Center for Theoretical Biological Physics

SEMINAR

"How the Genome Folds"

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12:30 - 1:30 PM

BRC, 10th Floor, Rm 1060 A/B

Abstract:

I describe Hi-C, a novel technology for probing the three-dimensional architecture of whole genomes. Developed together with collaborators at the Broad Institute and UMass Medical School, Hi-C couples proximity-dependent DNA ligation and massively parallel sequencing.

Our lab employs Hi-C to construct spatial proximity maps of the human genome. Using Hi-C, it is possible to confirm the presence of chromosome territories and the spatial proximity of small, gene-rich chromosomes. Hi-C maps also reveal an additional level of genome organization that is characterized by the spatial segregation of open and closed chromatin to form two genome-wide compartments. At the megabase scale, the conformation of chromatin is consistent with a fractal globule, a knot-free conformation that enables maximally dense packing while preserving the ability to easily fold and unfold any genomic locus. The fractal globule is distinct from the more commonly used globular equilibrium model. Our results demonstrate the power of Hi-C to map the dynamic conformations of whole genomes.