

# *Unveiling the Dynamic Nuclear Landscape: A Mini-Course on 3D Human Genome Modelling.*

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**Keywords:** 3D genome organization, Genome architecture, Chromatin conformation capture, ChIA-PET, long range chromatin interaction, chromatin spatial organization, CTCF, RNA polymerase II (RNAPII), Multidimensional scaling, graph distance, 3D modeling, multiscale properties, polymer physics.

**Abstract:** The Mini-Course on 3D Human Genome Modelling aims to provide participants with a comprehensive understanding of the cutting-edge techniques and computational approaches used in unraveling the complex spatial organization of chromatin within the human nucleus at the population scale. As advancements in genomic research have revealed the importance of higher-order chromatin structure in gene regulation, this course serves as a gateway to the fascinating realm of 3D chromatin modelling.

The Mini-Course on 3D Human Genome Modelling, led by Dariusz Plewczynski, aims to provide participants with a comprehensive understanding of cutting-edge techniques and computational approaches used in unraveling the complex spatial organization of chromatin within the human nucleus at the population scale. By exploring principles and methodologies behind 3D chromatin modeling, participants will delve into key concepts such as chromatin interactions, loop extrusion, and genome architecture. The course covers experimental and computational techniques including Hi-C, ChIA-PET, imaging methods, molecular dynamics simulations, and polymer models. Participants will gain hands-on experience with popular tools, datasets, and software used for 3D chromatin modeling, enabling them to interpret and visualize spatial chromatin contacts and 3D models.

The mini-course aims to equip participants with a solid foundation in nuclear biology and computational genomics, enabling them to understand the spatiotemporal organization of chromatin, and the role of chromatin structure in gene regulation, and contribute to the development of novel hypotheses and research directions. The course includes a detailed review of four papers selected to present a complete story on 3D chromatin modeling. These papers discuss the application of the ChIA-PET technique to study the 3D genome architecture of human B-lymphoblastoid cells, the introduction of 3D-GNOME as a computational pipeline for simulating 3D genome structures, the use of 3D-GNOME as a web service for generating and analyzing 3D genome structures, and the impact of genetic variants on chromatin folding and gene transcription regulation at the population scale.

By showcasing advancements in 3D chromatin modeling, from experimental techniques to computational tools, this mini-course highlights the significance of understanding genome organization and its implications in development and gene regulation. Participants will gain valuable insights into the complexity of genome organization and function, contributing to advancements in the field of 3D chromatin modeling.