

Microbiota amplicOn
CHaracterization Implement

MOCHI

User Guide

MOCHI

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MOCHI is a microbiota amplicon rRNA analytical tool for 16S and 18S microbiota. It is based primarily on QIIME2 (2021.4) and has a friendly web interface powered by the R package Shiny.

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BugReports https://github.com/v0369012/mochi_web_service

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CHAPTER 1: INSTALLATION OF LOCAL SERVICE

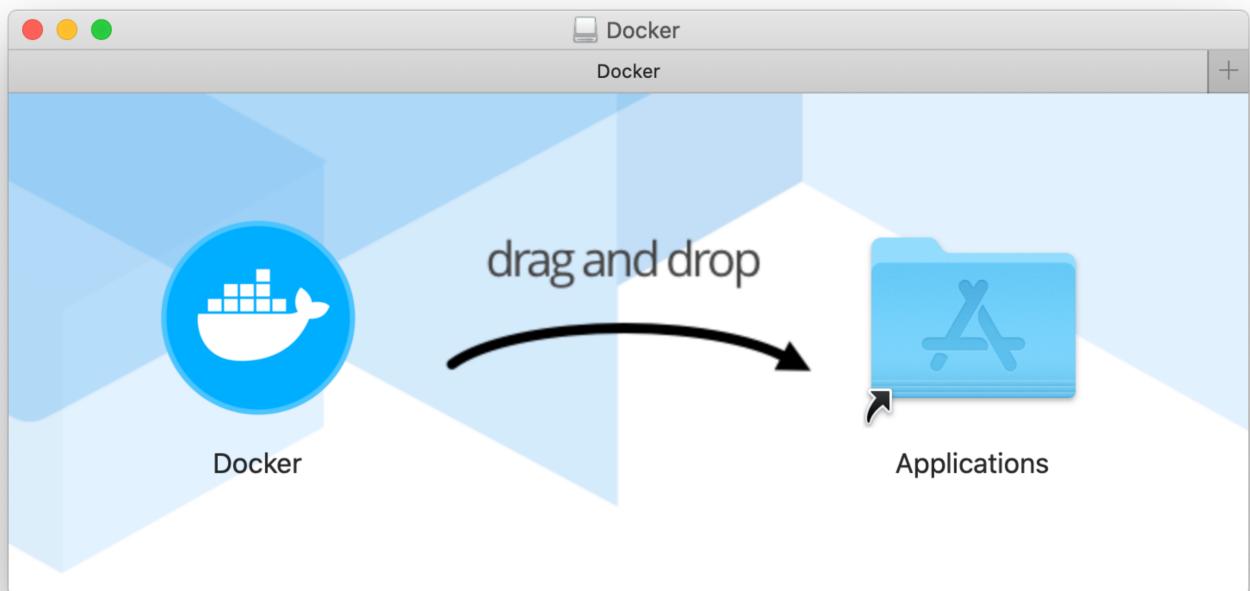
MacOS

(A) Install Docker

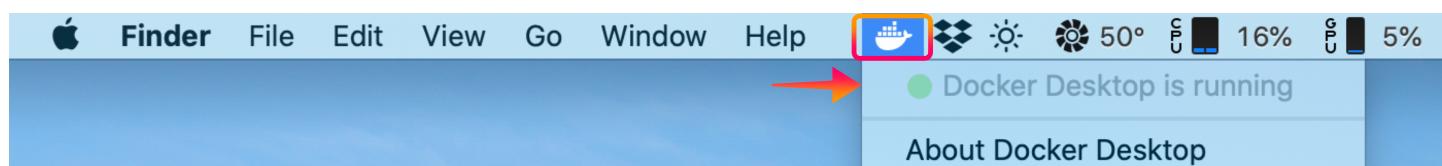
1. Download [Docker Desktop](#).



2. Open “**Docker.dmg**” file. Drag **Docker Desktop** app to the Applications folder.



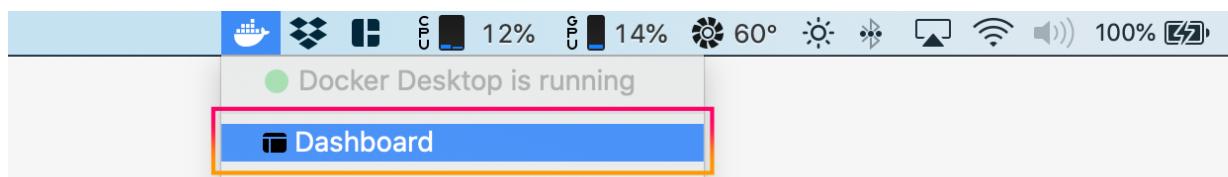
3. Start the Docker service by double clicking the Docker app. Wait for a few seconds to load, the docker icon should appear in the status bar.



