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Title: "From 1D to 3D and back: Explaining and exploiting genome structure"

Abstract: Hi-C is a molecular technique that allows high-throughput genome-wide measurement of pairs of loci that physically interact in vivo. In recent years, Hi-C experiments have led to the discovery of Topologically Associating Domains (TADs). TADs are Hi-C interaction patterns that have been suggested to represent a fundamental higher-order organization of chromatin such that each TAD constitutes an isolated regulatory micro-environment. However, it is currently unclear what TADs exactly are and how they are encoded in the 1D genome. In the first part of my talk, I will present recent results that may offer some answers to these questions. In the second part of my talk, I will present how, by using Hi-C, we can exploit our understanding of fundamental properties of chromatin organization to solve several outstanding problems in the field of genome assembly.