

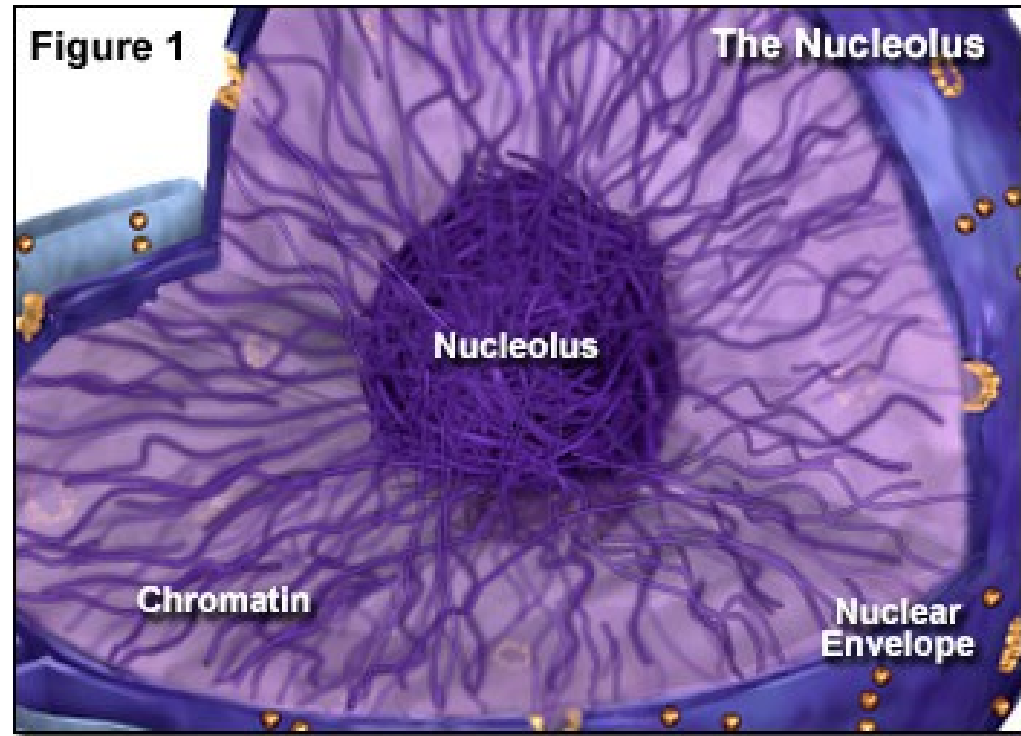
EPIGENETIC LANDSCAPES AND CHROMATIN ORGANIZATION

Mithun Kumar Mtra
Department of Physics, IIT Bombay

ISPC2018



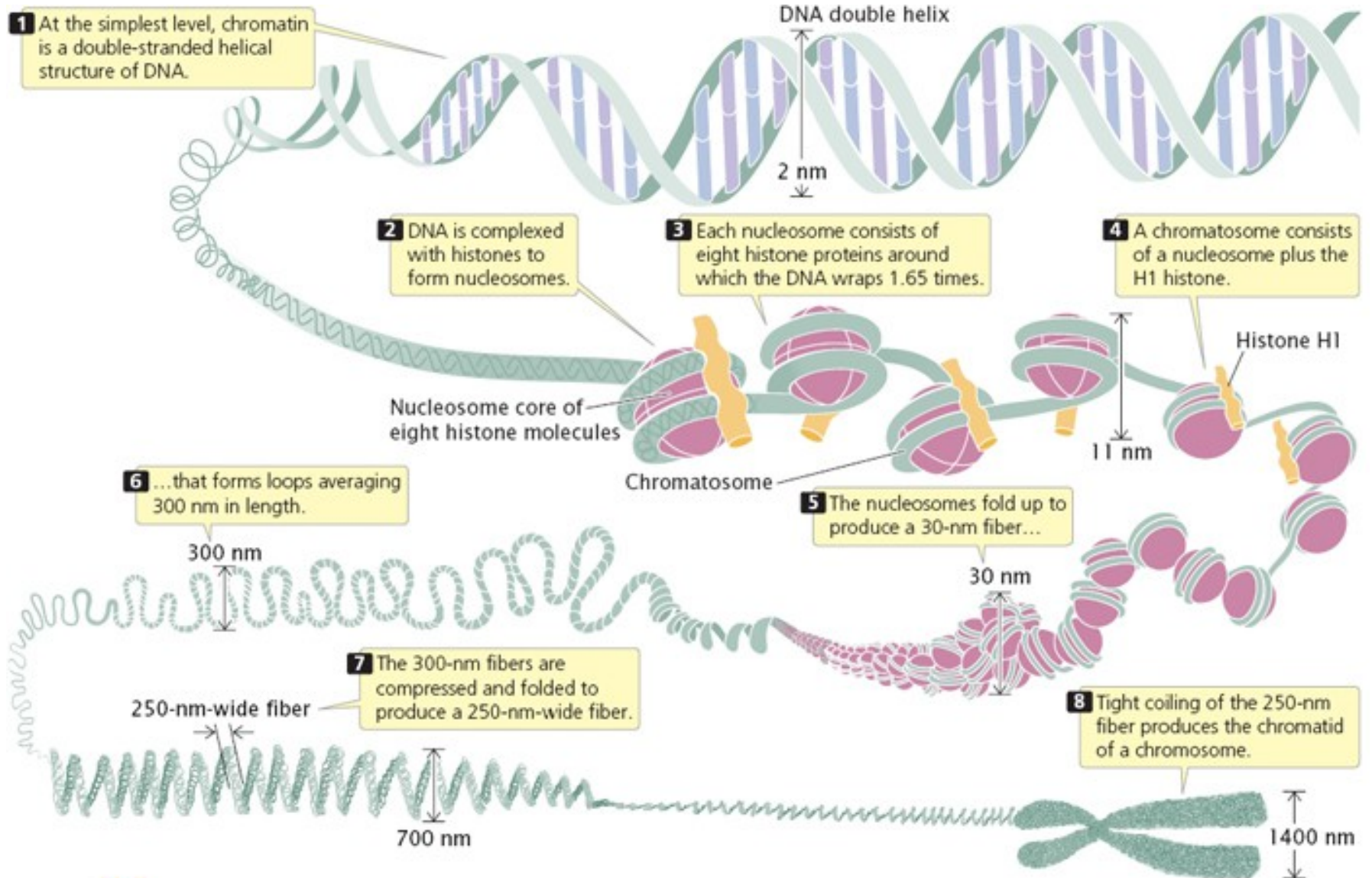
Packaging at multiple scales

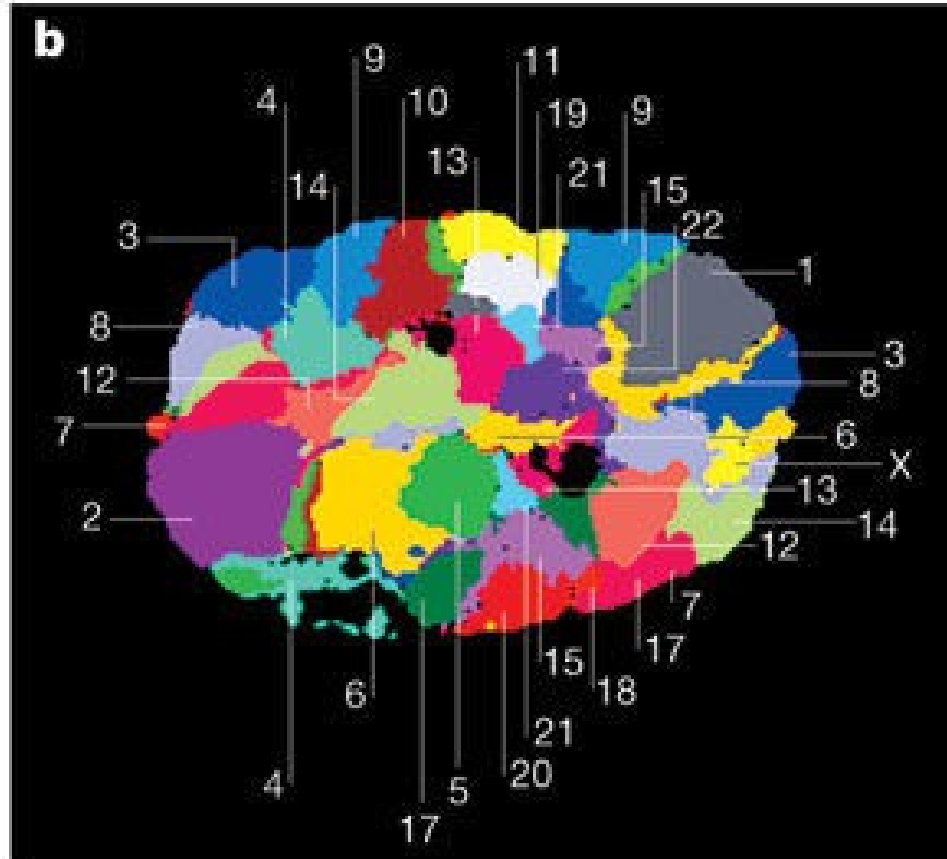
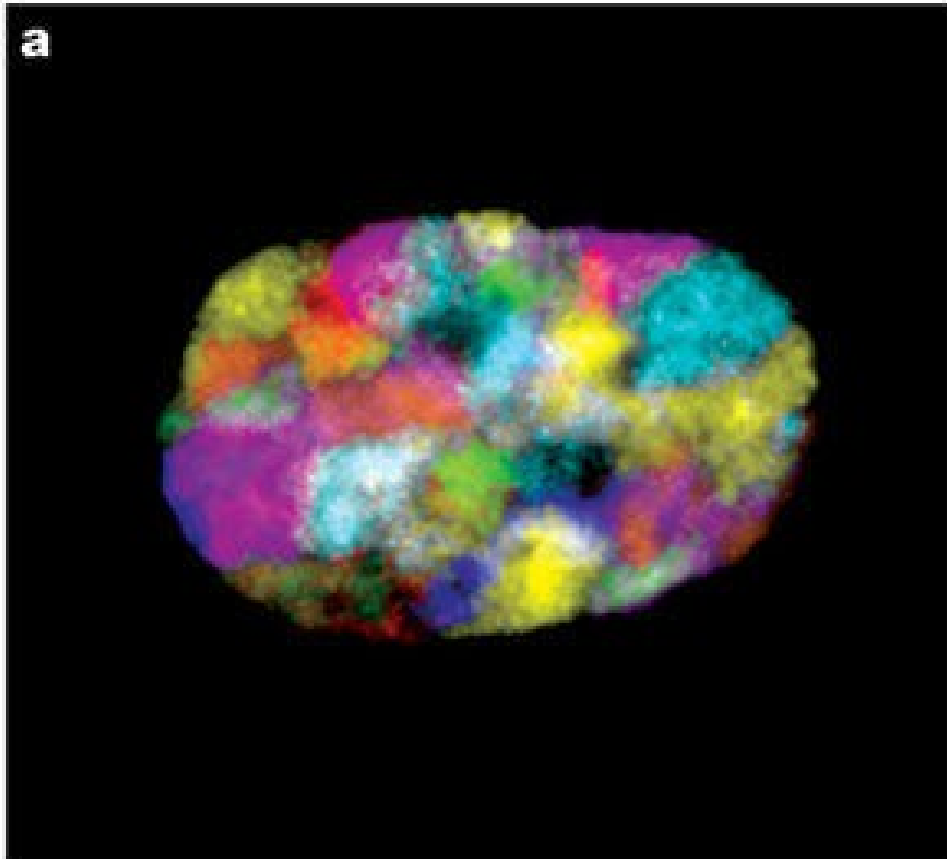


