



Saint Louis University

MicrobioSee v2.0, a desktop software for microbiome data visualization.

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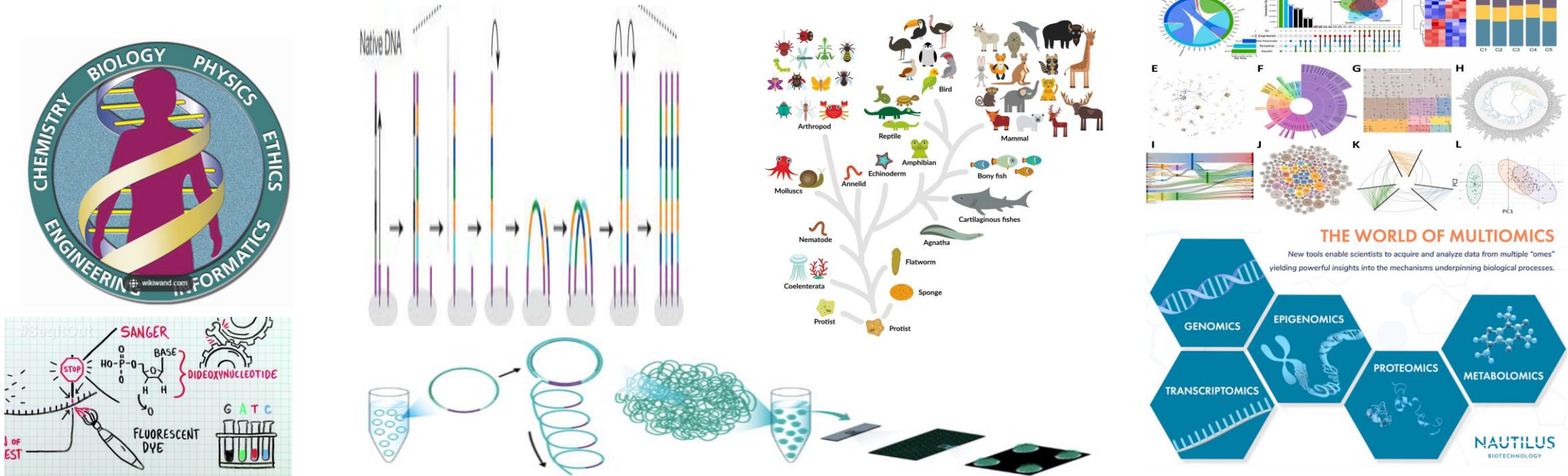
5/7/2024

Content

- **Background**
- **Method & Modules**
- **Demonstration of MicrobioSee & Discussion**

Background

- What is a bioinformatics engineer's main work?
 - Construct analyze pipelines and run it.
 - Visualize the result.
 - Develop the algorithms of mapping and clustering.
 - Build the database for searching mapping.
- Why bioinformatics are important?

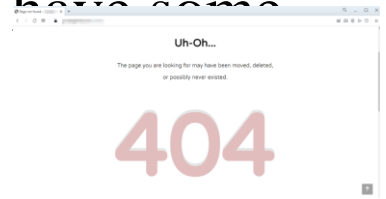


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Background

- Microbiome plays an important role in personal life.
- Many microbiologists can't master code techniques, include coding for visualization and developing a tool for visualization of microbiome data is very necessary.
- The interactive tools based on web technique that depend on the **network** and **have some visit restriction** due to the security policy of management.
- **Data security**. Some scientists don't want to upload their data in any website before publishing work, such as iDEP.
- The desktop tools existed **are expensive**, such as Origin and GraphPad Prism.



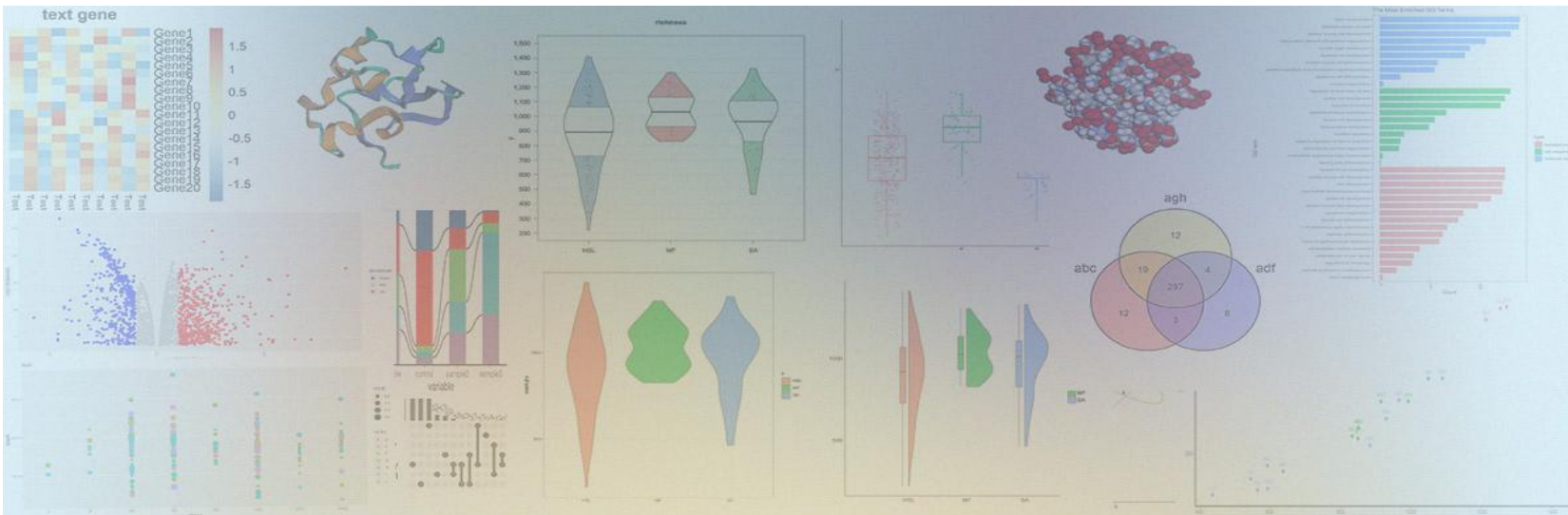
MicrobioSee2 (desktop version)

Microbio**See** = Microbiome + See

- The desktop version contain **12 visualization tools**.
- Form a developer community in github.
- Github: <https://github.com/jinhuili-lab/MicrobioSee2>
- User Guide: <https://microbiosee.github.io/>

