7.1	29.96	0.004
40	0.0391	6.05	23.67	
37	0.0494	5.45	20.25	0.03
32	0.0763	4.45	15.15	0.18
28	0.1139	3.62	11.60	0.41

For 5 kbp : 4001

L	Phi	k	Nk (kbp)	1 MCS ( $10^{-1}$ )
22	0.0939	5.00	44.76	0.004
18	0.1715	3.70	29.96	0.019, 0.020
16	0.2441	3.05	23.67	0.054
15	0.2963	2.70	20.80	0.066
11	0.7513	1.40	11.19	0.160

For 10 kbp : 2001

L	Phi	k	Nk (kbp)	1 MCS
14	0.1822	4.3	72.50	
11	0.3757	2.9	44.76	0.0188
9	0.6859	1.95	29.96	0.0423
8	0.9766	1.5	23.67	0.0381



# Entanglement Length

•Key parameters in our Model

•Bending stiffness :

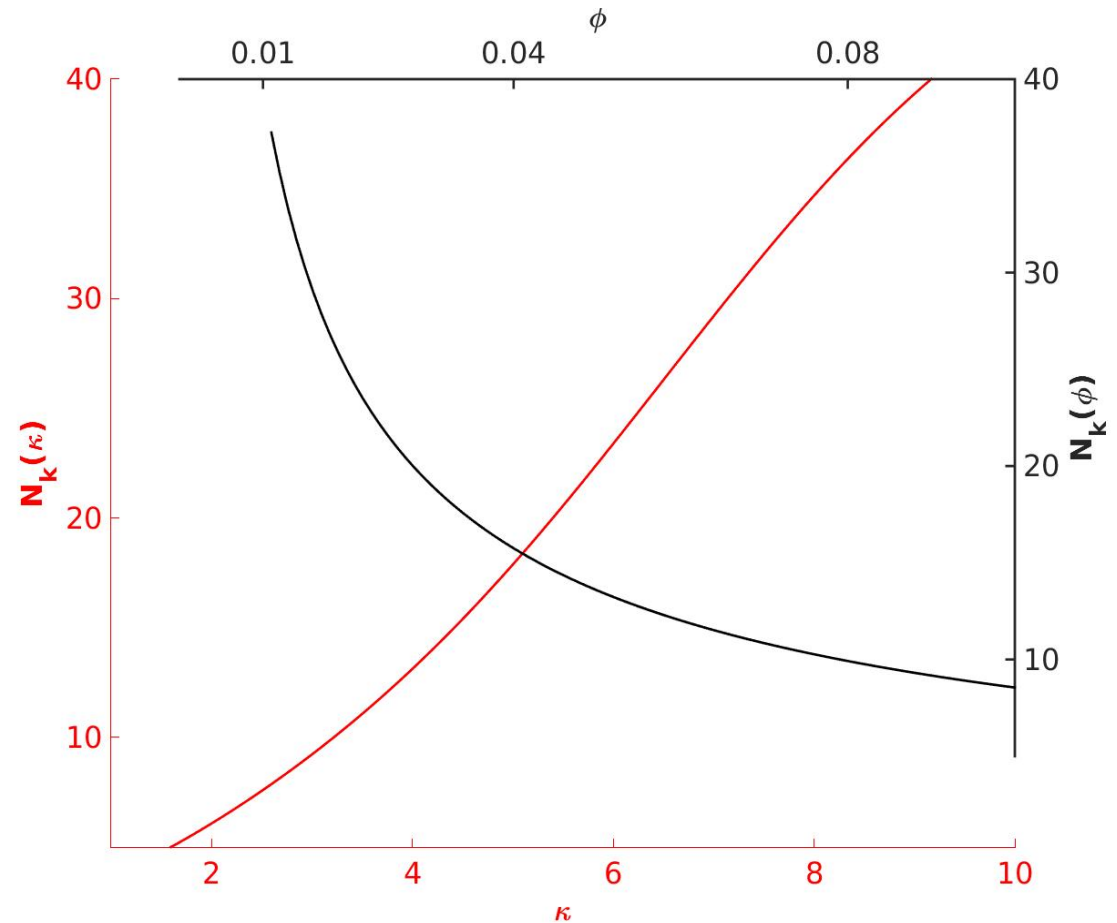
$\mathcal{K}$

$$N_k(\kappa) = n \frac{1 + x(\kappa)}{1 - x(\kappa)}$$

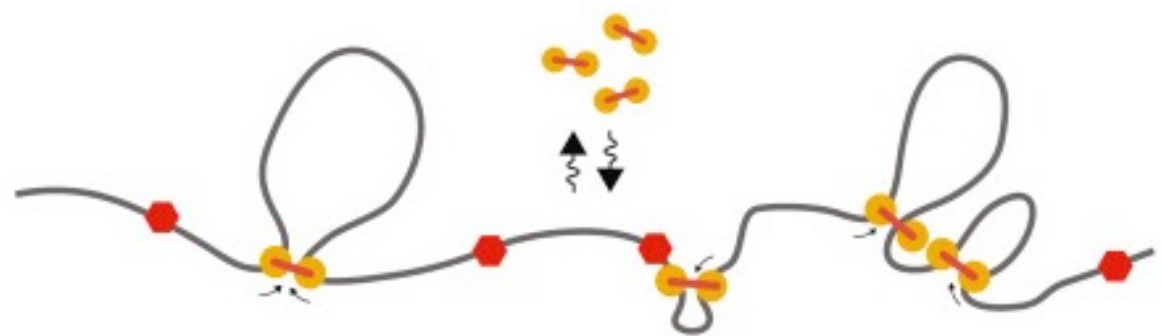
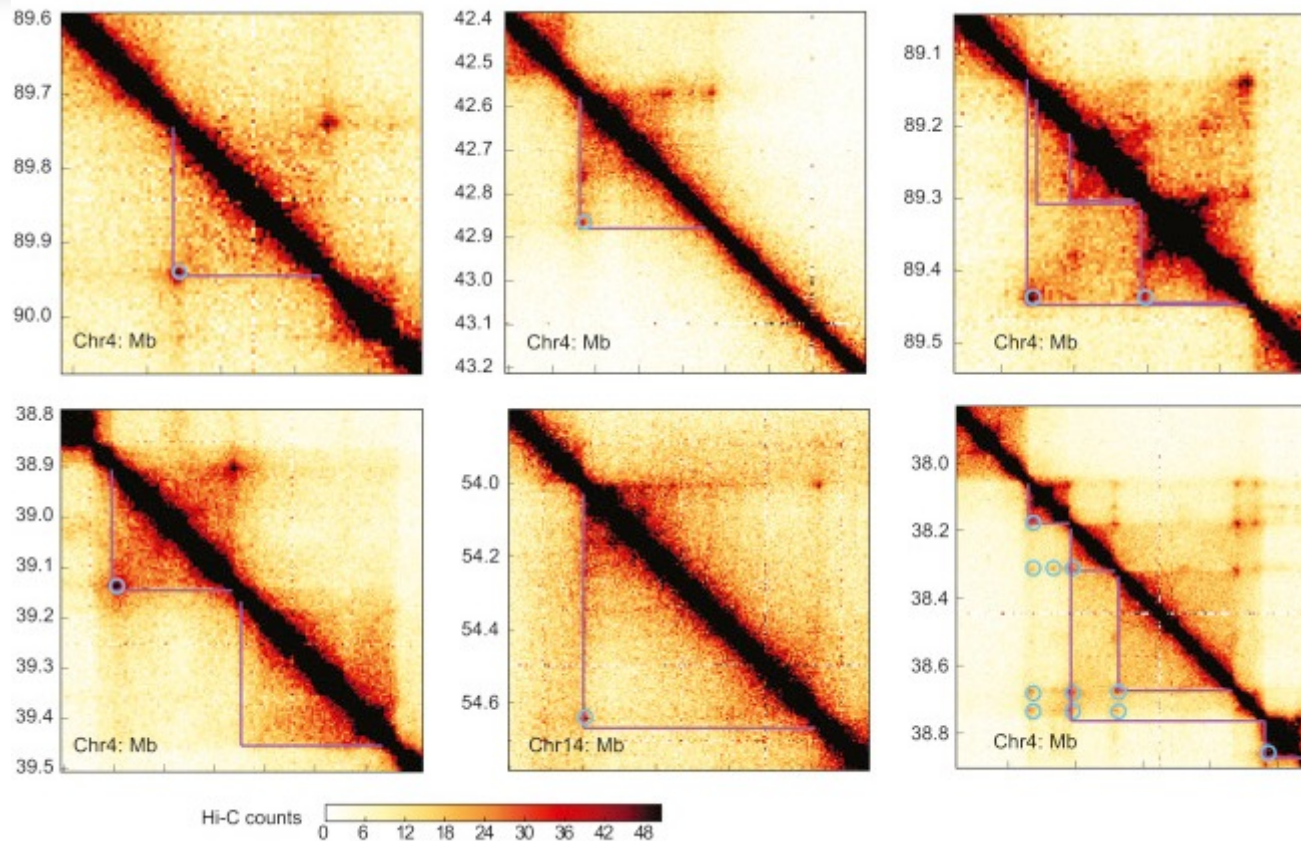
•Lattice density :