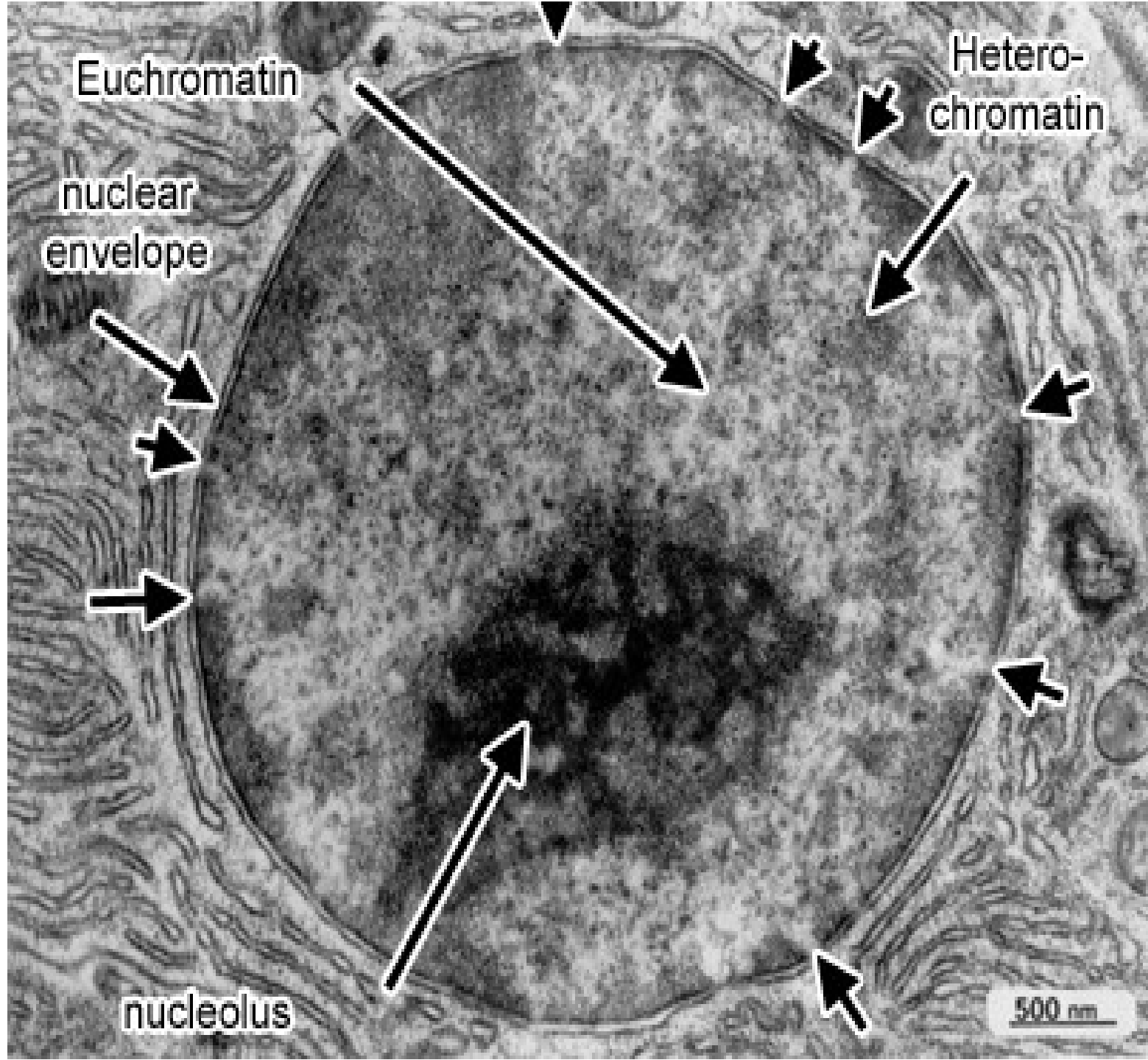
No. of base pairs in the human genome ~ 3 billion $\equiv 3 \times 10^9$

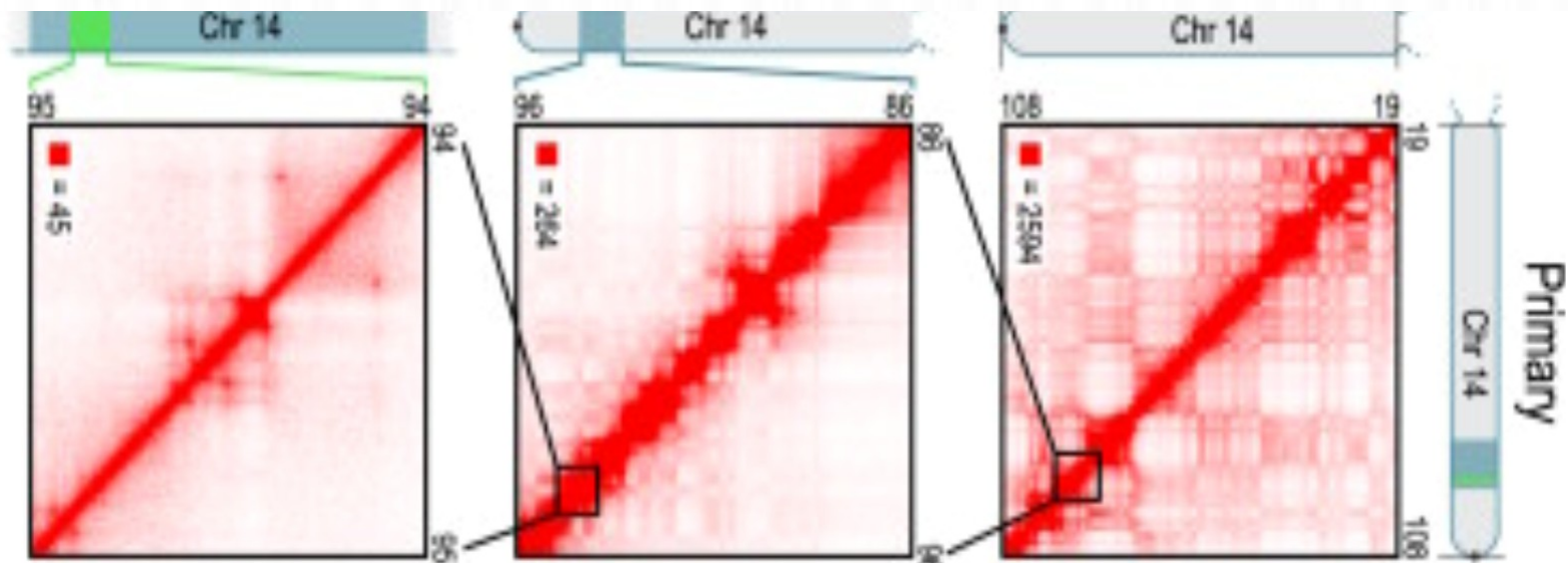
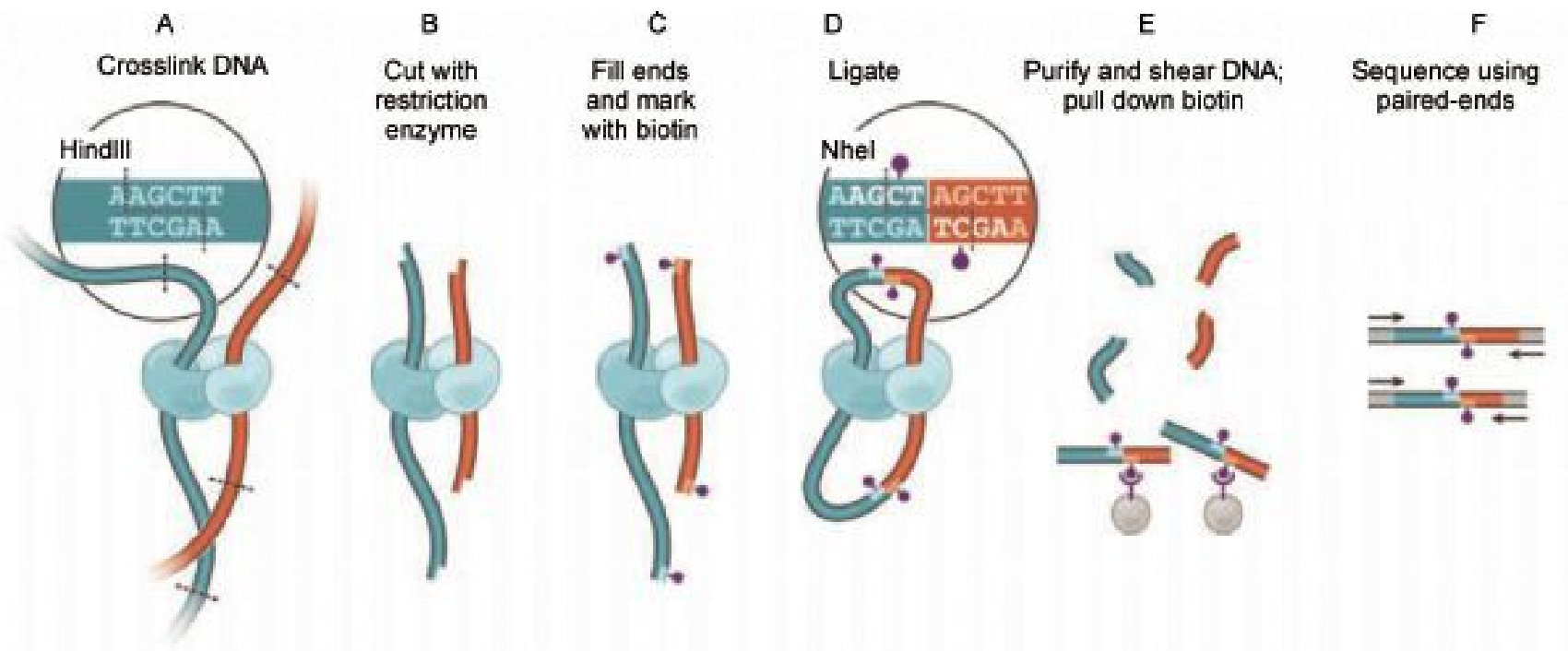
Linear size of the human genome ~ 3 - 6 m

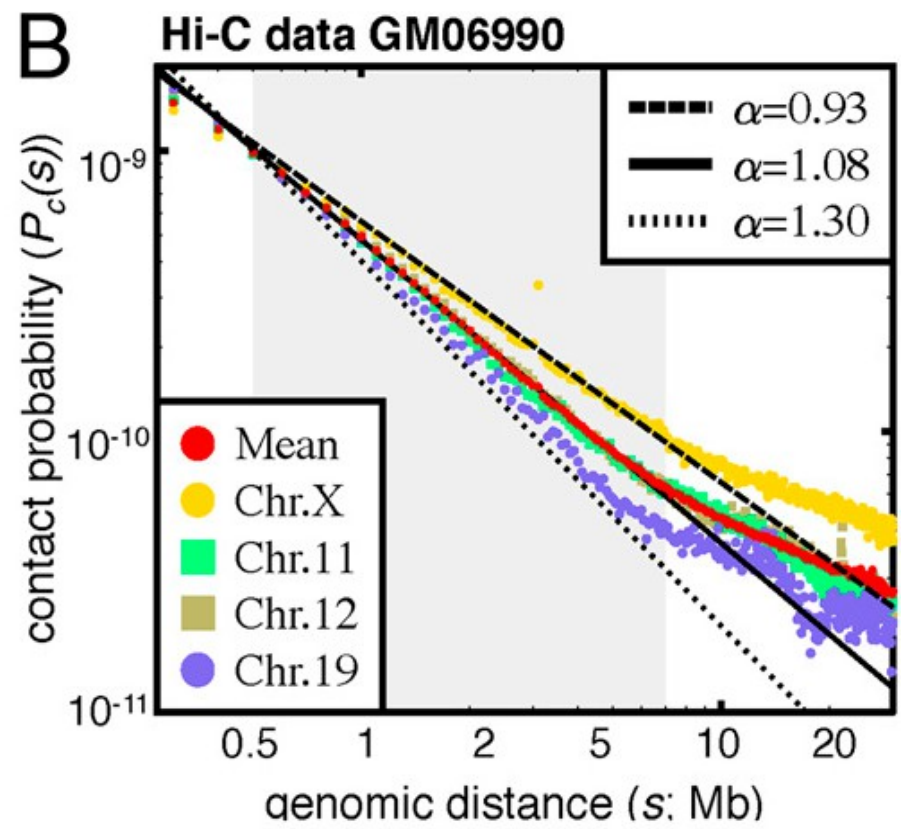
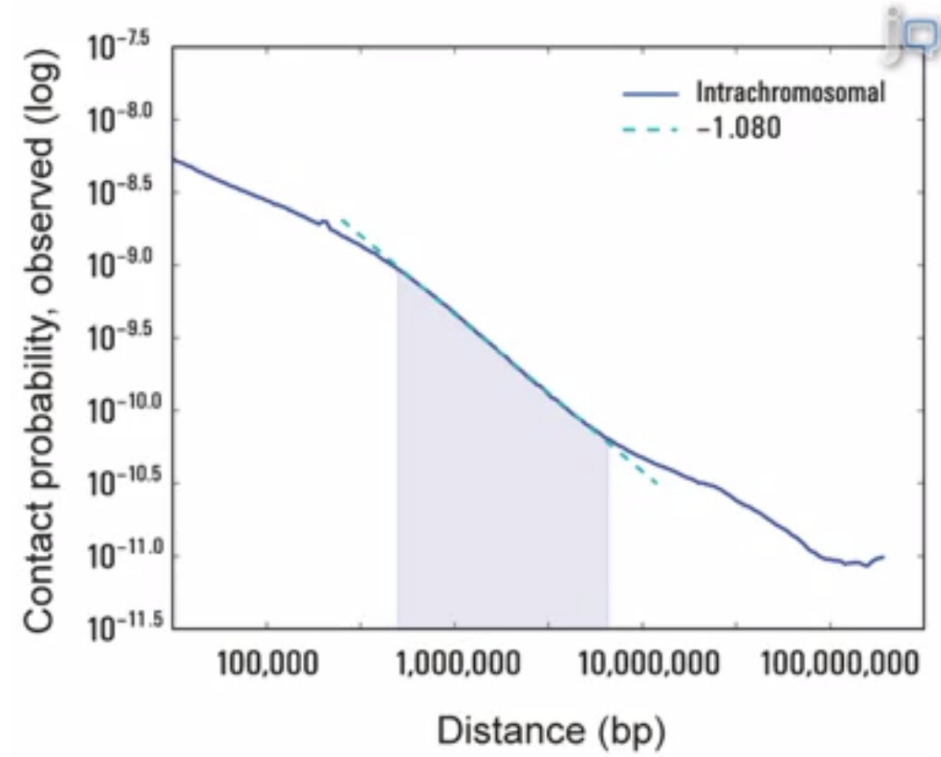
The Hierarchical Genome





