

PERSONAL DASHBOARD, MODULES & GUIDES

Once a job has been submitted to MetagenoNets, user is taken to a personal dashboard. Each dashboard is tagged to a trackable Dashboard ID, which is displayed on the top.

There are 4 analytical and visualization modules in MetagenoNets:

1. Categorical Network Analysis
2. Integrated (multi-omic) Network Analysis
3. Network Composition Analysis
4. Network Property Analysis

Info tags

Access the (i) tags at various sections of the modules to get assistive information

Multi-modular

Use this menu panel for Accessing multiple analysis and visualization Modules in the personal dashboard

All plots generated in MetagenoNets are **downloadable as Hi-Res images.**

PERSONAL DASHBOARD
Dashboard ID: 7909804a

CATEGORICAL NETWORKS

CHOOSE NETWORK TO CREATE [v] UPDATE

Parameters [i] UPDATE PARAMETERS

Algorithm [i] NAMAP [v]

INTEGRATED NETWORKS

Network [v] Module specific guides

Overlay Node MetaData [v]

VENN DIAGRAMS

Pan, zoom, reset Play with layouts

Simple Categorical

PROPERTIES

Global Property Value

Nodes Edges Diameter Density Avg. Degree

Change Layout

HIER CONC CIRC GRID COSE RAND

FILTRATION AND NORMALIZATION

Status terminal: [x]

Module specific guides

A step-by-step process guide is provided in each module (for executing a task), along-with basic plot-guides

Status terminal

Status terminal helps get Information about task outcomes

Dynamic data management

- Use this floating button to access Various filtration, normalization and transformation methods
- This option may be used multiple times, at any point in time.

Original: 108 Features

Current: 64 Features

EIGENVECTOR

Download Data

generate.

press update

goto Integrated

to be integrated

Change method [v]

Prevalence: 0.0001

Occurrence: 10

UPDATE

CLOSE

MODULE1: CATEGORICAL NETWORKS

MetagenoNets creates group level networks for each category (also called Environment) in the supplied meta-data . For example, for Geography environment, categorical groups can be India, US, Japan, Europe etc. MetagenoNets automatically infers all possible categorical groups in the meta-data and provides options to perform network analysis on each of such groups.

