EXPLORATION

COMPARISON

**CATEGORICAL NETWORKS**

Geo-1　　　　Geo-2

Node metadata and centrality mapped categorical networks

Correlograms

**INTEGRATED NETWORKS**

COMPLETE　　　Bi-partite

Microbe-1
Microbe-2
Microbe-3
Microbe-4

Age
Metabolite-2
Metabolite-1

**Bi-partite Sankey**

Data Filtration

Data Normalization
Transformation

Network inference
Algorithms
(e.g CCREPE, SPARCC)

**INPUT DATA**

Samples

Microbes | Primary Input
(e.g Taxonomic
profile)

Geo | Age

Samples | Primary Meta-Data
(e.g Geography,
Age)

Phylum | Pathogen

Microbes | Node Meta-Data
(e.g Phylum,
Pathogenicity)

Samples

Metabolites | Secondary Input
(e.g Metabolic
profile)

**COMPOSITIONAL VENNS**

**Node composition**
Venn diagram

**Edge composition**
Venn diagram

**NETWORK PROPERTIES**

Centrality Measures

Microbes

Centrality Measures

Microbes

**Property tables for all Categories**

Degree

Geo-1　Geo-2　Geo-3　Geo-4

Betweenness

Geo-1　Geo-2　Geo-3　Geo-4

**Grouped box-plots for all properties**

# MetagenoNets

Inference and **meta**-insights for microbial correlation **networks**

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
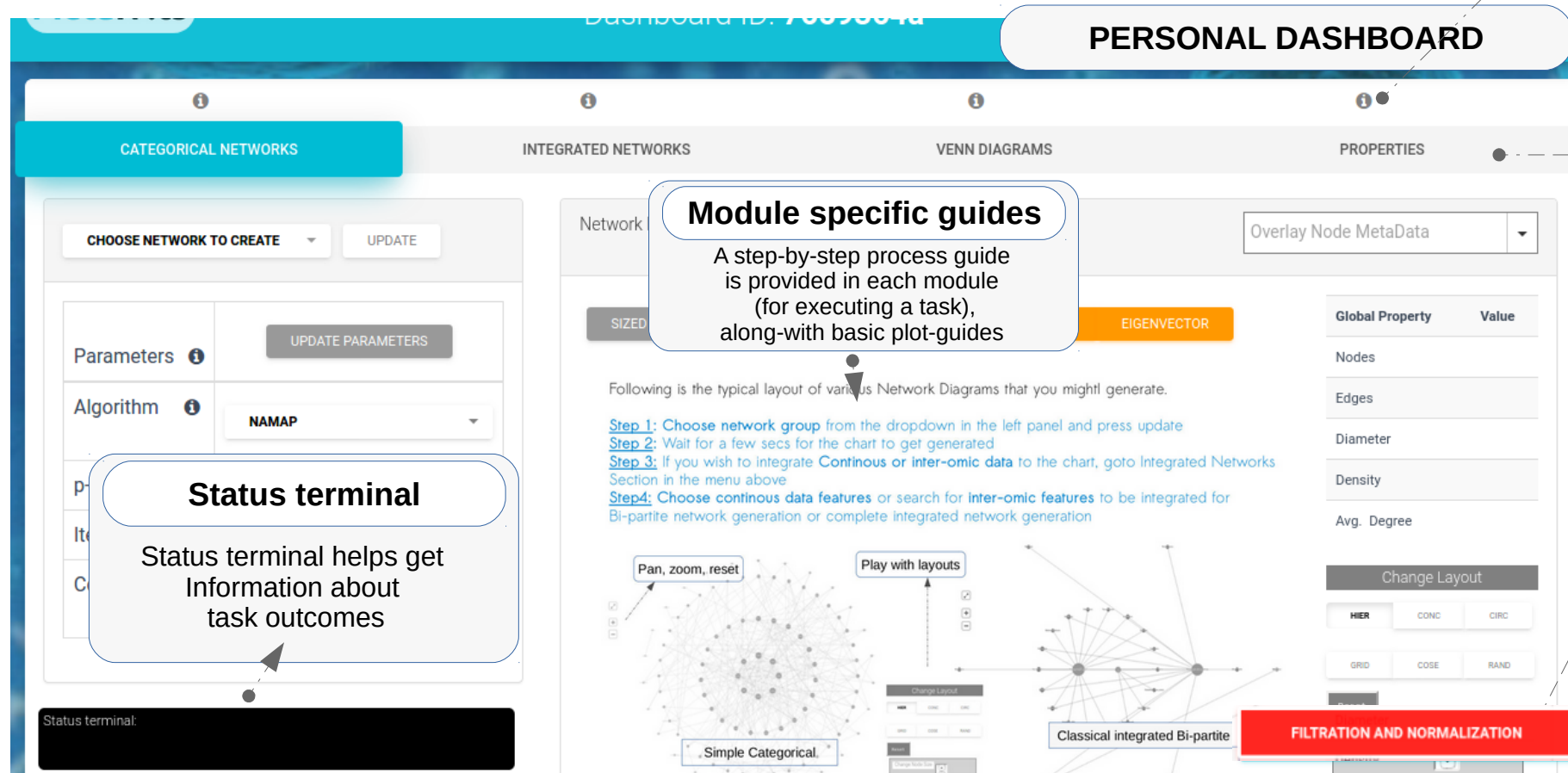3. Network Composition Analysis
4. Network Property Analysis