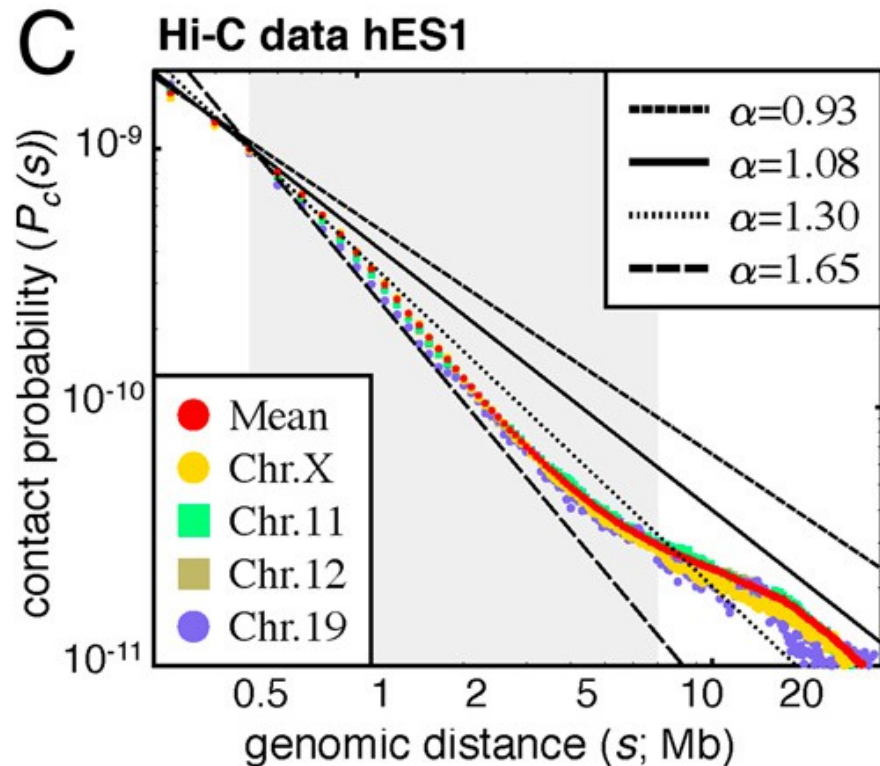
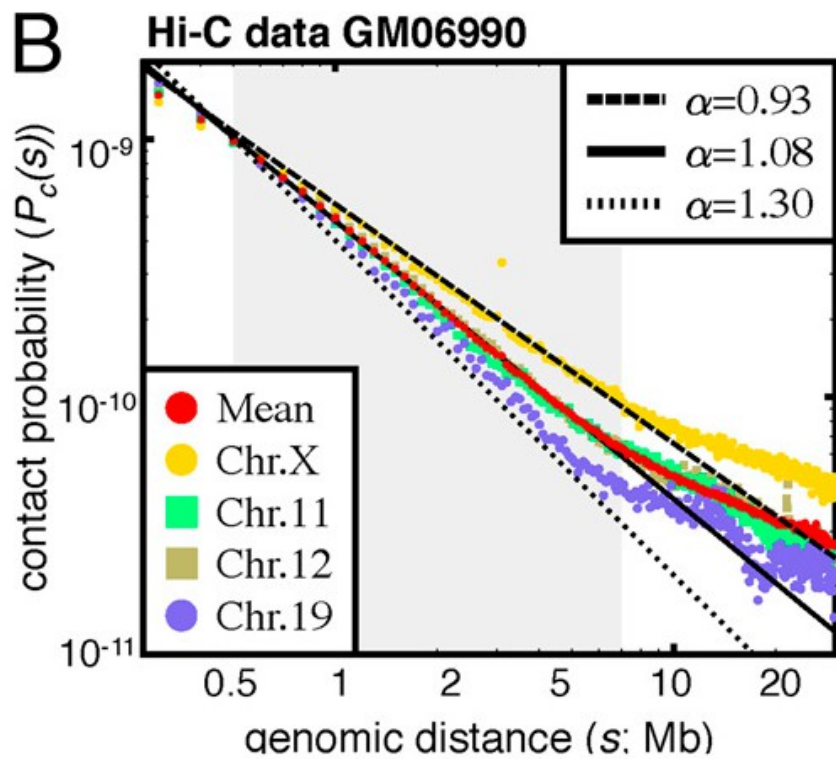






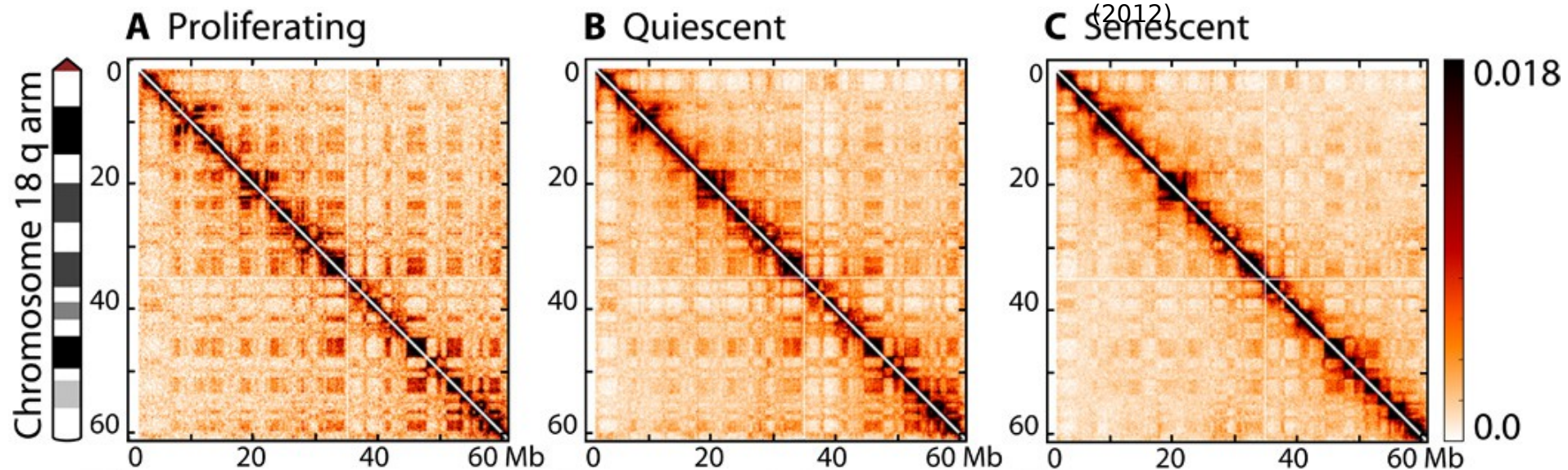
Nicodemi et. al. PNAS, 109, 16173 (2012)

$n(s) \propto 1/s$

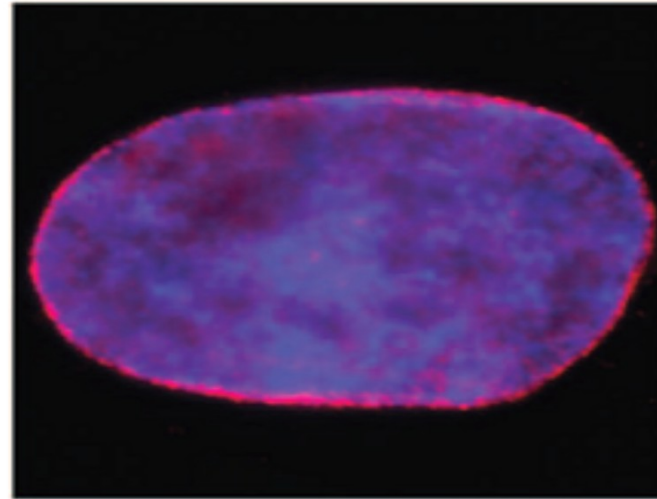
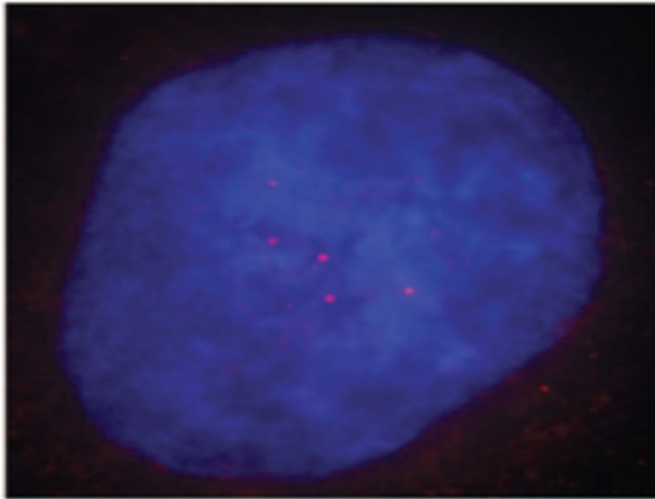


Nicodemi et. al. PNAS, 109, 16173

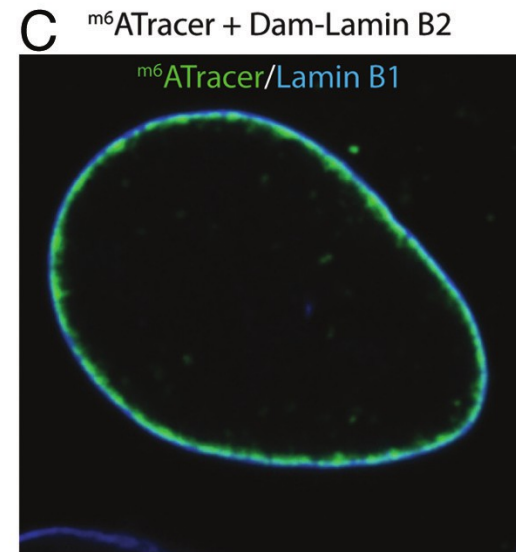
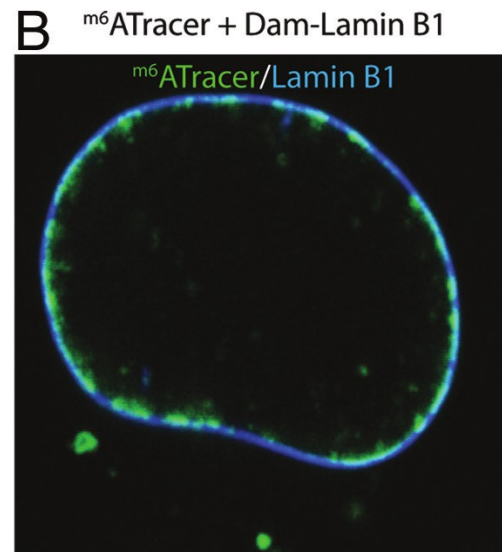
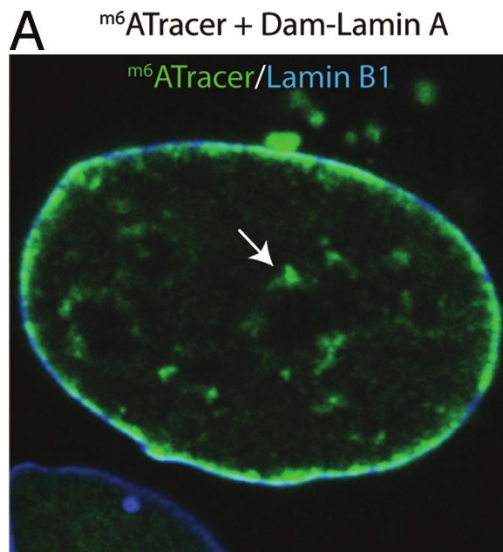
(2012)