$\phi$

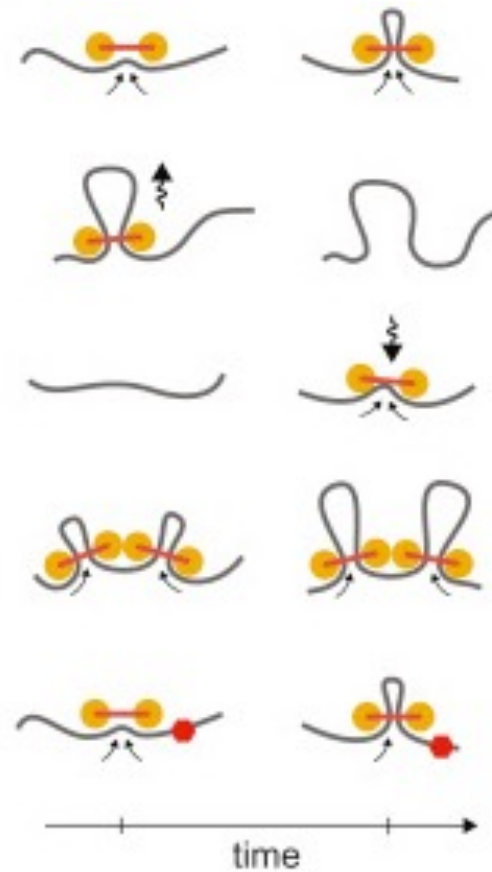
$$N_k(\phi) = \left( \frac{c^2 n^4}{N_e \phi^2} \right)^{\frac{1}{3}}$$



