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Physical biology of chromatin dynamics

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Cellular differentiation occurs during the development of multicellular organisms and leads to the formation of many different tissues where gene expression is modulated without modification of the genetic information. These modulations are in part encoded by chromatin-associated proteins or biochemical tags that are set down at the chromatin level directly on DNA or on histone tails, the so-called epigenome. These markers are directly or indirectly involved in the local organization and structure of the chromatin fiber, and therefore may modulate the accessibility of DNA to transcription factors or enzymatic complexes, playing a fundamental role in the transcriptional regulation of gene expression. Statistical analysis of the repartition of this epigenomic information along the chromosomes have shown that genomes of higher eukaryotes are linearly partitioned into domains of functionally distinct chromatin states. In particular, experimental evidence has shown that the pattern of chromatin markers along chromosomes is strongly correlated with the 3D chromatin organization inside the nucleus. This suggests a coupling between epigenomic information and large-scale chromatin structure. In this presentation, I will review our efforts to understand the physical and biological mechanisms behind this coupling. Using polymer and statistical physics, we develop models of chromatin organization and epigenomic regulation in close collaboration with experimentalists. Based on original physical concepts, these models allow us to explore different aspects of the 3D-1D coupling of chromatin from drosophila to human.

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