Biophysical principles for chromosome organisation

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I will describe some biophysical principles for genome organisation arising from Brownian dynamics simulations of chromatin fibres and whole chromosomes interacting with bivalent of multivalent (architectural) chromatin-binding proteins (transcription factors).

Chromatin binding mediates cooperative interactions between proteins which naturally leads to the creation of clusters. Such clusters are strikingly similar to some of the "nuclear bodies" and transcription factories found inside the nucleus of eukaryotic organisms. The model also yields chromatin domains and an organisation into active and inactive compartments which recapitulates that observed in high-throughput chromosome conformation capture experiments, Hi-C.

Recent experiments have shown that some chromosomal loops, involving the CTCF and cohesin proteins, show a puzzling bias favouring a convergent arrangement of the CTCF binding sites on the base of the loop. This bias is accounted for by the recent "loop extrusion model" which postulates a motor activity associated to cohesin. We show that the bias can also be understood by including in our simulations molecular slip links representing the cohesin complexes, in the absence of any motor activity.