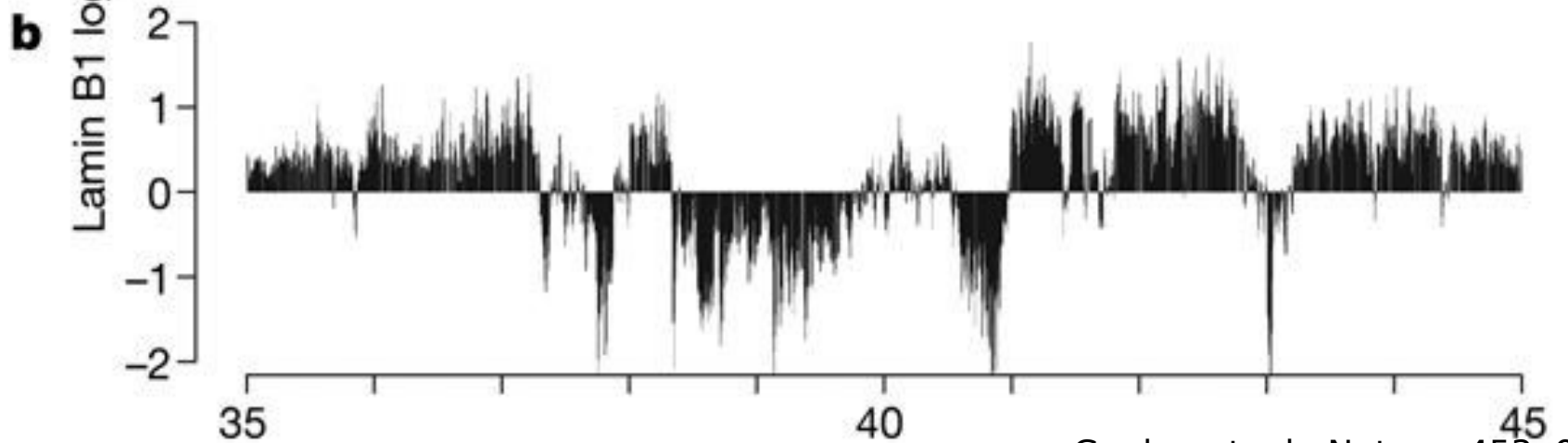
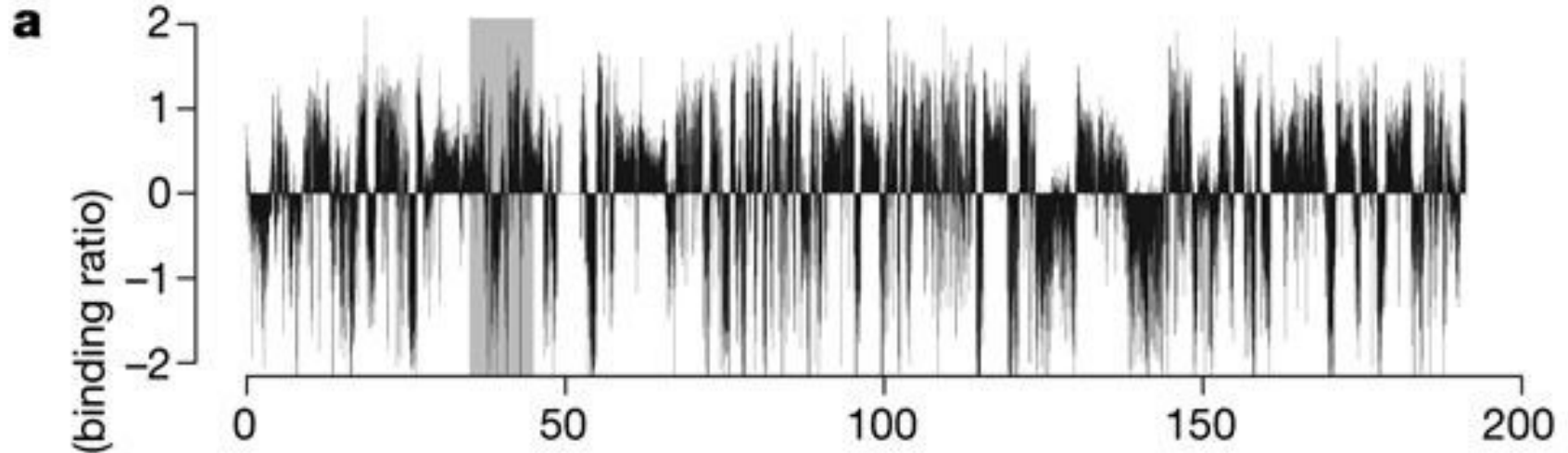
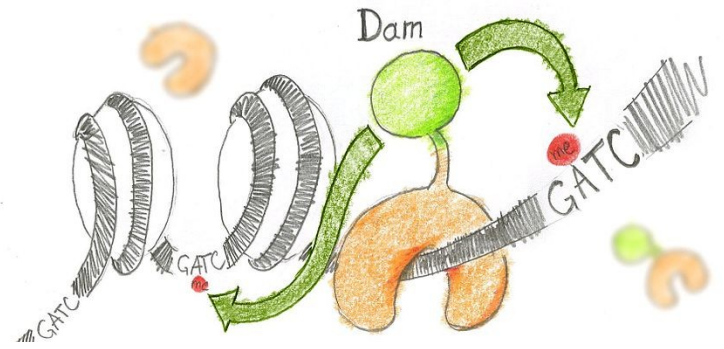
NUCLEAR LAMIN PROTEINS

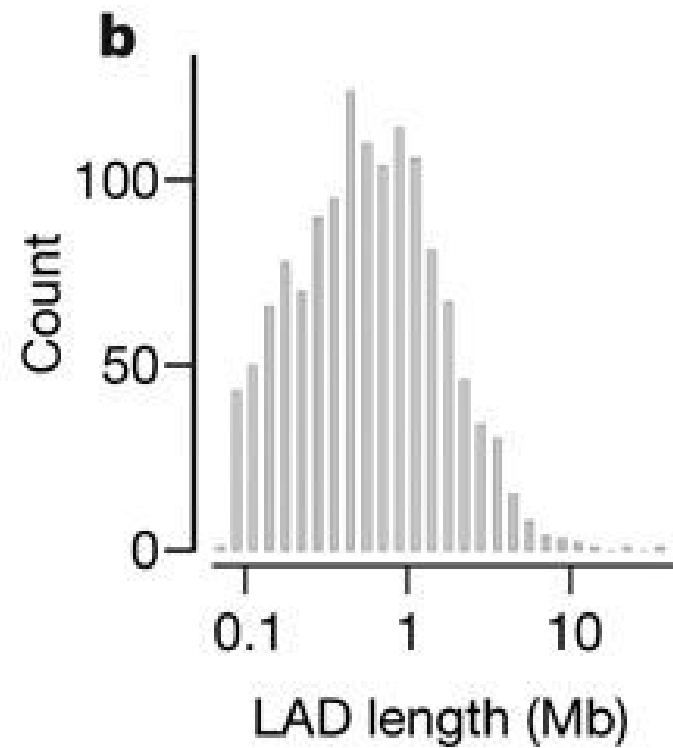
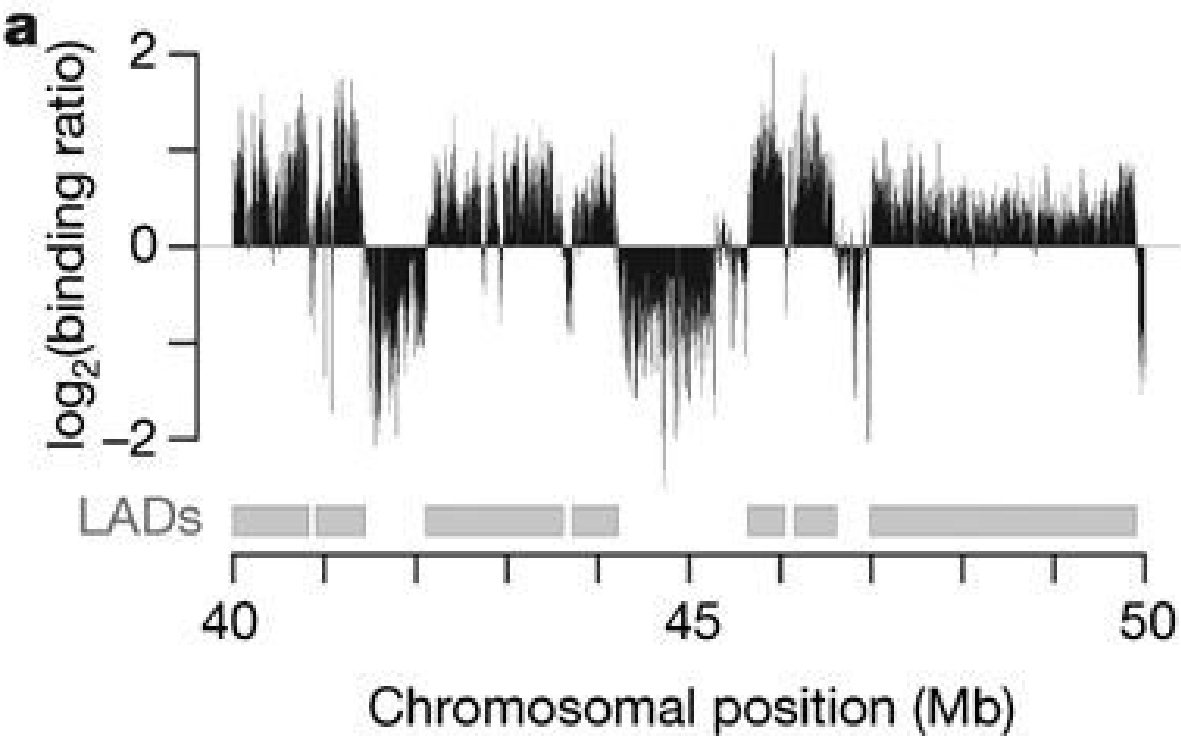


Morris et. al. Cell Biology of Stem Cells, eds. Meshorer&Plath (2010)

