

Seminar

Integrative modelling of *Escherichia coli* chromosome and cytoplasm

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E. coli, despite its seemingly simple appearance and a genome much smaller than the human genome, presents a complex challenge in understanding the organisation of its single circular chromosome within a sub-micron-sized volume. In this presentation, I will discuss our endeavours to illuminate the intricacies of *E. coli*'s chromosome organisation through in-silico modelling of its in-vivo configuration. We establish a comprehensive modelling protocol, employing a polymer-physics based model, and conduct simulations to generate a data-enriched ensemble of chromosome conformations at a 5000 base pair resolution. Rigorous validation of the model and protocol is followed by the capture and in-depth analysis of macrodomain segregation and loci movement during chromosome replication. Our exploration extends to the investigation of the roles played by two nucleoid associated proteins in chromosome organisation. Subsequently, we refine the model by incorporating more extensive experimental data, achieving hyper-branched chromosome conformations at a resolution of 500 base pairs. Utilising this refined model, we challenge the widely accepted assumption that ribosomes act as inert-crowders to the nucleoid, disproving this notion. Lastly, we delve into the localisation patterns of transcribing and non-transcribing regions of the chromosome, re-examining chromosome-ribosome segregation to decipher how these preferential localisations contribute to the bacterium's survival and metabolic optimisation.

Friday, May 24th 2024

16:00 Hrs (Tea / Coffee 15:45 Hrs)

Auditorium, TIFR-H