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Diffusion-driven looping provides a consistent framework for chromatin organization DIETER HEERMANN, MANFRED BOHN, University of Heidelberg — Chromatin looping seems to play a dominant role both in transcriptional regulation as well as in chromatin organization and has been assumed to be mediated by long-range interactions in many polymer models. However, it remains a crucial question which mechanisms are necessary to make two chromatin regions become co-located, i.e. have them in spatial proximity. We demonstrate that the formation of loops can be accomplished solely on the basis of diffusional motion. The probabilistic nature of temporary contacts mimics the effects of proteins, e.g. transcription factors, in the solvent. We establish testable quantitative predictions by deriving scale-independent measures for comparison to experimental data. In this Dynamic Loop (DL) model, the co-localization probability of distant elements is strongly increased compared to linear non-looping chains. The model correctly describes folding into a confined space as well as the experimentally observed cell-to-cell variation. Most importantly, at biological densities, model chromosomes occupy distinct territories showing less inter-chromosomal contacts than linear chains. Thus, dynamic diffusion-based looping, i.e. gene co-localization, provides a consistent framework for chromatin organization in eukaryotic interphase nuclei.

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