Unwinding dynamics of double stranded polymers

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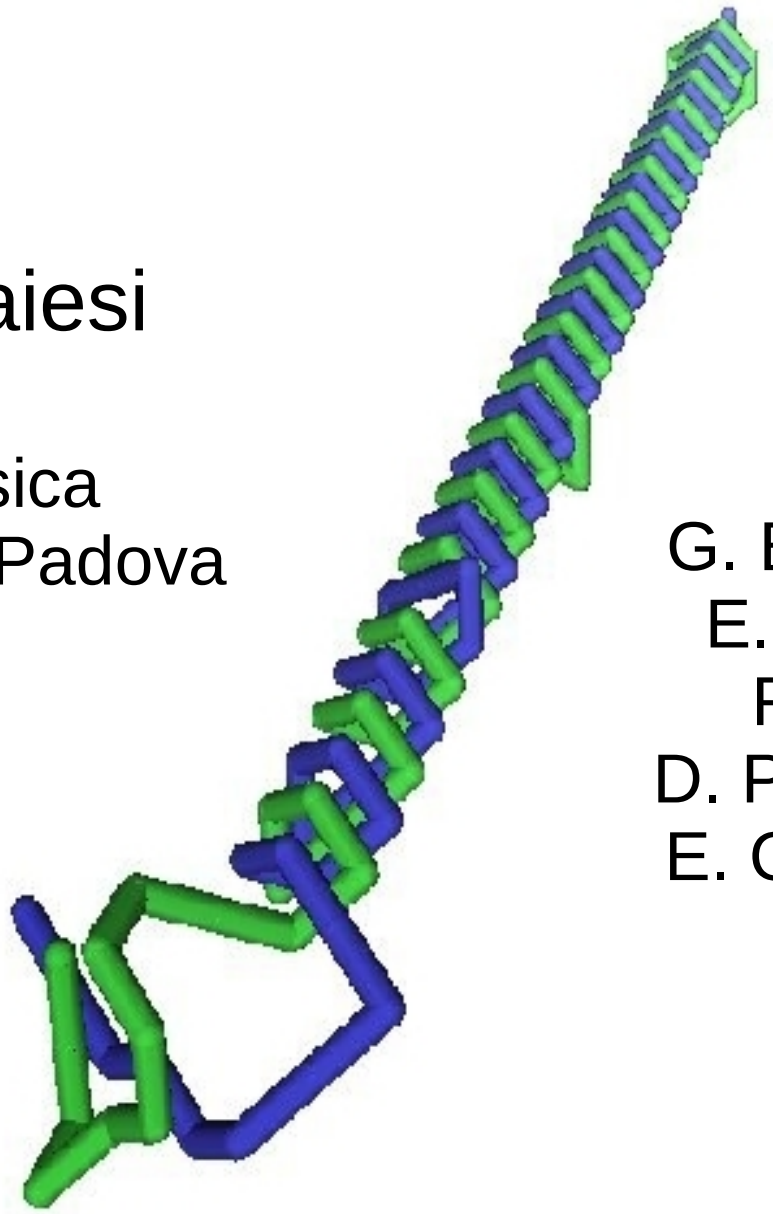


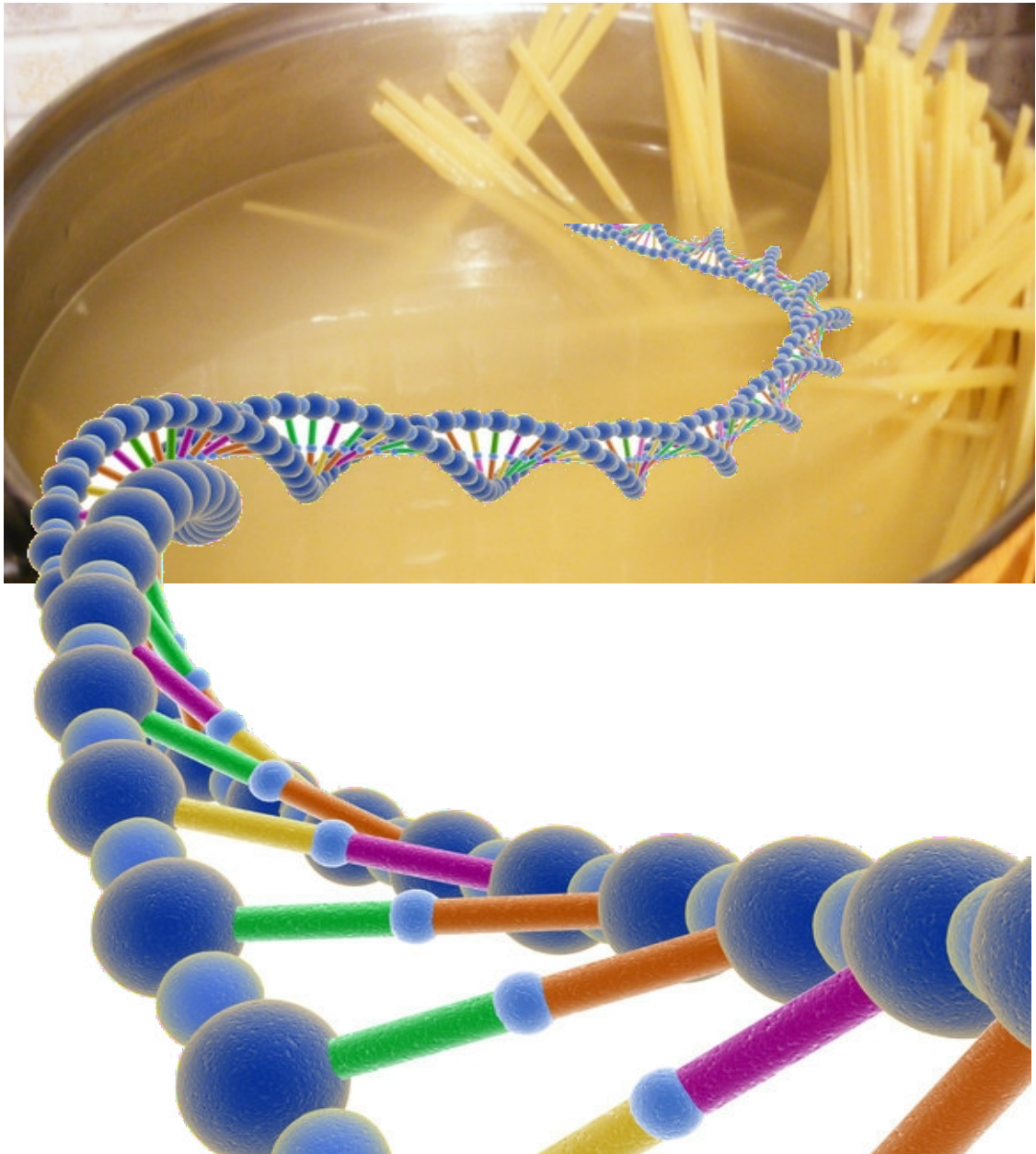
G. Barkema (Utrecht)
E. Carlon (Leuven)
R. Livi (Firenze)
D. Panja (Amsterdam)
E. Orlandini (Padova)

Unwinding of DNA

If we throw DNA in hot water, the bonds between the two strands break, and the strands disentangle

How long does it take?

It depends on the DNA length...



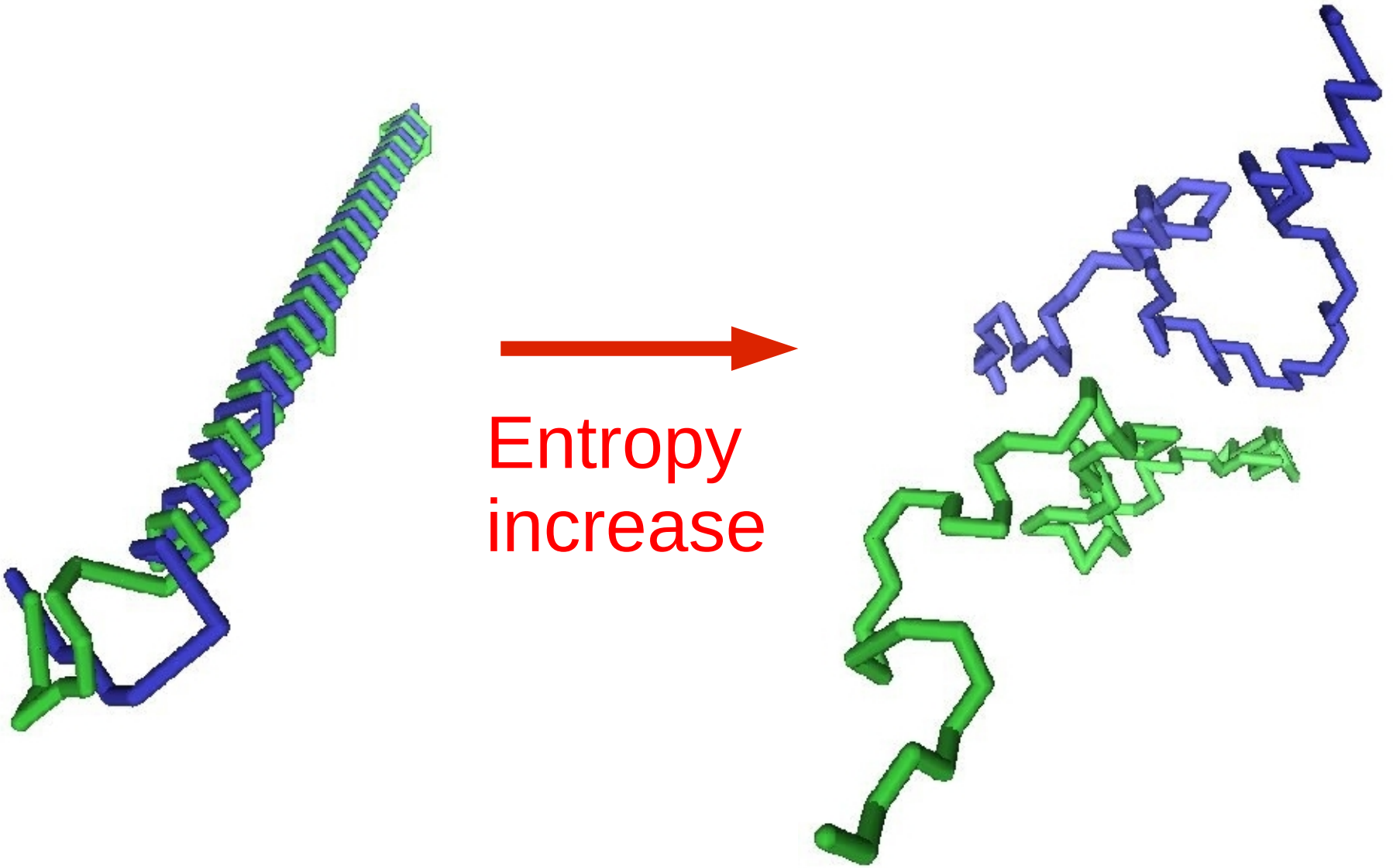
Scaling properties

- We want to study the time τ of DNA thermal denaturation as a function of the DNA length L