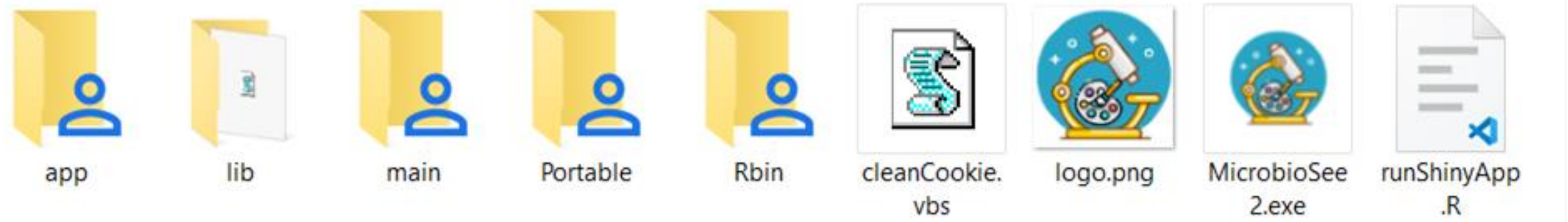


MicrobioSee logo



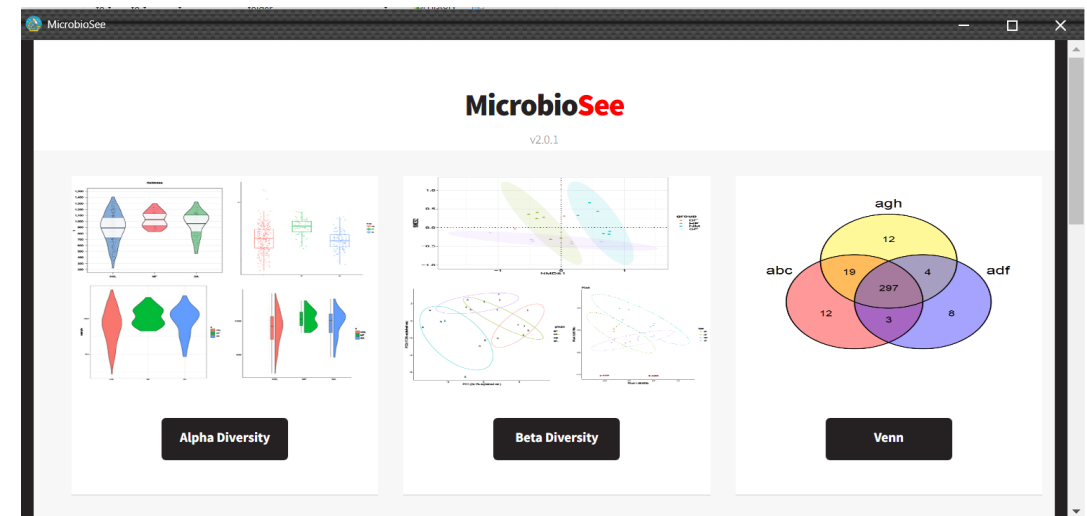
MicrobioSee2 logo

MicrobioSee2



- App: modules
- Lib: some library file
- Main: core program
- Portable: dependence
- Rbin: R packages
- CleanCookie.vbs: Clean cookie
- Logo.png: logo png
- **MicrobioSee2.exe**: Executable program and entrance
- runShinyApp.R: hook

Shiny + VBS + Chromecore + HTML = Desktop version



Comparative analysis

	Origin	MicrobioSee v1.3	MicrobioSee v2.0
Without network dependence	√		√
Responding speed	Faster	depend on network	Faster
Free		√	√
Interactive visualization	√	√	√

Modules

- Alpha

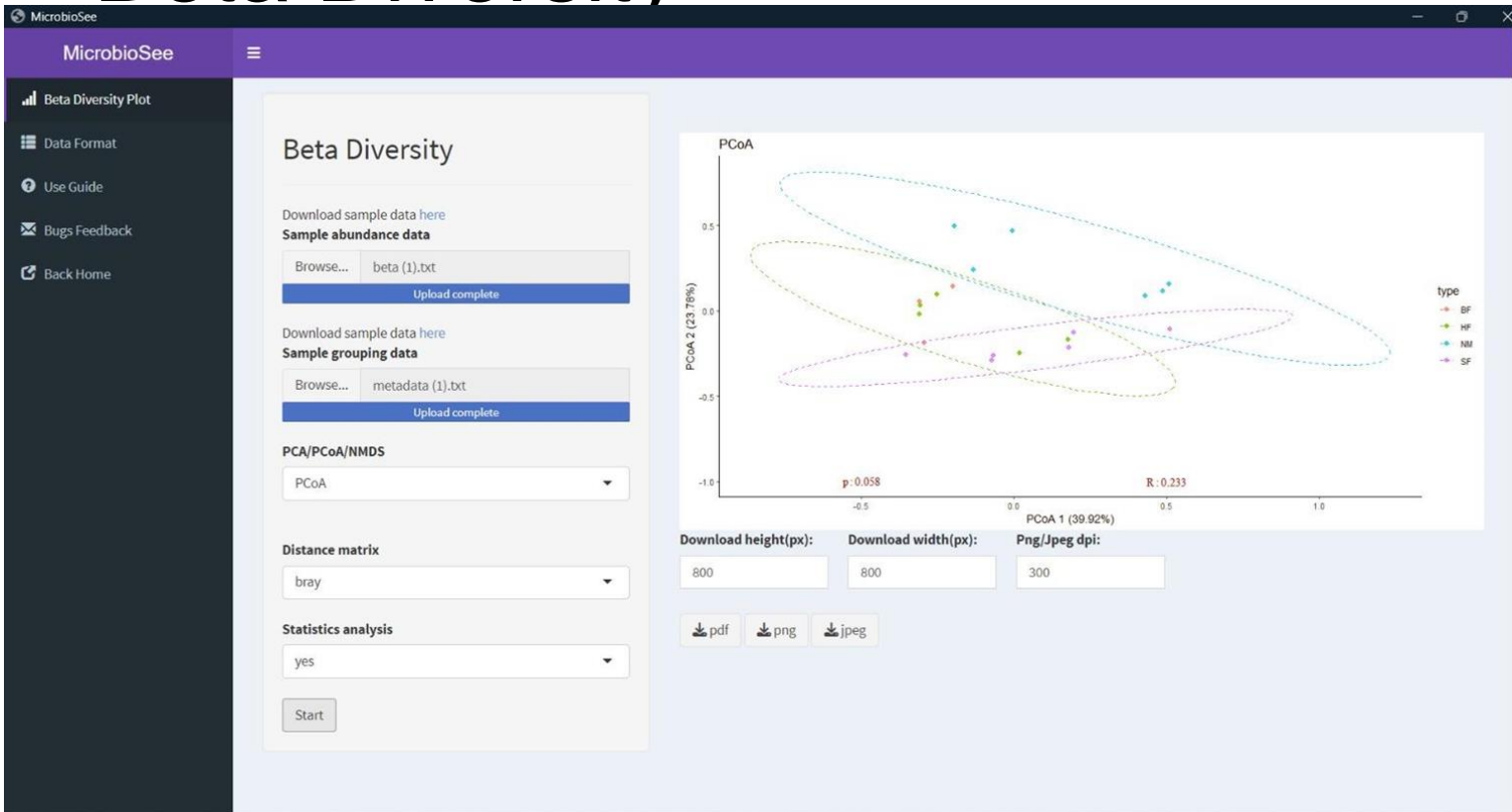
The screenshot shows the MicrobioSee v2.0.1 web application interface. On the left is a dark sidebar with navigation links: Alpha Plot, Data Format, Use Guide, Bugs Feedback, and Back Home. The main content area is titled 'Alpha Plot' and contains several input sections. The first section, 'Input alpha diversity result:', has a 'Browse...' button and a 'No file selected' status. The second section, 'Input metadata file:', also has a 'Browse...' button and a 'No file selected' status. Below these is a 'Select the alpha diversity result:' dropdown menu with the value '2'. The 'Statistical method:' dropdown menu is set to 'T-test/ANOVA'. The 'Select plot type:' dropdown menu is set to 'box-plot'. At the bottom left of the main area is a 'Start' button. On the right side of the main area, there are three input fields for 'Download height(px):' (800), 'Download width(px):' (800), and 'Png/Jpeg dpi:' (300). Below these fields are three buttons for downloading the plot: 'pdf', 'png', and 'jpeg'.