# TAD : Topologically associated domain



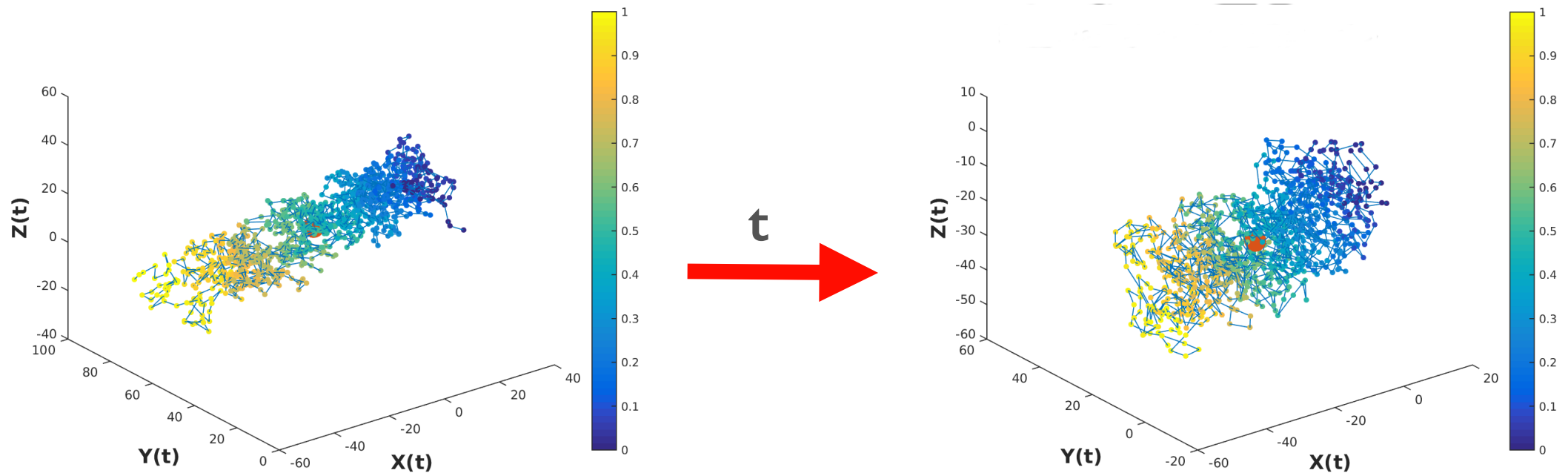
# TAD : Topologically associated domain



# Key physical quantity to measure

## I. Mean squared displacement : MSD

$$MSD(t) = \langle (x - x_0)^2 \rangle = \frac{1}{N} \sum_1^N (x_n(t) - x_n(0))^2$$

