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Forces shaping chromatin in the nucleus

Vittore Scolari

(Institut Curie, CNRS «Dynamique du noyau», CNRS «Physico-Chimie Curie»)

Introduction, prof. **Guido Raos** (Politecnico di Milano, DCMIC)

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live | online

link will be emailed to registered participants

Registration Form

The physics of genome dynamics is an emerging field at the interface between biology, bioinformatics and polymer physics. The description of how chromatin is folded inside the nucleus is necessary to understand its functions. Being a dynamic and well organised object, it requires innovative out-of-equilibrium modelling approaches. The cell nucleus, from the most basic chemical reactions to evolutionary timescales of billions of years, strives to counteract disorder in order to be healthy, consuming energy, being alive. My objective is to develop a physical theory able to describe intranuclear dynamics, with the ambition of reaching a quantitative understanding of the two essential processes of gene regulation and DNA recombination. In particular, I investigate: (i) how 3D chromosome conformation is shaped by specific biological processes. Particularly loop extrusion and the formation of foci – or phases – for heterochromatin and transcription, and (ii) the fundamental implications of thee mechanisms on control and reliability of the biological processes of transcriptional induction, gene silencing, and evolution. In this talk I will present my original approach to simulate loop extrusion, an active process central in regulating the shape of chromatin in vivo. The “gold standard” currently uses molecular dynamics simulations: while very flexible, this limits our possibility (i) to explore the parameter space in an efficient manner and (ii) to dissect the observed effects under the lenses of a coherent analytical theory. I will show my original approach that exploits the analytical solution of the Einstein-Smoluchowski equation for the Rouse model affected by the action of extruders simulated in 1D.

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