Uses:

- Visualizing species richness and diversity within samples
- Assessing evenness and relative abundance of species
- Identifying dominant or most abundant species
- Comparing diversity patterns across samples/environments

Modules

- Beta Diversity

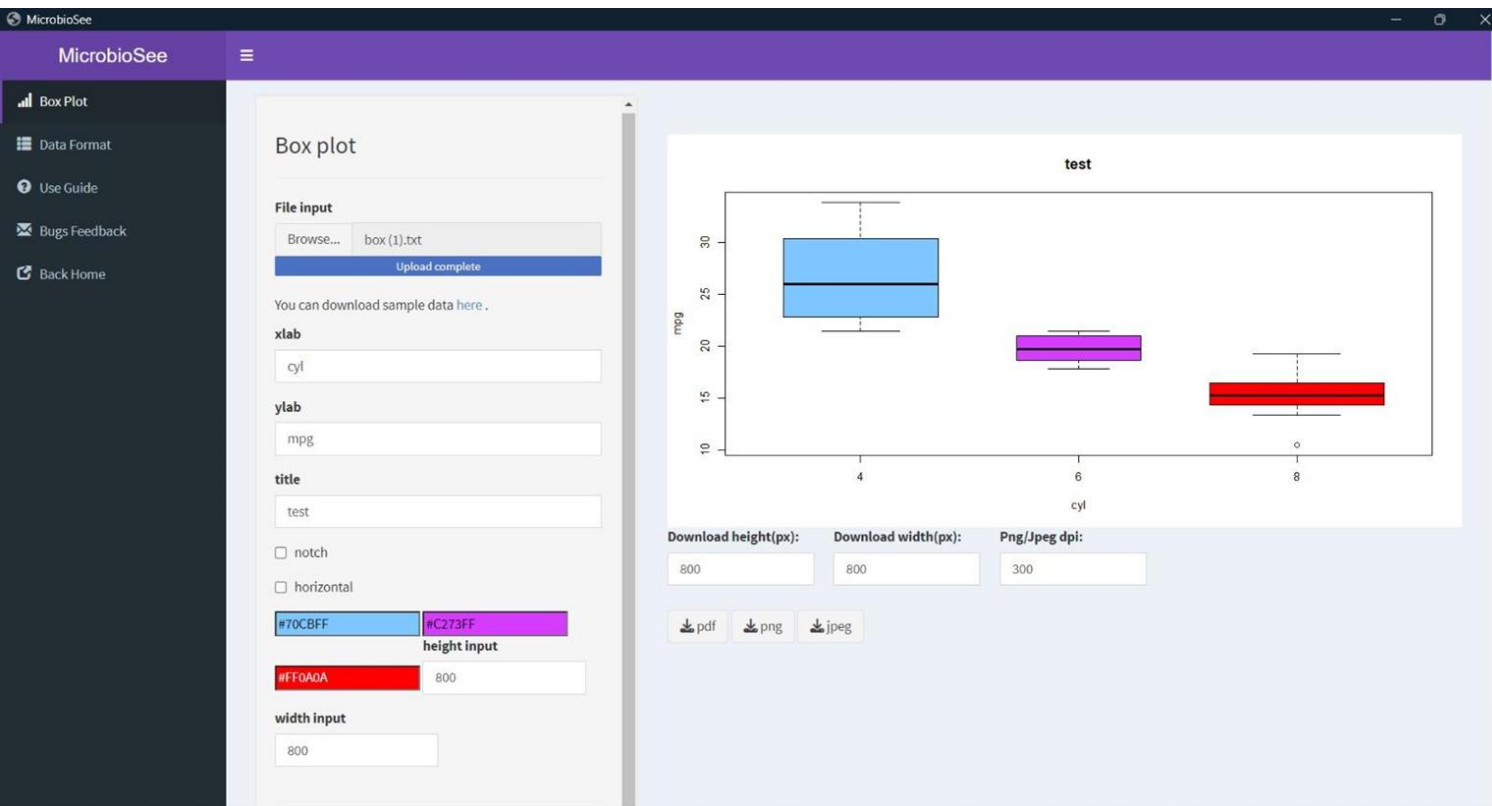


Uses:

- Comparing microbial community compositions across samples/environments
- Identifying environmental drivers shaping community structures
- Assessing ecological processes influencing community assembly
- Monitoring dynamics and responses to perturbations