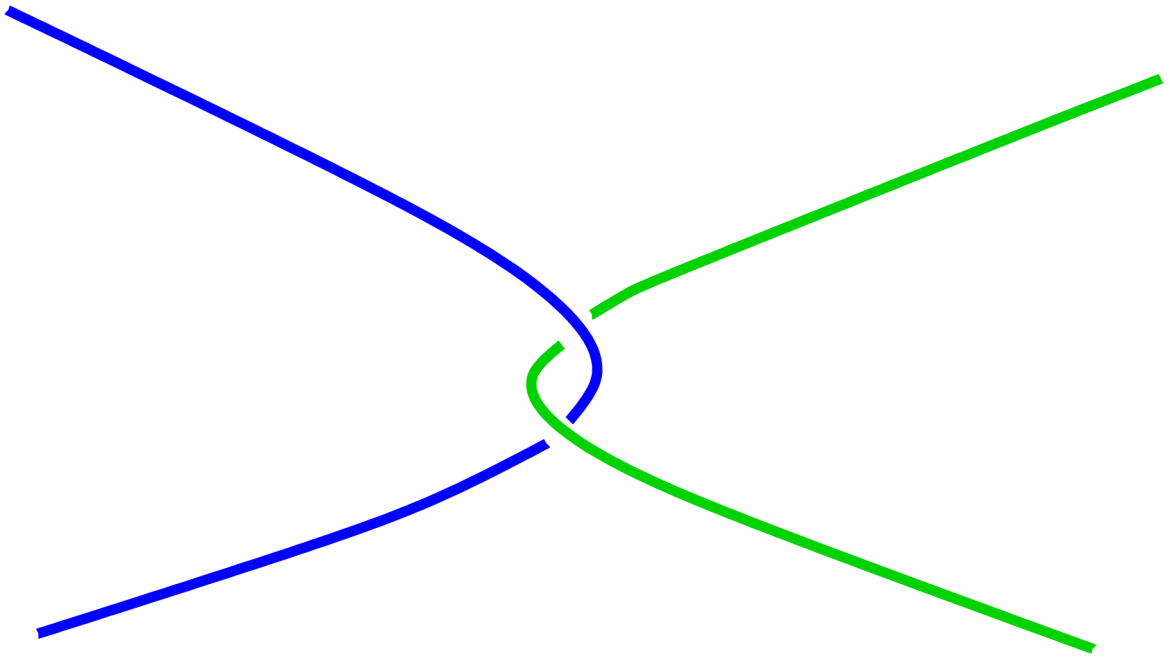
$$\tau \sim L^{z}$$

- We use simplified models, no microscopic details
  - Poland-Scheraga
  - Self-avoiding walks on 3d lattice

A lot of twist needs to be released



The main point:
no crossings of the two strands

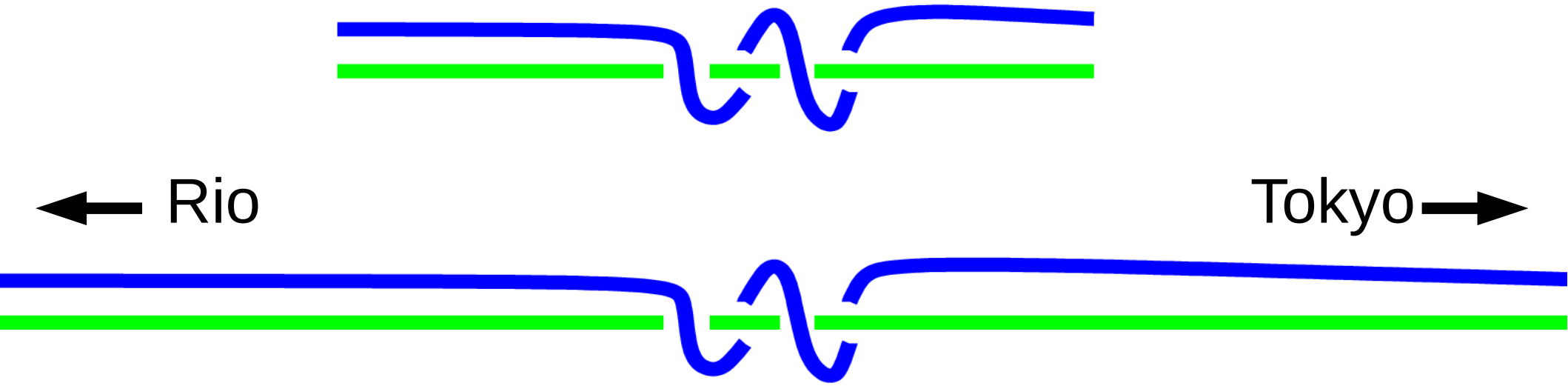


Polymer locally **cannot** overlap or temporarily break their continuity to cross each other

In our body there are enzymes (topoisomerases) that allow portions of DNA strands to cross each other, removing knots or other unsuitable topologies

unwinding is a non-local problem

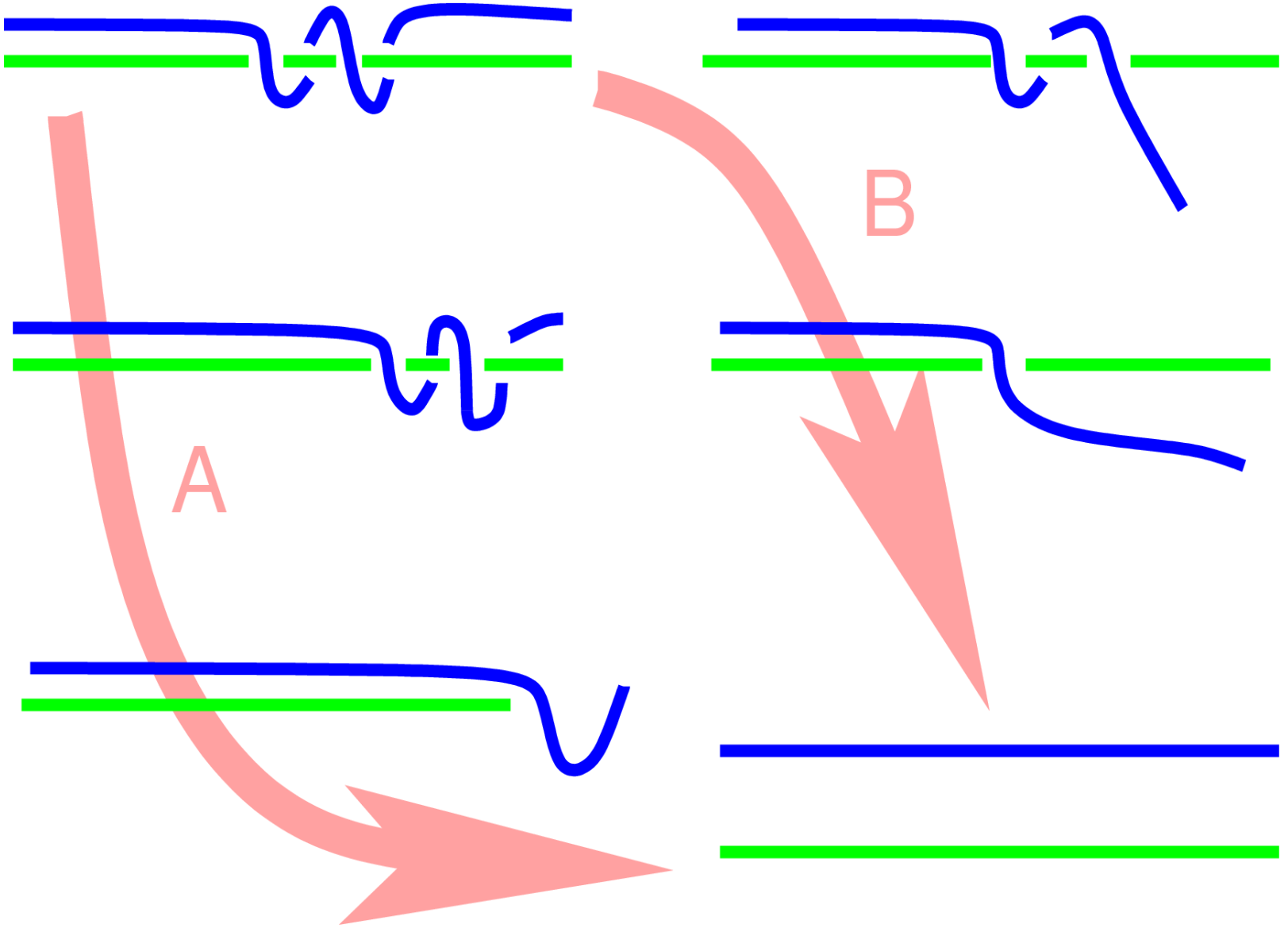
the chain length matters



Same linking, but
in the second case there is
a longer portion of the chain
to be moved / traveled...