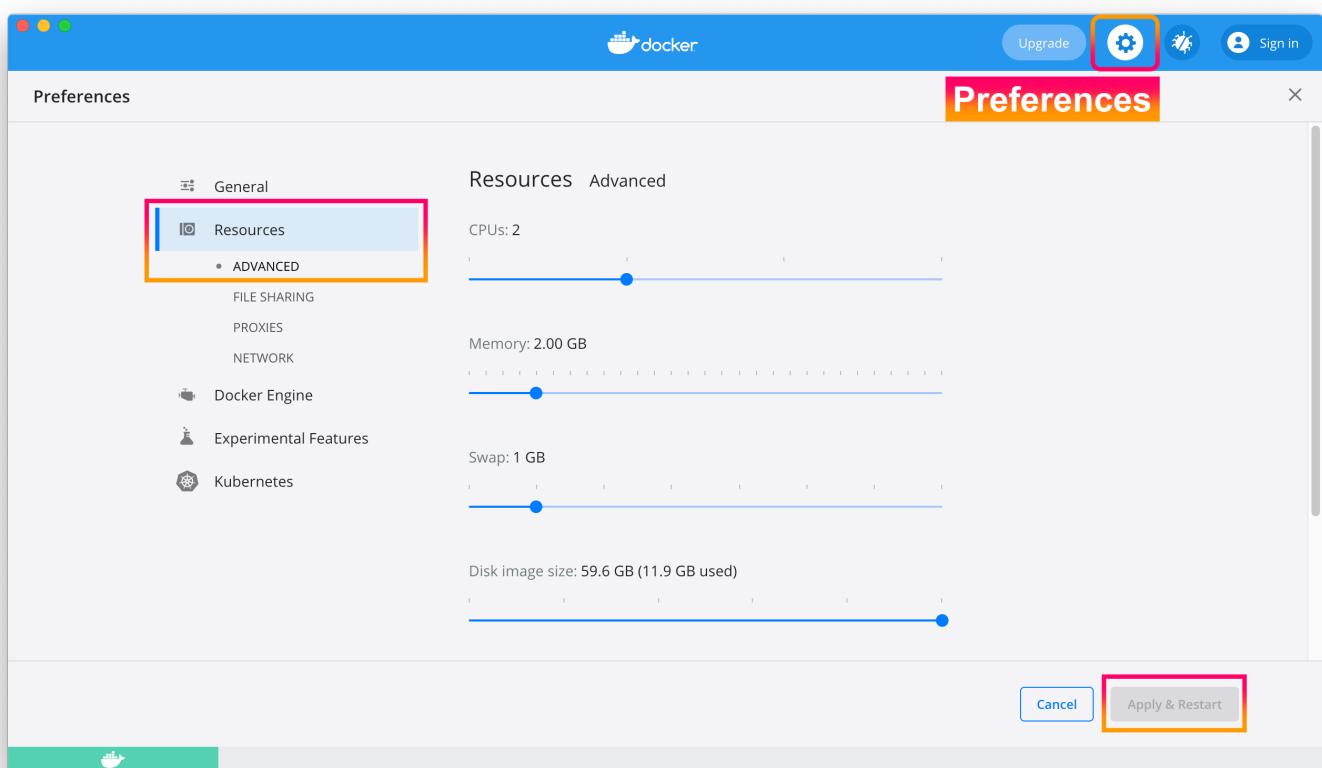
4. (Optional) In MacOS, the computational resources are preset in Docker app. To optimize the efficiency of analysis, the user can adjust the settings with the following instruction. We recommend settings **above 4 CPUs** and **8-16 GB memory** (by default, MOCHI only uses a maximum of 16 GB memory).

⚠ Assigning all of the resources to Docker may cause your system to delay or crash.

4.1. Open the Docker dashboard from the drop-down menu in the status bar.



4.2. Go to **Preference / Resources / Advanced**. Adjust the resources using the rolling bar. Press “Apply & Restart”. Waiting for Docker to restart.