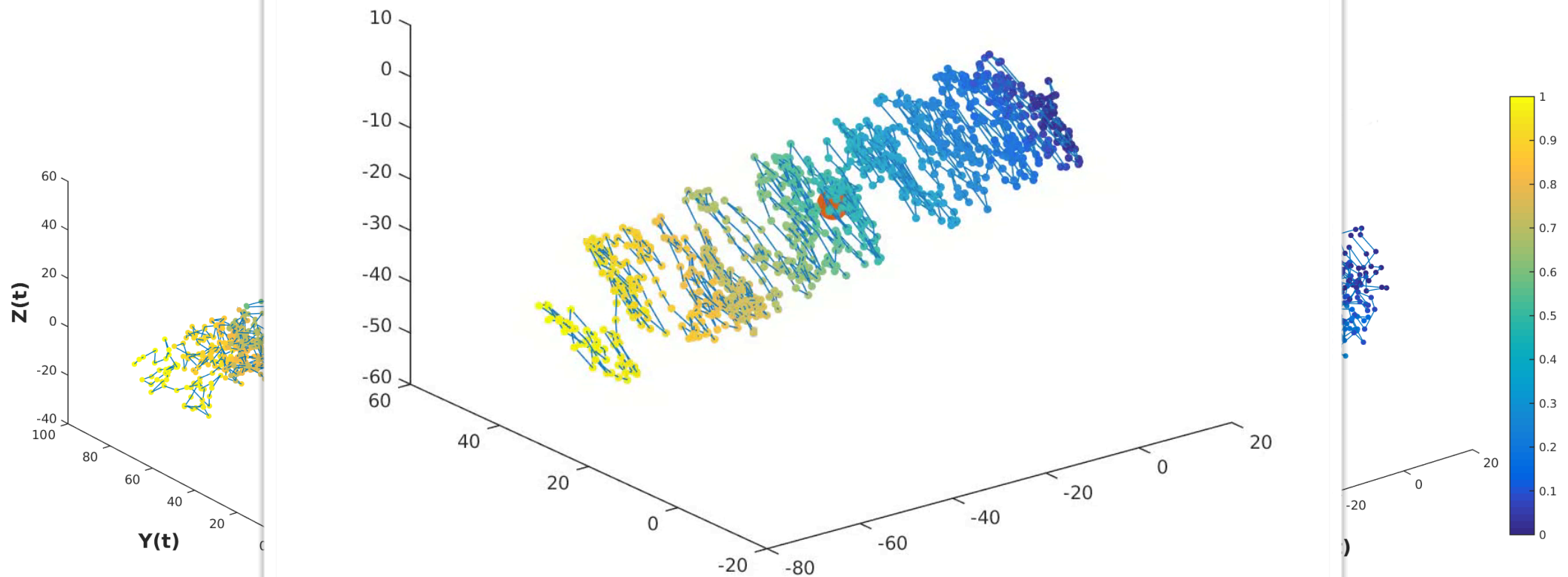




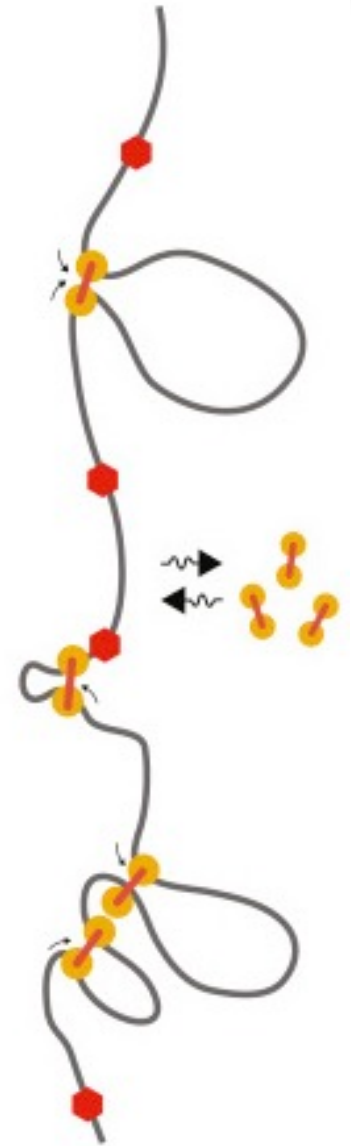
