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Abstract for an Invited Paper  
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**Polymer models of chromosome (re)organization**

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Chromosome Conformation Capture technique (Hi-C) provides comprehensive information about frequencies of spatial interactions between genomic loci. Inferring 3D organization of chromosomes from these data is a challenging biophysical problem. We develop a top-down approach to biophysical modeling of chromosomes. Starting with a minimal set of biologically motivated interactions we build ensembles of polymer conformations that can reproduce major features observed in Hi-C experiments. I will present our work on modeling organization of human metaphase and interphase chromosomes. Our work suggests that active processes of loop extrusion can be a universal mechanism responsible for formation of domains in interphase and chromosome compaction in metaphase.