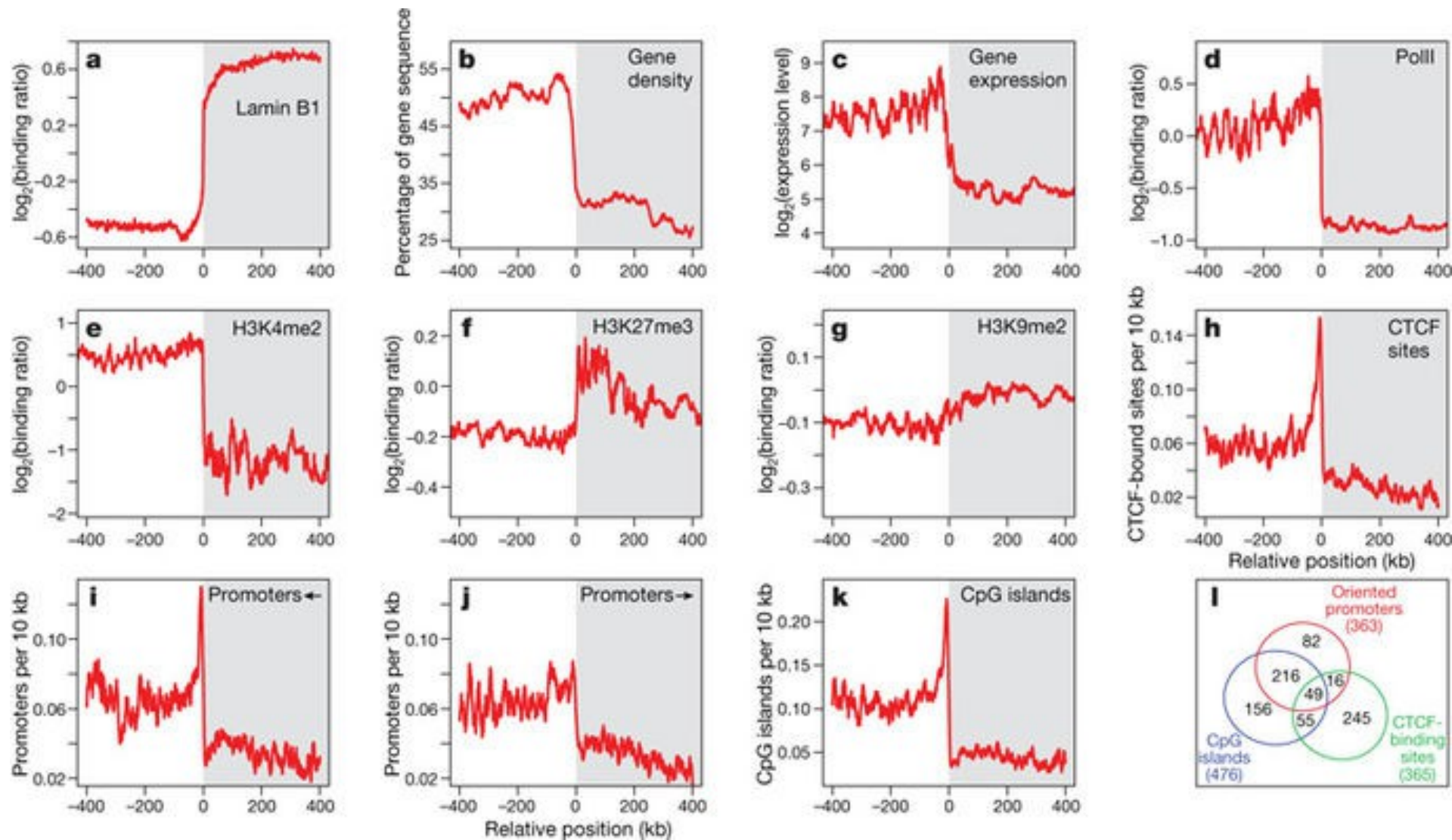


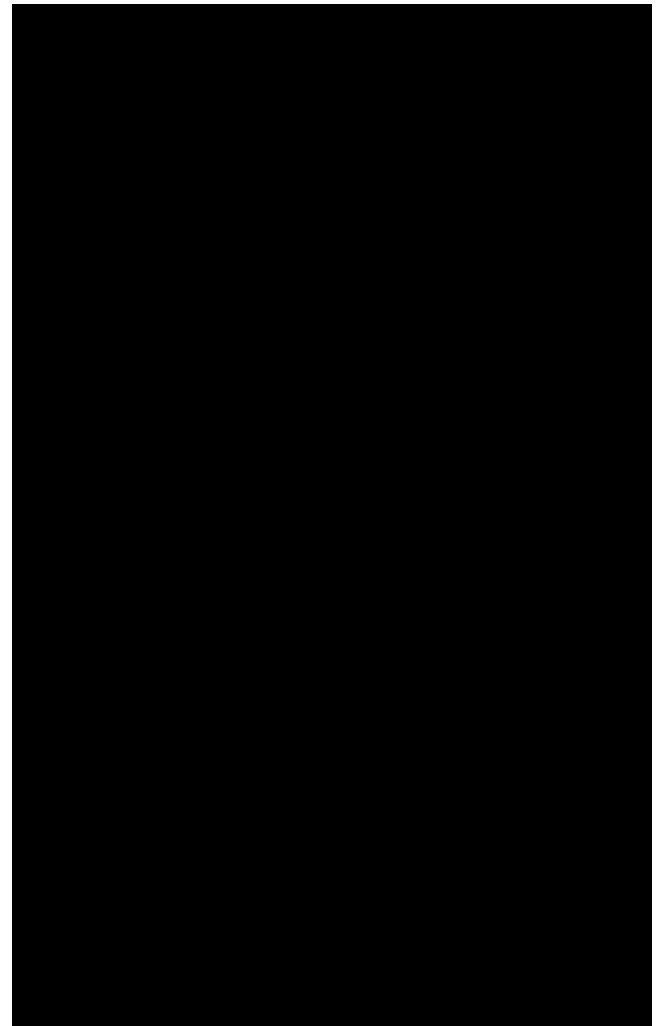
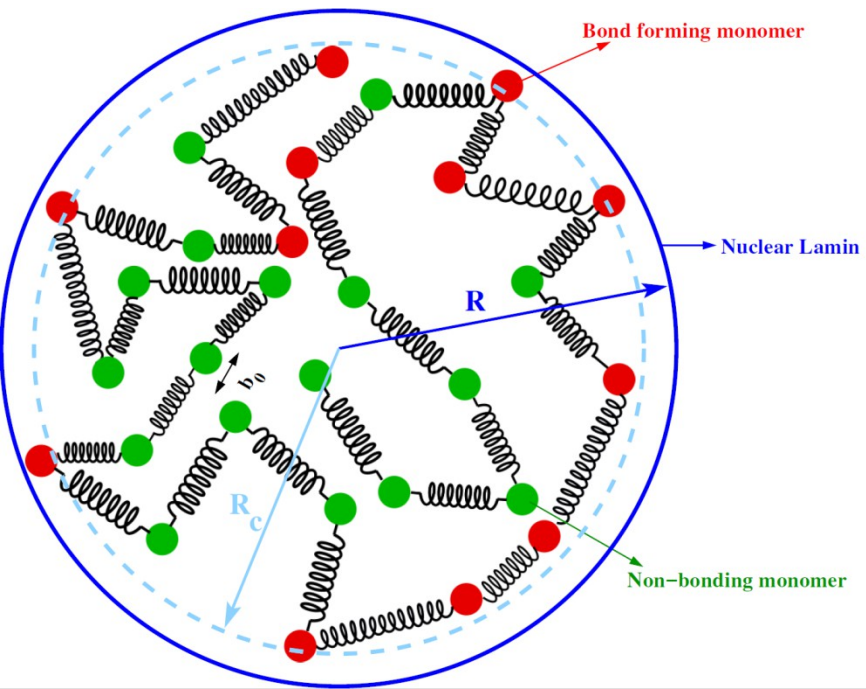
DAVID M_{ps}



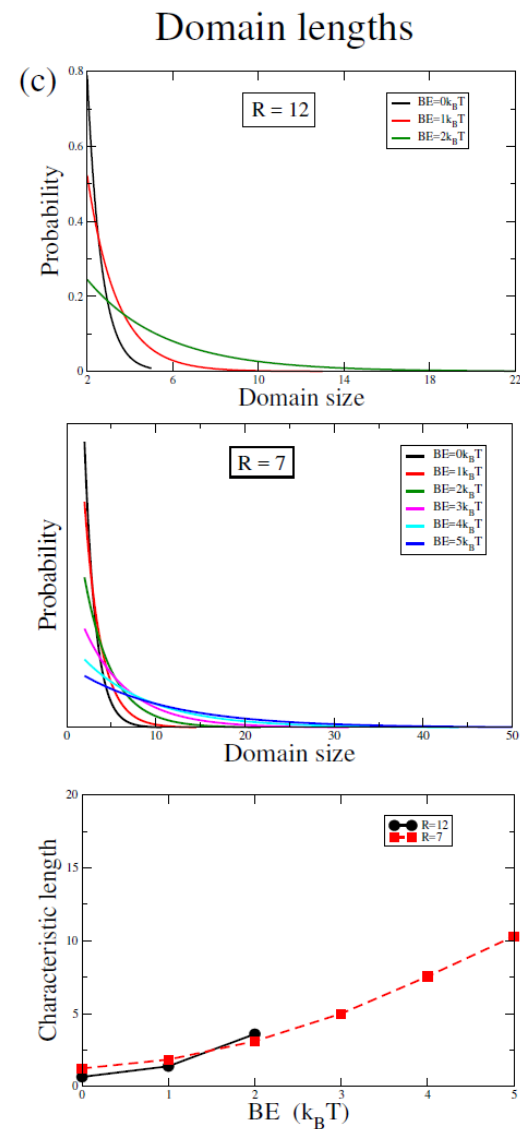
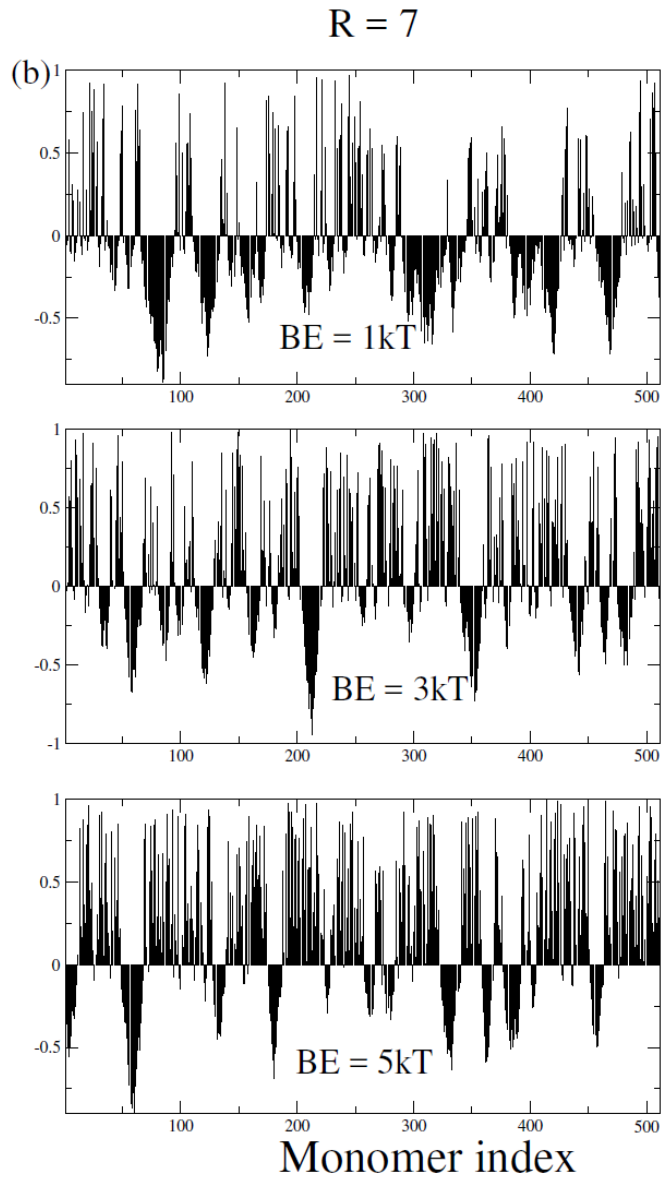
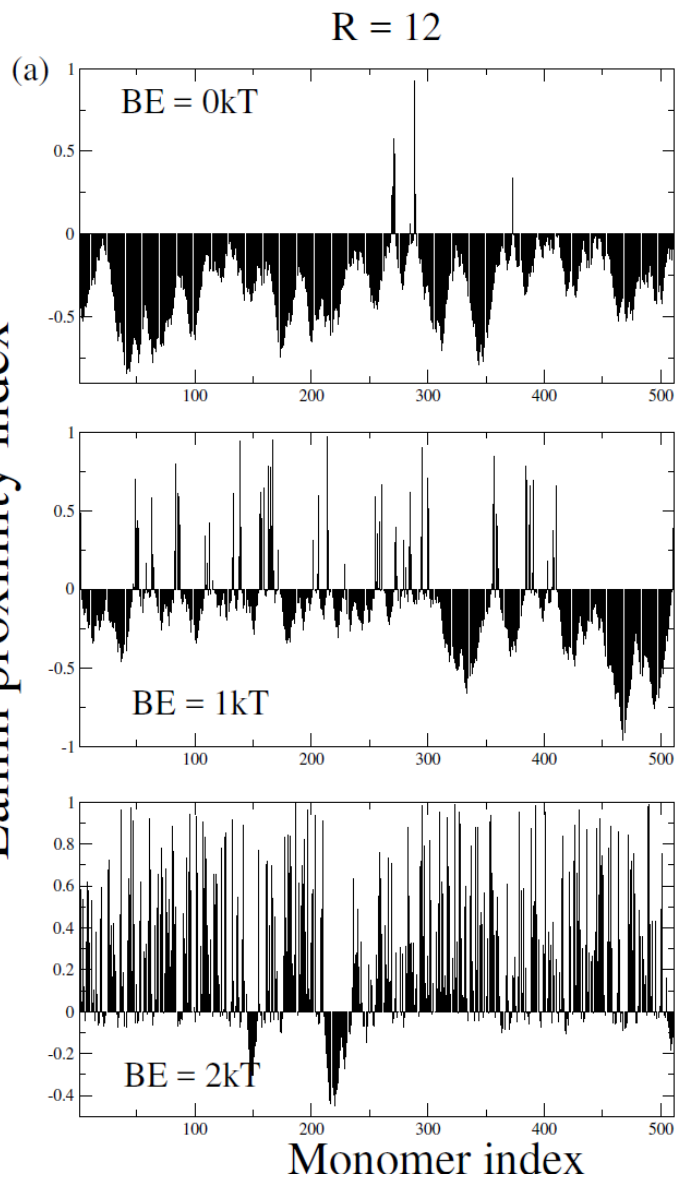