**Info tags** ⓘ

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

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

**PERSONAL DASHBOARD**

**Multi-modular**

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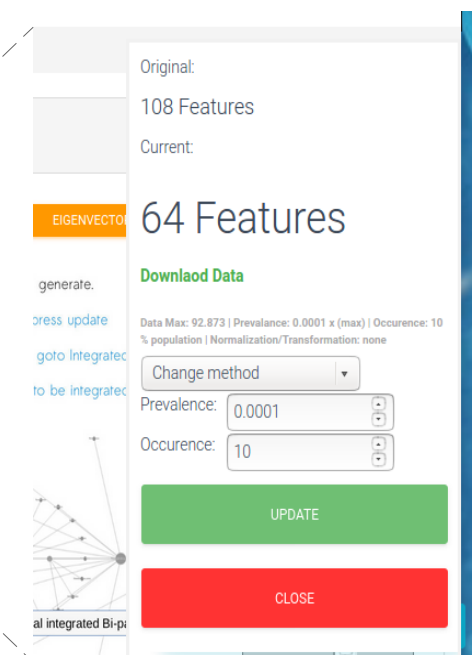


**Module specific guides**

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.

# 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.
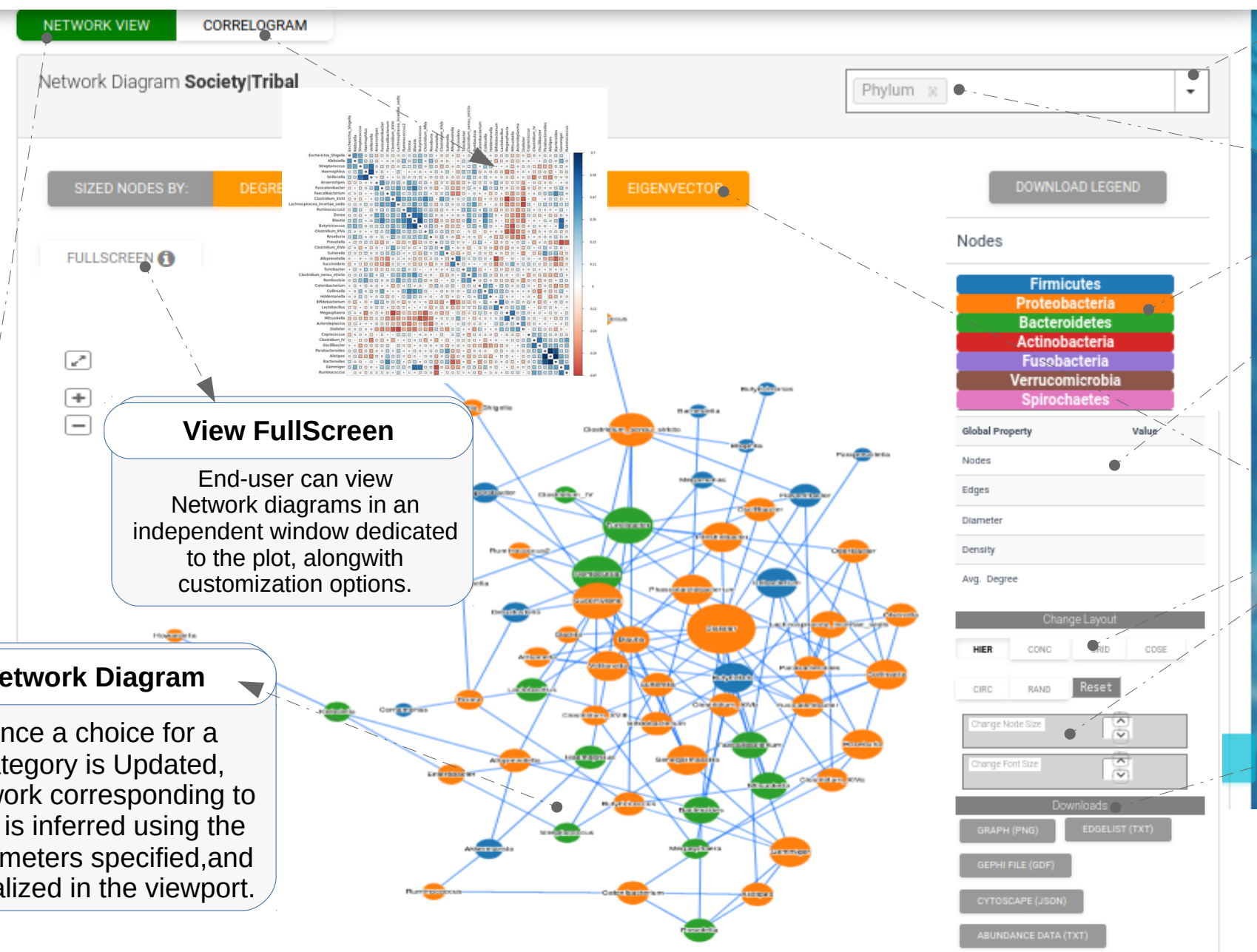


**Refer Next Slide**

**Node meta-data**

Dropdown option to overlay Node meta-data

**Global Properties**

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

**View FullScreen**

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

**Customizations**

- **Layouts**
- Property **mapping**
- Node and Font sizes

**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

**Download Options**

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

TRIBAL ▼

Environment: Society
Tribal
Urban

Environment: Geography
Assam
Andhra
Sikkim
Manipur
Ahmedabad

Environment: Sex
Male
Female

Environment: Diet
Non_Vegetarian
Vegetarian
Unknown

TRIBAL ● ▼    UPDATE

Parameters ❶    UPDATE PARAMETERS

Algorithm ❶    NAMAP W/ SPEARMAN ▼

p-value ❶

Iterations ❶

Corr. cutoff ❶    CRITICAL-R ▼

Algorithm ❶    NAMAP W/ SPEARMAN ▼

p-value ❶

Iterations ❶    NAMAP w/ Spearman

Corr. cutoff ❶    NAMAP w/ Pearson
SparCC
ReBoot (CCREPE)
CCLasso
Permuted (Resample) Spearman
Permuted (Resample) Pearson
Permuted (Reshuffle) Spearman
Permuted (Reshuffle) Pearson
Pearson (vanilla)
Spearman (vanilla)

