

# MicrobiomeAnalyst 2.0

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Comprehensive statistical, functional and  
integrative analysis of microbiome data

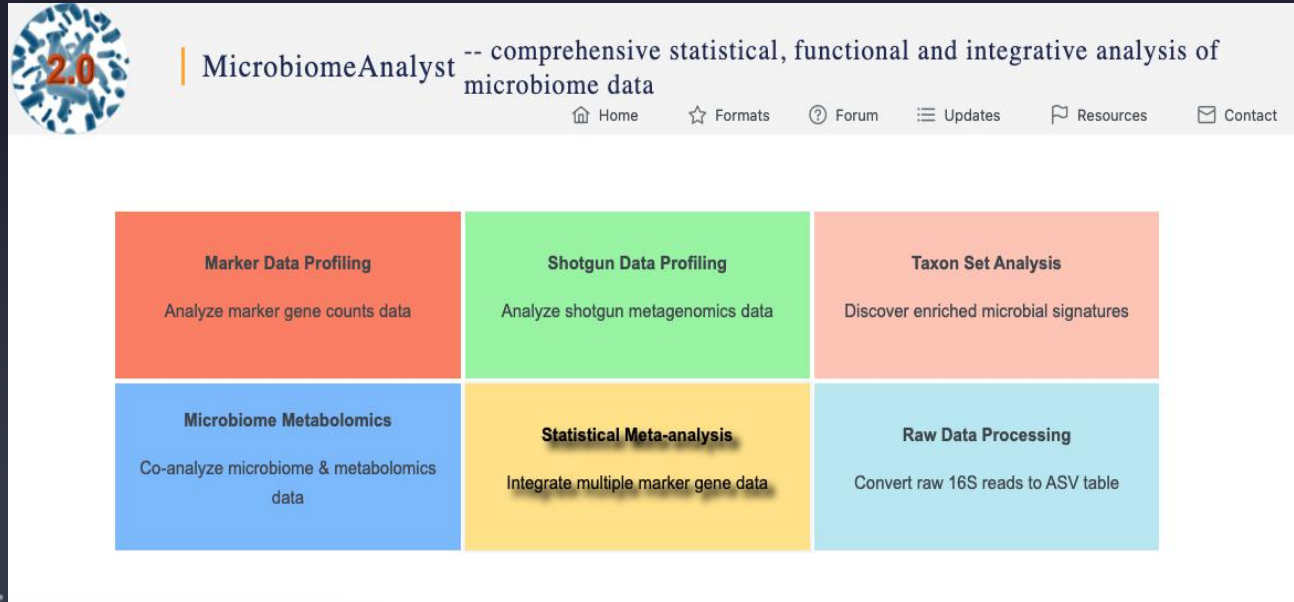


# Motivation for version 2.0 development :

- ❖ 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



The image shows the web interface of MicrobiomeAnalyst 2.0. At the top left is a circular logo with a blue and white pattern and the number '2.0' in red. To its right is the text 'MicrobiomeAnalyst' followed by a subtitle '-- comprehensive statistical, functional and integrative analysis of microbiome data'. Below this is a navigation bar with links: Home, Formats, Forum, Updates, Resources, and Contact. The main content area features a 2x3 grid of colored boxes, each representing a different analysis tool. The top row includes 'Marker Data Profiling' (orange), 'Shotgun Data Profiling' (green), and 'Taxon Set Analysis' (light orange). The bottom row includes 'Microbiome Metabolomics' (blue), 'Statistical Meta-analysis' (yellow), and 'Raw Data Processing' (light blue). Each box contains a brief description of the tool's function.