unwinding is a non-local problem

the chain length matters



Poland-Scheraga model

1 = bound segment →

energy E →

weight exp[-E/kT]

0 = bubble portion

000000 = bubble of length n → weight $b^n n^{-c}$

c = 3/2 (random walk)

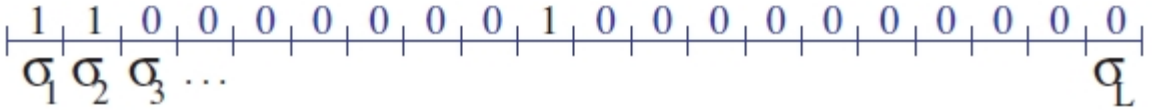
c = 1.76 (self-avoiding polygon)

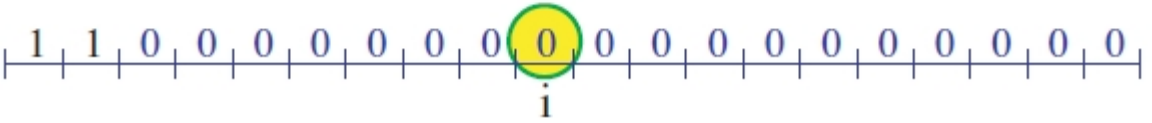
c = 2.14 (Kafri-Mukamel-Peliti, we use this one)

A configuration: 0000101001111010111111101000

Partition function: $Z = \left(b^{n_1} n_1^{-c}\right) \ldots \left(b^{n_q} n_q^{-c}\right) \exp\left[-E_{tot}/kT\right]$

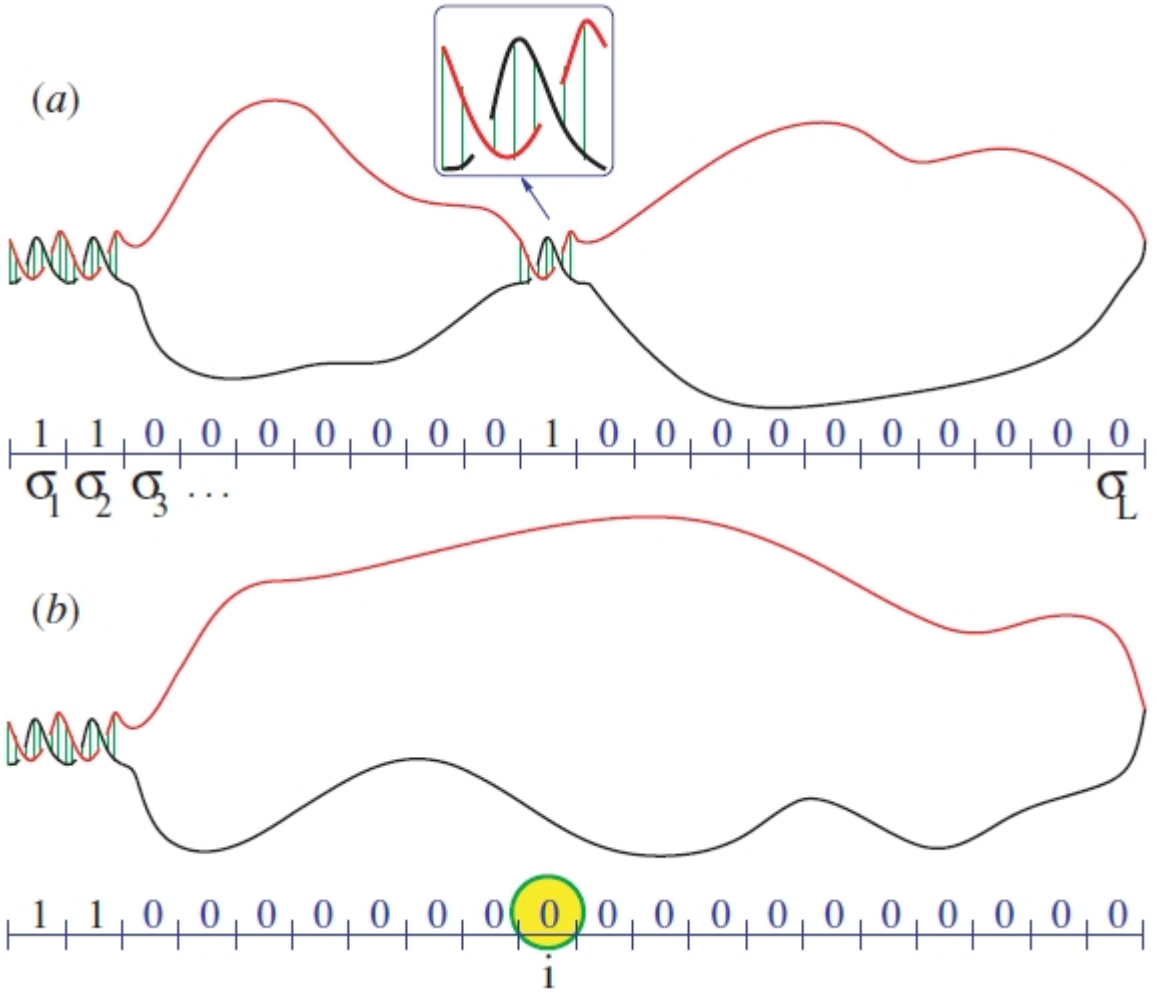
Poland-Scheraga model





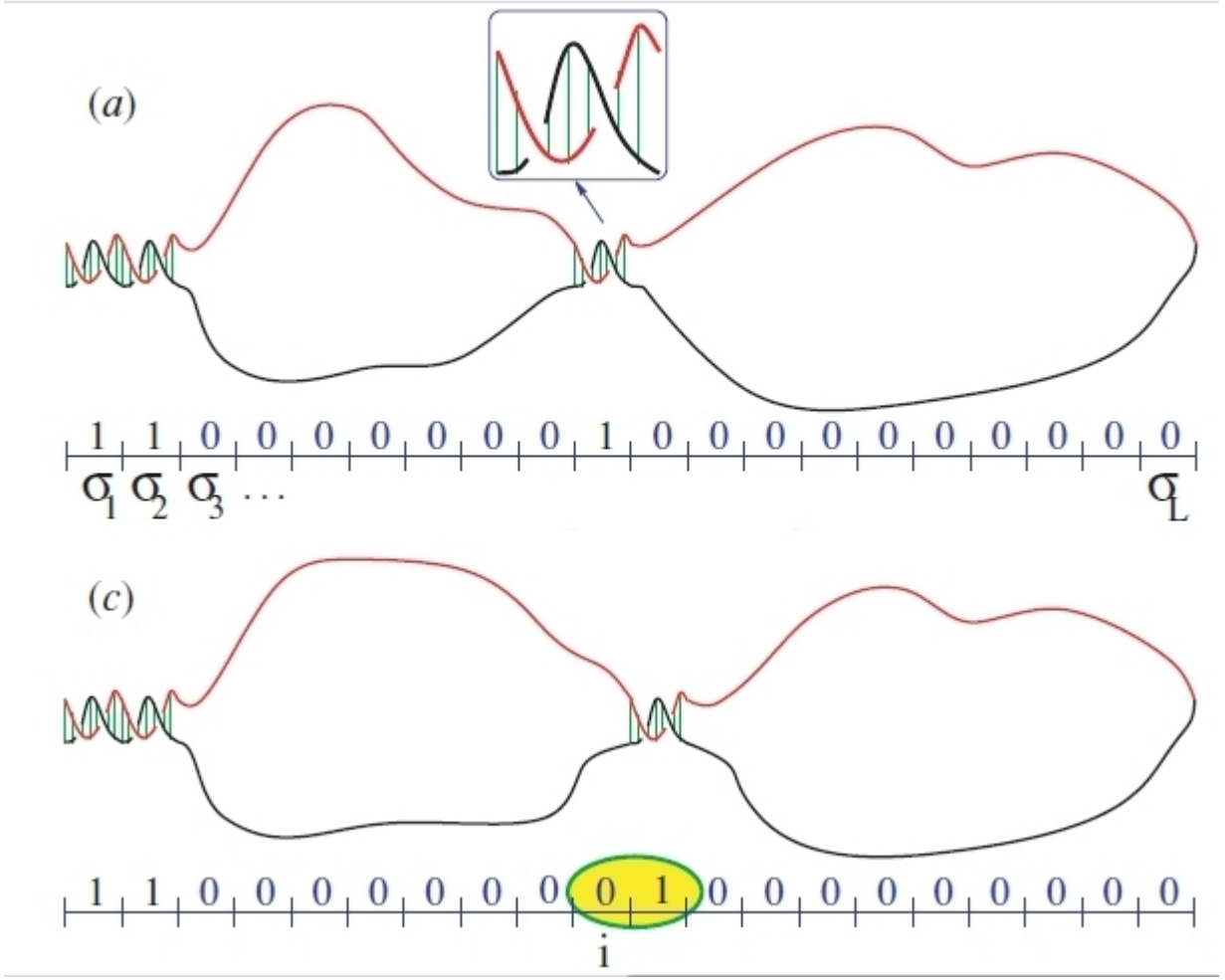
It is tempting to change a 1 to a 0 as a Glauber move in the Ising model

Poland-Scheraga model



...but a simple 1 → 0 change corresponds to a **non-local** rearrangement of the chain!