**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.

**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
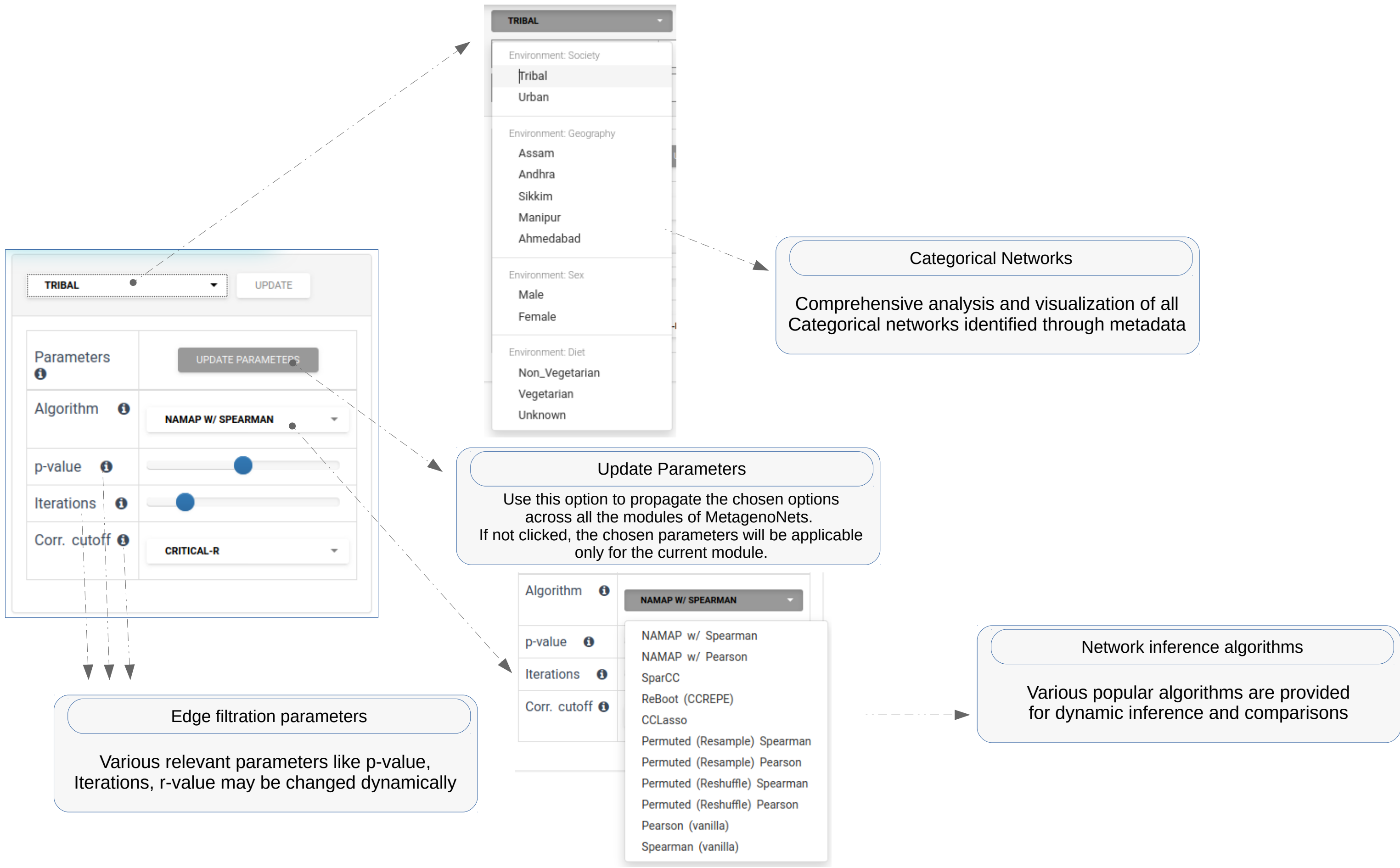
# MODULE2: INTEGRATED NETWORKS

**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.



**Continous 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

**Bi-partite plots**

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

**Searchable inter-omic data**

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

# 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.



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

CATEGORICAL NETWORKS    INTEGRATED NETWORKS    VENN DIAGRAMS    PROPERTIES

Geography ×

Class
Tribe_name
Sex
Age_Range_yrs
Diet_Vegetarian_or_Non_Vegetarian
BMI_RANGE

Update

UPDATE PARAMETERS

p Value
Iterations
Corr. cut-off    CRITICAL-R

Venn Diagram for networks in **Geography** environment

Change view mode:  CLASSIC    EDWARDS

Venn of **Nodes**

CHOOSE NETWORK COMPONENT▾

Download options

Download PNG image
Download SVG image
Download CSV lists

Number of chosen components in each Network

**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

# MODULE4: 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.



**Switch Mode**

Switch to box-plot Comparison mode

**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.