Marker Data Profiling	Shotgun Data Profiling	Taxon Set Analysis
Analyze marker gene counts data	Analyze shotgun metagenomics data	Discover enriched microbial signatures
Microbiome Metabolomics	Statistical Meta-analysis	Raw Data Processing
Co-analyze microbiome & metabolomics data	Integrate multiple marker gene data	Convert raw 16S reads to ASV table

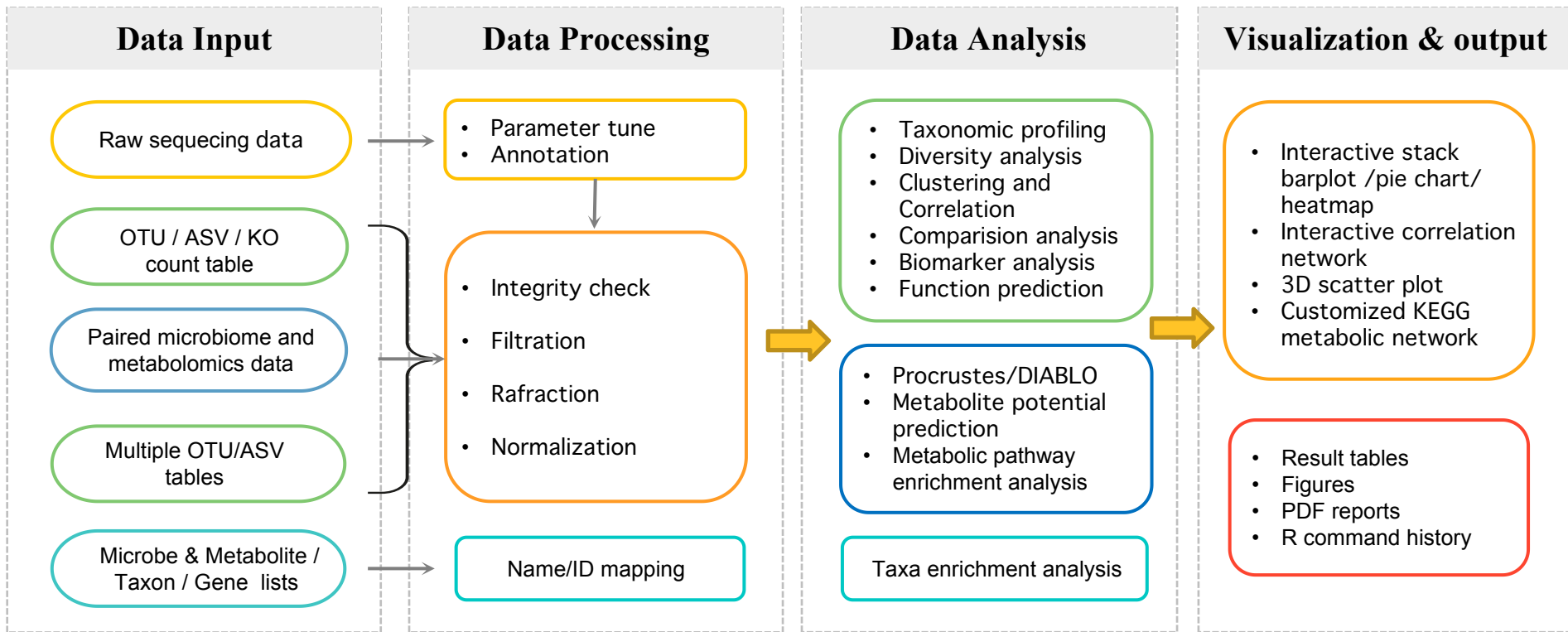
# New modules in MicorbiomeAnalyst 2.0:

- ❖ 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:

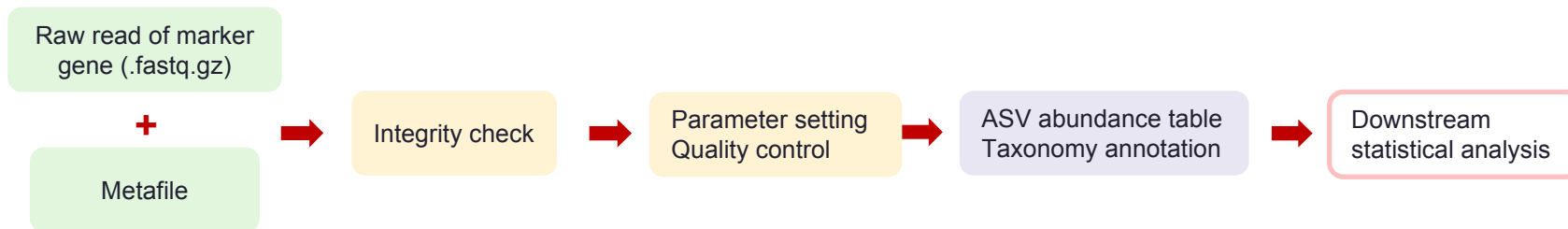
- ❖ Editable metadata and multi-factor comparison analysis
- ❖ Updated approaches for marker gene function prediction and correlation network
- ❖ Enhanced visualization: interactive barplot and heatmap, KEGG metabolic network
- ❖ **Expanded taxon set libraries for taxa enrichment analysis**

