

Markov state modeling of chromatin hierarchical 3D reconstruction

Enrico GUARNERA - *Bioinformatics Institute - Agency for Science, Technology and Research, Singapore*

Chromatin is the result of the packing of two meters long DNA into few micrometers constraint of cell nucleus. With the development of the chromosome conformation capture protocols, it has become possible to study chromatin interactions between distant genomic loci and conformational organization. In this talk I will show how to explore chromatin organization by exploring the interaction network between genomic loci associated with Hi-C experimental data. Combining a Machine Learning approach with Energy Landscape theory, a Markov process is introduced to describe the random motion of traveling probes in chromatin media, mimicking the exploration of a biomolecules involved in chromatin function. By studying the dynamical properties of the associated Markov State Model, a multiscale description of the chromatin hierarchical structure is obtained. As a result, a stochastic embedding procedure is introduced for the multiscale chromatin 3D reconstruction, which allows to analyze and discuss chromatin conformational hallmarks in health and disease.