Modules

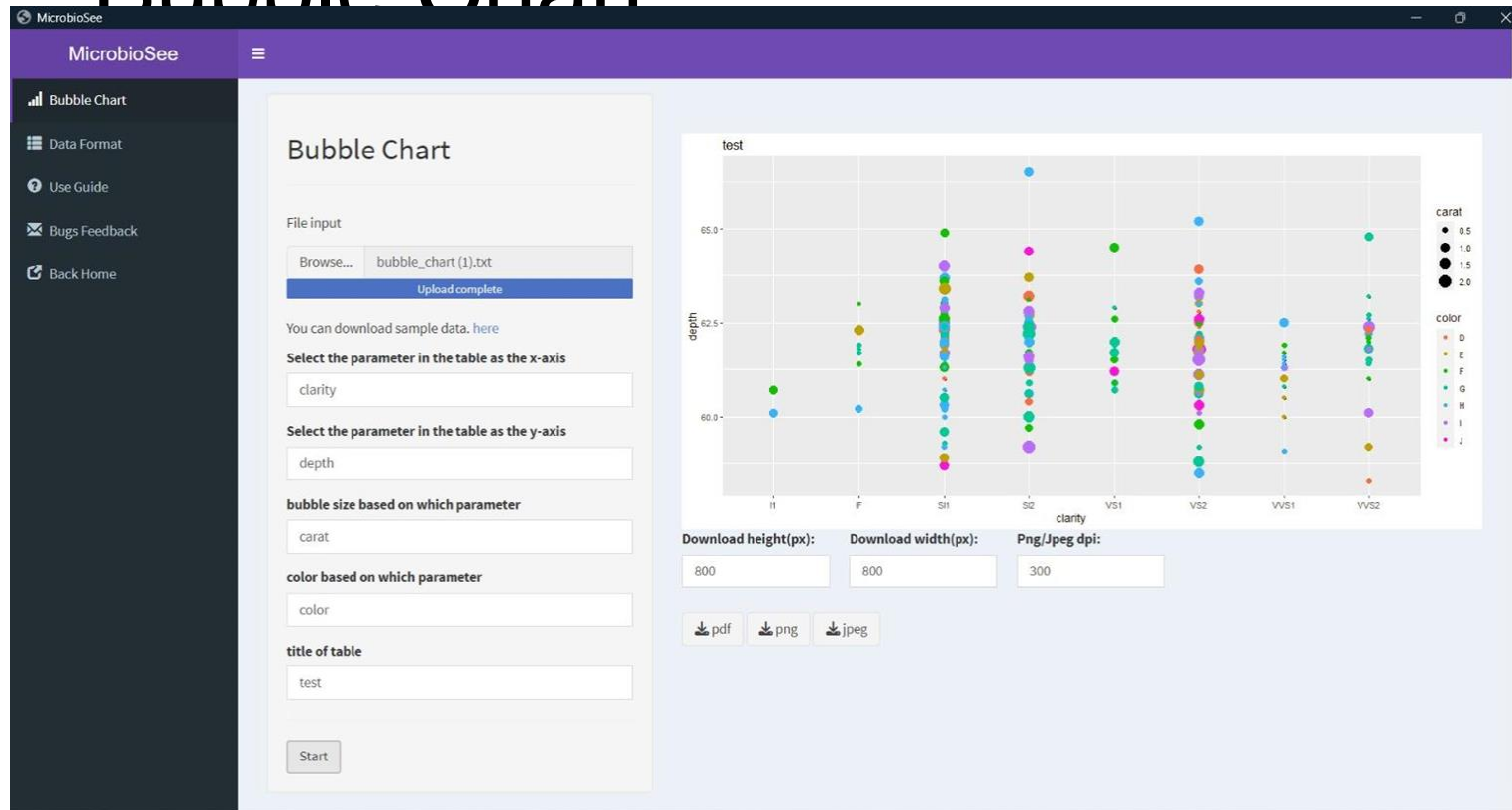
- Box Plot



- Comparison of central tendencies and dispersion
- Identification of statistically significant differences
- Detection of outliers or anomalies
- Exploration of patterns and hypothesis generation

Modules

• Bubble Chart

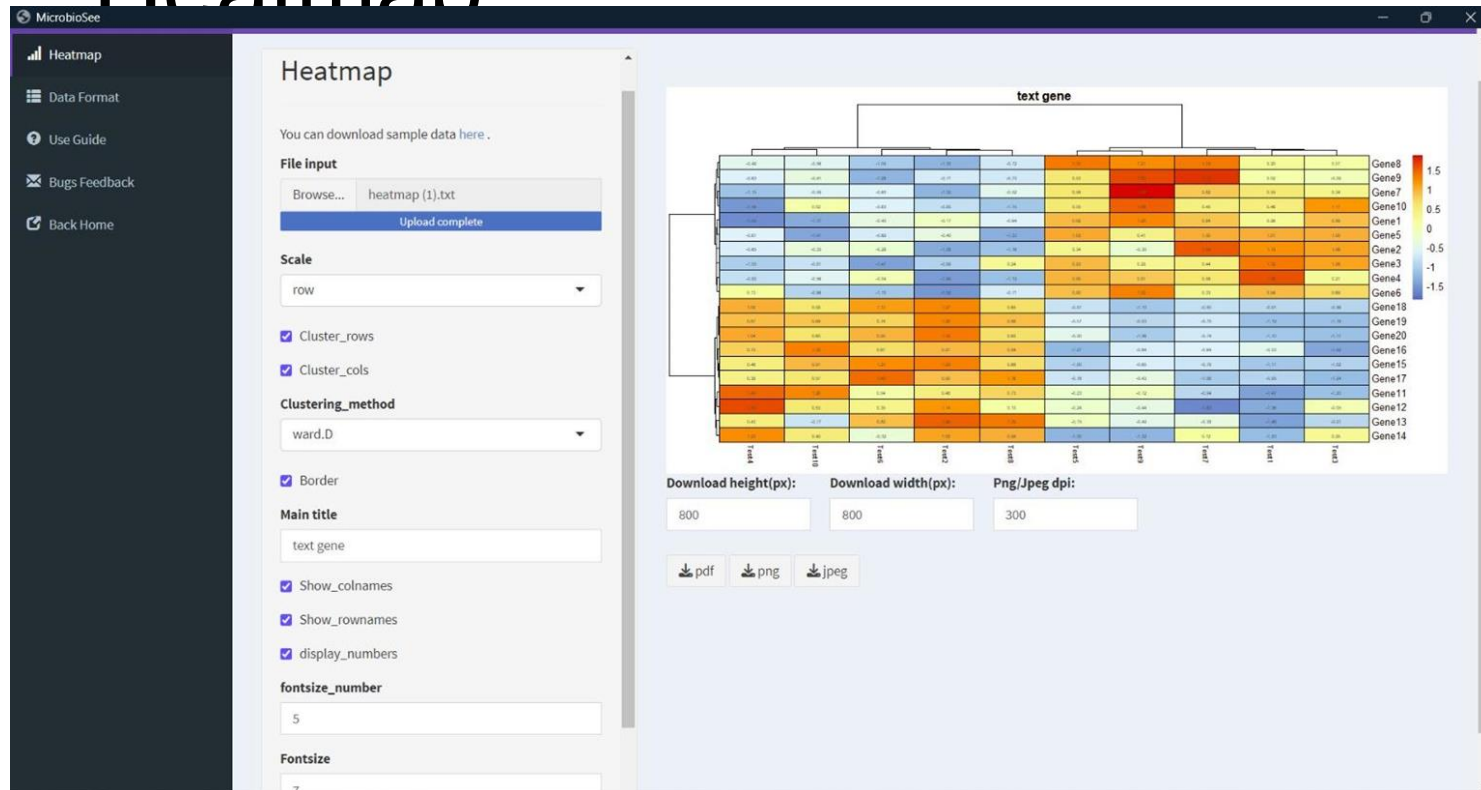


Uses;

