

# MicrobiomeAnalyst 2.0

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Comprehensive statistical, functional and  
integrative analysis of microbiome data

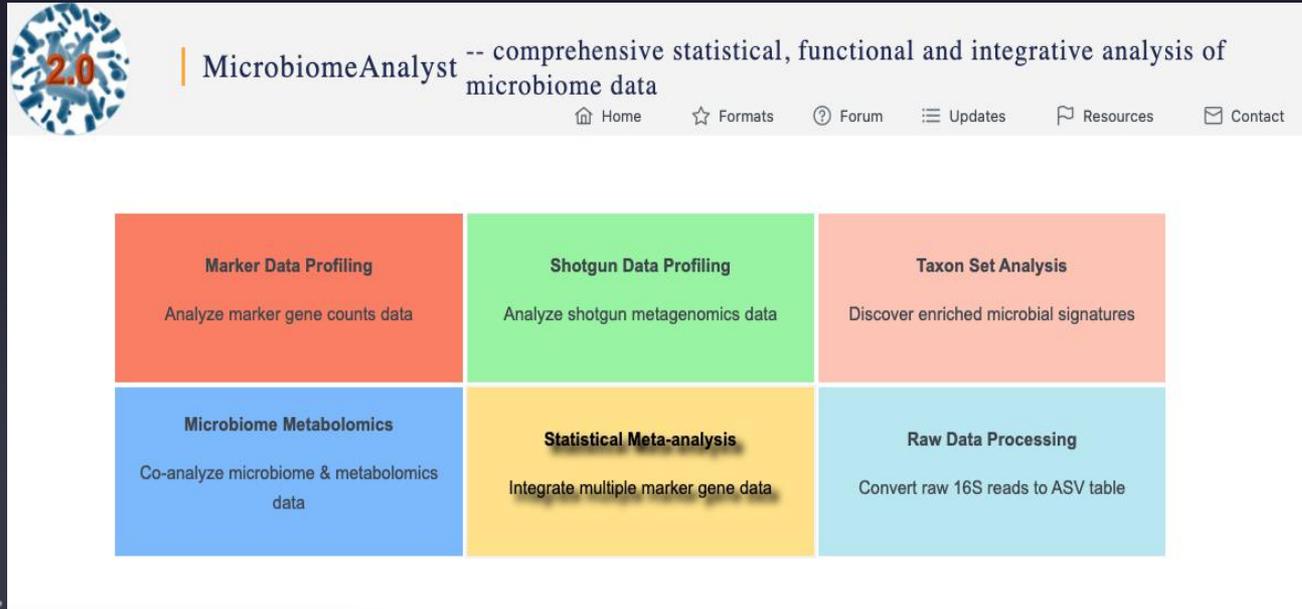


# Motivation for version 2.0 development :

- ❖ 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 MicrobiomeAnalyst 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 screenshot displays the MicrobiomeAnalyst 2.0 website. At the top left is a circular logo with a blue and white pattern and the number '2.0' in red. To the right of the logo, the text reads 'MicrobiomeAnalyst -- comprehensive statistical, functional and integrative analysis of microbiome data'. Below this is a navigation bar with icons and labels for 'Home', 'Formats', 'Forum', 'Updates', 'Resources', and 'Contact'. The main content area features a 2x3 grid of colored boxes, each representing a different analysis tool:

