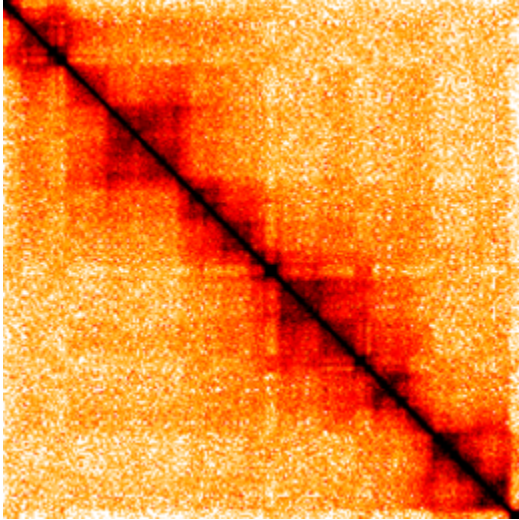


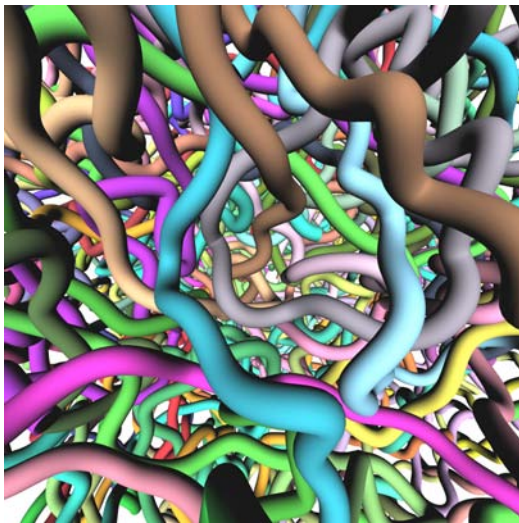
3D genome: a double seminar

<http://journals.plos.org/plosbiology/article?id=info:doi/10.1371/journal.pbio.003015>



Noam Kaplan, U.Mass Medical School Encoding and decoding 3D genome organization

Hi-C is a recent molecular biology technique that allows simultaneous measurement of millions of physical pairwise interactions between DNA loci across the genome. After an overview of Hi-C technology I will describe how we can proceed beyond descriptive statistics to more mechanistic predictive models. I will focus on structures known as Topological Associating Domains (TADs), which may constitute a new conserved higher-order chromatin structure that defines elementary regulatory units. Specifically, I will propose a probabilistic model which both explains TAD structure and can predict the effects of genomic rearrangements on TAD structure and gene regulation.



Courtesy of E.Likhtman



Alexander Grosberg, New York U. Nuclear Chromodynamics

The human cell nucleus contains two meters of DNA. Swollen chromosomes have an interface: chromosomes occupy separate territories, unlike any regular polymer system, where chains intermix. I will argue that territorial segregation is in fact a generic property of a concentrated system of polymers with topological constraints, the latter arising simply from the fact that DNA is too long. I will further argue that a useful insight is gained by considering a concentrated system of unconcatenated rings. These indeed form territories, with interesting fractal properties of the surfaces separating them. I will show that fractal dimension of these surfaces is directly related to the results of HiC measurements. Active (driven) hydrodynamics of chromatin and dynamics of rings will be also discussed, if time permits.



Monday, January 11, 1:45-5:00 pm,
Kohn Hall Auditorium
More at sheets16.wikispaces.com

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