3D Genome Structure Modeling by Lorentzian Objective Function

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ABSTRACT
Reconstructing 3D structure of a genome from chromosomal conformation capturing data such as Hi-C data has emerged as an important problem in bioinformatics and computational biology in the recent years. In this talk, I will present our latest method that uses Lorentzian function to describe distance restraints between chromosomal regions, which will be used to guide the reconstruction of 3D structures of individual chromosomes and an entire genome. The method is more robust against noisy distance restraints derived from Hi-C data than traditional objective functions such as squared error function and Gaussian probabilistic function. The method can handle both intra- and inter-chromosomal contacts effectively to build 3D structures of a big genome such as the human genome consisting of a number of chromosomes, which are not possible with most existing methods.

We have released the Java source code that implements the method (called LorDG) at GitHub (https://github.com/BDM-Lab/LorDG), which is being used by the community to model 3D genome structures. We are currently further improving the method to build very high-resolution (e.g. 1KB base pair) 3D genome and chromosome models.

CCS CONCEPTS  
• Bioinformatics → Genomics

KEYWORDS
3D genome; modeling; optimization; Lorentzian function; chromosomal conformation capturing; Hi-C

ACM Reference format:
T. Trieu and J. Cheng. 2017. 3D Genome Structure Modeling by Lorentzian Objective Function. In Proceedings of the 8th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics, Boston, MA, USA, August 2017, 1 page.