TRIBAL UPDATE

Parameters UPDATE PARAMETERS

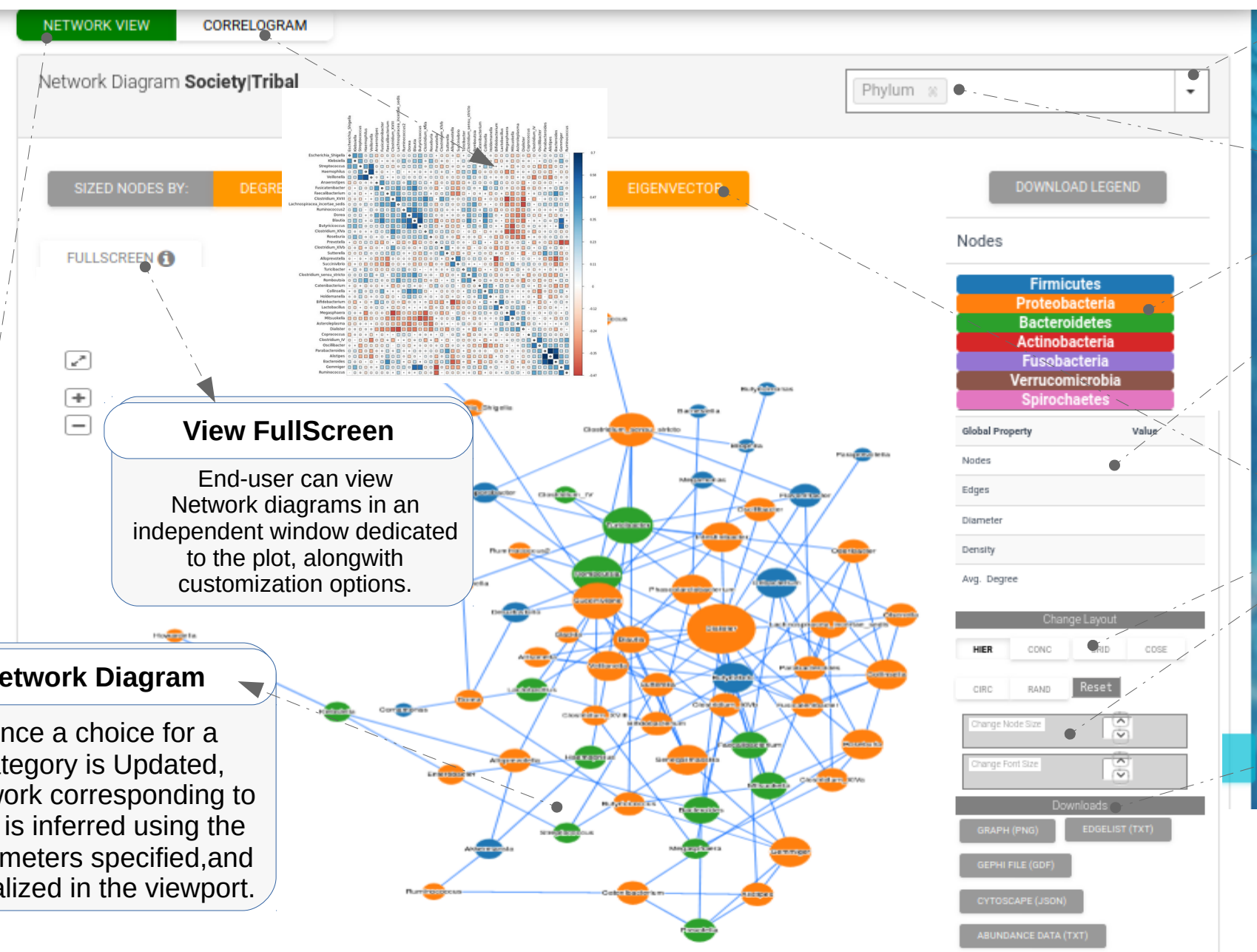
Algorithm NAMAP W/ SPEARMAN

p-value

Iterations

Corr. cutoff CRITICAL-R

Refer Next Slide



Node meta-data
Dropdown option to overlay Node meta-data

Overlay Node MetaData
Median_Abandance
Phylum

Global Properties
Tabulated summary of the key global Properties of the network being analysed.

Customizations

- Layouts
- Property mapping
- Node and Font sizes

Download Options

- Plot Downloads
- Cytoscape and Gephi compatible files
- Edgelist
- Abundance Data

View FullScreen
End-user can view Network diagrams in an independent window dedicated to the plot, alongwith customization options.

Network Diagram
Once a choice for a category is Updated, Network corresponding to that is inferred using the parameters specified, and visualized in the viewport.

Status terminal
Status terminal helps get Information about task outcomes

```
Status terminal:
Network processed!
```

TRIBAL

Parameters	<input type="button" value="UPDATE PARAMETERS"/>
Algorithm	NAMAP W/ SPEARMAN
p-value	<input type="range"/>
Iterations	<input type="range"/>
Corr. cutoff	CRITICAL-R

TRIBAL

Environment: Society

- Tribal
- Urban

Environment: Geography

- Assam
- Andhra
- Sikkim
- Manipur
- Ahmedabad

Environment: Sex

- Male
- Female

Environment: Diet

- Non_Vegetarian
- Vegetarian
- Unknown

Categorical Networks

Comprehensive analysis and visualization of all Categorical networks identified through metadata

Update Parameters

Use this option to propagate the chosen options across all the modules of MetagenoNets. If not clicked, the chosen parameters will be applicable only for the current module.

