

Internal Webinar

Computational Elucidation of self-organization of E. coli chromosome underlying HI-C data

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The chromosome of archetypal bacteria *E. coli* is riddled with multifaceted complexity and its multiscale organization is slowly getting recognised. The emergence of chromosome conformation capture techniques such as Hi-C and super-resolution microscopy are providing newer ways to explore chromosome organisation, chromosome dynamics and its effect on gene expression. Here we combine a beads-on-a-spring polymer model and recently reported high-resolution Hi-C data for *E. coli* chromosome to develop a comprehensive model of its chromosome at 5 kbp resolution. The Hi-C data-integrated chromosome model elucidates a self-organised structure of *E. coli* chromosome into multiple macrodomains within ring-like architecture, with *oriC* locus located at the mid-cell position. The model also predicts that a majority of the genetic loci are linearly organised, except *Ter* macrodomain. The distance profiles, extracted from the model are in quantitative agreement with data from FISH and DNA-recombination assay experiments. Additionally, a genome-wide fine-grained radius of gyration map captures multiple chromosomal interaction domains (CIDs) and identifies the location of *rrn* operons. Finally, via a mutation-based analysis, the model quantifies the role of multiple nucleotide-associated proteins (NAPs) like *Hu*, *Fis* and *MatP* in controlling the chromosome architecture.

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