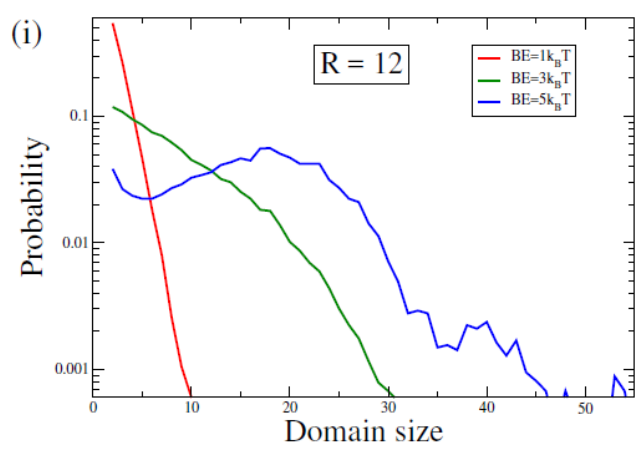
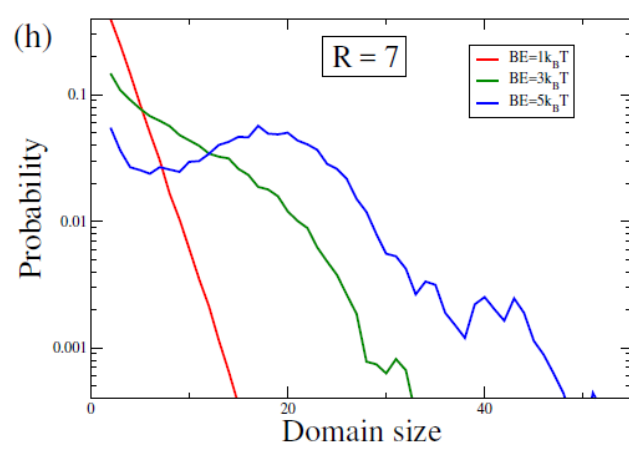
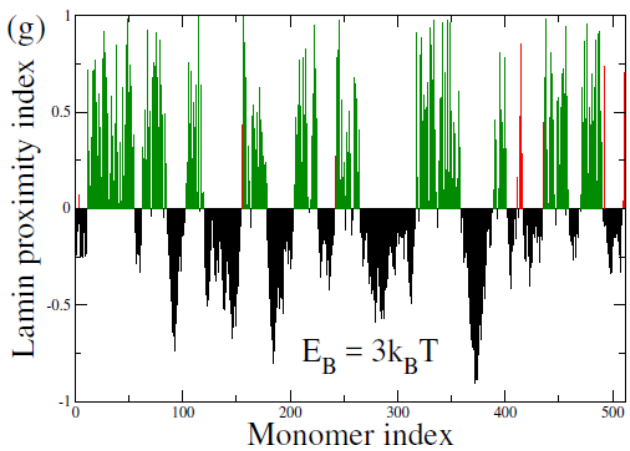
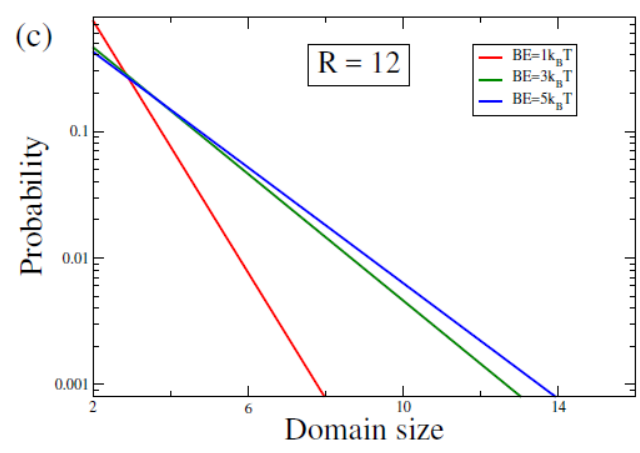
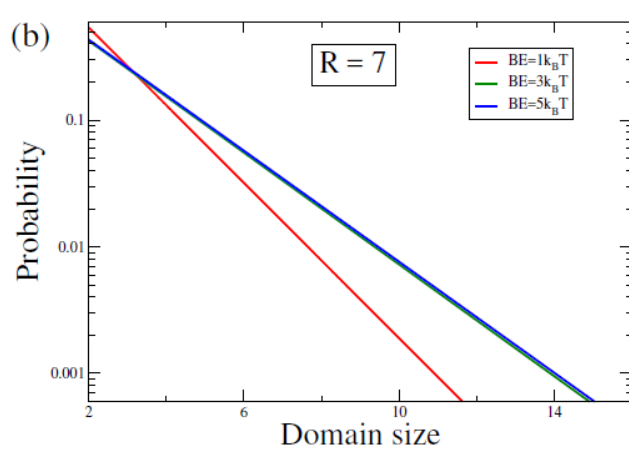
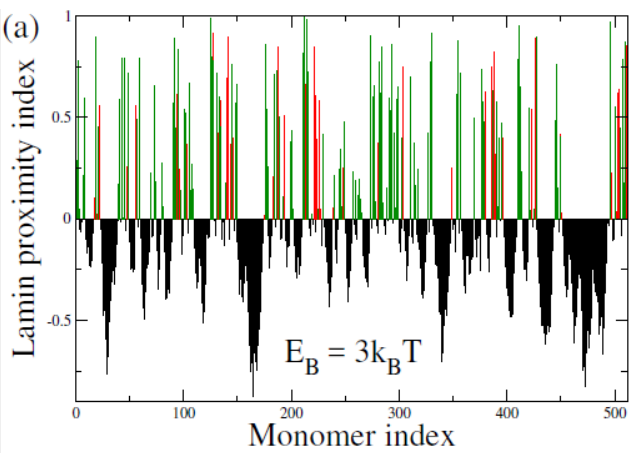
Guelen et. al., Nature, 453, 948
(2008)

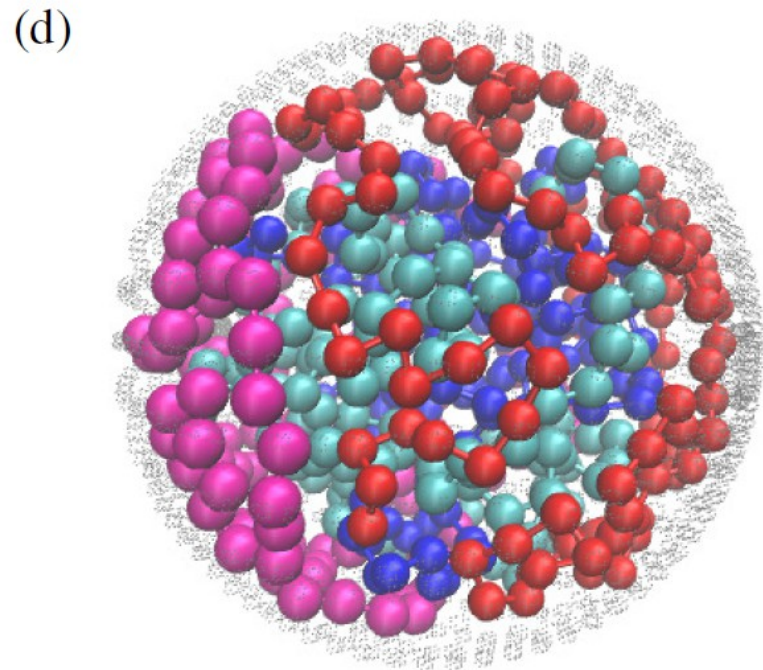
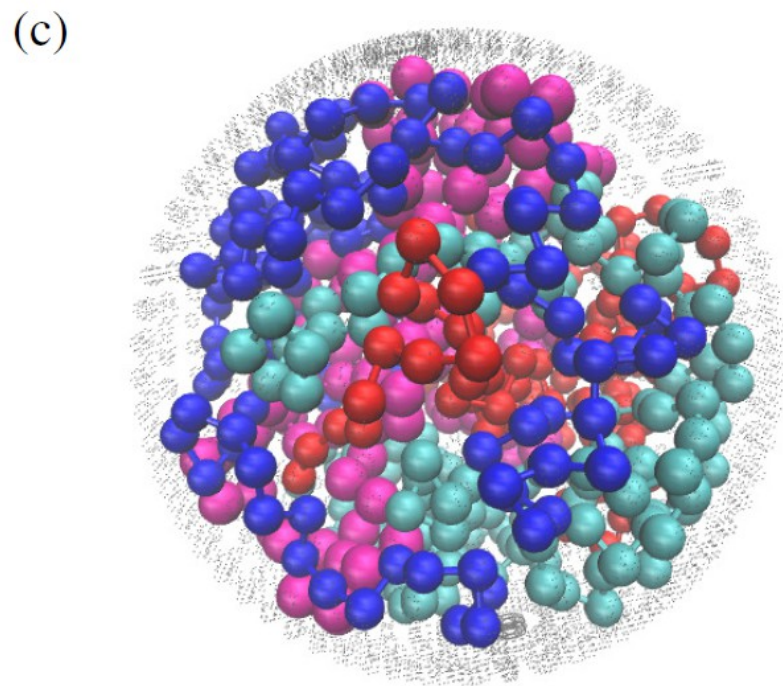
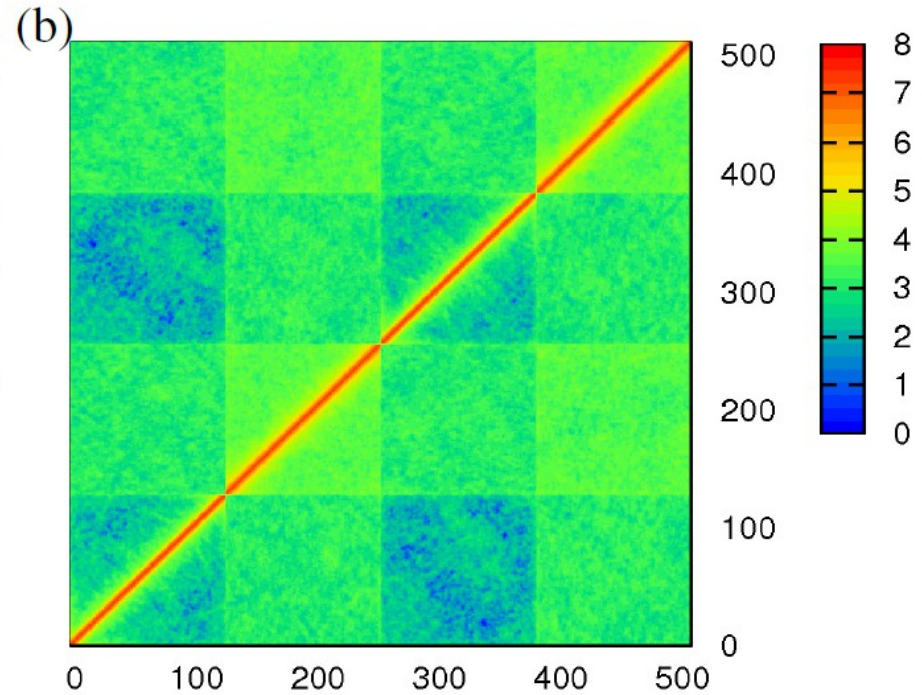
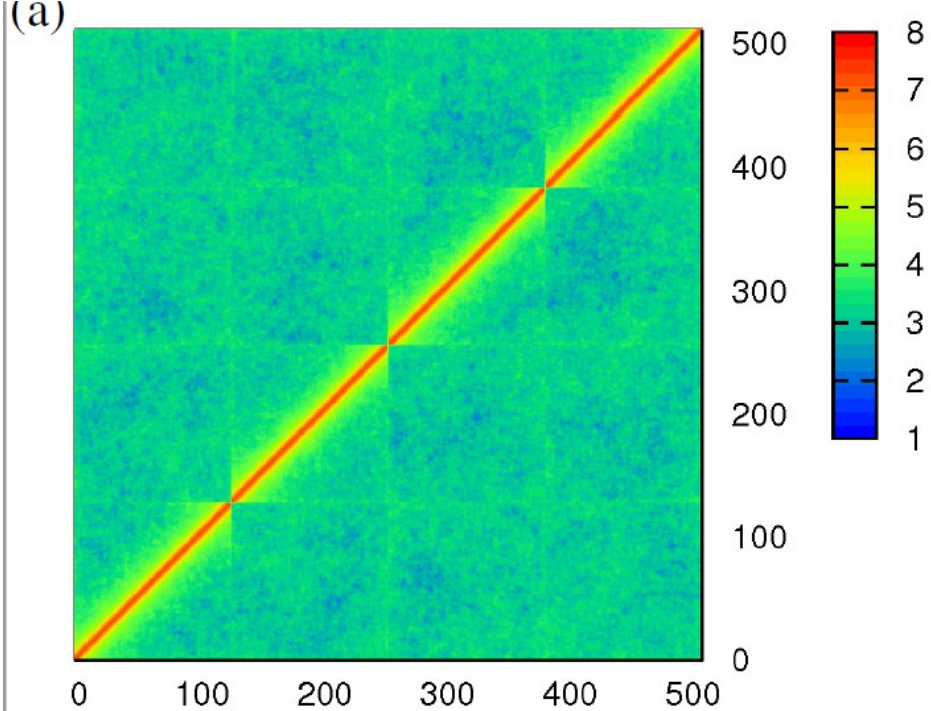




