MicrobiomeAnalyst 2.0

Comprehensive statistical, functional and integrative analysis of microbiome data

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Motavition for version 2.0 development :

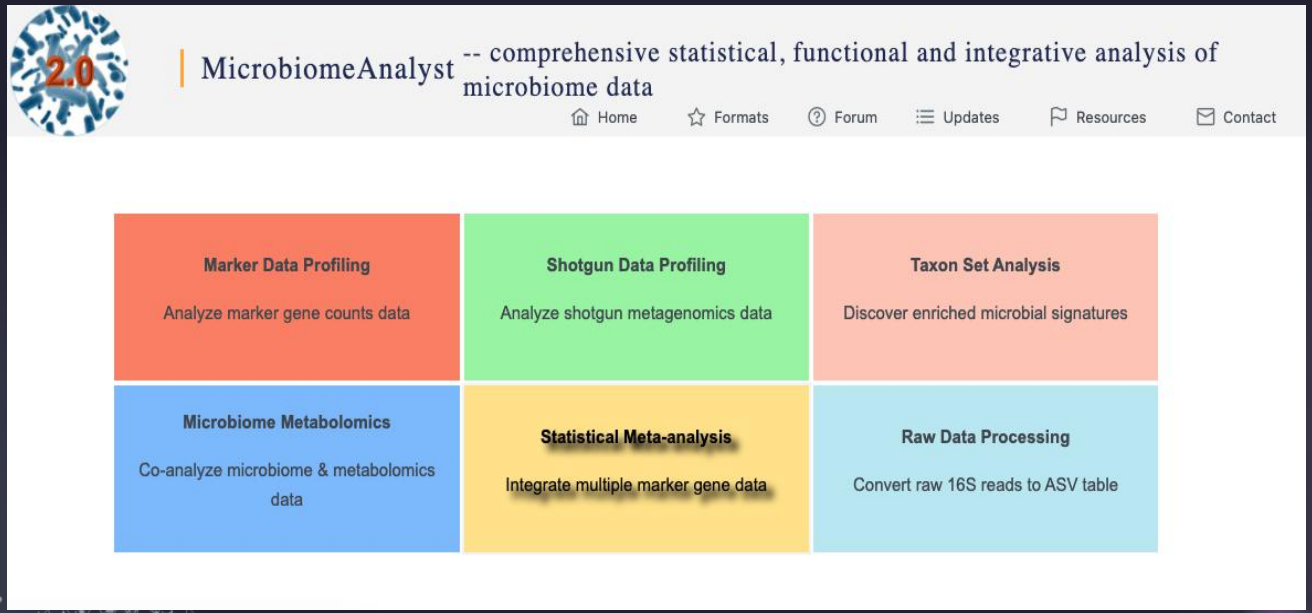
- The microbiome is a critical player in human health, sustainable agriculture and environmental sciences.

- The fast expanding of microbiome data and advancing multi-omics techniques call for update methods for comprehensive and integrative analysis to better understand the role of the microbiome.

- The previous version of MicorbiomeAnalyst did not support raw data processing, multi-omics integration and statistical meta-analysis.

Introducing MicrobiomeAnalyst 2.0

Goal: to support comprehensive statistics, visualization, functional interpretation, and integrative analysis of common data formats from microbiome studies



