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Boost-HiC: computational enhancement of long-range contacts in chromosomal contact maps

Abstract
Motivation

Genome-wide chromosomal contact maps are widely used to uncover the 3D organization of genomes. They rely on collecting millions of contacting pairs of genomic loci. Contacts at short range are usually well measured in experiments, while there is a lot of missing information about long-range contacts.
Results

We propose to use the sparse information contained in raw contact maps to infer high-confidence contact counts between all pairs of loci. Our algorithmic procedure, Boost-HiC, enables the detection of Hi-C patterns such as chromosomal compartments at a resolution that would be otherwise only attainable by sequencing a hundred times deeper the experimental Hi-C library. Boost-HiC can also be used to compare contact maps at an improved resolution.
Availability and implementation

Boost-HiC is available at https://github.com/LeopoldC/Boost-HiC.

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