- Visualizing relative abundances of taxa across samples
- Identifying dominant and rare taxa within communities
- Comparing taxonomic compositions between different samples or conditions

Modules

• Heatman

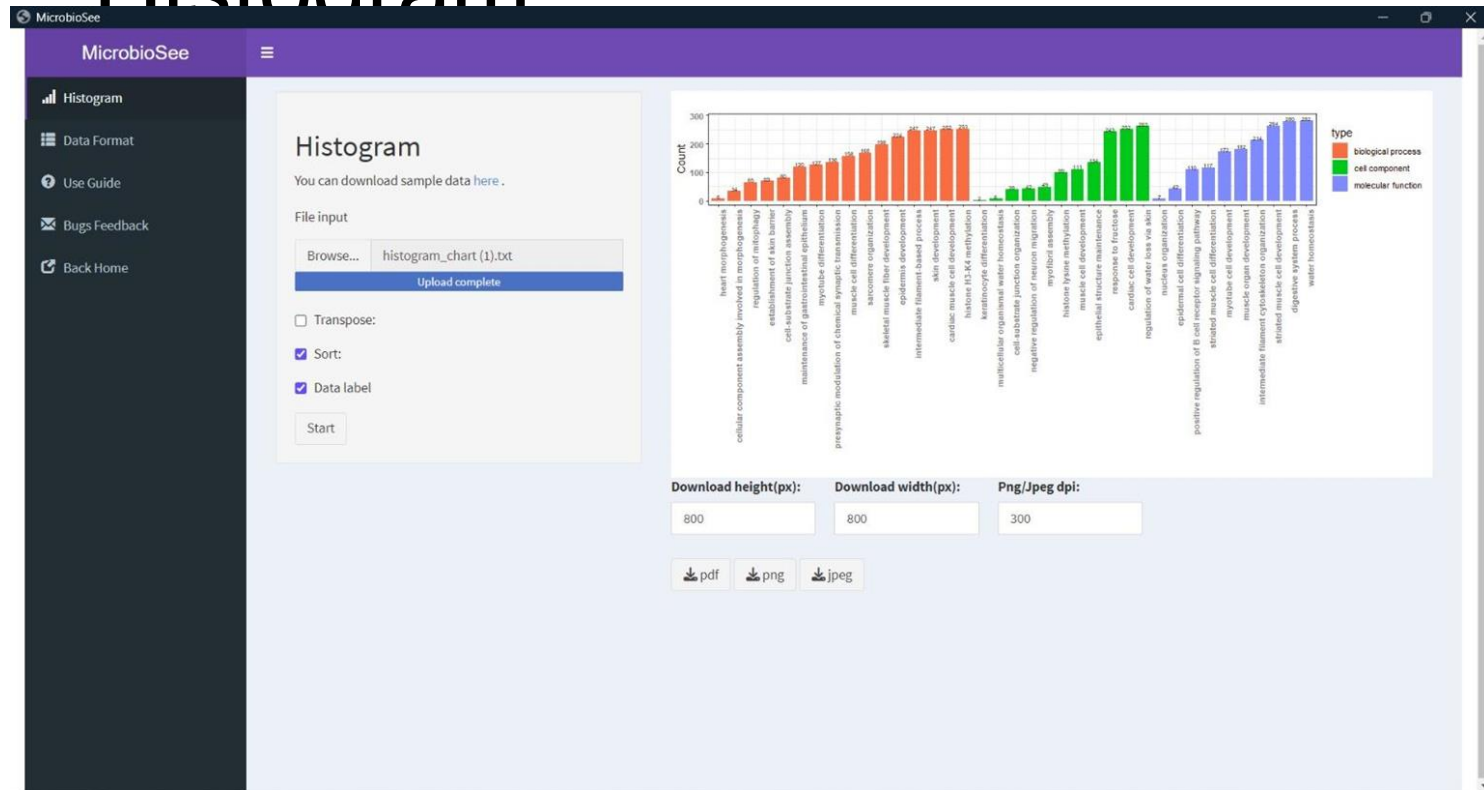


Uses:

- Visualizing and comparing the abundance patterns of taxa across multiple samples
- Identifying clustering patterns or similarities in community compositions
- Exploring relationships between taxa and environmental/experimental variables
- Detecting hotspots or areas of high or low abundance