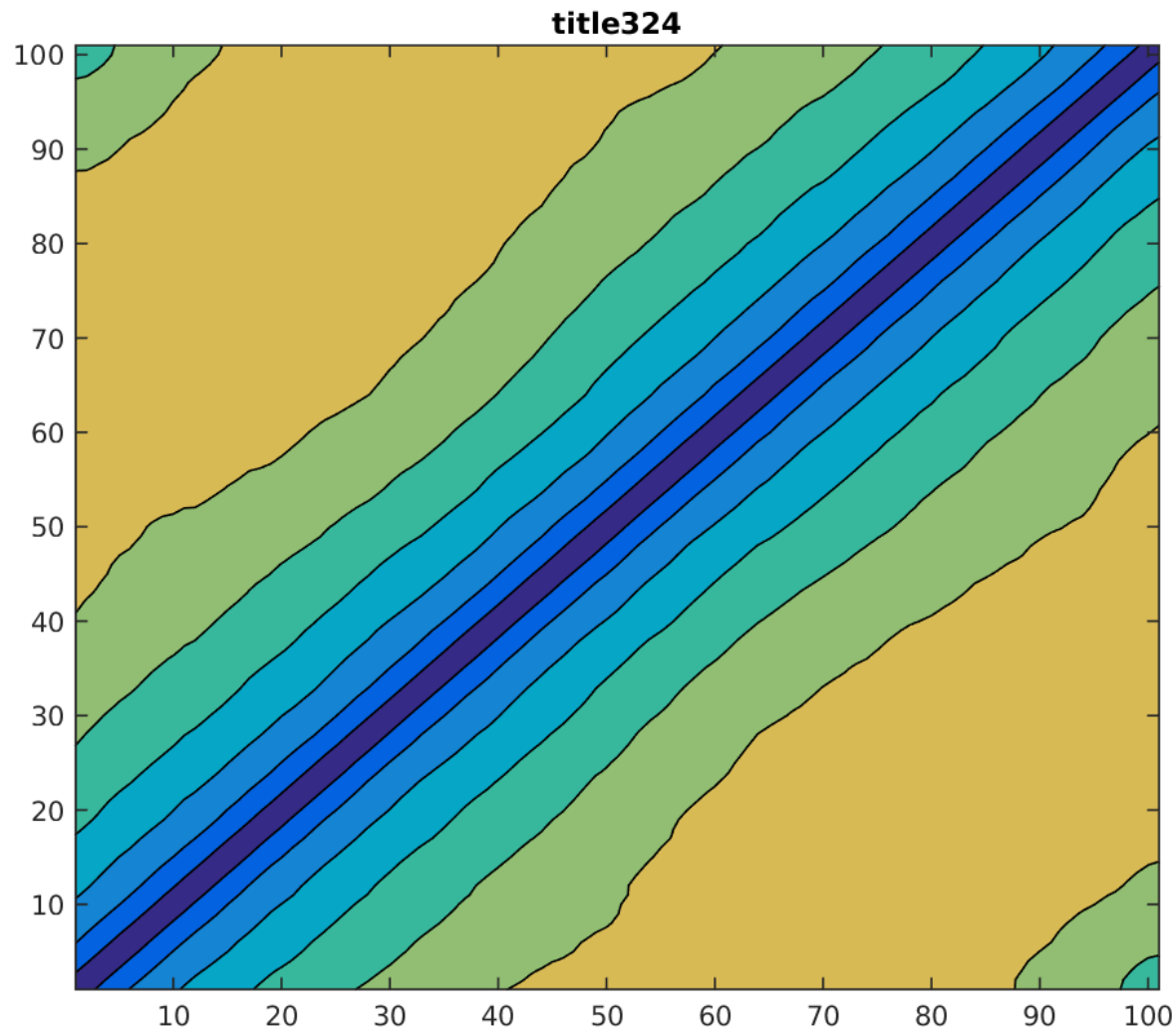
# Key physical quantity to measure

