**Tata Institute of Fundamental Research**
Survey No. 36/P, Gopanpally Village, Serilingampally, Ranga Reddy Dist., Hyderabad – 500 046

# Seminar

## Scaling and memory in the epigenetic regulation of gene expression

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Multicellular organisms utilise epigenetic modifications of their genomes in order to develop different cell types starting from an undifferentiated cell. The last few decades of research focused on the role of DNA methylation in controlling gene expression during development. The DNA methylation on gene bodies has been demonstrated to repress gene expression by obstructing the movement of polymerases on the gene. At the same time, the polymerase bound on the gene in turn impacts the methylation landscape of the gene by inhibiting the binding of the methyltransferases/methyl binding proteins to the CpG's. In order to investigate the nature of these interactions, we take recourse to the scM&T-seq data providing both transcriptome and DNA-methylation profiles in individual mouse embryonic stem cells. Quantification of transcription elongation rate using a stochastic gene expression model shows a scaling relation between the length of genes and transcription elongation rates. The average methylation levels of the genes are also found to scale with the length of genes. A biophysical model suggests that the collective movement of multiple polymerases on the gene mediates the information of local nearest neighbour interactions to extended regions of the genome which finally leads to the observed scaling between the DNA methylation and gene length. Our study offers a data driven general theoretical framework to delineate the role of interplays between DNA methylation and gene expression in entailing scaling and memory in epigenetic patterns.

***Friday, Aug 18th 2023***

***4:00 PM (Tea / Coffee 03.45 PM)***

***Auditorium, TIFR-H***