Poland-Scheraga model



One should move the 1's only **locally**

- Kawasaki
- ~~Glauber~~

The dynamics

- Metropolis acceptance ratio

$$P(x \to y) = min(1, Z_y / Z_x)$$

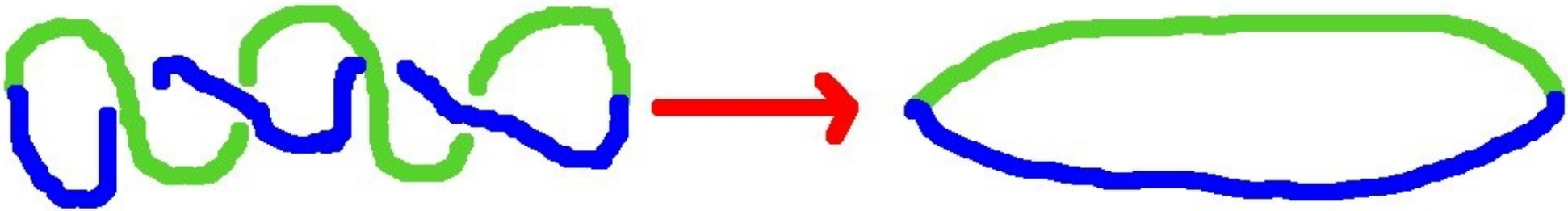
- Kawasaki in the bulk $01 \leftrightarrow 10$
  Glauber at end sites $0 \to 1$ or $1 \to 0$

- L sites, all 1's at time t=0

- Time step = L local updates
  (Glauber / Kawasaki)

The simulation

- Number of open sites (0's) = δ
- Number of bubbles = ν
- Closed boundaries (one loop with two strands)
- High temperature
- Thus: we start with a lot of 1's (double helix) and we wait until we have almost all 0's (giant bubble)



Comparison of the two dynamics

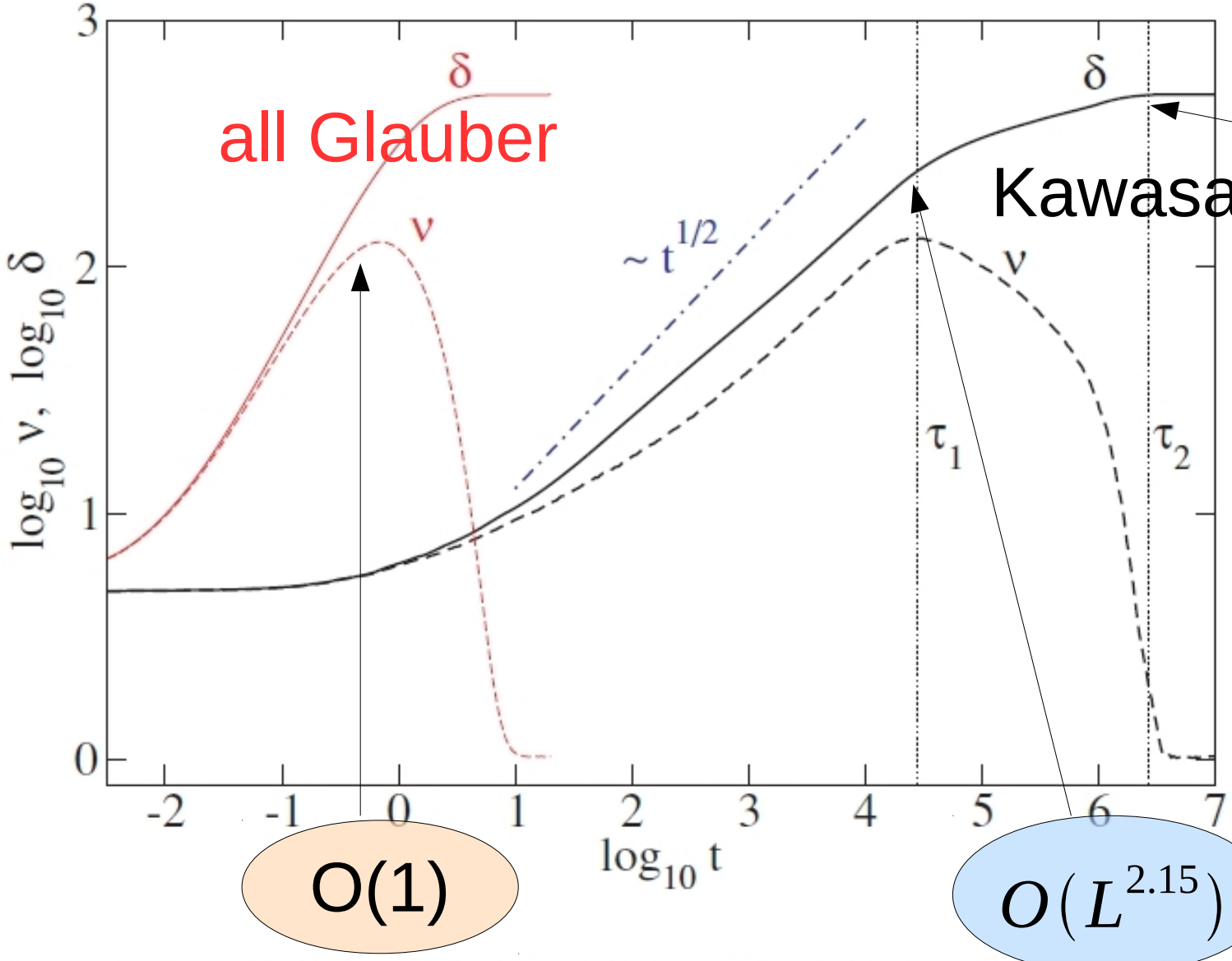
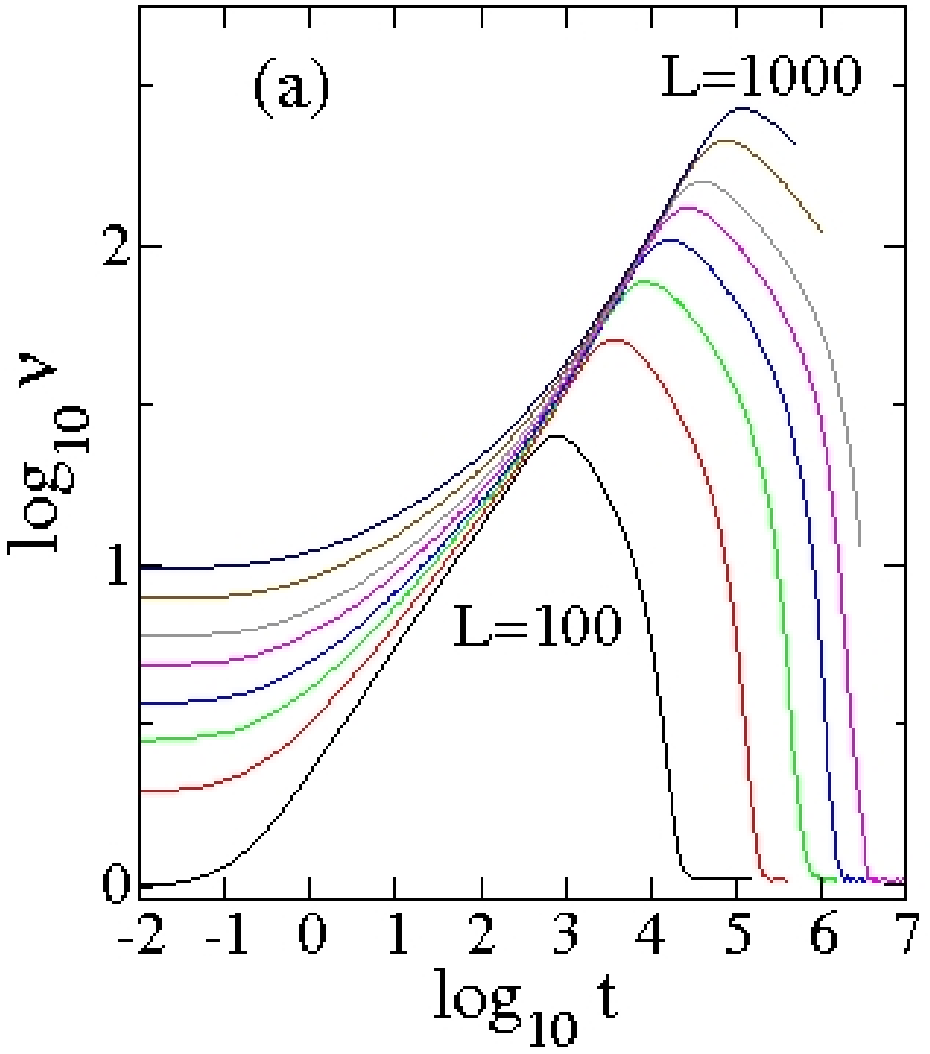


