

Chromatine 3D structure and Hi-C data analysis

Abstract

The three-dimensional conformation of the genome in the nucleus has a major impact on its functioning, affecting key processes such as cell differentiation, embryonic development and organism survival in animals and plants. It is well known that the 3D structures regulating these processes are organized hierarchically at various scale levels: DNA loops, topological domains, genomic compartments, chromosomal territories. However, little is known about the multi-scale dynamics of these structures and their interactions, limiting our understanding of the links between genome structure and function. Recent advances in molecular biology have changed the way we can study the spatial organization of chromosomes, thanks in particular to the Hi-C (High-throughput chromosome conformation capture) sequencing technology. A particular feature of Hi-C experiments is that they generate data in the form of arrays, counting interactions between genome regions close to each other in the 3D space of the nucleus. Analysis of such a matrix of interactions enables the detection of 3D structures (loops, domains, compartments) present within a biological sample, and provides new interdisciplinary challenges in cell biology, mathematics and statistics, bioinformatics and computer science, or polymer physics.

The aim of the mini-symposium is to bring together an interdisciplinary community to promote scientific exchange around the comparative analysis of 3D genomics data, in order to present the challenges and methods of Hi-C data analysis to better understand the links between genome structure and function.

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Program

14h-14h15 : Sylvain Foissac (GenPhySE, INRAE, Toulouse) & Jean-Marc Victor (LPTNC, CNRS, Paris)

Presentation of ChrocoNet and GDR ADN networks on 3D chromatine structure

14h15-14h50 : Yad Ghavi-Helm (IGFL, CNRS, Lyon)

Regulating gene expression in 3D during Drosophila development

14h50-15h25 : Salari Hossein (LPENS, CNRS, Lyon)

Chromosome stiffening with loop-extrusion activity

15h25-16h00 : Jacques Serizay (Institut Pasteur X ENS, Paris)

Integrating Hi-C data in multi-omics studies

