**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:**  
MetaHiCNet accommodates both new and returning users with tailored input requirements:

* **New Users:** The platform requires four key input files:  
  a) **Contig Information File:** Details about contigs.  
  b) **Raw Contact Matrix File:** Hi-C contact data between contigs.  
  c) **Binning and Category Information File:** Bin assignments and contig categories (e.g., virus, plasmid, chromosome)..  
  d) **Taxonomy File:** Taxonomic annotations or custom labels for bins.
* **Returning Users:** Upload previously generated normalized or unnormalized files to retrieve visualizations.

**Output:**  
The output is a dynamic visualization of microbial Hi-C interaction networks. This includes histograms, treemaps, and Cytoscape graphs that represent relationships between microbial elements at various taxonomic levels. The visualizations allow users to explore and interact with the data, such as selecting and filtering by taxonomic levels, bins, or contigs.

**Processing Method:**  
The app implements a three-step workflow:  
a) **Preparation:** Validates user inputs for consistency.  
b) **Normalization:** Applies different normalization techniques to enhances interpretability and reliability.  
c) **Visualization:** Interactive charts and graphs provide multifaceted analyses of microbial interactions.

**Complete Citations:**  
(Need to be updated.)

**Keywords:**

* Microbial Network Visualization
* Meta Hi-C Interaction Data
* Data Normalization
* Interactive Graphs

**Software and Third-Party Dependencies:**  
MetaHiCNet uses several open-source libraries, including Dash, Redis, and Cytoscape for visualization. All libraries are free and open to use, ensuring full accessibility and compliance with open-source standards.