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

Seminar

Expansion in situ Genome Sequencing (ExIGS): linking nanoscale nuclear architecture to genome function & aging

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The 3D nanoscale architecture of the genome determines its function, and its disruption is a hallmark of aging and disease. Existing imaging and genomics methods fail to link specific nanoscale defects to genomic consequences at single-cell resolution. Here we introduce Expansion in situ Genome Sequencing (ExIGS), which combines expansion microscopy with in situ DNA sequencing to simultaneously read DNA sequences and visualise nuclear proteins in physically expanded nuclei. In Hutchinson–Gilford Progeria Syndrome fibroblasts, ExIGS reveals that nanoscale lamin defects create local hotspots of aberrant chromatin localisation proximal to internal lamin nanotubes and suppress transcription which leads to erosion of cell identity. More broadly, ExIGS offers a generalised platform to map and quantify nanoscale nuclear defects and connect them to gene regulation across tissues.

Tuesday, Dec 2nd 2025

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

Auditorium, TIFRH