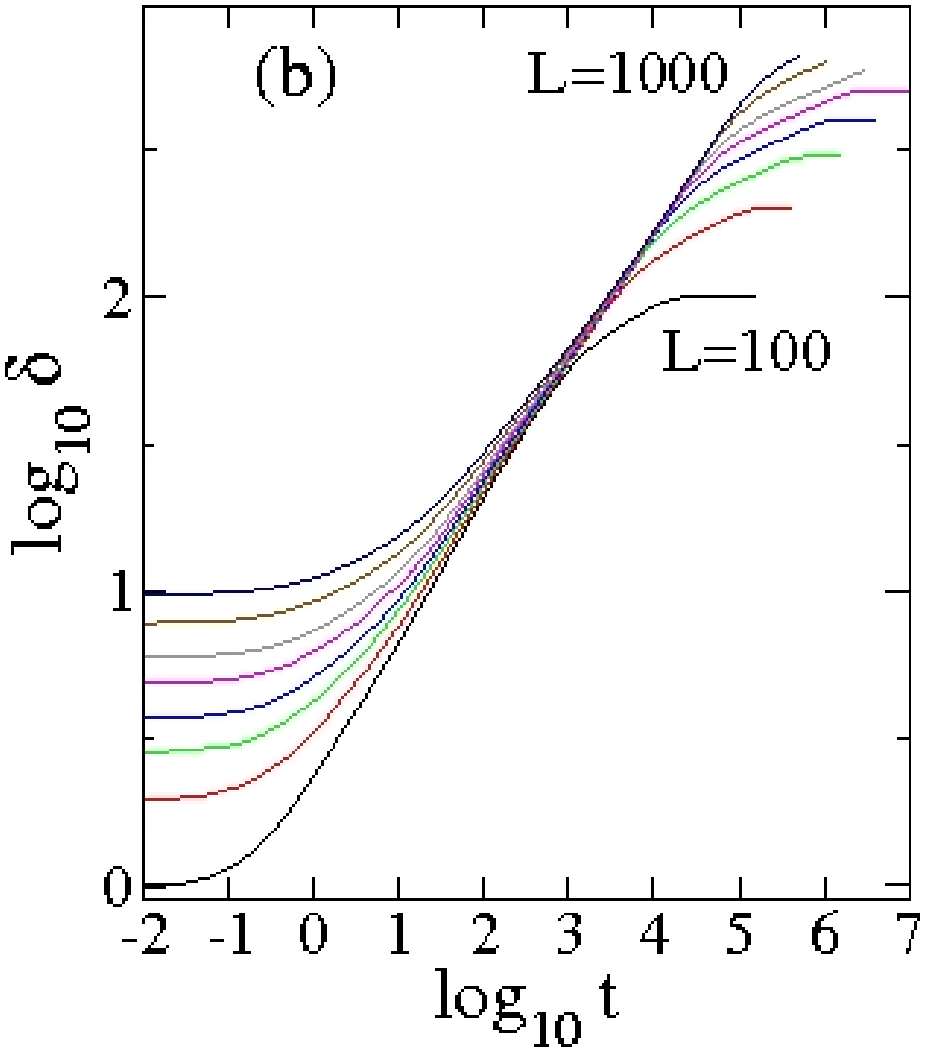
Figure 2. Log–log plot of the number of open sites δ (dense lines) and of the number of bubbles ν

Scaling with L

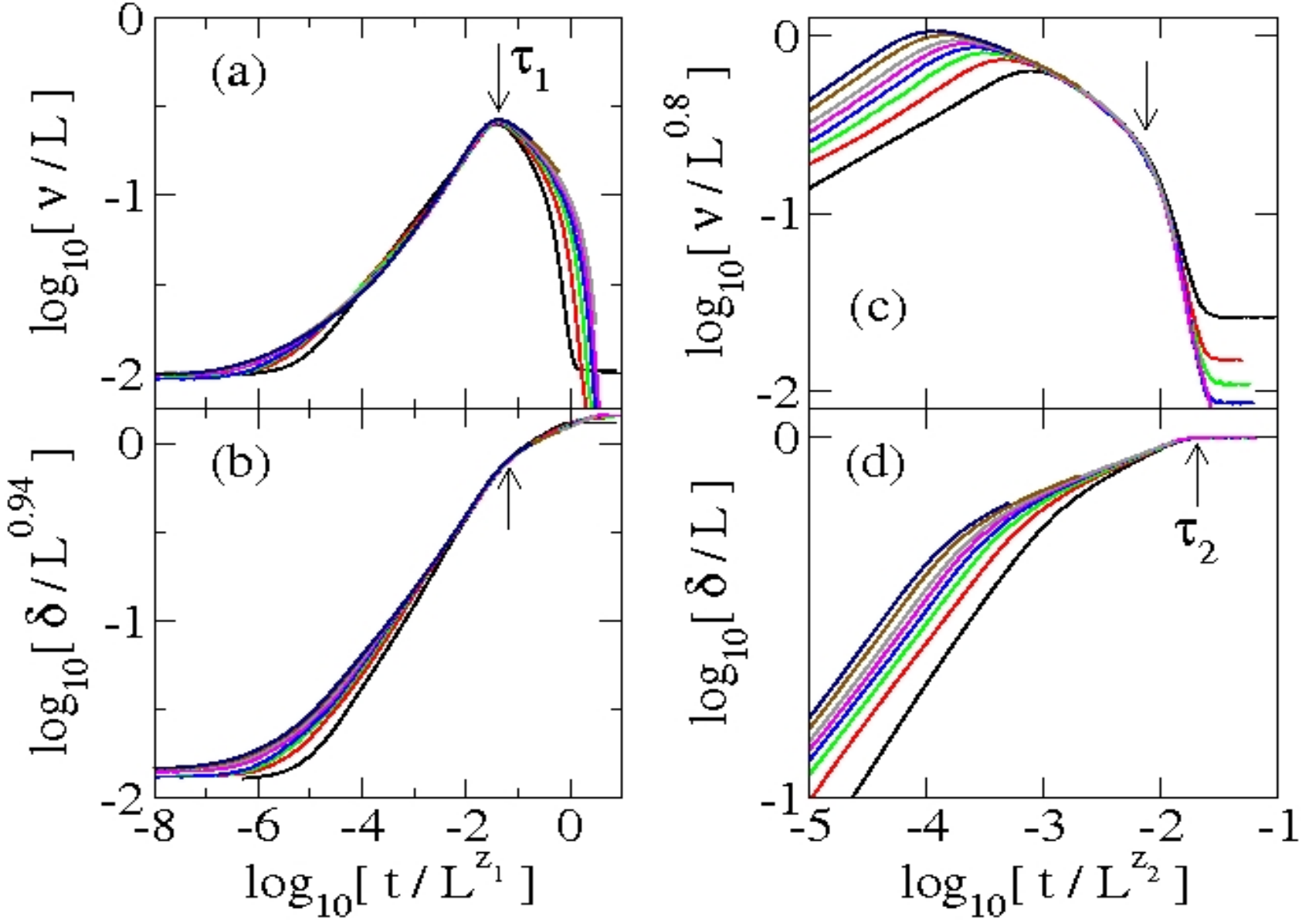
bubbles

unbound sites





Two time-scales τ_1, τ_2



First regime:
1's escape from borders

- 11111111111111111111111111
- 01111111111111111111111110
- 01011111111110111111111100
- 00011111111100111001010
- .....
- 00000001111111000000000

TIME

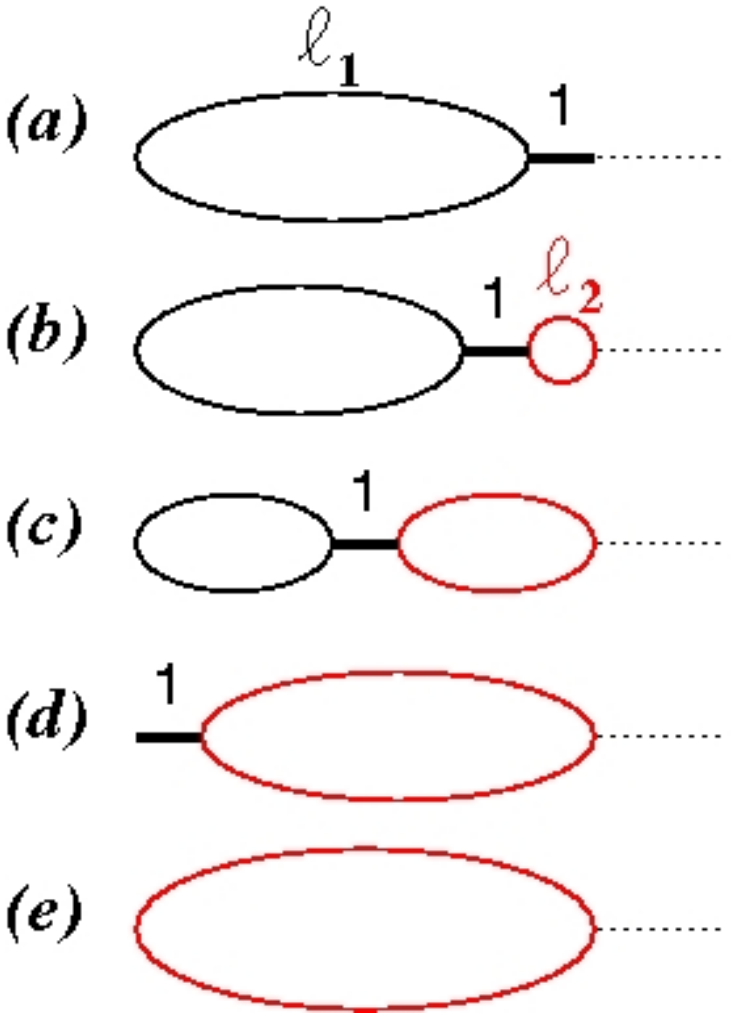
Random 1-0 swaps lead to a diffusion like time-scale L^2