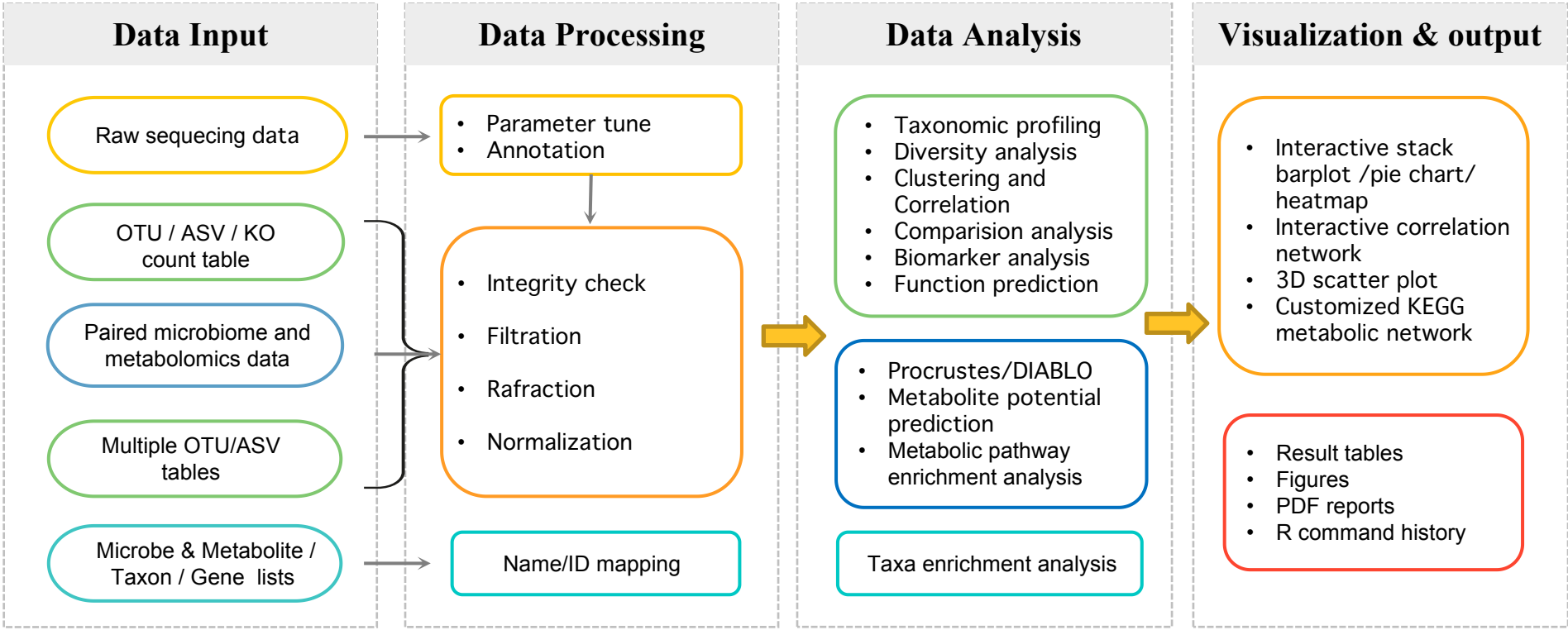
New modules in MicorbiomeAnalyst 2.0:

- Raw data processing module that links directly to downstream analysis
- Microbiome metabolomics module for co-analysis of microbiome and metabolomics data
- Statistical meta-analysis module for integrative analysis of multiple marker gene datasets

Enhanced features in MicorbiomeAnalyst 2.0:

- Editable metadata and multi-factor comparison analysis
- Updated approaches for marker gene function prediction and correlation network
- Enhanced visualization: interactive barplot and heatmap, KEGG metabolic network
- **Expanded taxon set libraries for taxa enrichment analysis**

Workflow


Data Input
Raw sequecing data
OTU / ASV / KO count table
Paired microbiome and metabolomics data
Multiple OTU/ASV tables
Microbe & Metabolite / Taxon / Gene lists
Data Processing
Parameter tune
Annotation
Integrity check
Filtration
Rafraction
Normalization
Name/ID mapping
Data Analysis
Taxonomic profiling
Diversity analysis
Clustering and Correlation
Comparision analysis
Biomarker analysis
Function prediction
Procrustes/DIABLO
Metabolite potential prediction
Metabolic pathway enrichment analysis
Taxa enrichment analysis
Visualization & output
Interactive stack barplot /pie chart/ heatmap
Interactive correlation network
3D scatter plot
Customized KEGG metabolic network
Result tables
Figures
PDF reports
R command history

Overview of amplicon sequencing data processing

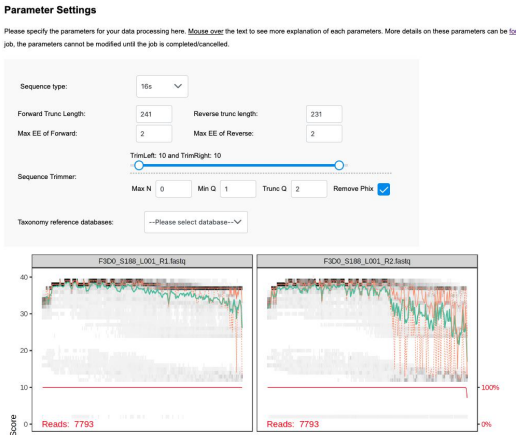
The raw sequece processing is based on the DADA2 pipeline:

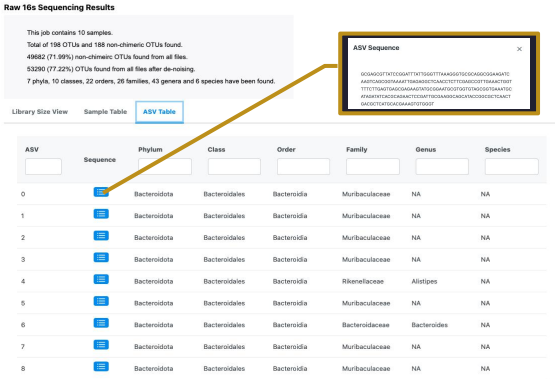
Raw read of marker gene (.fastq.gz)

+

Metafile

→ Integrity check → Parameter setting Quality control → ASV abundance table Taxonomy annotation → Downstream statistical analysis



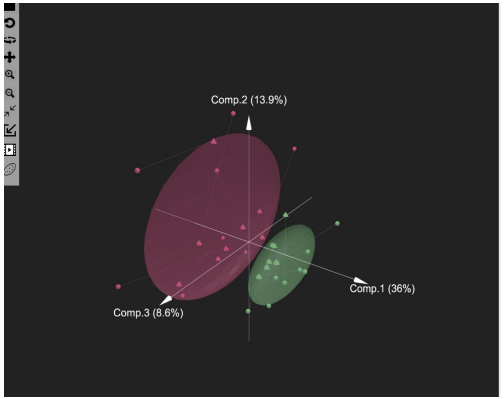


Overview of microbiome metabolomics

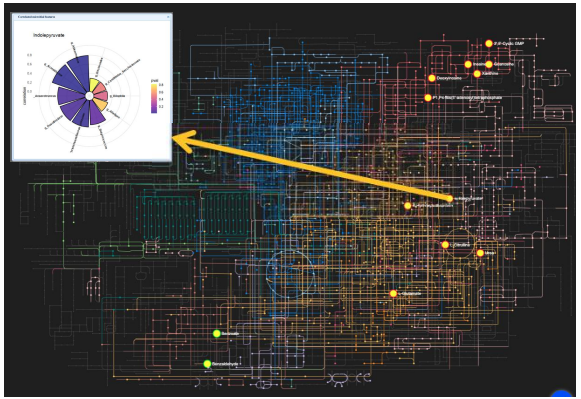
Paired microbiome-metabolimics **abundance tables** → Integrity check → Filtering Normalization → Differential analysis → ① ② ③

Paired microbiome-metabolimics **lists** → Name mapping → ② ③

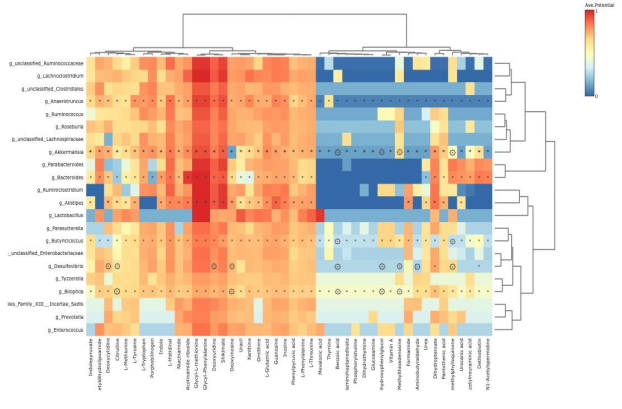
① Dimensionality reduction



② Metabolic network analysis



③ Correlation analysis



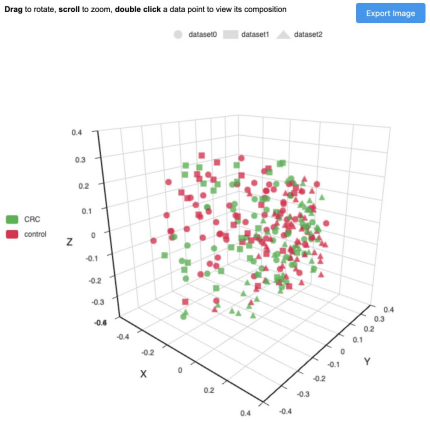
Overview of statistical meta-analysis:

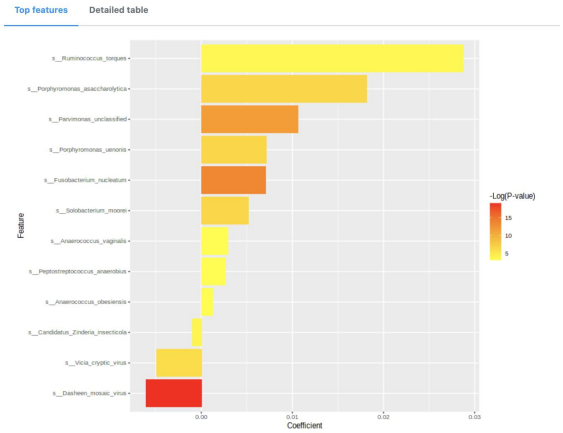
Multiple marker gene data table → Integrity check → Filtering Normalization → Differential analysis → ①②③

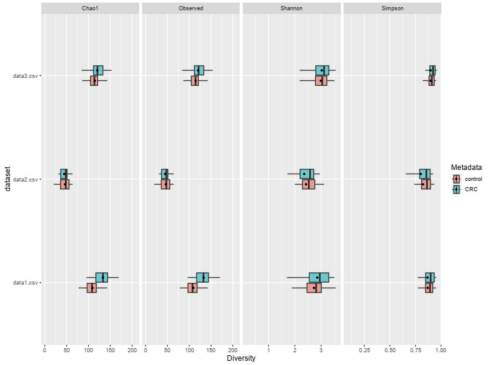
① Visual exploration

② Biomarker meta-analysis

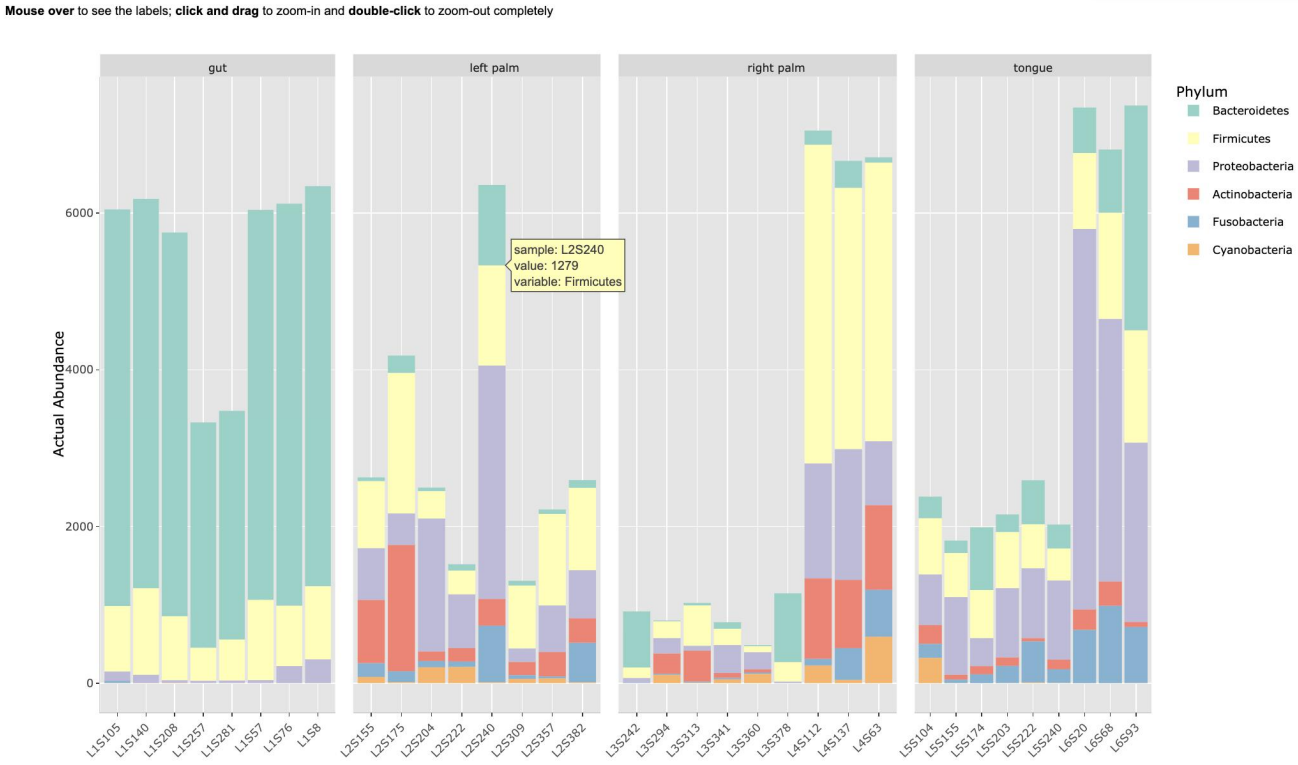
③ Diversity meta-analysis.