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

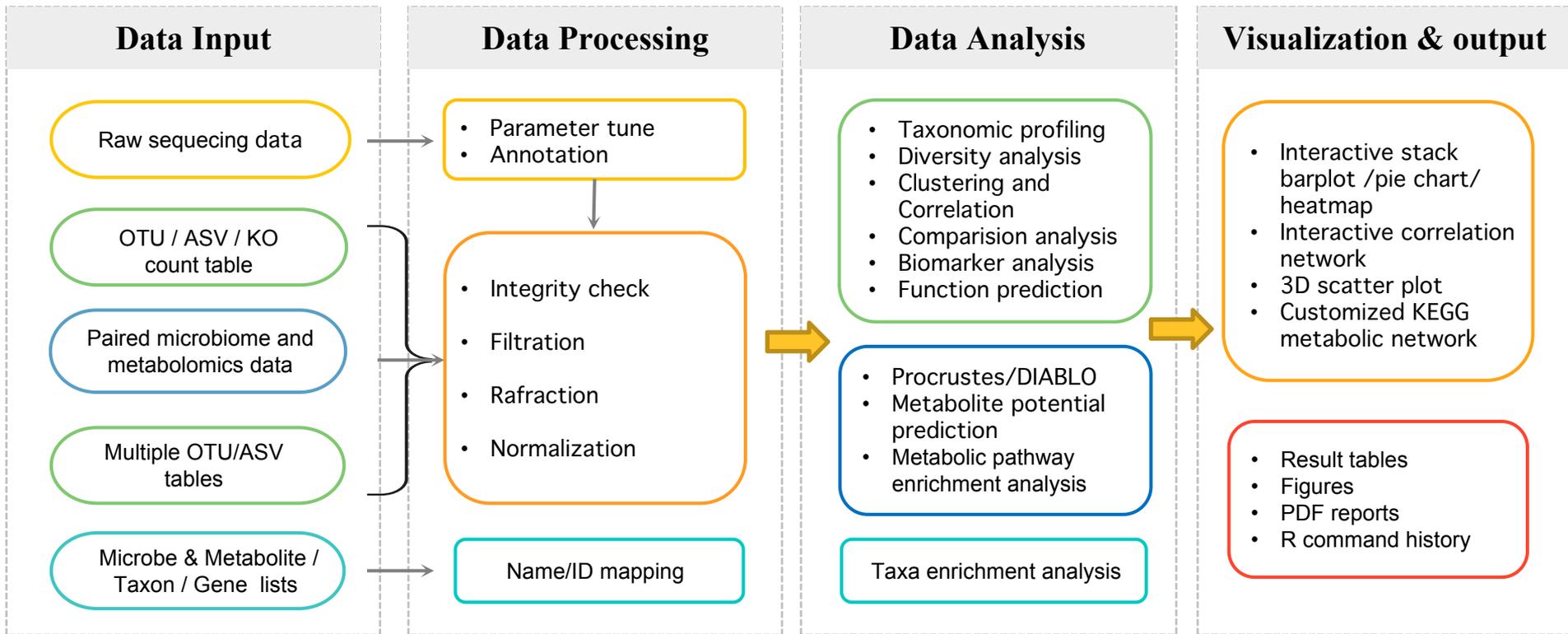
# New modules in MicorbiomeAnalyst 2.0:

- ❖ 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:

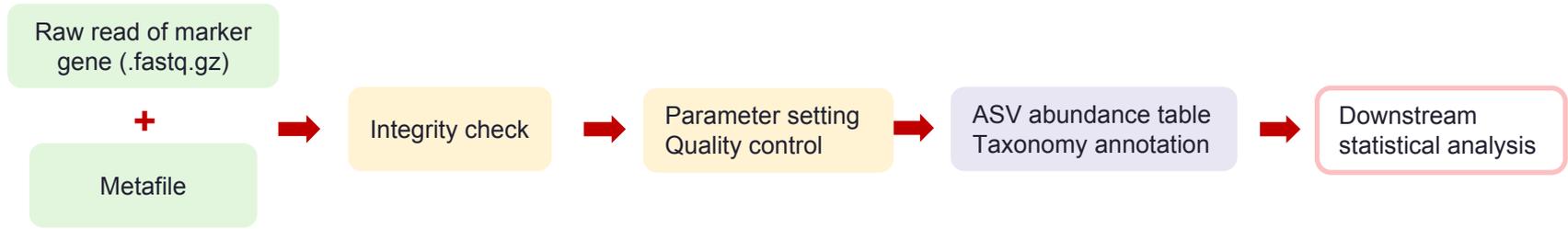
- ❖ Editable metadata and multi-factor comparison analysis
- ❖ Updated approaches for marker gene function prediction and correlation network
- ❖ Enhanced visualization: interactive barplot and heatmap, KEGG metabolic network
- ❖ **Expanded taxon set libraries for taxa enrichment analysis**

# 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/canceled.

Sequence type:

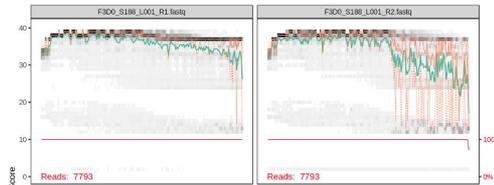
Forward Trunc Length:  Reverse trunc length:

Max EE of Forward:  Max EE of Reverse:

Trim Left: 10 and Trim 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

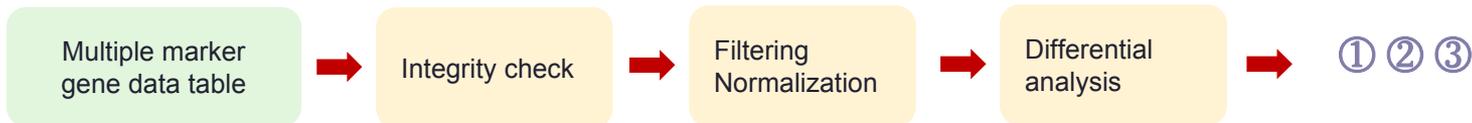
ASV	Sequence	Phylum	Class	Order	Family	Genus	Species
0		Bacteroidota	Bacteroidales	Bacteroidia	Muribaculaceae	NA	NA
1		Bacteroidota	Bacteroidales	Bacteroidia	Muribaculaceae	NA	NA
2		Bacteroidota	Bacteroidales	Bacteroidia	Muribaculaceae	NA	NA
3		Bacteroidota	Bacteroidales	Bacteroidia	Muribaculaceae	NA	NA
4		Bacteroidota	Bacteroidales	Bacteroidia	Rikenellaceae	Allistipes	NA
5		Bacteroidota	Bacteroidales	Bacteroidia	Muribaculaceae	NA	NA
6		Bacteroidota	Bacteroidales	Bacteroidia	Bacteroidaceae	Bacteroides	NA
7		Bacteroidota	Bacteroidales	Bacteroidia	Muribaculaceae	NA	NA
8		Bacteroidota	Bacteroidales	Bacteroidia	Muribaculaceae	NA	NA