## I. Mean squared displacement : MSD

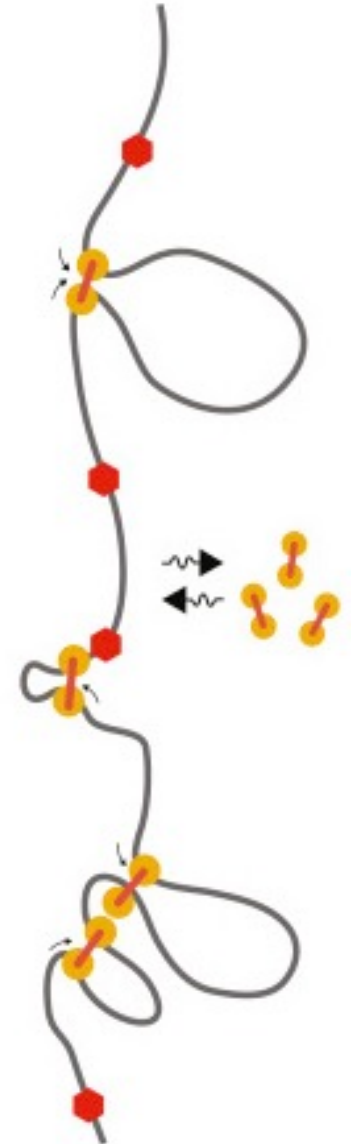
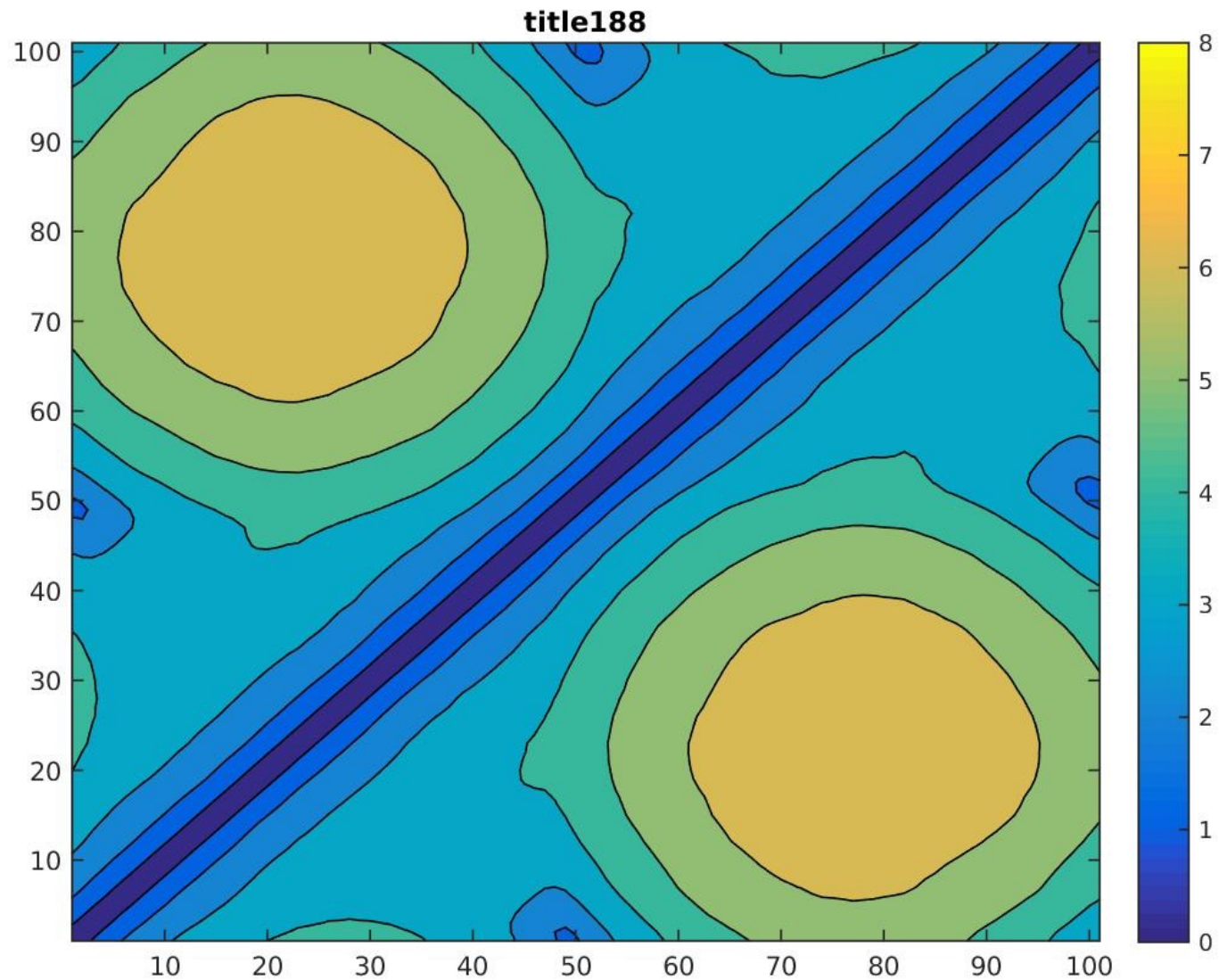
$MSD(t)$