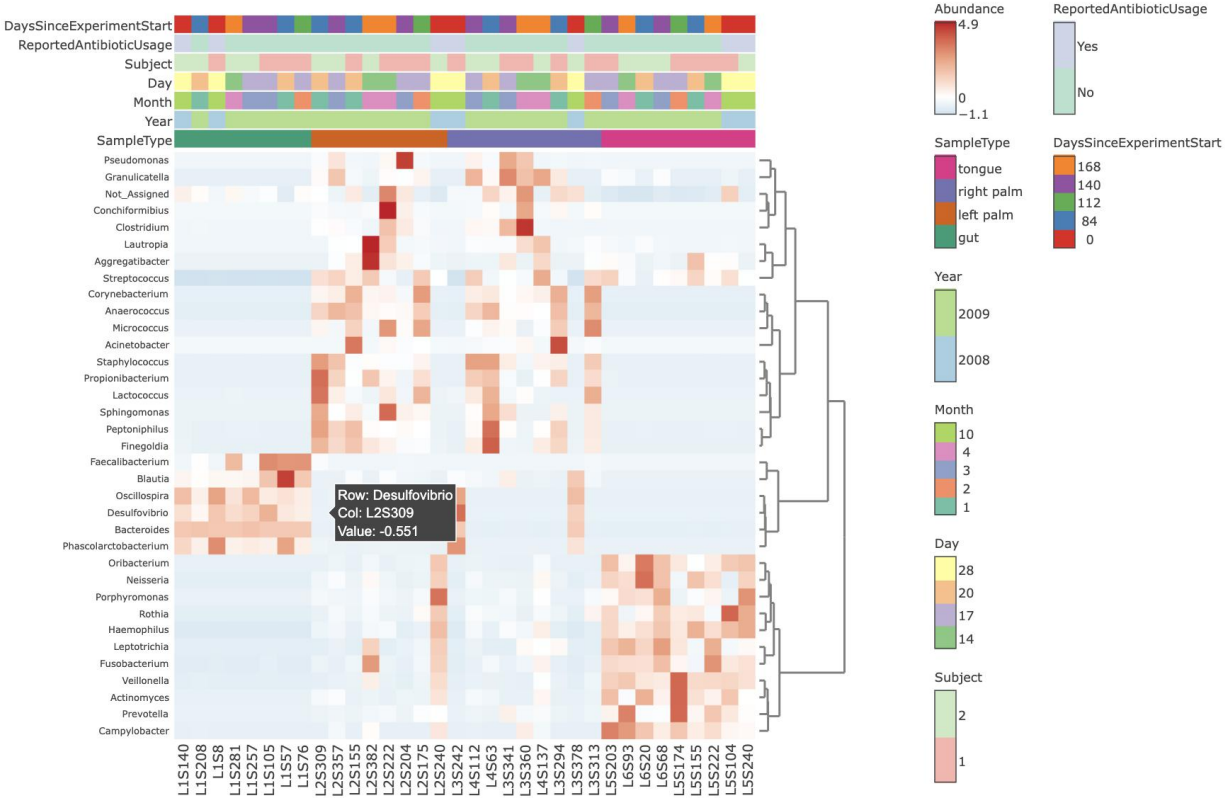




Interactive Stack Barplot :



Interactive Heatmap :



The End

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Also visit our forum for FAQs on www.omicsforum.ca