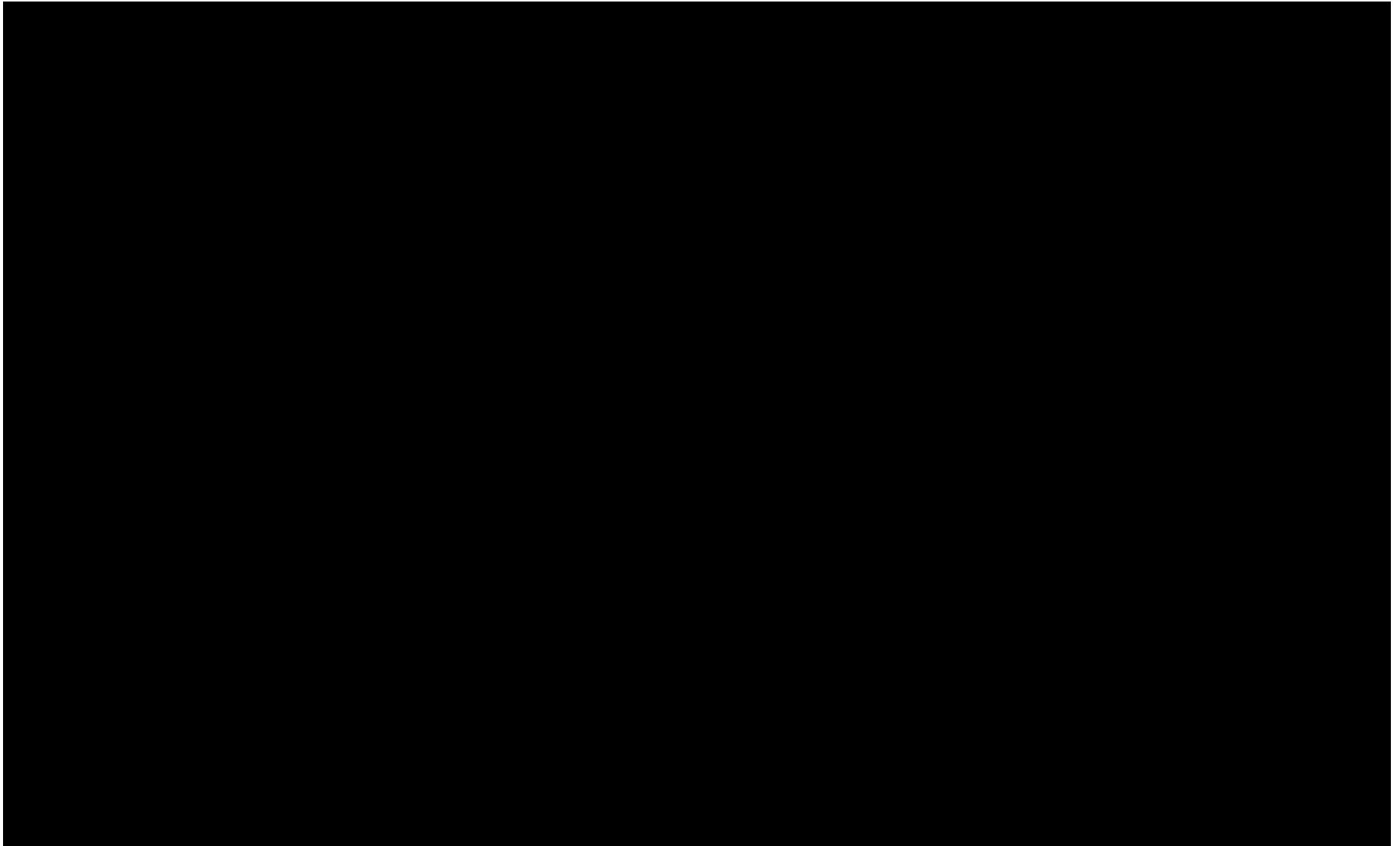
Lamin proximity index



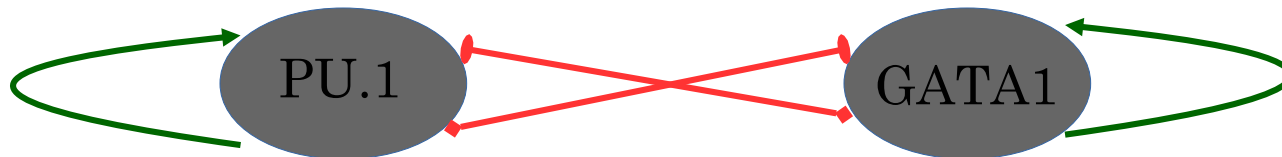
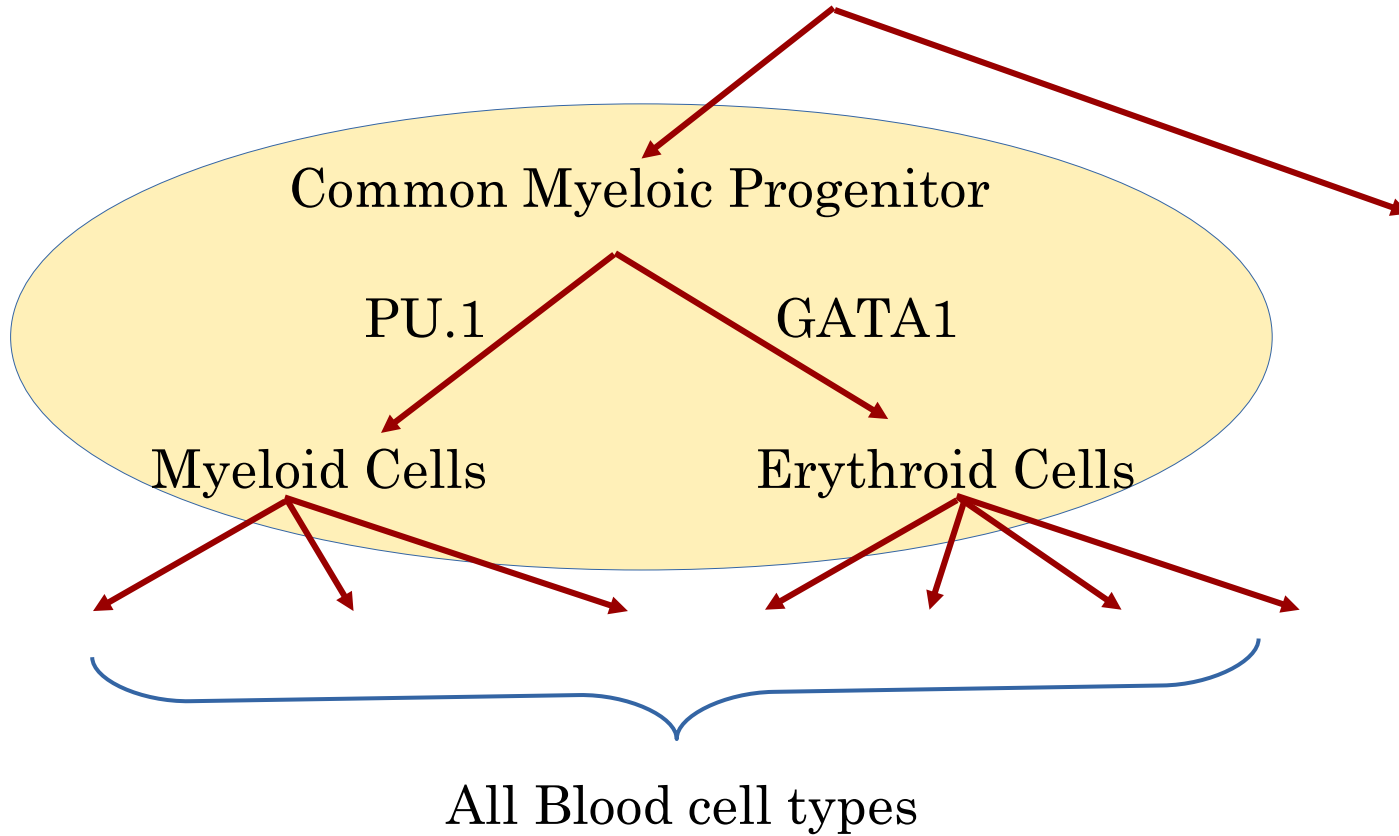




Waddington's EPIGENETIC LANDSCAPE



GENE REGULATORY NETWORKS

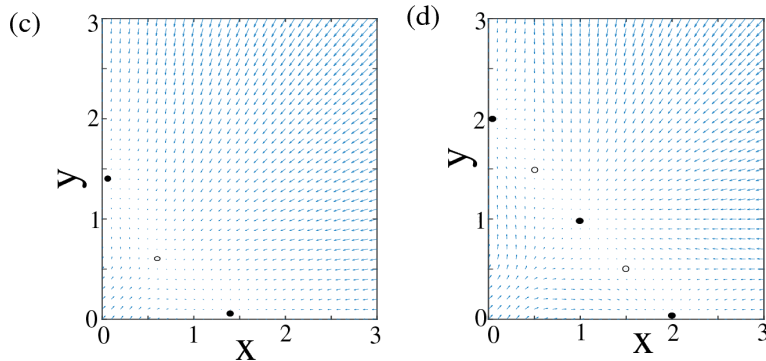
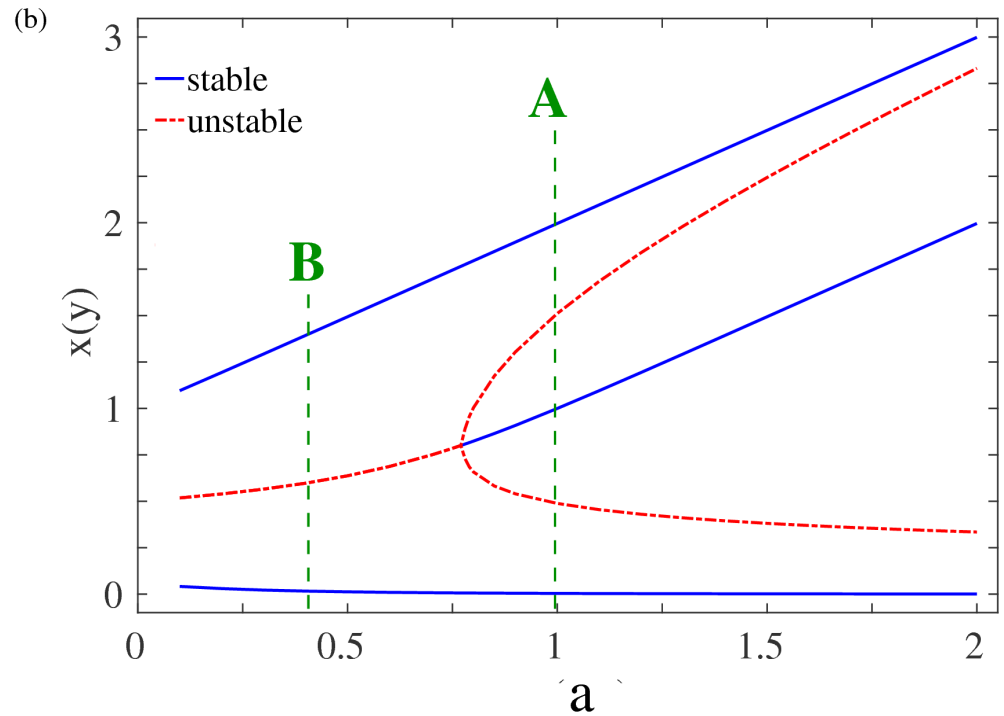
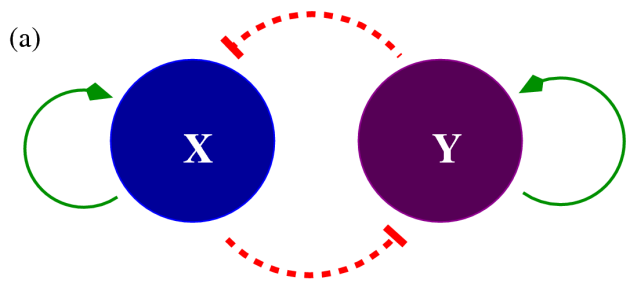