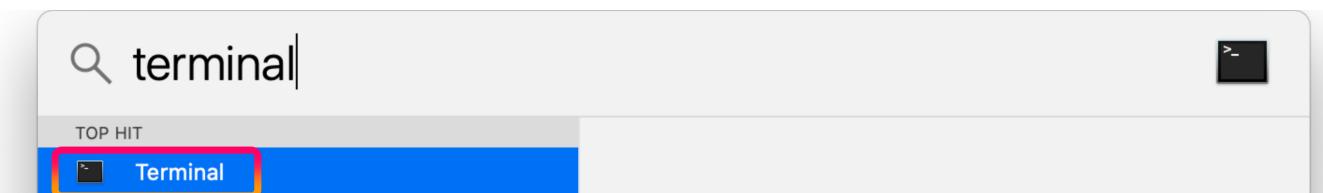


(B) Start MOCHI service

1. Download “**docker-compose.yml**” from [NCTU website](#), and place it under a folder named “**MOCHI**”.



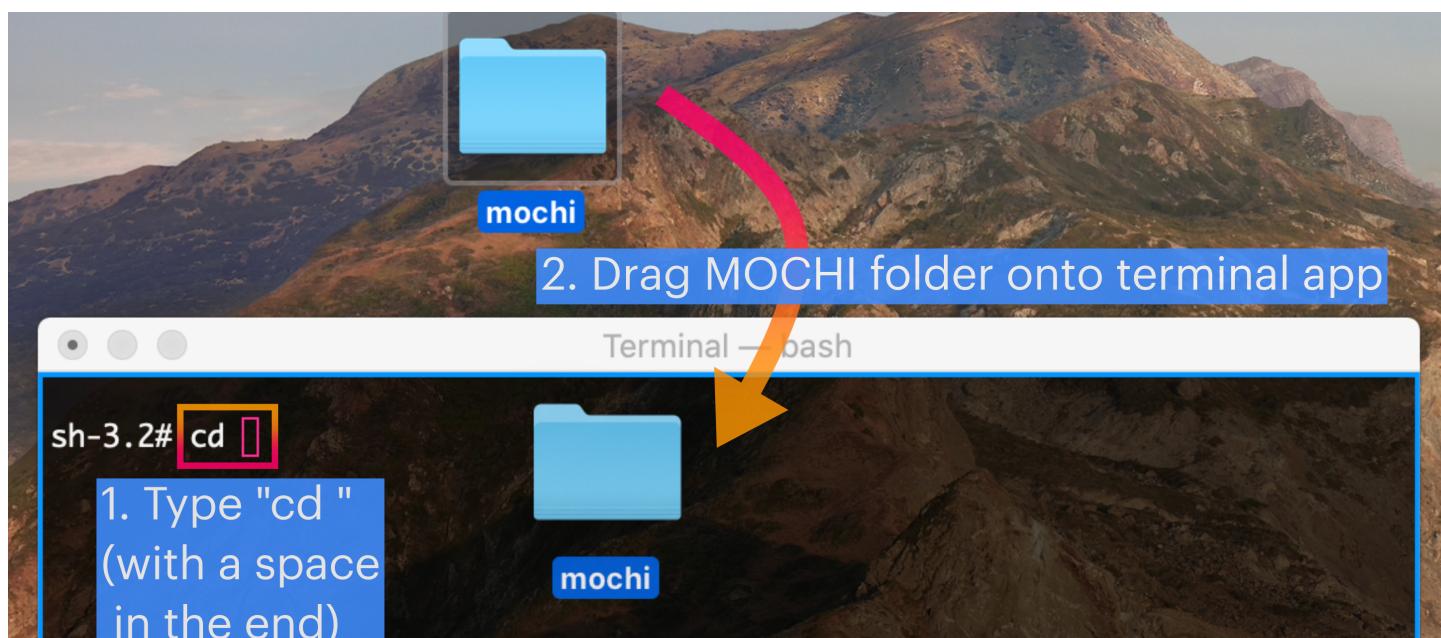
2. Open the **Terminal** app. (Press “Command + Space” to open Spotlight and type “terminal”.)



