Do Single-Cell Hi-C Data Follow a Power-Law Decay?

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Hi-C, a chromosome conformation capture-based method, allows researchers to interrogate chromatin interactions between any two genomic loci in a bulk of cells and study the spatial arrangement of chromatin collectively, which plays crucial roles in gene expression regulation, DNA replication, and repair. With the development of single-cell technologies, single-cell Hi-C was developed to study chromatin three-dimensional structure at the single-cell resolution. With the aid of visual diagnostics, it is generally believed that the frequency of bulk Hi-C data and genomic distance follow a power law decay. However, for single-cell Hi-C data this property has been underexplored, much less rigorously examined by quantitative statistical analysis. In this research, the frequency of chromatin interactions and genomic distance in single cells is analyzed. This is important because it provides an insight into the development of new computational methods on single-cell Hi-C data and improves our understanding of the organization and function of the genome.

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