But at some point some larger bubbles start to trap the 1's

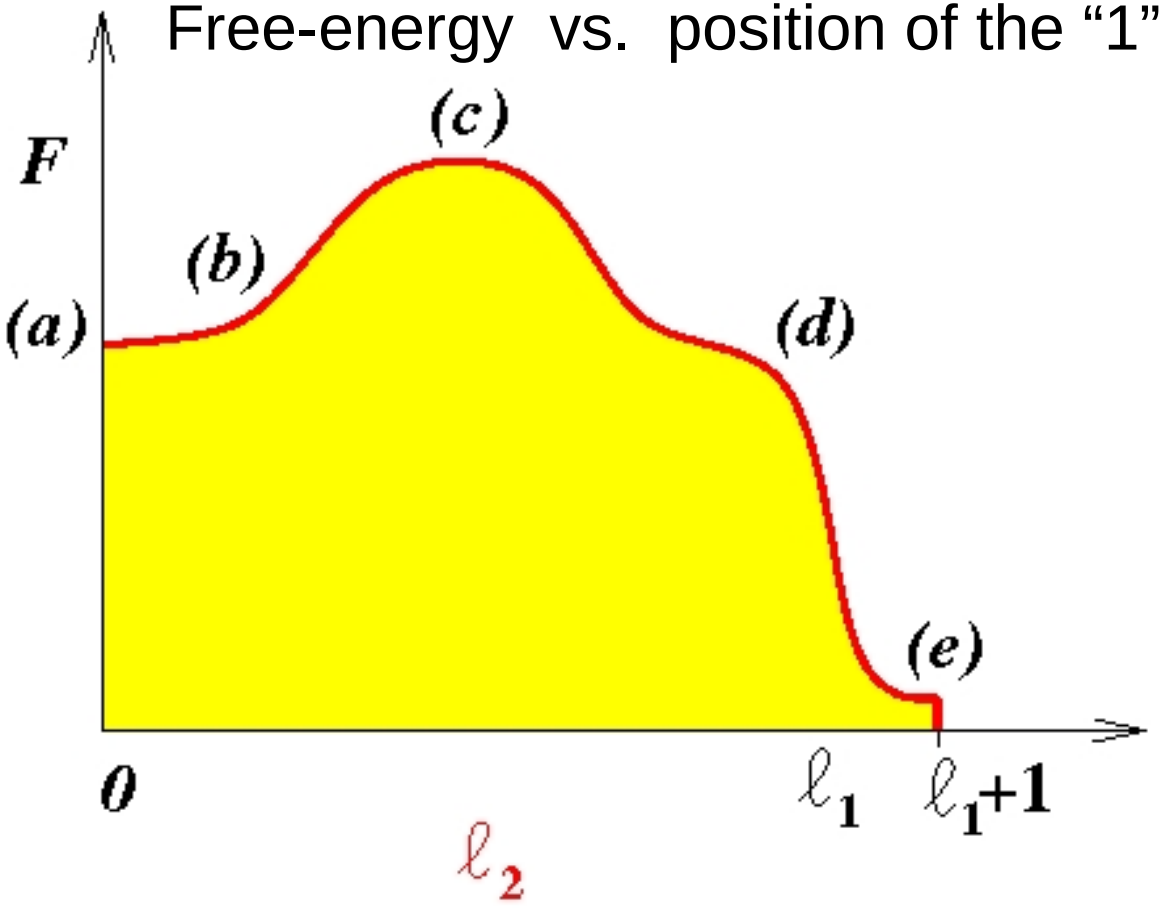
Numerically:

$$\tau_1 \sim L^{z_1} \quad with \quad z_1 \simeq 2.15$$

2nd regime: bound segments (1's) must overtake entropic barriers



Free-energy vs. position of the "1"



$$Z = \left(b^{n_1} n_1^{-c}\right) \ldots \left(b^{n_q} n_q^{-c}\right) \exp\left[-E_{tot}/kT\right]$$

Scaling of the 2nd time-scale

A single escape of a bound segment from an entropic barrier from a bubble of length x takes a time ~ x^c

Summing over all lengths x<L/2, one expects an exponent

$$z_2 = c + 1 \simeq 3.1$$

Numerically

$$\tau_2 \sim L^{z_2} \ with \ \ z_2 \simeq 3$$

Noticeable approximations

1) One assumes jumps between states described by equilibrium quantities (partition functions)

2) Pairing between homologous bases is forced

3) Inertia neglected

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1) One assumes jumps between states described by equilibrium quantities (partition functions)

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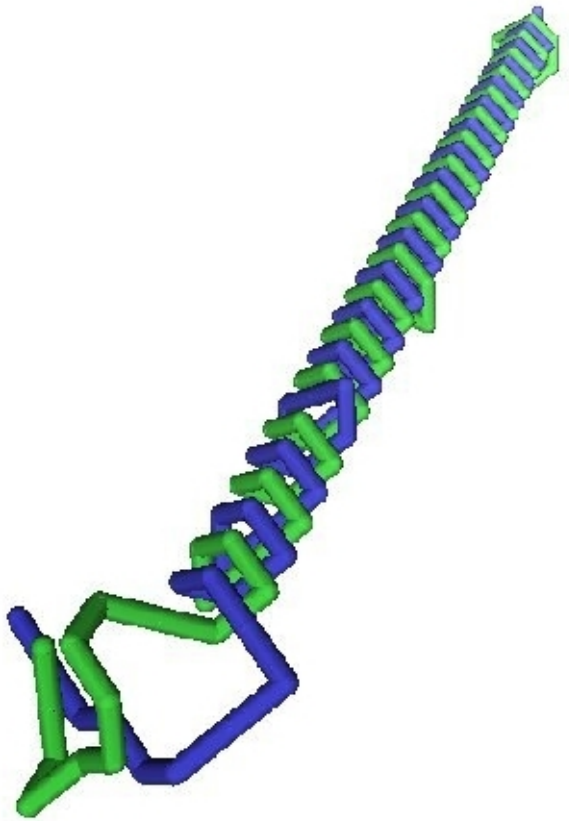
Let's try a 3d simulation

