Computational methods to elucidate chromatin topological structures using 3D genomic maps

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Abstract: T The chromosome conformation capture (3C) technique and its variants have been employed to reveal the existence of a hierarchy of structures in three-dimensional (3D) chromosomal architecture, including compartments, topologically associating domains (TADs), sub-TADs and chromatin loops. In this talk, I am going to introduce three methods on deciphering 3D genomic maps: (1) a mixed-scale dense convolutional neural network model (HiCMSD) to enhance low-resolution Hi-C interaction map for deciphering accurate multi-scale topological structures; (2) a generic and efficient method to identify multi-scale topological domains (MSTD), including cis- and trans-interacting regions, from a variety of 3D genomic datasets; (3) a powerful and robust circular trajectory reconstruction tool CIRCLET without specifying a starting cell for resolving cell cycle phases of single cells by considering multi-scale features of chromosomal architectures.

[1] Ye Y, Gao L, **Zhang S**. MSTD: an efficient method for detecting multi-scale topological domains from symmetric and asymmetric 3D genomic maps. **Nucleic Acids Research** (2019), 47: e65.

[2] Ye Y, Gao L, **Zhang S**. Circular trajectory reconstruction uncovers cell-cycle progression and regulatory dynamics from single-cell Hi-C maps. **Advanced Science** (2019), doi:10.1002/advs.201900986