MetaHiCNet: A Platform for Normalizing and Visualizing Microbial Hi-C Interaction Networks

This website is free and open to all users and there is no login requirement.

Input Data:

Two required files (Contig Information and Raw Contact Matrix) and two optional files (Binning Information and Taxonomy Information) are expected. The first three files can be directly obtained from common Meta Hi-C analysis pipelines, while the taxonomy information file can be generated using genome annotation tools like GTDB-TK.

Output:

Users can check data quality by access processed interaction matrices and Pearson correlation metrics. A set of dynamic, interactive visualizations (e.g., histograms, treemaps, Cytoscape-compatible graphs) can help user explore microbial Hi-C networks in various taxonomic level.

Processing Method:

MetaHiCNet offers multiple normalization and spurious contacts removal methods [1-4] for adjusting raw Hi-C contact matrices, aiming to reduce systematic biases. Visualizations are generated using Cytoscape for in-depth network analysis [5].

Complete Citations:

[1] Baudry, L., Foutel-Rodier, T., et al. (2019). MetaTOR: a computational pipeline to recover high-quality metagenomic bins from mammalian gut proximity-ligation (meta3C) libraries. Frontiers in genetics, 10, 753.  
[2] DeMaere, M. Z., & Darling, A. E. (2019). bin3C: exploiting Hi-C sequencing data to accurately resolve metagenome-assembled genomes. *Genome biology*, 20, 46.  
[3] Du, Y., & Sun, F. (2023). MetaCC allows scalable and integrative analyses of both long-read and short-read metagenomic Hi-C data. *Nature Communications*, 14, 6231.  
[4] Du, Y., Laperriere, S. M, et al. (2022). Normalizing metagenomic Hi-C data and detecting spurious contacts using zero-inflated negative binomial regression. *Journal of Computational Biology*, 29 (2), 106-120.   
[5] Kohl, M., Wiese, S., et al. (2011). Cytoscape: software for visualization and analysis of biological networks. *Data mining in proteomics: from standards to applications*, 291-303.

Keywords:

MetaHi-C Contact Normalization  
Spurious Contact Detection  
Microbial Network Visualization