Two polymers on the *fcc* lattice



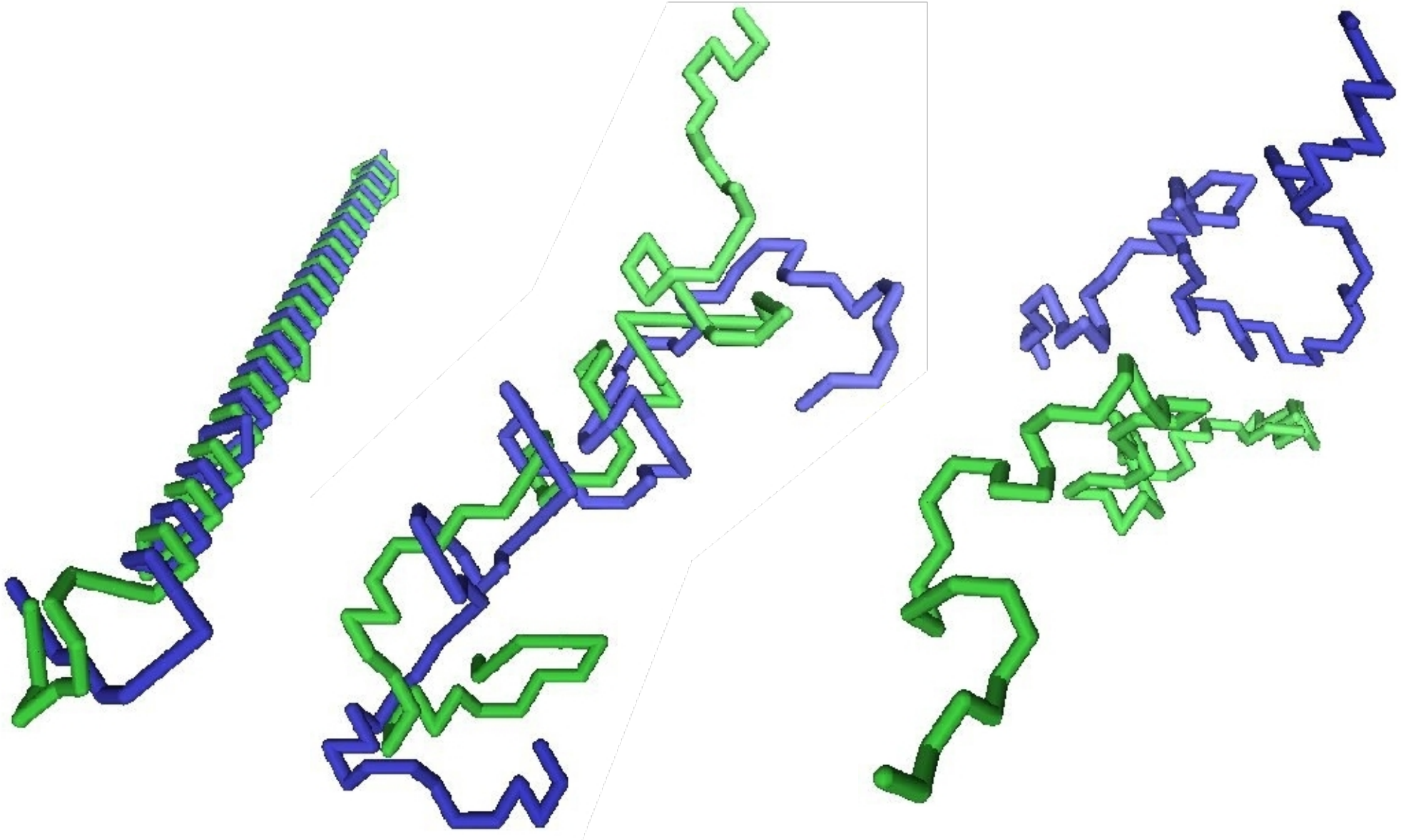
Initial double helix

No interaction, only self- and mutual-avoidance

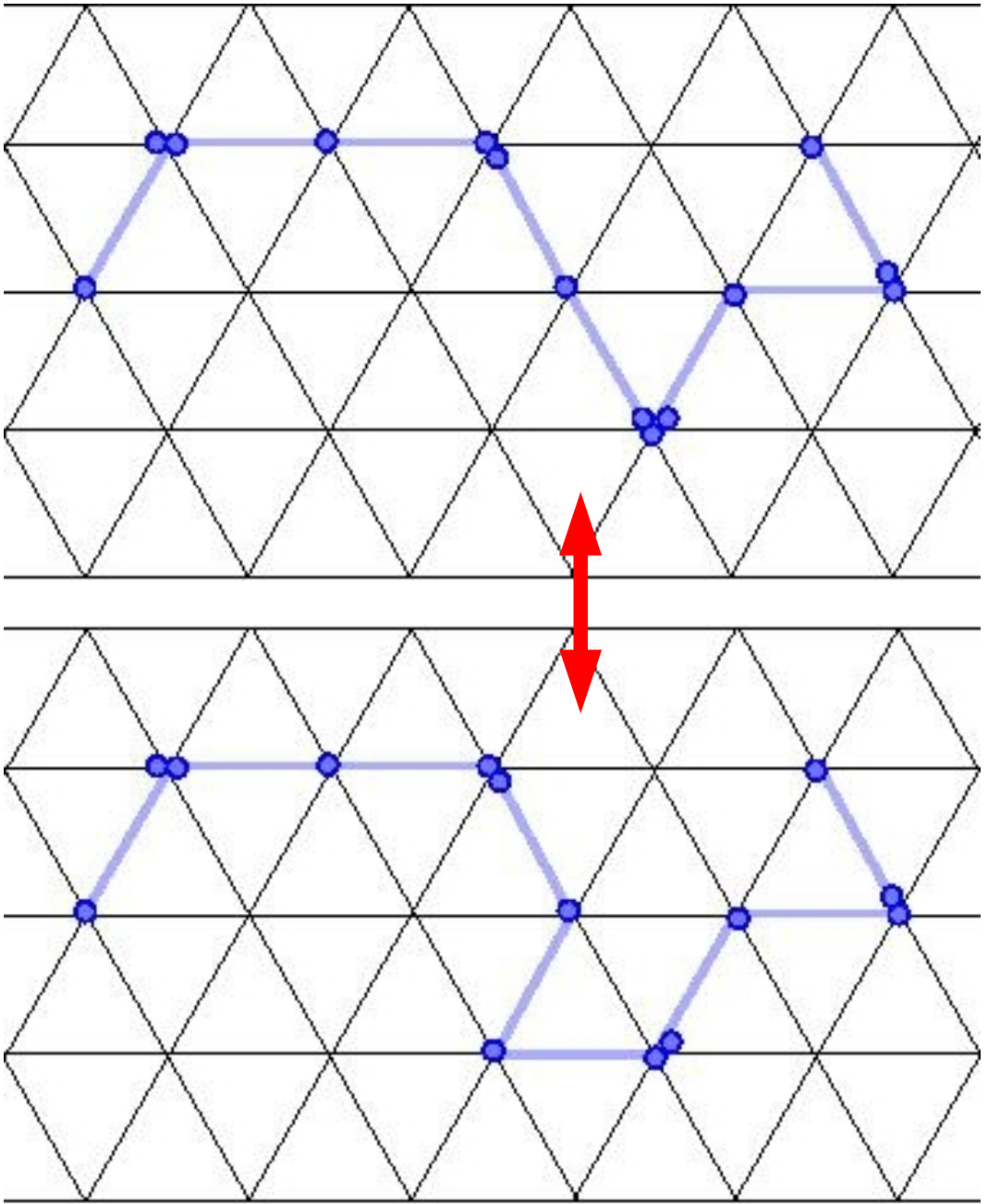
Each of the L sites can host one or more consecutive monomers (not visible)

Total N ≥ L monomers

~N local moves per time step t



Local moves



N=14, L=9

Among local moves, we have displacements of accumulated monomers, and vicecersa

N=14, L=10

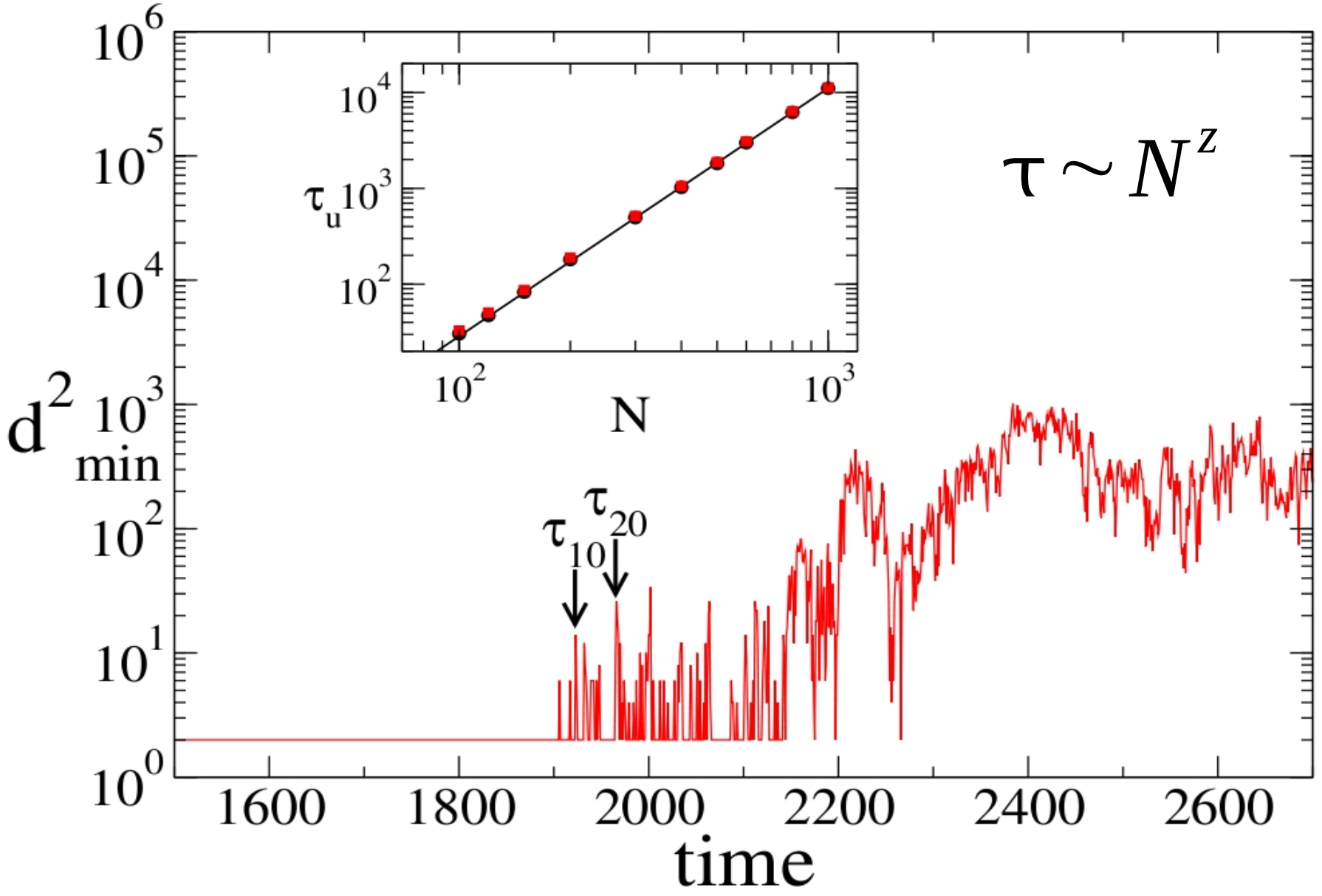
Elastic Lattice Polymers (ELP)

This model has been named ELP

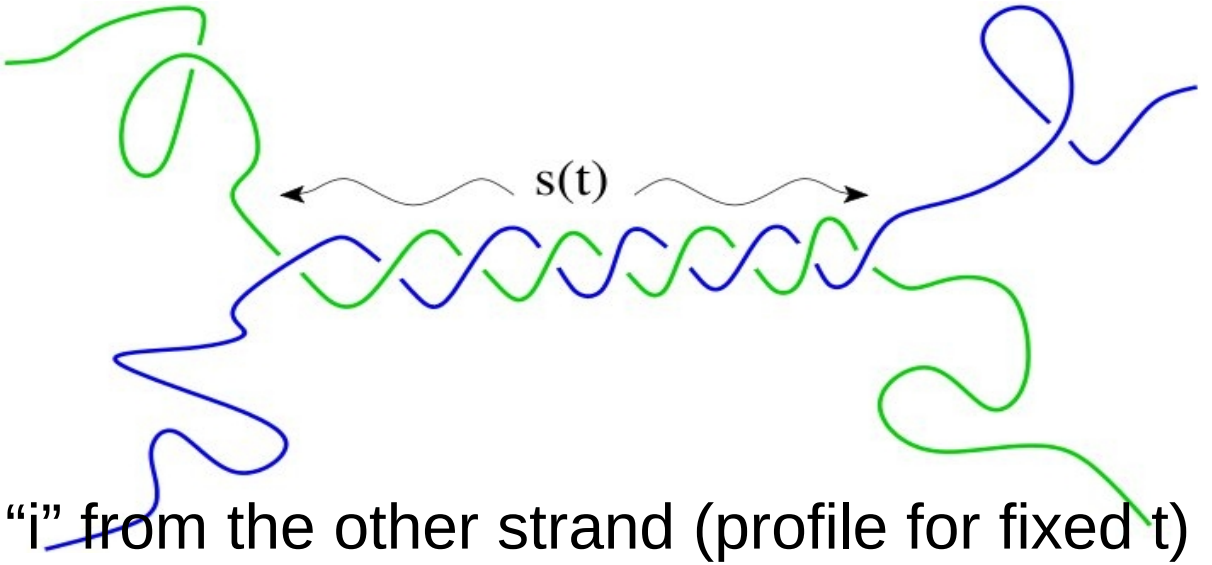
Its equilibrium properties studied recently
Baiesi, Barkema, Carlon, Phys.Rev.E. 2010