**ASV Sequence**

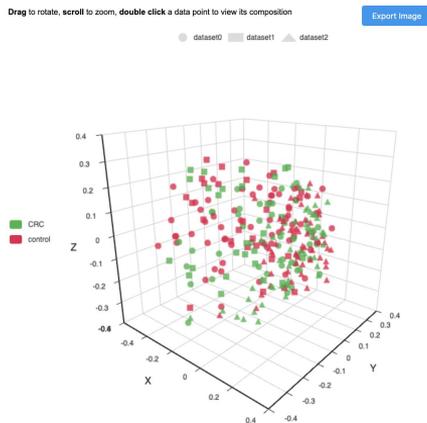
```
GGGAGGTTTCGGATTCTTGTTTGAAGGATGTCGAGGCGAGGAGT  
AATTCAGGCGAATTAATTAAGAGTCAGCTCTTGAGAGGCTTGAATTTT  
TTCTTCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG  
AATATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG  
AGAGGTTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
```



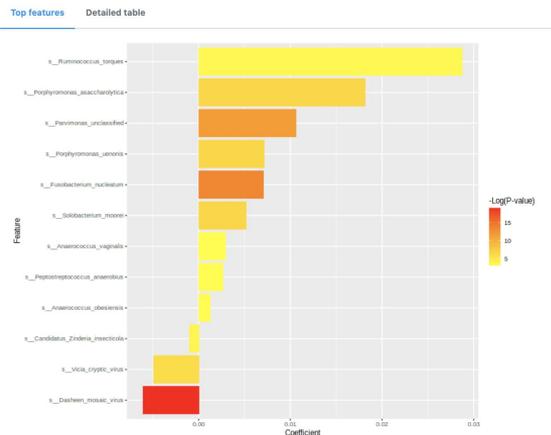
# Overview of statistical meta-analysis:



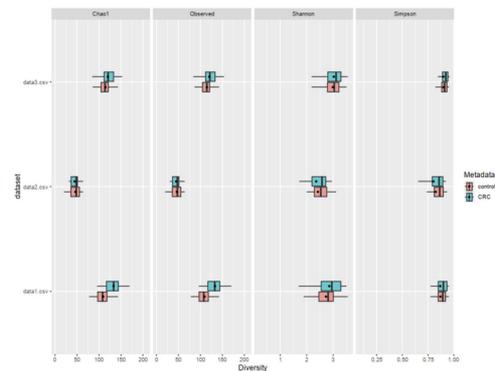
## ① Visual exploration



## ② Biomarker meta-analysis

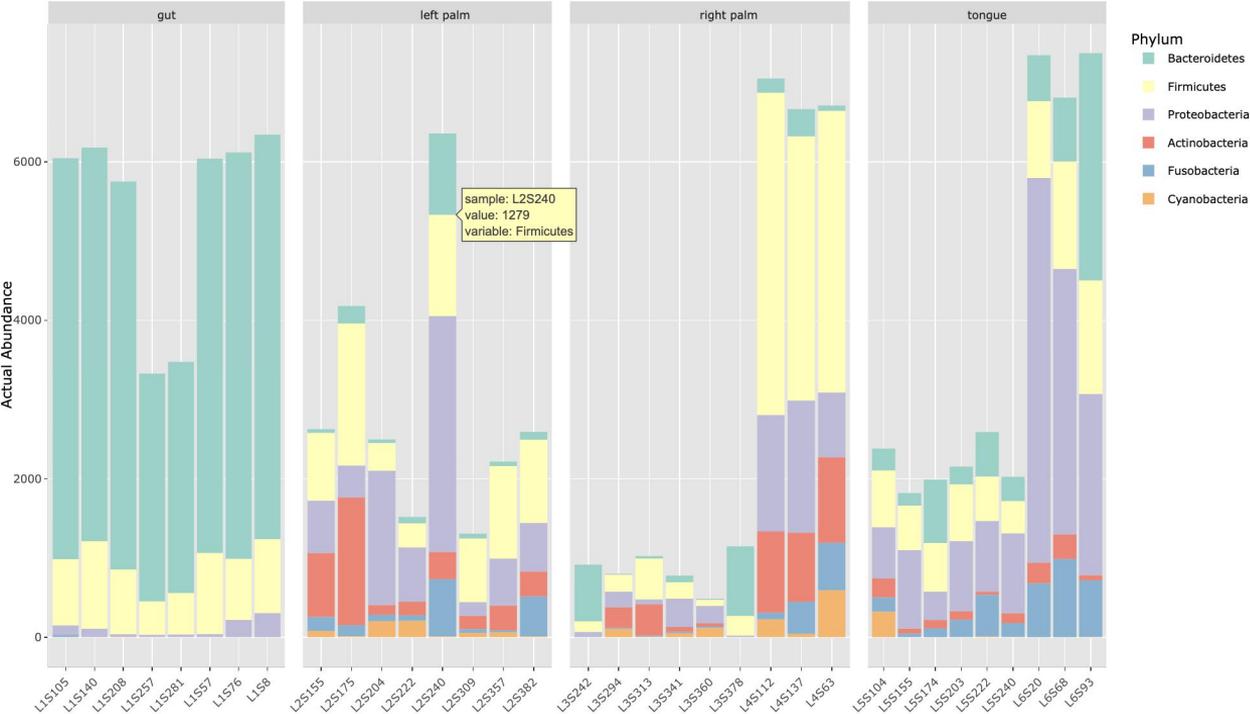


## ③ Diversity meta-analysis.

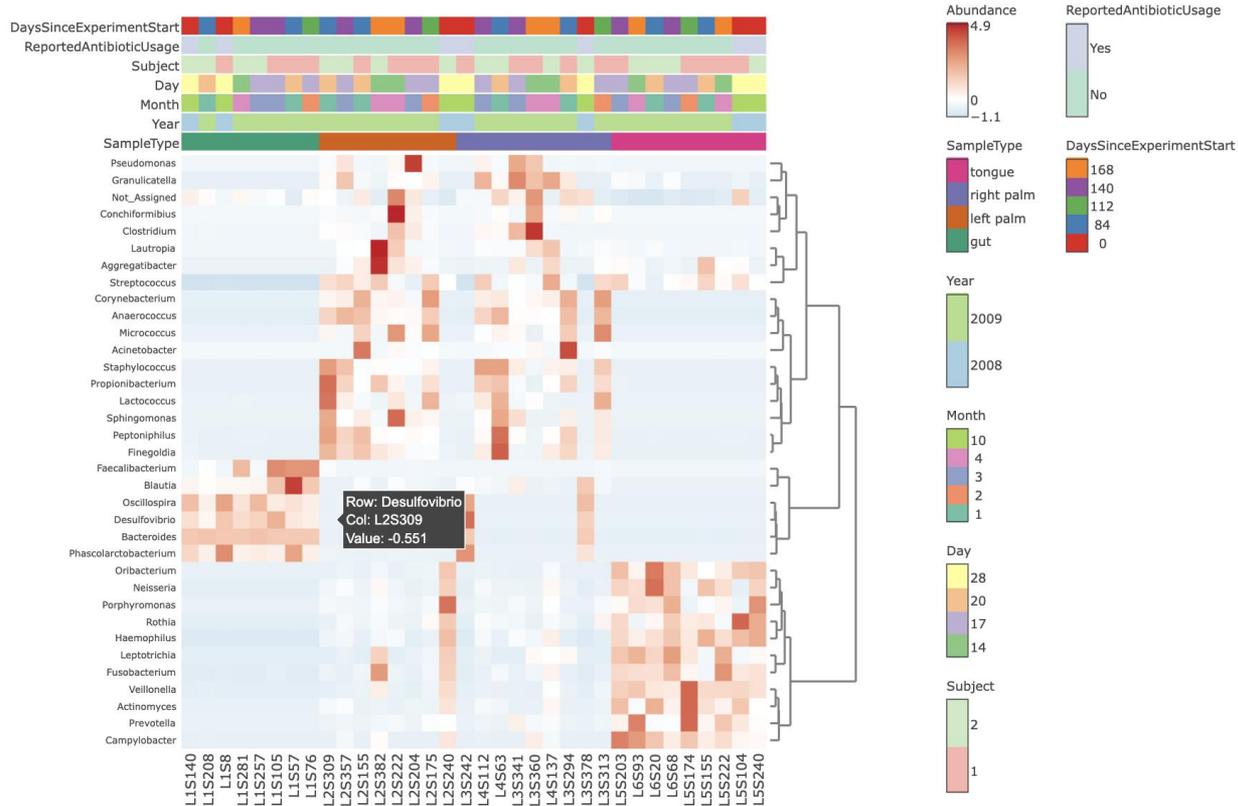


# Interactive Stack Barplot :

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)