Algorithm

NAMAP W/ SPEARMAN

p-value

Iterations

Corr. cutoff

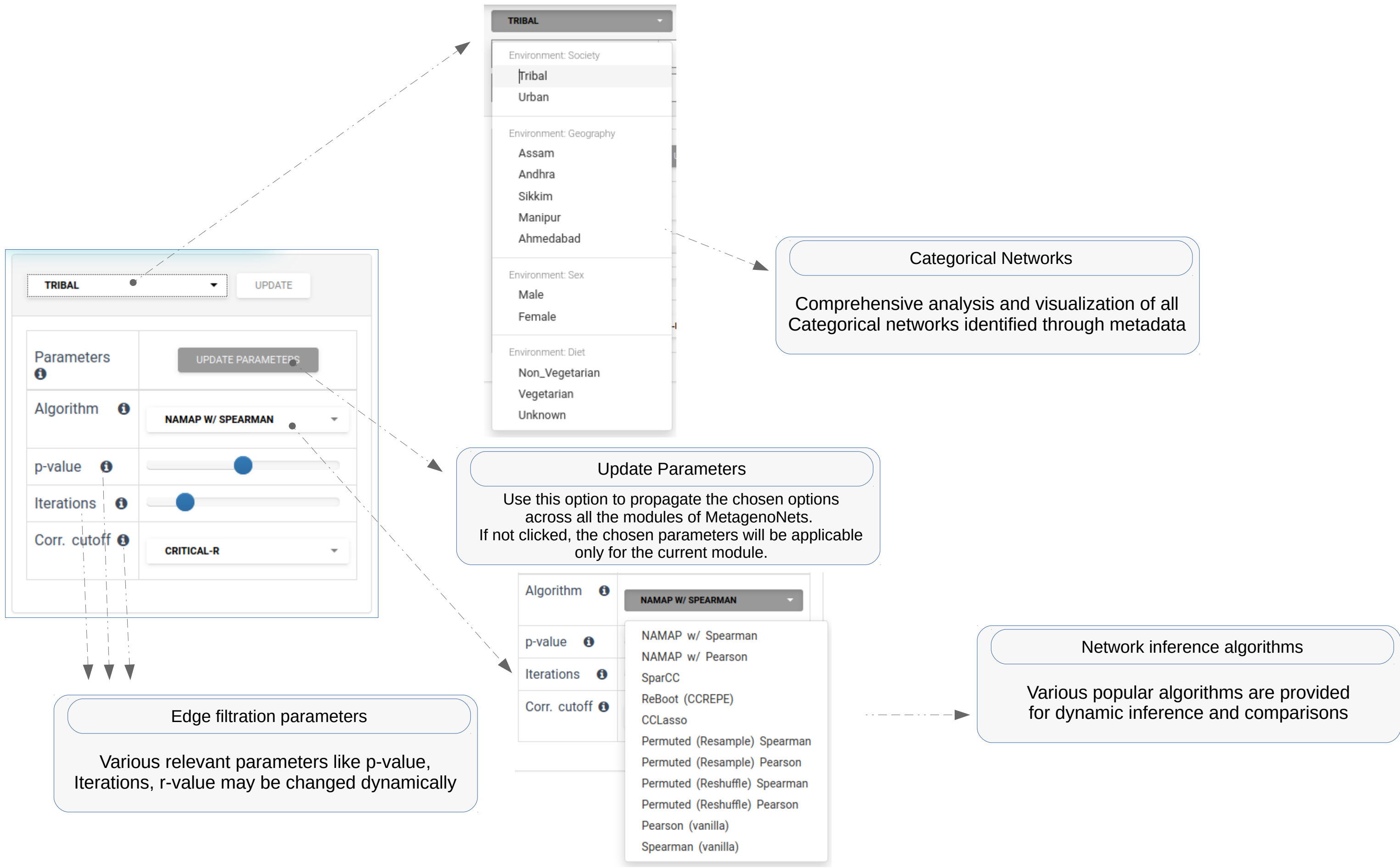
- NAMAP w/ Spearman
- NAMAP w/ Pearson
- SparCC
- ReBoot (CCREPE)
- CCLasso
- Permuted (Resample) Spearman
- Permuted (Resample) Pearson
- Permuted (Reshuffle) Spearman
- Permuted (Reshuffle) Pearson
- Pearson (vanilla)
- Spearman (vanilla)

Network inference algorithms

Various popular algorithms are provided for dynamic inference and comparisons

Edge filtration parameters

Various relevant parameters like p-value, Iterations, r-value may be changed dynamically



MODULE 2: INTEGRATED NETWORKS

Integrated Networks are created for a categorical group by combining continuous groups/ features having continuous values from Primary Metadata and/ or Secondary Input data to create a complex or inter-omic view of the microbiome associations. User can also change the layouts and reset the node sizes as required.

The screenshot displays the 'INTEGRATED NETWORKS' section of a software interface. It includes a sidebar for selecting metadata (e.g., BMI, Age) and metabolic pathways (e.g., Glycolysis_Gluconeogenesis, Citrate_cycle_TCA_cycle). The main area shows a network diagram with nodes and edges, and a 'Bi-partite plots' visualization. A terminal window at the bottom left shows the command: 'Network processed! Society/Tribal using namap at p-val: 0.05'. Callout boxes provide detailed explanations of the 'Inter-omic options', 'Continuous Metadata', and 'Searchable inter-omic data' features.