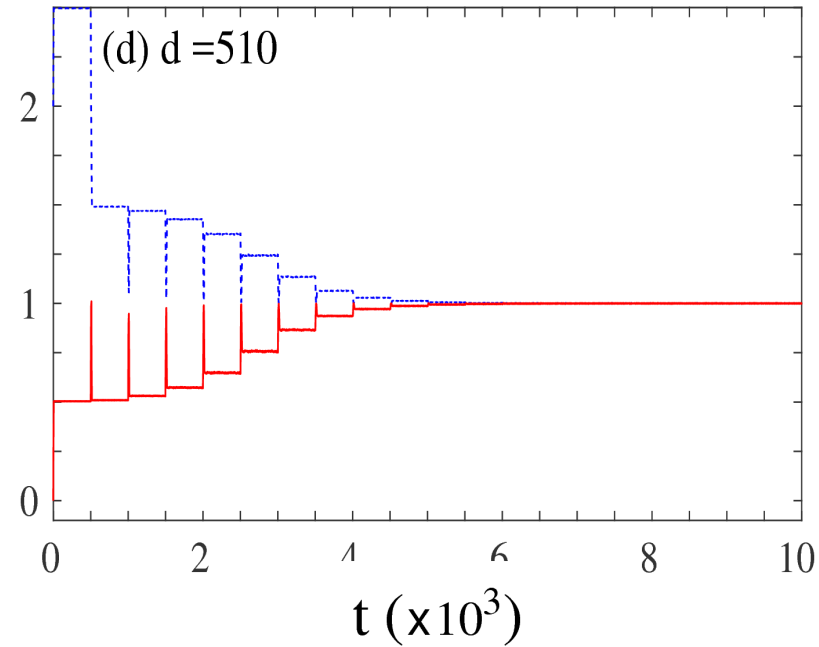
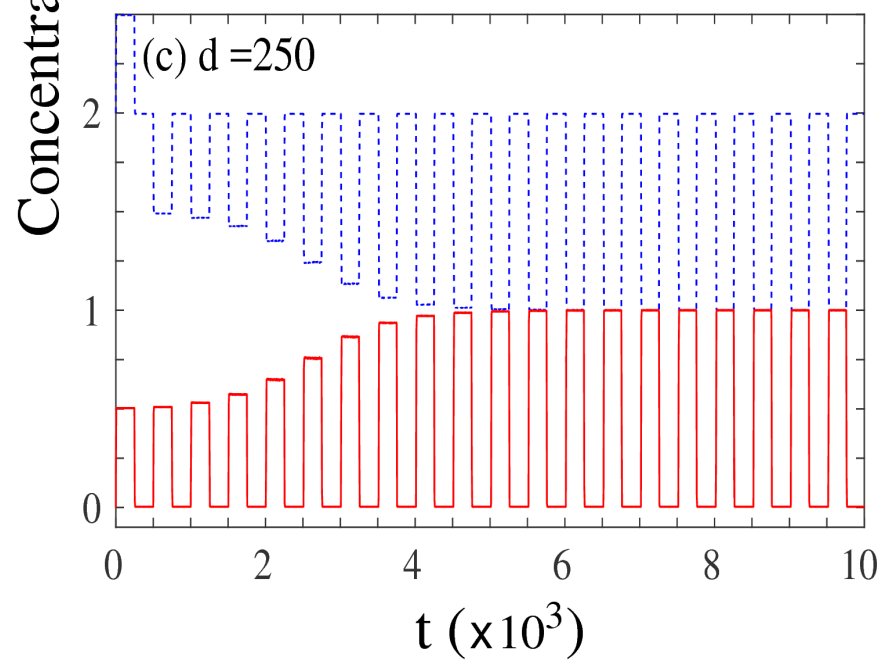
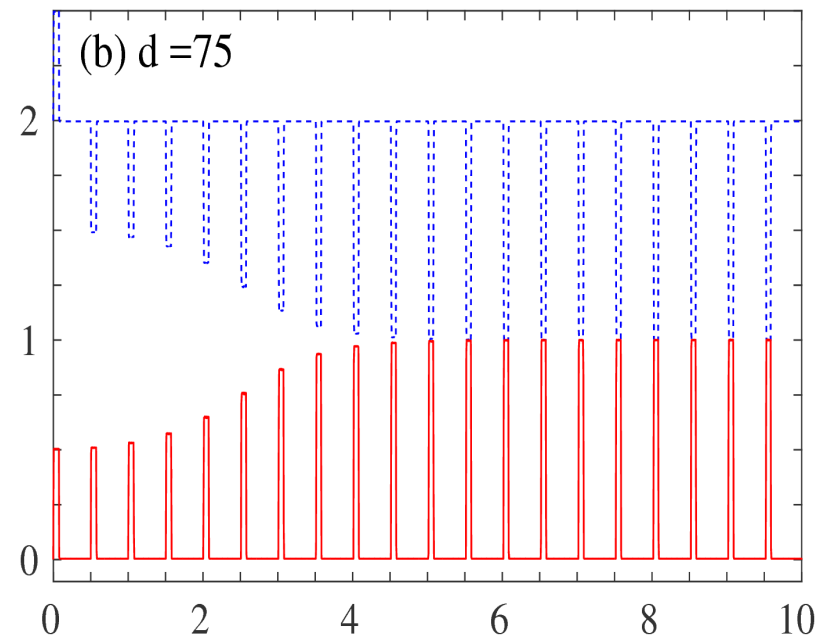
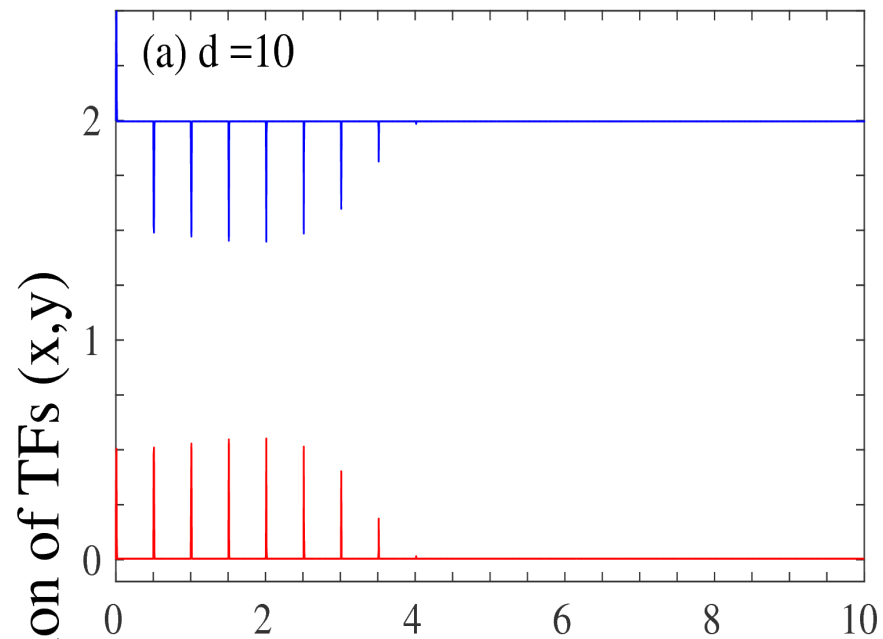
Self-activating and mutually inhibiting

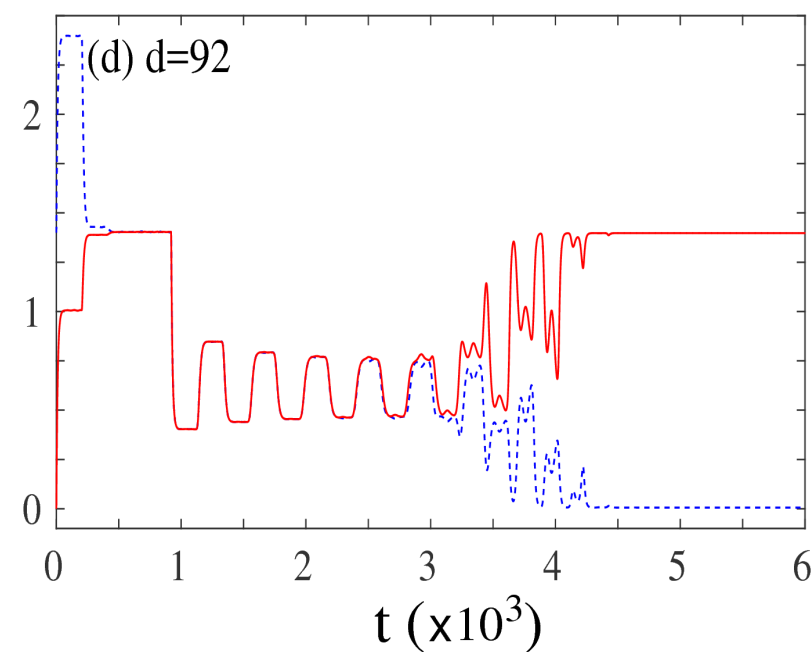
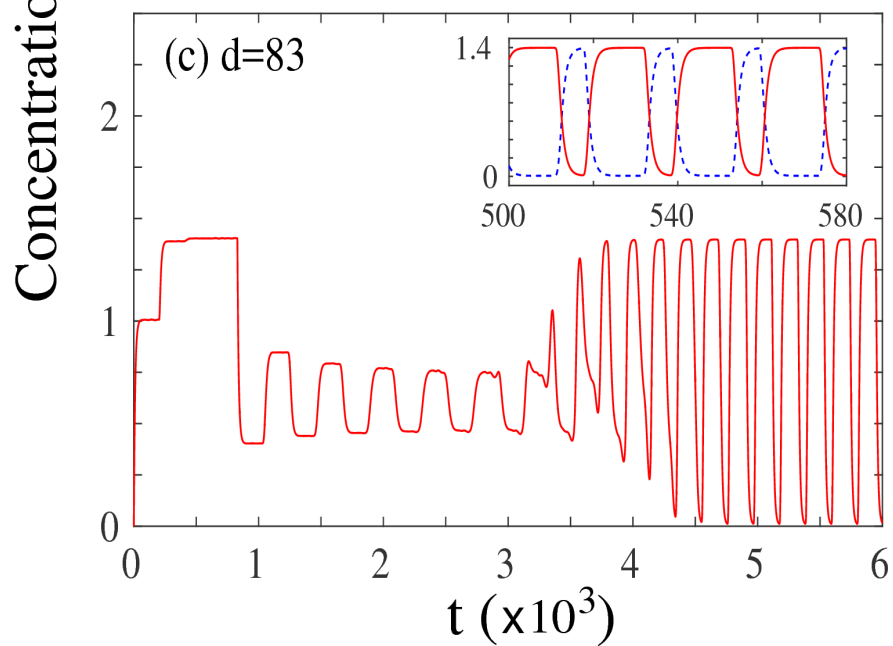
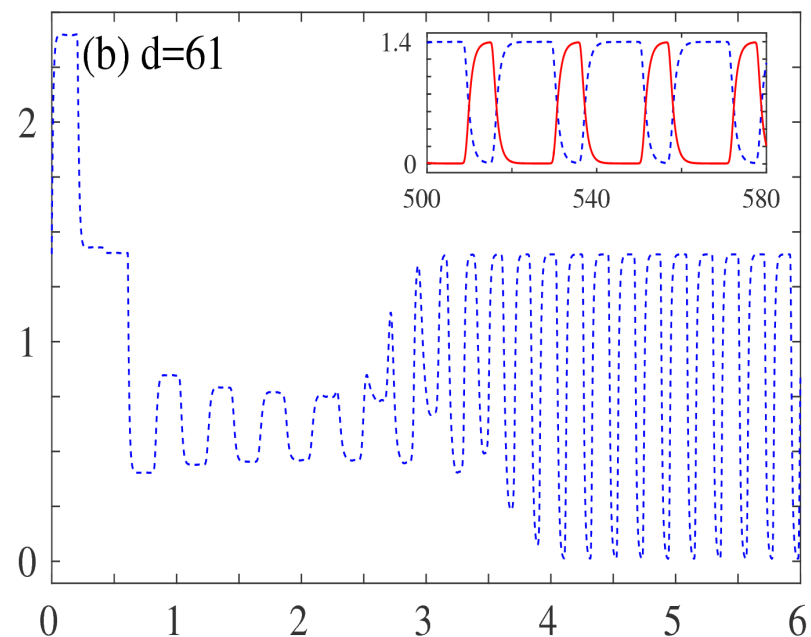
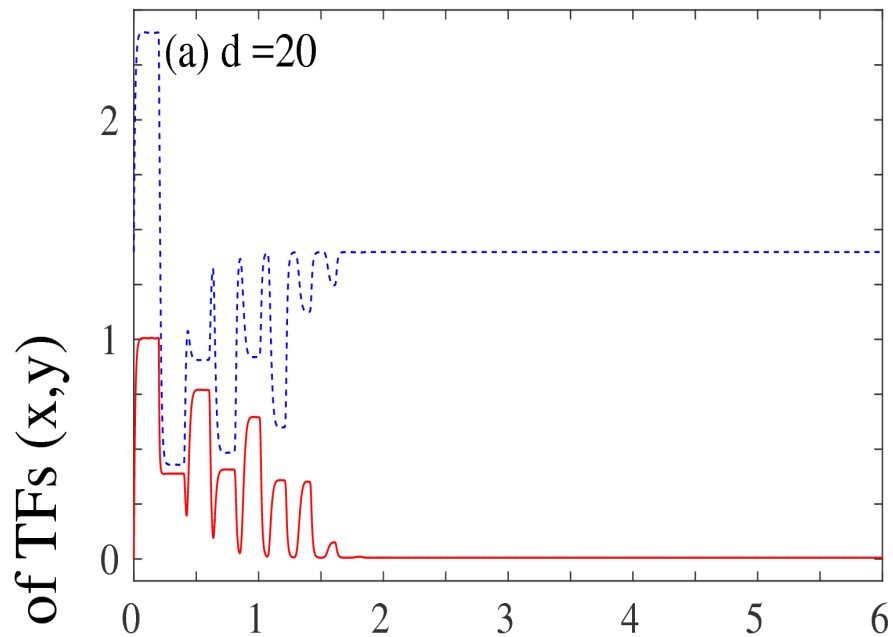
THE TWO GENE NETWORK

$$\frac{dx_1}{dt} = a_0\Theta(d - t) + \frac{a_1x_1^n(t - \tau_1)}{S^n + x_1^n(t - \tau_1)} + \frac{b_1S^n}{S^n + x_2^n(t - \tau_2)} - k_1$$

$$\frac{dx_2}{dt} = a_0\Theta(d - t) + \frac{a_2x_2^n(t - \tau_2)}{S^n + x_2^n(t - \tau_2)} + \frac{b_1S^n}{S^n + x_1^n(t - \tau_1)} - k_2$$







The structure of a folded chromatin fiber has implications for the regulation of gene expression. The folded structure is determined by interactions with various proteins such as CTCF and nuclear lamin proteins.

The epigenetic landscapes that describes the path of a cell during differentiation can be interpreted using the dynamics of the underlying gene regulatory network. The incorporation of time-delayed feedback in these networks leads to oscillatory states and trans-differentiation.



**Bivash Kaity,
IIT Bombay**



**Ajoy Maji,
IIT Bombay**



**Jahir Ahmed
Pune
University**



**Ratan Sarkar, IISc
Bangalore**



**Subhankar Roy,
IISER Kolkata**



**Buddhapriya Chakrabarti,
University of Sheffield**

Funding: DST, IIT-B