Modules

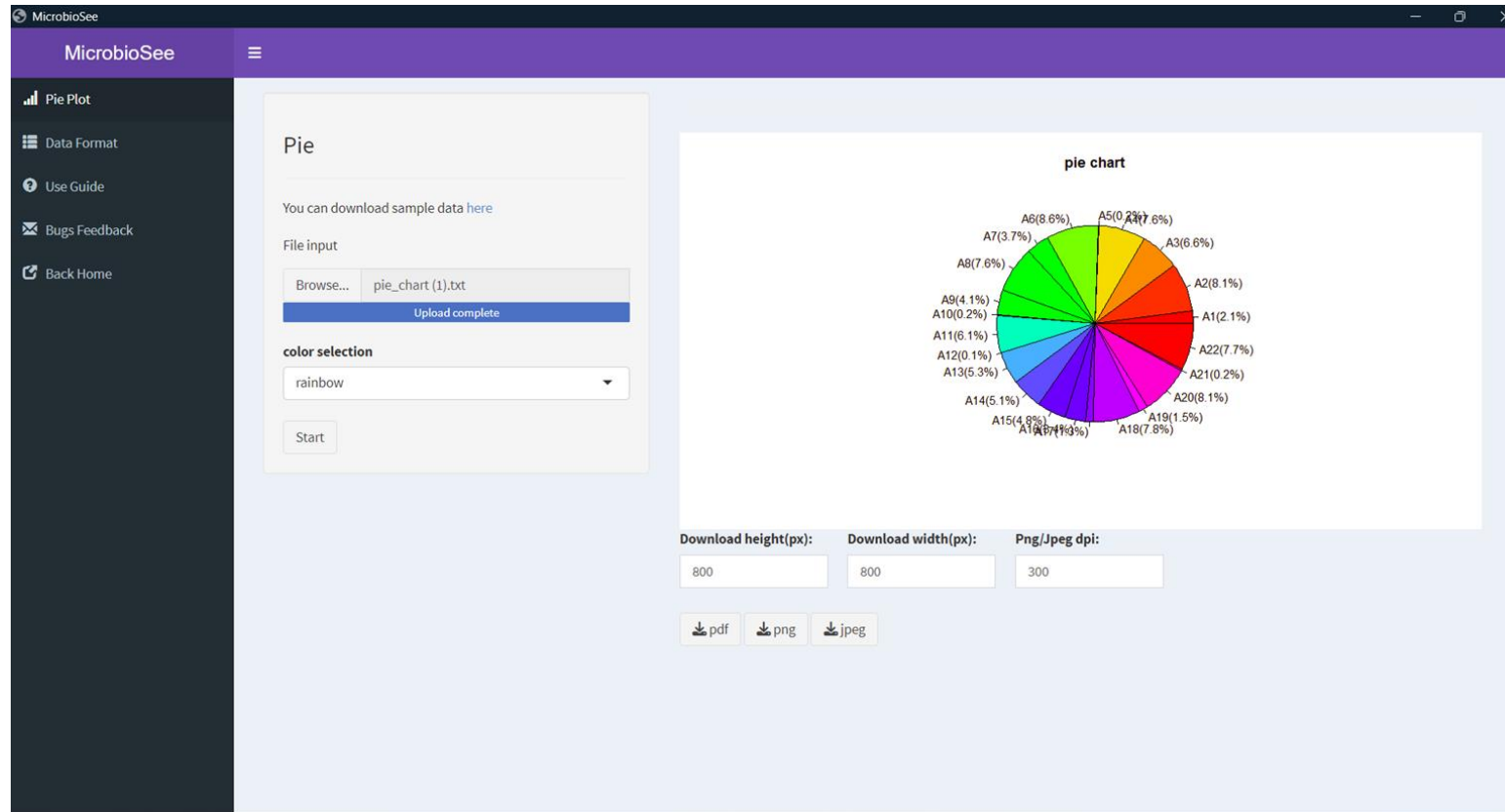
• Histogram



- Summarize metagenomic data distribution, aiding in understanding its characteristics.
- Help to detect errors and contamination, ensuring data reliability.
- Illustrate taxonomic abundance, revealing the composition and diversity of microbial communities.
- Enable comparison of features across samples, highlighting differences or similarities in microbial communities.

Modules

- Pie chart

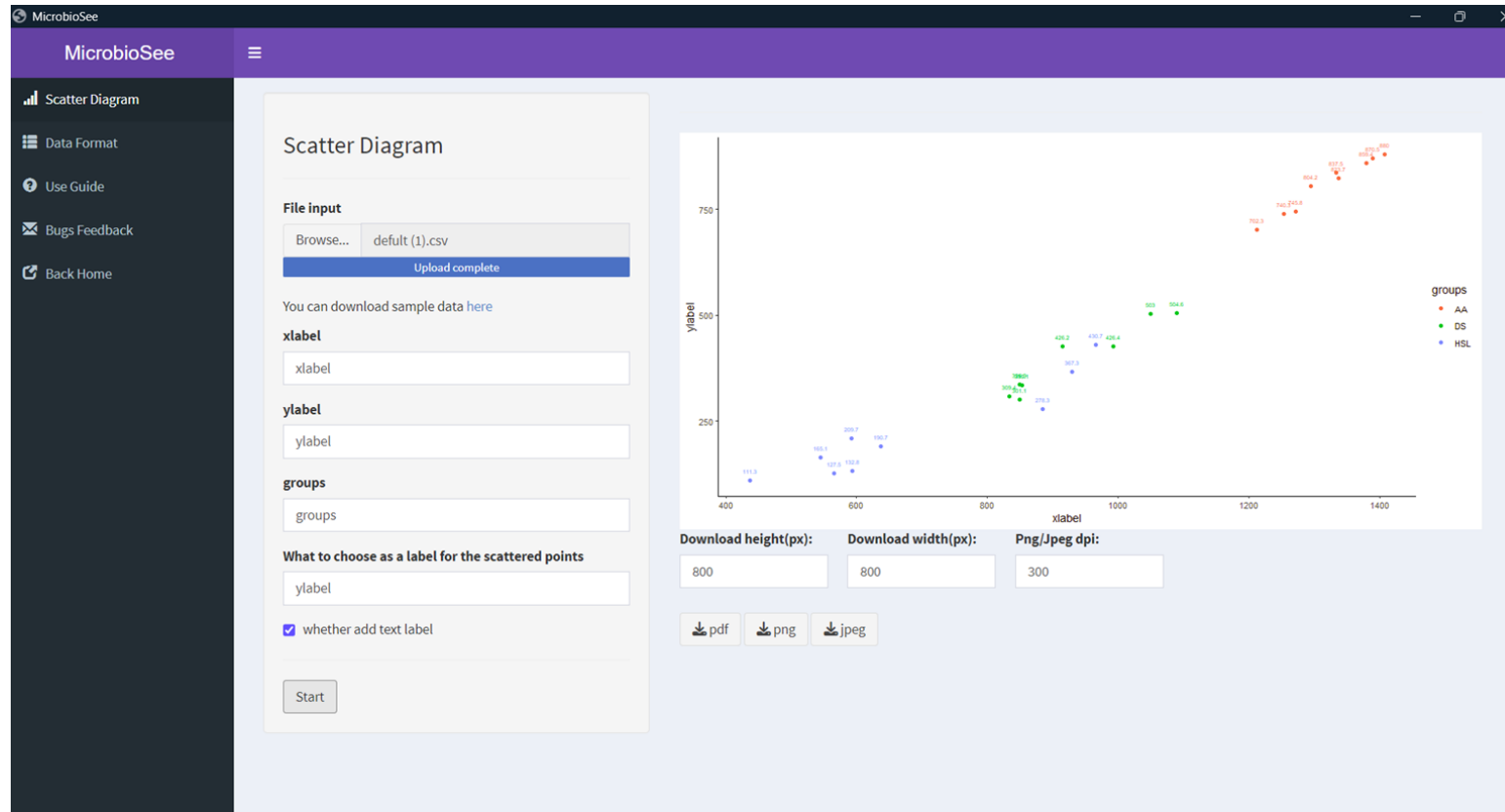


Uses:

- Relative representation of taxonomic composition
- Visualizing distribution of metabolic pathways
- Identify spatial trends

Modules

- Scatter plot

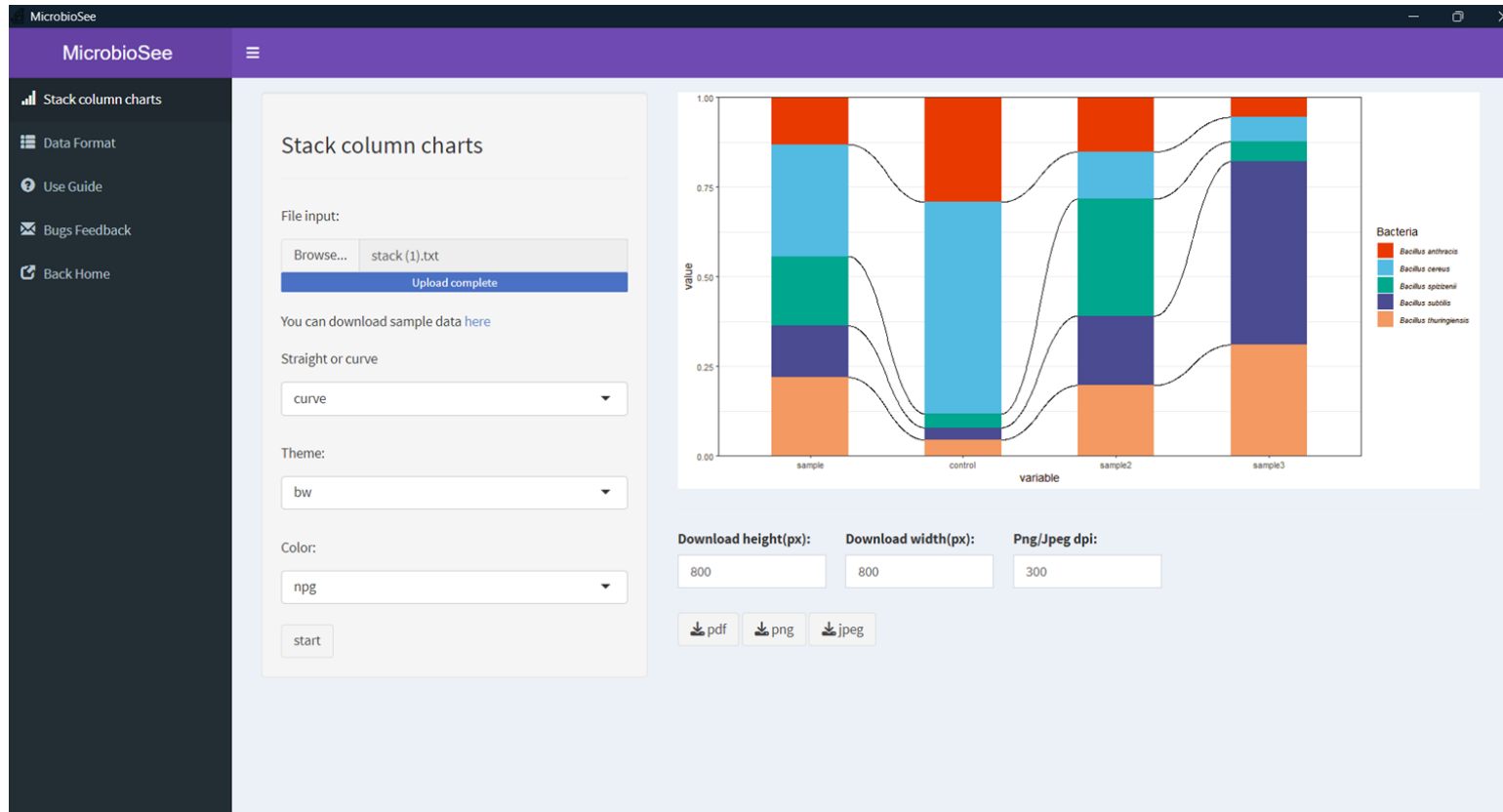


Uses:

- Identifying evolutionary relationships between microbial communities.
- Detect outliers by identifying unusual compositions.
- Compare metagenomic profiles across different conditions