# Workflow



# Overview of amplicon sequencing data processing

The raw sequence processing is based on the DADA2 pipeline:



## Parameter Settings

Please specify the parameters for your data processing here. [Mouse over](#) the text to see more explanation of each parameter. More details on these parameters can be [found](#) here. The parameters cannot be modified until the job is completed/cancelled.

Sequence type:

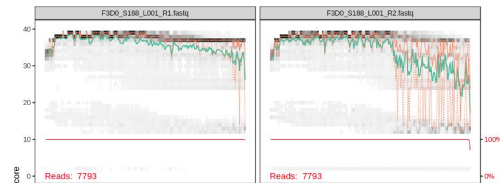
Forward Trunc Length:  Reverse trunc length:

Max EE of Forward:  Max EE of Reverse:

Time Left: 10 and Time Right: 10

Sequence Trimmer:    ☒ Remove PhiX

Taxonomy reference databases:



## Raw 16s Sequencing Results

This job contains 10 samples.  
Total of 198 OTUs and 188 non-chimeric OTUs found.  
49682 (71.96%) non-chimeric OTUs found from all files.  
53290 (77.22%) OTUs found from all files after de-noising.  
7 phyla, 10 classes, 22 orders, 26 families, 43 genera and 6 species have been found.

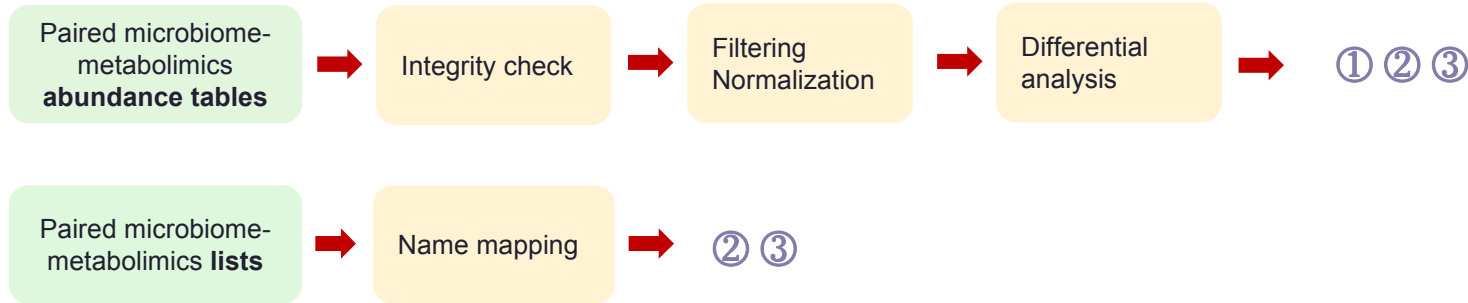
Library Size View Sample Table [ASV Table](#)

ASV	Sequence	Phylum	Class	Order	Family	Genus	Species
0	<a href="#">View</a>	Bacteroidota	Bacteroidales	Bacteroidia	Muribaculaceae	NA	NA
1	<a href="#">View</a>	Bacteroidota	Bacteroidales	Bacteroidia	Muribaculaceae	NA	NA
2	<a href="#">View</a>	Bacteroidota	Bacteroidales	Bacteroidia	Muribaculaceae	NA	NA
3	<a href="#">View</a>	Bacteroidota	Bacteroidales	Bacteroidia	Muribaculaceae	NA	NA
4	<a href="#">View</a>	Bacteroidota	Bacteroidales	Bacteroidia	Rikenellaceae	Aliitiger	NA
5	<a href="#">View</a>	Bacteroidota	Bacteroidales	Bacteroidia	Muribaculaceae	NA	NA
6	<a href="#">View</a>	Bacteroidota	Bacteroidales	Bacteroidia	Bacteroidaceae	Bacteroides	NA
7	<a href="#">View</a>	Bacteroidota	Bacteroidales	Bacteroidia	Muribaculaceae	NA	NA
8	<a href="#">View</a>	Bacteroidota	Bacteroidales	Bacteroidia	Muribaculaceae	NA	NA