Interesting quantity: **stored length density**
(N-L)/N
Its scaling is related to critical exponents

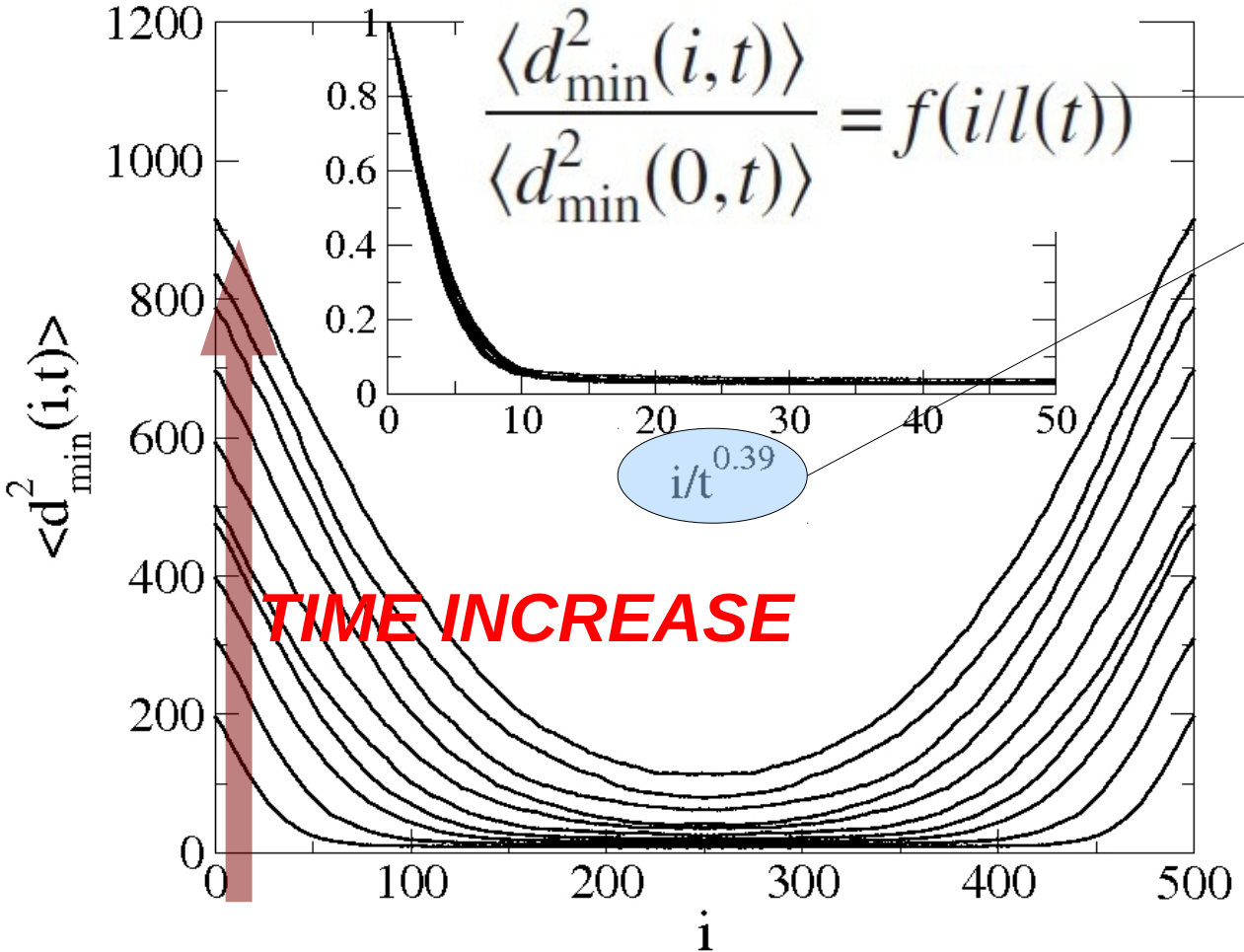
Unbinding time: exponent z=2.57(3)



Opening from the ends



Mean distance of monomer “i” from the other strand (profile for fixed t)

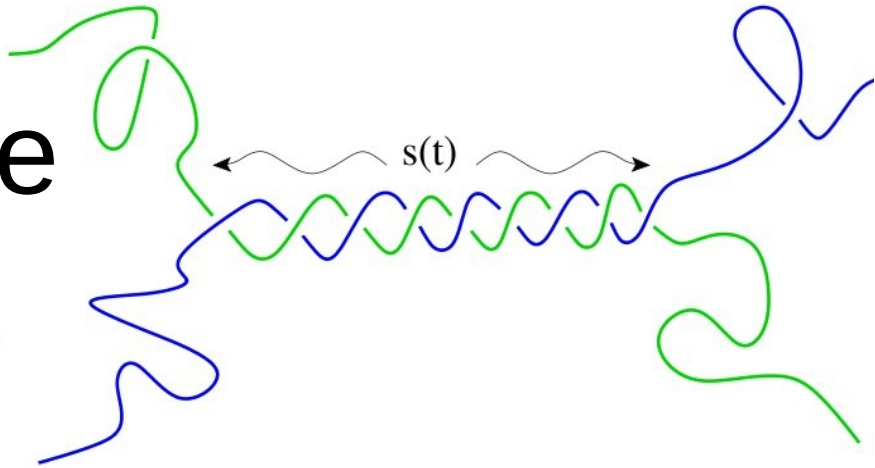


$$l(t) \sim t^{0.39}$$

0.39 = 1 / 2.57

This opening is not imposed: It comes from the physics of the process

If it was equilibrium-like



$$Z_{\text{helix}} \sim \mu_h^s \qquad Z_{\text{coil}} \sim \mu_c^{N-s}$$

$$\beta F = -\, s\, \log(\mu_h) - 2(N-s)\log(\mu_c)$$

$$dF = -\, \beta^{-1}\, \log(\mu_c^2/\mu_h)ds \equiv -\, K_1 ds$$

$$R_v \sim (N-s)^{\nu}$$

$$dr \propto R_v ds \propto (N-s)^{\nu} ds$$

$$dW = \gamma \dot{r} dr = \gamma R_v^2 \dot{s} ds$$

$$\gamma \propto N - s$$

$$K_2 (N-s)^{1+2\nu} \dot{s} ds \leq K_1 ds$$

$$K_1/K_2 = -\,[N - s(t)]^{2\nu+1} \frac{ds}{dt}$$

$$\tau_u \sim N^{2\nu+2} = N^{3.18}$$

Too large exponent z=3.18 > 2.57

- A similar exponent >3 found by Baumgärtner & Muthukumar (1985) in a less asymptotic simulation

- Assumption of equilibrium meta-states is not supported by our simulations

- Configurations can have spiral-like shapes
- Though not easy to define spirals between two polymers → Need to try polymer+bar

Summary

- DNA denaturation is not a desorption problem, we must take into account the chain entanglement

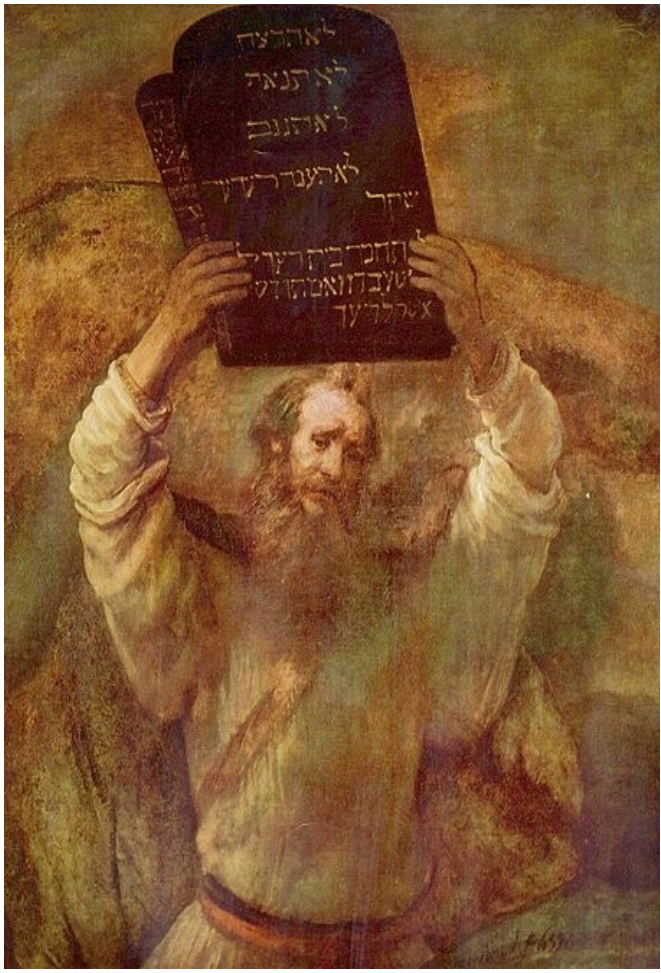
- If we do, the time-scales of disentangling scale at least as a power-law of DNA length, with exponent at least 2.57

- Need to clarify the occurrence of multiple time-scales and the kind of dynamics, and find more explanations for the numbers

Quite not prophetic

Baumgärtner and Muthukumar, 1985

gen bonding interactions. The second step of disentangling of two interpenetrating chains requires a characteristic time proportional to $N^{3.3 \pm 0.2}$. Although this process is, in principle, related to the relaxation mechanism of a chain in a dense polymer solution or melt,[1] it is not at present obvious what this relation is. Nevertheless, our observation of two-stage disentangling and the molecular weight dependence of the corresponding characteristic times was unexpected and will hopefully create interest. The issue of how the above results



References

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M. Baiesi, G. T. Barkema, E.Carlon, and D. Panja,
J. Chem. Phys. 133, 154907 (2010).