3. Run **cd /path/to/MOCHI** to navigate to the MOCHI directory.

```
sh-3.2# cd /Users/Mac/Desktop/mochi
```

Hint: If you do not know the folder path of MOCHI, type **cd** and then a space, and then drag the MOCHI folder into the terminal window. The folder path should appear in the terminal automatically.



4. Run `docker-compose up -d` to download and start the MOCHI image from Docker Hub. (The download process will only run during the first setup. The size of the MOCHI image is around 10 GB, and the running time depends on the download speed.)

```
[powang@MacBook-Pro--PoWang mochi % docker-compose up -d
WARNING: Some services (mochi_server) use the 'deploy' key, which will be ignored. Compose does not support 'deploy' configuration - use `docker stack deploy` to deploy to a swarm.
Creating network "mochi_default" with the default driver
Pulling mochi_server (dockerjjz/mochi_local:...
latest: Pulling from dockerjjz/mochi_local
f15005b0235f: Pull complete
1901fd813023: Pull complete
a92940affedf: Pull complete
dbebda29cb22: Pull complete
3c63b26b92fd: Pull complete
e0c15c0b4e0b: Pull complete
Digest: sha256:1501a145eb826f9f799239964eb064170fdc5be8abcd7b04fd9a61c888b9dee
Status: Downloaded newer image for dockerjjz/mochi_local:latest
Creating mochi_server ... done]
```

5. Open the browser, and type **127.0.0.1:3811** in the address bar. A MOCHI interactive webpage will appear and you will be able to begin your analysis.

Welcome to MOCHI! (Microbiota amplicon CHaracterization Implement)

MOCHI is a 16S or 18S microbiota amplicon rRNA analytical tool for microbiota based primarily on QIIME2 with a friendly web interface powered by the R package of Shiny. MOCHI may also be downloaded and operated locally.

Overview of MOCHI

The MOCHI pipeline consists of three main steps:

- Sequence Preprocessing:** This step includes a sequence summary (read counts, read quality) and sequence denoising (DADA2) (sequence table, alpha rarefaction).
- Taxonomy Analysis:** This step includes a taxonomy table, Krone, bar plot, heatmap, alpha diversity, box plot, PCoA plot, ANCOM, comparison between groups, and post hoc analysis.
- Function Analysis:** This step includes FAPROTAX, functional annotation table, and bar plot.

The advantages of MOCHI

- Friendly user interface: point-and-click and fill-in inputs, no programming required.
- Cross-platform: simple set-up with Docker containers on Linux, Windows, or Mac OS.
- Local computing resource: runs on your premise with privacy, not subject to network reliability and limitation.
- Compatible with other downstream analytical tools
- Publishable plots and charts generated with chosen parameters

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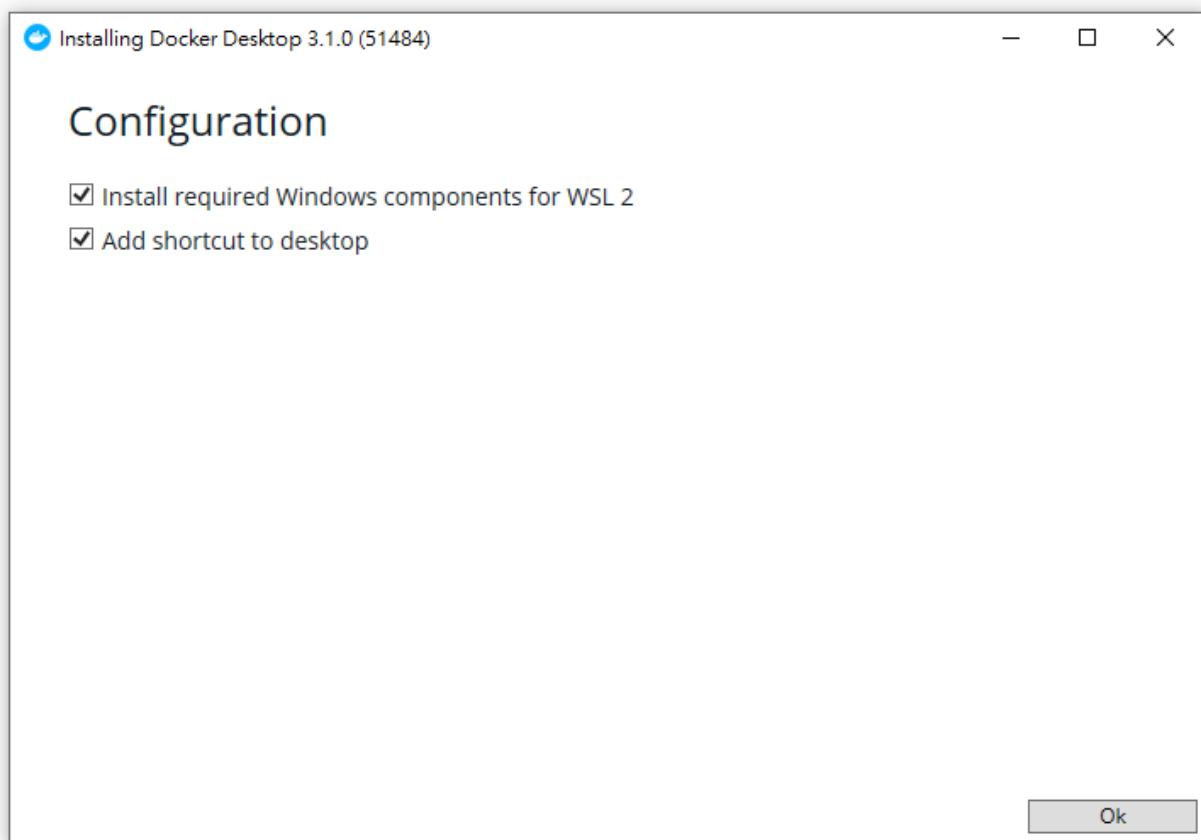
Windows 10

