

HONG KONG INSTITUTE FOR DATA SCIENCE POSTDOC ASSOCIATES AND STUDENTS SEMINAR

A Lightweight Framework for Chromatin Loop Detection at the Single-Cell Level

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Abstract

Single-cell Hi-C (scHi-C) has made it possible to analyze chromatin organization at the single-cell level. However, scHi-C experiments generate inherently sparse data, which poses a challenge for loop calling methods. The existing approach performs significance tests across the imputed dense contact maps, leading to substantial computational overhead and loss of information at the single-cell level. To overcome this limitation, a lightweight framework called scGSLoop is proposed, which sets a new strategy for scHi-C loop calling by adapting the training and inferencing strategies of graph-based deep learning to leverage the sequence features and 1D positional information of genomic loci. With this framework, sparsity is no longer a challenge, but rather an advantage that the model leverages to achieve unprecedented computational efficiency. Compared to existing methods, scGSLoop makes more accurate predictions and is able to identify more loops that have the potential to play regulatory roles in genome functioning. Moreover, scGSLoop preserves single-cell information by identifying a distinct group of loops for each individual cell, which not only enables an understanding of the variability of chromatin looping states between cells, but also allows scGSLoop to be extended for the investigation of multi-connected hubs and their underlying mechanisms.

Biography

Fuzhou Wang is a Ph.D candidate in the Department of Computer Science at City University of Hong Kong, where he is advised by Dr. Ka-Chun Wong. His research interests reside at the intersection of Regulatory Genomics and Machine Learning. Specifically, Fuzhou's work has focused on investigating the three-dimensional organization of the human genome and its role in regulatory functions. To achieve this, he develops cutting-edge computational tools for analyzing genome-wide 3D genomics data. He also explores efficient deep learning methods to gain insights into the dynamics of genome structures latent within large-scale single-cell genomics data. With the single-cell lens, Fuzhou aims to shed light on the interplay of genome organizations in different biological processes.