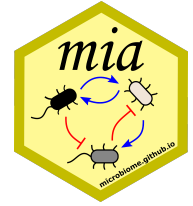


Orchestrating Microbiome Analysis with Bioconductor



In this session, we will cover the recent advances in microbiome data science in R/Bioconductor — an open-source project dedicated to developing tools for bioinformatics and computational biology. Software development in Bioconductor is based on data containers which are structured formats to store and manage complex data. The most common data container in Bioconductor is *SummarizedExperiment* that is optimized for biological data analysis. This data container is further extended to a broad range of fields from metabolomics to metagenomics.

TreeSummarizedExperiment data container enables microbiome data science in the large *SummarizedExperiment* ecosystem. It is highly scalable and it supports integration of diverse multi-omics datasets. To support microbiome-specific operations, we have developed *mia* (Microbiome Analysis) family of packages, offering tools for data processing, analysis, and visualization. This ecosystem is further enhanced by contributions from independent developers, and thanks to a shared data container — *SummarizedExperiment* — a wide range of interoperable methods is readily available.

To help users and to promote the best practices in the field, we have developed an online book [Orchestrating Microbiome Analysis with Bioconductor \(OMA\)](#). This book and methods are products of collaborative development, and we are excited to keep developing them together with the community. To support this, we offer multiple channels for participation.

Pre-requisites

- Basic knowledge of R coding
- Basic knowledge of microbiome research

Goals and objectives

Learning goals

- **Methods for microbiome analysis:** Learn to harness *SummarizedExperiment* ecosystem in your project.
- **Data structure:** Understand how to utilize the *TreeSummarizedExperiment* class for effective microbiome data analysis.
- **Access resources:** Get familiar with additional tools and resources, including the OMA online book.

Learning objectives

- **Analyze and apply methods:** Apply the framework to process and analyze microbiome data.
- **Create visualizations:** Generate and interpret visualizations.
- **Explore documentation:** Use the OMA to explore additional tools and methods.