(A) Install Docker

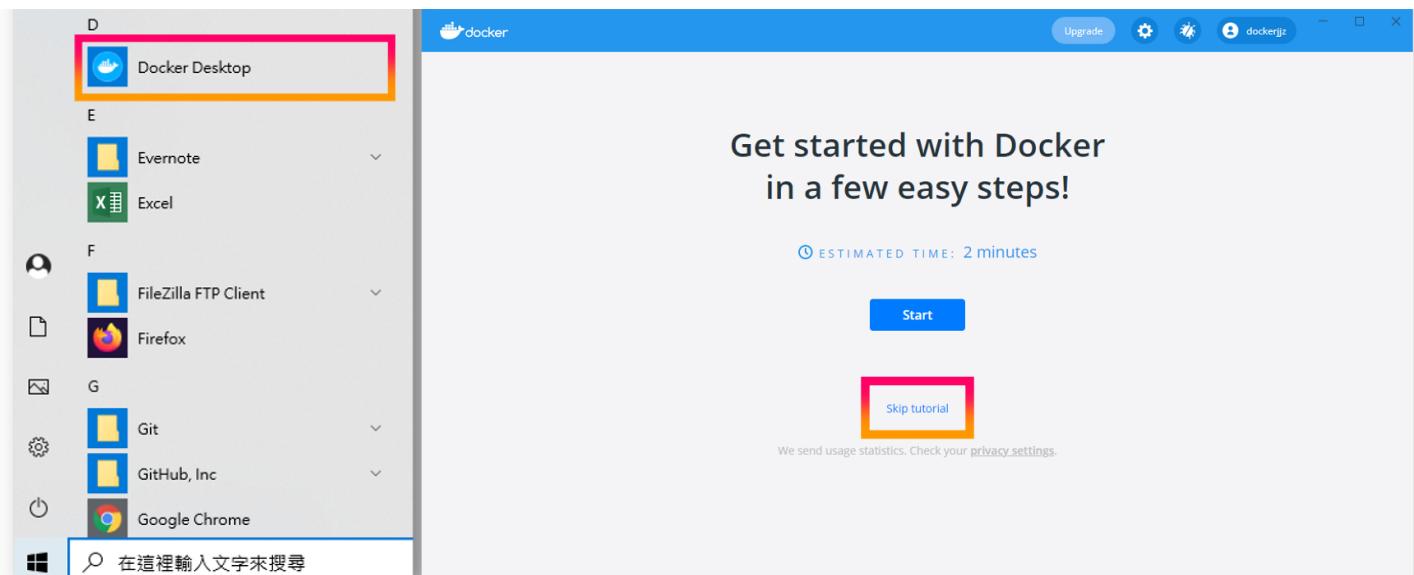
6. Download [Docker Desktop](#).



