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Modeling the human genome through polymer physics

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In the nucleus of cells, chromosomes have been discovered to self-organize into a complex spatial architecture that serves vital functional purposes as, for instance, genes have to establish specific physical contacts with their distal DNA regulators to control transcriptional activities. However, how the system self-assembles to shape the folding of our genome and its functions is only poorly understood. In this talk, I discuss principled models of interacting polymers from statistical mechanics to investigate the mechanisms whereby distal DNA sequences recognise and interact with each other. Those theories are validated against independent experiments, opening to new tools for real-world applications, such as the prediction of the effects of disease-associated mutations, linked to congenital disorders or cancer, on genome 3D structure.

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