Continuous Metadata

Integrate continous meta-data with primary data for finding correlating taxa against Continous factors

Inter-omic options

Switch between Complete and Bi-partite Integrated inter-omic networks

Searchable inter-omic data

Search and specify inter-omic features of interest for integrating into network inference

Bi-partite plots

Edges exclusively between the inter-omic data and continous metadata groups can be visualized through highly intuitive Bi-partite plots

MODULE3: NETWORK COMPOSITIONS (VENN DIAGRAMS)

This module allows group level comparisons for each environment in the MetaData, in terms of **Node and Edge compositions** of various networks in the environmental category. This is enabled through interactive Venn diagrams for node and edge composition of all networks in a chosen Environment. This visualisation may take some time to load. Please be patient.

CATEGORICAL NETWORKS
INTEGRATED NETWORKS
VENN DIAGRAMS
PROPERTIES

Geography Update

Class

Tribe_name

Sex

Age_Range_yrs

Diet_Vegetarian_or_Non_Vegetarian

BMI_RANGE

Iterations

Corr. cut-off

CRITICAL-R

Venn Diagram for networks in **Geography** environment

Change view mode:

CLASSIC
EDWARDS

Assam

Ahmedabad

Manipur

Number of chosen components in each Network

State	Number of Nodes
Assam	86
Andhra	88
Sikkim	72
Manipur	81
Ahmedabad	94

Venn of Nodes

CHOOSE NETWORK COMPONENT

Download options

Download PNG image

Download SVG image

Download CSV lists

Compositional Comparisons

Compare networks of various groups within a Category of Metadata (e.g networks of all states in a given Geography), in terms of their Node and Edge composition

Dynamically generated Venn Diagrams for Node as well as Edge composition of various network groups in an environment

MODULE 4: NETWORK PROPERTIES

This module of MetagenoNets allows computation and analysis of network properties (centrality measures) for each of the network in an environment using selected algorithm and associated parameters. There are two methods of analysis and visualization available:

- 1). Tabulated view (sortable, searchable and exportable tables)
- 2). Grouped Boxplots of properties for all networks in an environment, thereby enabling comparison.

The screenshot displays the 'PROPERTIES' tab of the MetagenoNets application. The interface is divided into two main sections: a control panel on the left and a data visualization area on the right.

Control Panel (Left): Features a dropdown menu for 'Sex' (set to 'MALE') and an 'Update' button. Below it, a 'Class' dropdown menu is open, showing options like 'Geography', 'Tribe_name', 'Age_Range_yrs', 'Diet_Vegetarian_or_Non_Vegetarian', and 'BML_RANGE'. A 'Switch Mode' button is also present, with a tooltip that says 'Switch to box-plot Comparison mode'. The 'Switch Output Type' is set to 'TABLES', and the 'Switch property' is set to 'DEGREE'.

Table View (Center): A table with 8 columns: Node_Index, Label, Degree, Cluster_Coeff, Closeness, Betweenness, Eigen_Vector, and Eccentricity. The data is as follows:

Node_Index	Label	Degree	Cluster_Coeff	Closeness	Betweenness	Eigen_Vector	Eccentricity
1	Acidaminococcus	7	0.333333	0.150746	0.247722	1.534740e-02	4
2	Anaerobiospirillum	2	1.000000	0.134130	0.000000	1.674160e-03	5
3	Bifidobacterium	15	0.285714	0.162119	0.659270	8.504360e-02	4
4	Clostridium_XIVa	8	0.535714	0.155624	0.190473	1.652360e-02	4
5	Faecalibacterium	10	0.533333	0.158805	0.116501	6.225580e-02	4
6	Megamonas	5	0.600000	0.153263	0.062776	2.460040e-02	4
7	Megasphaera	6	0.266667	0.147445	0.565031	1.130090e-02	5
8	Sutterella	11	0.327273	0.156832	0.173658	4.289290e-02	4

Box Plot View (Right): A grouped box plot showing the distribution of 'DEGREE' for five geographical regions: Assam, Andhra, Sikkim, Manipur, and Ahmedabad. The y-axis represents 'Values' ranging from 0 to 24. The plot shows the median, quartiles, and range for each region. A 'Layout' menu at the bottom offers options: CLASSIC, NOTCHED, VIOLIN, BEAN, BEESWARM, and SCATTER. A 'Download' button is also visible.

Annotations:

- Network Properties:** Interactive, searchable and exportable network property tables for each group of an environment.
- Network Properties Box Plots:** Interactive, downloadable, trend enabled, boxplots (and variants) for each network property, for each group of an environment.
- Graph type and trend lines:** Use the buttons to change graph type Or overlay trend-lines for better comparison. Download option available as well.