**MicrobioSee2: a powerful desktop software designed for microbiome data visualization.**

**Jinhui Li, Kaarunya Nachimuthu, and Abdur Rahman Syed Ali**

1. **Department of Biology, St Louis University, St Louis, MO, USA. Email: jinhui.li@slu.edu**
2. **Program of Bioinformatic and Computational Biology, St Louis University, St Louis, MO, USA**

**Abstract**

The microbiome plays an important role in personal life, but Many microbiologists can’t master code techniques, including coding for visualization. Developing a tool for visualization of microbiome data is very necessary. The interactive tools are based on web techniques that depend on the network and have some visit restrictions due to the security policy of management. Some scientists don’t want to upload their data to any website. MicrobioSee v2.0 is a desktop application that offers 12 different visualization tools for microbiome data analysis. MicrobioSee v2.0 simplifies the process of exploring and analyzing microbiome data. MicrobioSee v2.0 can be available at <https://github.com/jinhuili-lab/MicrobioSee2>.

**Keywords**: MicrobioSee, Microbiome, Data Visualization, Desktop Software, Bioinformatics, Data Analysis

**Background**

The microbiome plays a crucial role in various aspects of life, and its analysis is essential for understanding its impact on various domains. However, many microbiologists lack advanced coding skills, making it challenging to visualize and interpret microbiome data effectively. Existing web-based visualization tools often depend on network connectivity and may have security limitations ( Li, et al. 2022). Also, the potential risk of Privacy data revealing preventing researchers from uploading sensitive data before publication, such as iDEP(Ge et al. 2018). Additionally, commercial desktop tools for data visualization can be expensive, making them inaccessible to some researchers (Seifert et al. 2014).

MicrobioSee v2.0 addresses these challenges by providing a comprehensive desktop solution for microbiome data visualization. Its development was driven by the need for a network-independent, secure, and cost-effective tool that empowers microbiologists to explore and analyze their data without relying on web-based platforms or expensive commercial software. Unlike web-based tools that require internet access and may have security concerns, this software is a standalone solution that ensures data privacy and independence from network constraints. The software combines the power of Shiny, VBS (Visual Basic Script), Chromecore, and HTML to deliver an interactive and seamless experience. MicrobioSee v2.0 is available as a free and open-source project, hosted on GitHub, with a dedicated developer community and comprehensive user guide. MicrobioSee v2.0 is a powerful desktop software designed for microbiome data visualization. Developed by Jinhui Li, Kaarunya Nachimuthu, and Abdur Rahman Syed Ali at Saint Louis University, this tool aims to address the challenges faced by microbiologists who may not have advanced coding skills. With its user-friendly interface and comprehensive set of visualization modules, MicrobioSee v2.0 simplifies the process of exploring and analyzing microbiome data.

**Methods and Structure**

MicrobioSee v2.0 is a desktop application that integrates various technologies to deliver a seamless and interactive experience. The software leverages the power of Shiny, a package in R for creating interactive web applications, combined with Visual Basic Script (VBS) and Chromecore for executing the application on Windows operating systems without network dependency. We will develop the MacOS version in the future.

The software's architecture consists of several components:

1. App: Contains the visualization modules and user interface elements.
2. Lib: Includes necessary library files.
3. Main: Houses the core program files.
4. Portable: Stores dependencies required for portability.
5. Rbin: Contains R packages utilized by the application.
6. Additional files: CleanCookie.vbs (for cleaning cookies), Logo.png (application logo), MicrobioSee2.exe (executable program and entry point), and runShinyApp.R (hook for running the Shiny application).

**Modules**

MicrobioSee v2.0 offers a comprehensive suite of 12 visualization modules (Fig. 1), each designed to address specific analytical needs in microbiome data analysis.

1. Alpha Diversity: Visualizes species richness, diversity within samples, evenness, relative abundance, and dominant species, and allows comparison across samples/environments.

2. Beta Diversity: Compares microbial community compositions, identifies environmental drivers shaping structures, assesses ecological processes influencing community assembly, and monitors dynamics/responses to perturbations.

3. Box Plot: Enables comparison of central tendencies, dispersion, identification of significant differences, and detection of outliers.

4. Bubble Chart: Visualizes relative abundances of taxa across samples, identifies dominant and rare taxa, and compares taxonomic compositions between conditions.

5. Heatmap: Visualizes and compares abundance patterns of taxa, identifies clustering patterns/similarities, explores relationships between taxa and variables, and detects hotspots.

6. Histogram: Summarizes data distribution, aids in error/contamination detection, illustrates taxonomic abundance, and enables comparison across samples.

7. Pie Chart: Represents relative taxonomic composition, visualizes the distribution of metabolic pathways, and identifies spatial trends.

8. Scatter Plot: Identifies evolutionary relationships between communities, detects outliers, and compares metagenomic profiles across conditions.

9. Stack: Visualizes the proportion of different microbes within a sample and explores patterns among complex hierarchies.

10. Upset Plot: Visualizes complex and larger datasets, represents different organisms across variable conditions, and shows relative abundance of communities.

11. Venn: Compares genetic material across species, provides quantitative information on shared and unique features, and illustrates overlaps among communities.

12. Volcano Plot: Aids in generating hypotheses about microbial roles, represents magnitude of change and significant differences, and identifies activity/abundance of microbes.

白板上写着字

描述已自动生成

Fig. 1. The modules in MicrobioSee 2.

The development process involved challenges related to installing dependencies, ensuring reactiveness with Shiny, and constructing a network-independent application. The team plans to introduce additional features, such as building machine learning models and visualizing receiver operating characteristic (ROC) curves.

图形用户界面, 应用程序

描述已自动生成

Fig. 2 The user interface of MicrobioSee 2.

**Result and Discussion**

We developed MicrobioSee v2, which is a desktop version of software for microbiome data visualization. The development of MicrobioSee v2.0 involved overcoming several challenges: Installing target package versions and all their required complex dependencies, often encountering numerous errors. Testing until the app adapted to the reactiveness caused by the usage of Shiny. Constructing the application to be network-independent by running a Shiny app in Windows OS based on VBS code. Shiny is a very useful package in R for creating interactive applications. Documenting the necessary packages and their corresponding versions across different environments is crucial. Utilizing devtools and BiocManager can streamline the installation of packages, while VBS can be used for creating Windows scripts.

The developers plan to introduce additional functionalities to MicrobioSee v2.0, such as building machine learning models and visualizing receiver operating characteristic (ROC) curves, further enhancing its capabilities in microbiome data analysis.

**Availability**

MicrobioSee v2.0 can be available at <https://github.com/jinhuili-lab/MicrobioSee2>.

**Acknowledge**

Thanks to Sen Zeng and Yimeng Sang, who are the co-authors of the first version.

**Funding**

No funding support.

**Reference**

Li J, Sang Y, Zeng S, Mo S, Zhang Z, He S, Li X, Su G, Liao J and Jiang C (2022) MicrobioSee: A Web-Based Visualization Toolkit for Multi-Omics of Microbiology. Front. Genet. 13:853612. doi: 10.3389/fgene.2022.853612.

Ge, S.X., Son, E.W. & Yao, R. iDEP: an integrated web application for differential expression and pathway analysis of RNA-Seq data. BMC Bioinformatics 19, 534 (2018). https://doi.org/10.1186/s12859-018-2486-6

Seifert, E. “OriginPro 9.1: scientific data analysis and graphing software-software review.” Journal of chemical information and modeling vol. 54,5 (2014): 1552. doi:10.1021/ci500161d