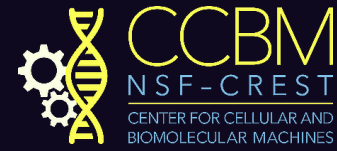




Soft Living Active and Adaptive Matter



Data-driven reconstruction of 3D genome from experimental data

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Abstract:

The principles that govern the organization of genomes, which are needed for a deeper understanding of how chromosomes are packaged and function in eukaryotic cells, could be deciphered if the three-dimensional (3D) structures are known. Recently, single-cell imaging experiments have determined the 3D coordinates of a number of loci in a chromosome. Here, we introduce a computational method, based on the maximum entropy principle, with experimental pair-wise distances between loci as constraints, to generate a unique ensemble of 3D chromatin structures. Using the ensemble of structures, we quantitatively account for the distribution of pair-wise distances, three-body co-localization and higher-order interactions. We demonstrate that our method can be applied to both small length-scale and chromosome-scale imaging data to quantify the extent of heterogeneity and fluctuations in the shapes on various length scales. Furthermore, we show that our method can be extended to predict the changes in 3D structures from structural variations. Our method also reveals quantitative differences between the 3D structures inferred from Hi-C and the ones measured in imaging experiments. Finally, the physical interpretation of the parameters extracted from our method provides insights into the origin of phase separation between euchromatin and heterochromatin domains.

Date:
09/26/2022

Time:
9:00 AM-10:15 AM (PT)
12:00 PM-1:15 PM (ET)

About the speaker:

Dr. Guang Shi is a postdoctoral research associate at the University of Illinois at Urbana-Champaign. He is broadly interested in the physical principles that underlie genome organization and biomolecular condensates and their biological functions. He is currently working with Prof. Kenneth S. Schweizer on the phase behavior and rheology of biomolecular condensates using theoretical approaches.

Dr. Shi earned his Ph.D. in Biophysics from the University of Maryland at College Park, under the supervision of Prof. Devarajan (Dave) Thirumalai, where he studied the structures and dynamics of the genome using both coarse-grained modeling and data-driven approaches.



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