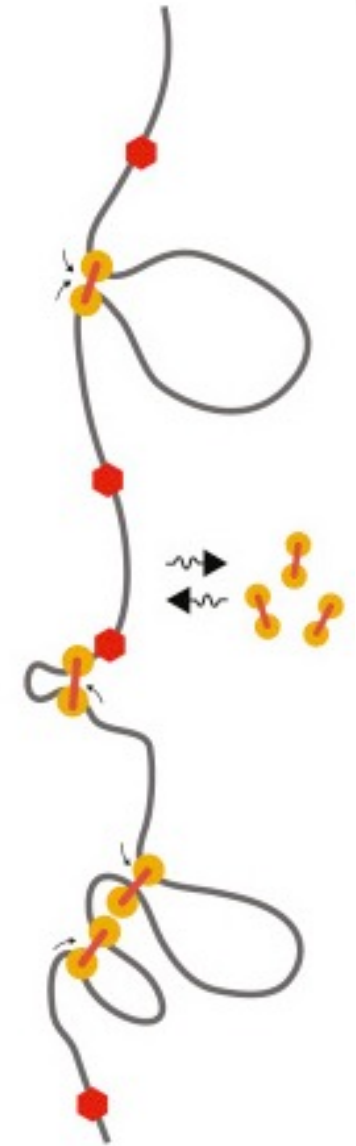
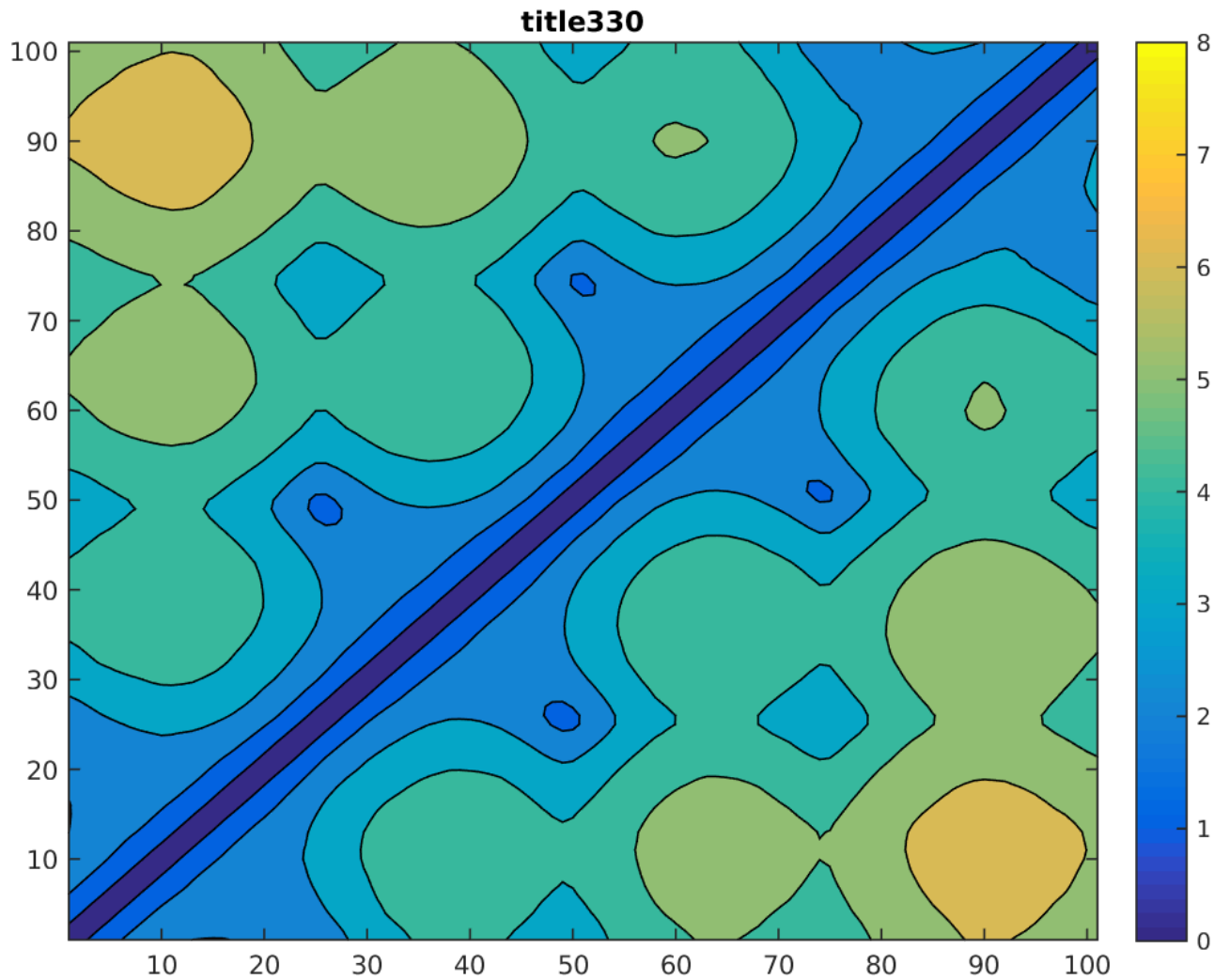
# Normal Polymer : No extruder



# Normal Polymer : With extruder



# Normal Polymer : With extruder , more boundary





# Polymer : with extruder, more boundary