Modules

- Stack

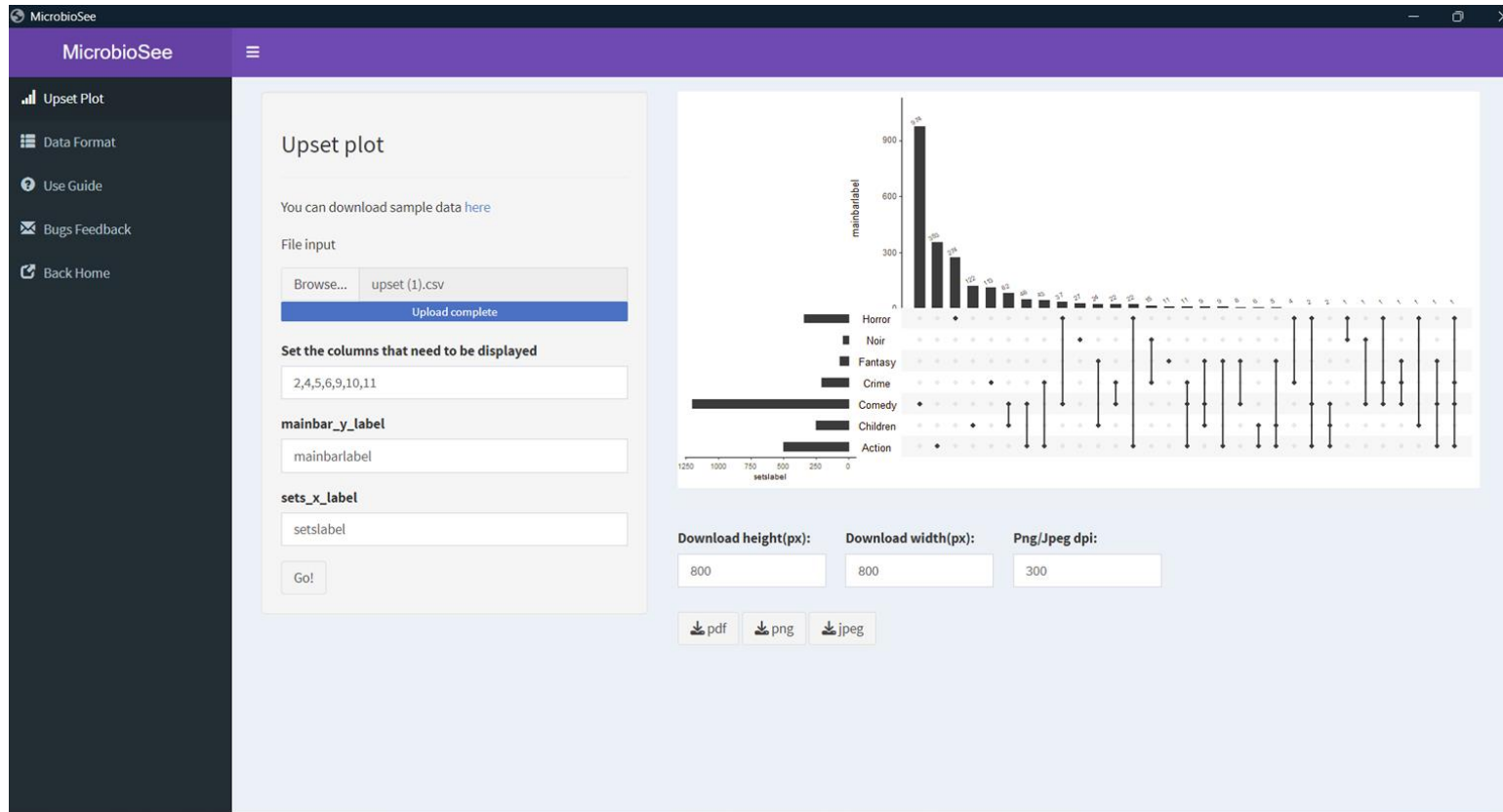


Uses:

- Visualize the proportion of different microbes within a sample.
- The layered representation helps to explore different patterns among complex hierarchies.

Modules

- Upset Plot

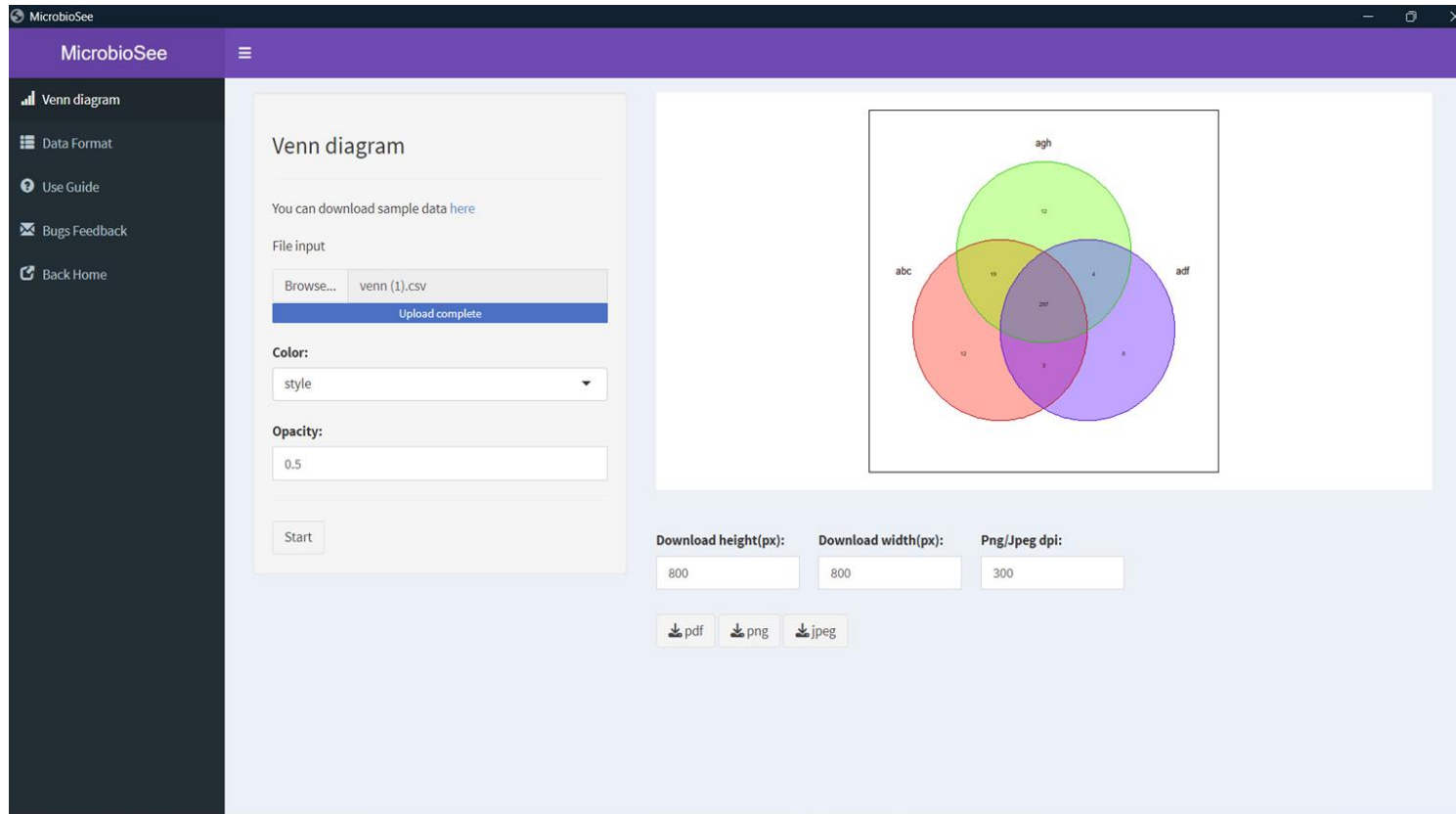


Uses:

- Better at visualizing complex and bigger datasets in comparison with traditional plotting methods
- Represent different organisms detached at variable conditions.
- Represent relative abundance of microbial communities.

Modules

- Venn



Uses:

- Often used to compare genetic material across different species.
- Provide quantitative information about the number of shared and unique features.
- Illustrate overlaps among microbial communities.

Modules

- Volcano Plot

- Aid in generating hypothesis regarding the roles of microbes in different conditions.
- Represent the magnitude of change and statistically significant differences among different observed samples.
- Identify the activity or abundance of different microbes in a sample.



Discussion

Challenges:

- Install target package **versions and** all their required **complex dependencies** and with many errors.
- Testing until the app gets adapted to the reactivity caused by usage of Shiny.
- Construct without network-independent. Run a shiny in Windows OS based on VBS code.

Future:

- More functions can be added in MicrobioSee2, such as **building Machine Learning model and visualizing the ROC.**

How to use MicrobioSee v2 ?

1. Installation
2. Usage Guide
3. Bug Feedback