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Inferring chromatine structure from m-FISH data: A unified picture from human and mouse cells

We analyze multiplexed fluorescence in situ hybridization (m-FISH) data for human and mouse cell lines. The m-FISH technique uses fluorescently-labeled single-stranded probes which hybridize to specific chromosomal regions, thereby allowing the measurement of the spatial positions of up to tagged sites for several thousands of interphase chromosomes. Our analysis focuses on a wide range of different cell lines and two distinct organisms and provides a unified picture of chromatin structure for scales ranging from 5 kb (kilobases) up to 2 Mb (megabases), thus covering a genomic region of almost three orders of magnitude. Confirming recent analysis [Remini et al., Phys. Rev. E 109, 024408 (2024)], we show that there are two characteristic arrangements of chromatin referred to as phase α (crumpled globule) and phase β (looped domain) and discuss the physical properties of these phases. We show that a simple heterogeneous random walk model captures the main behavior observed in experiments and brings considerable insights into chromosomal structure.

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