**Title:** *Mechanisms of 3D chromatin re-structuring in healthy and pathogenic genomes*

**Abstract**

*The research focuses on understanding quantitatively the structural re-arrangements of genome architecture associated to pathogenic contexts. Within the cell nucleus of eukaryotic organisms, chromosomes are organized in a complex, non-random three-dimensional (3D) spatial structure, which is intimately linked to vital functional purposes. Indeed, a correct folding allows an efficient communication between genes and their distal regulatory elements while, if altered, can cause severe diseases.*

*In this project, we will integrate omics databases with computational approaches based on Physics, in particular Polymer theory, combined with Molecular Dynamics simulations and Machine Learning to quantitatively investigate the complexity of 3D organization of real genomes and how such structure is rewired during disease development, with a special focus on viral infections. In this way, accurate and descriptive computational models will be developed to realistically describe those systems and investigate the physical-chemical mechanisms, such as phase-separation of molecular aggregates and polymer adsorption on nuclear membrane, that regulate them.*

*Overall, taking advantages of such models, we will be able to understand how the alteration of these physical processes can be linked to the genome activity alteration in viral infected genomes and can be used to investigate, as main case of study, aberrant looping and chromatin re-wiring caused by SARS-CoV-2 and avian Influenza A H5N1 virus.*

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