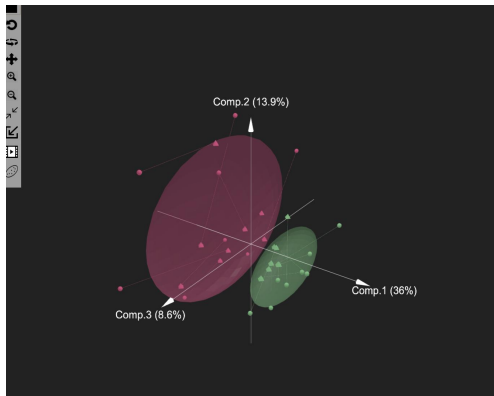
**ASV Sequence**

```
GGGAGTGTTCGGATTTTGGTTTGAAGGTTGTCGAGGCGGAGATC  
AAGTACGAGGAAATTAAGAGTTCAGCTTGTGAGGCGTTCAGTCTT  
TTCTTCTTGAAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
ATGATATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
```

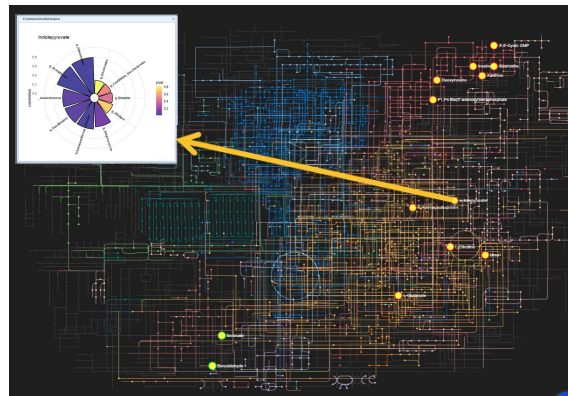
# Overview of microbiome metabolomics



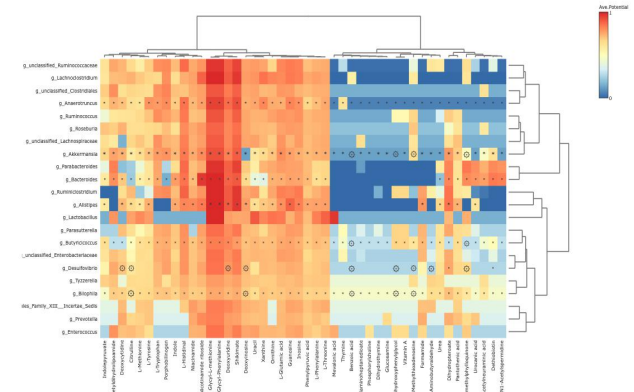
## ① Dimensionality reduction



## ② Metabolic network analysis

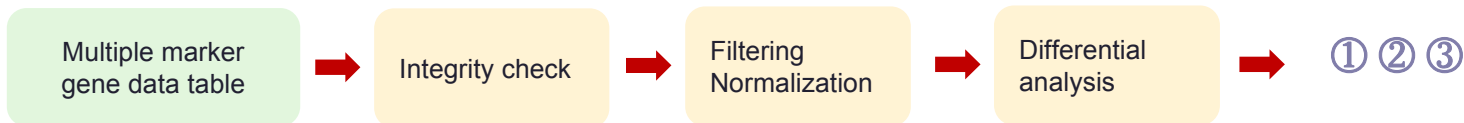


## ③ Correlation analysis

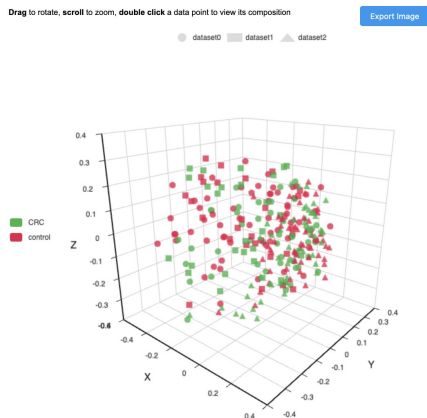




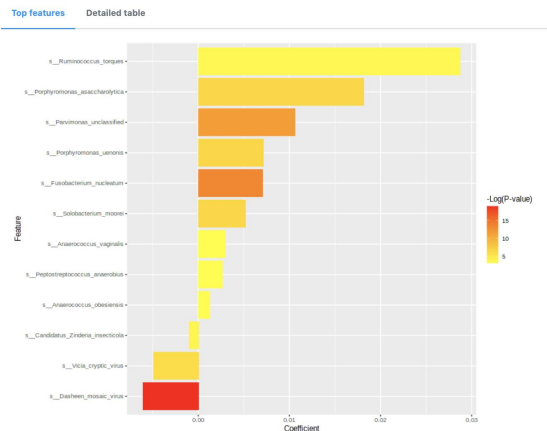
# Overview of statistical meta-analysis:



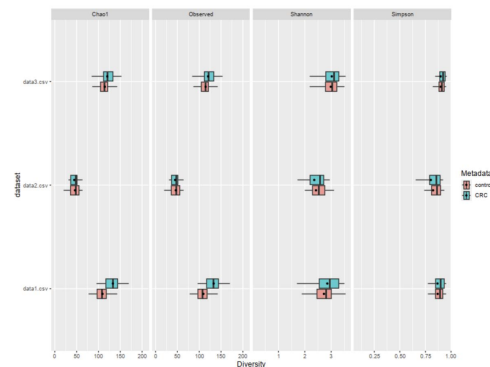
## ① Visual exploration



## ② Biomarker meta-analysis

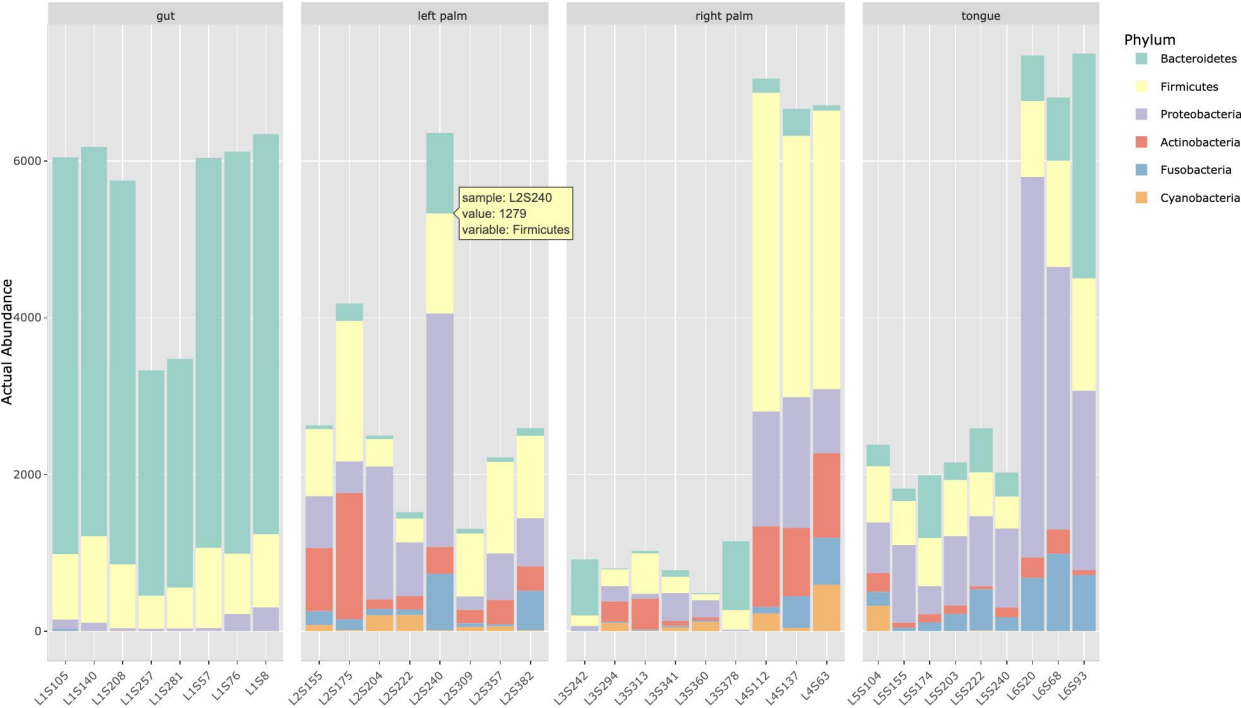


## ③ Diversity meta-analysis.

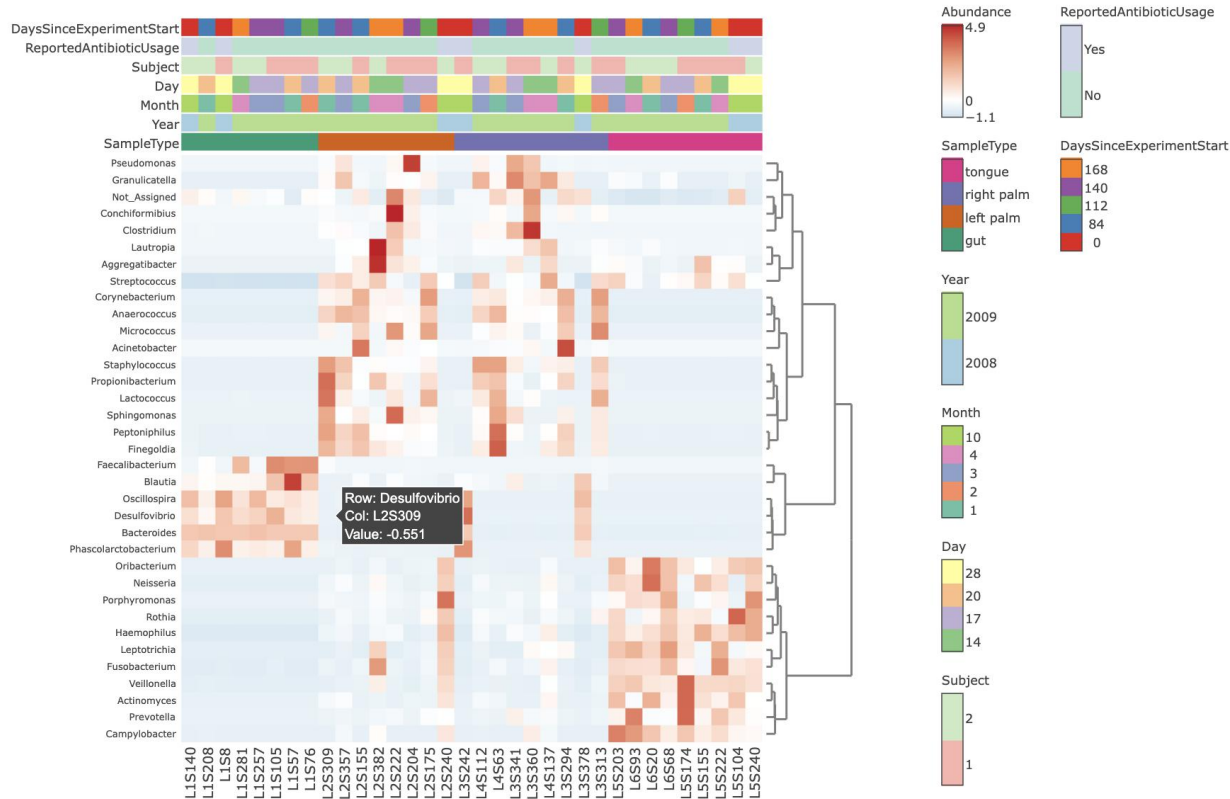


# Interactive Stack Barplot :

Mouse over to see the labels; click and drag to zoom-in and double-click to zoom-out completely



# Interactive Heatmap :



# The End



For more information, visit Tutorials, Resources  
and Contact pages on [www.microbiomeanalyst.ca](http://www.microbiomeanalyst.ca)  
Also visit our forum for FAQs on [www.omicsforum.ca](http://www.omicsforum.ca)