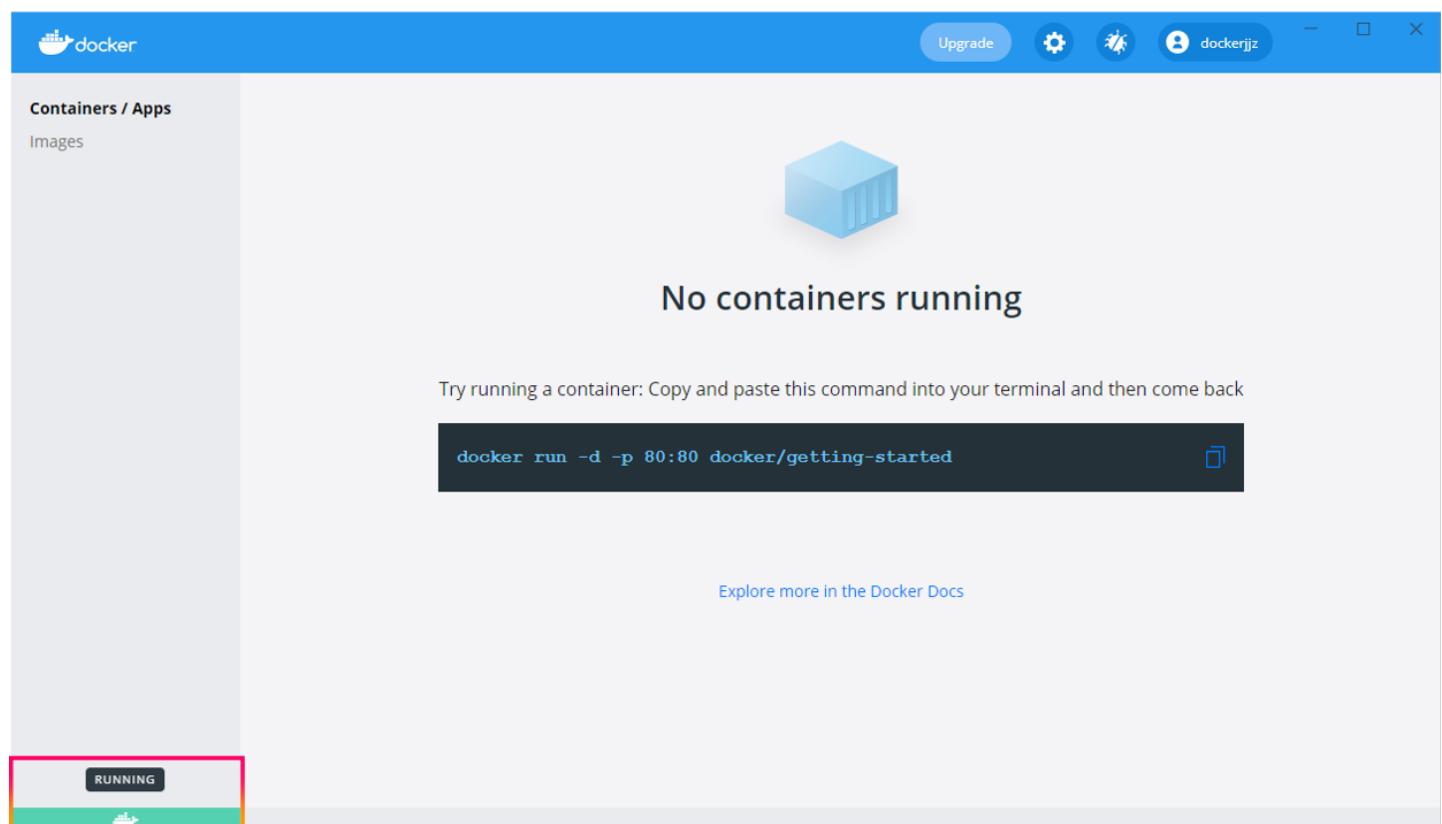
7. Run "**Docker Desktop Installer.exe**" and follow the instructions for setup. (You may be asked whether to install WSL2 Engine. By default, it is installed along with Docker to speed up the performance but is not required for running MOCHI. Use the default setting if you don't know what to choose.)



8. Start Docker by **clicking the Docker icon**. Press “Skip tutorial”.



9. If the Docker service has been successfully turned on, a green indicator will appear on the bottom-left in the Docker window.

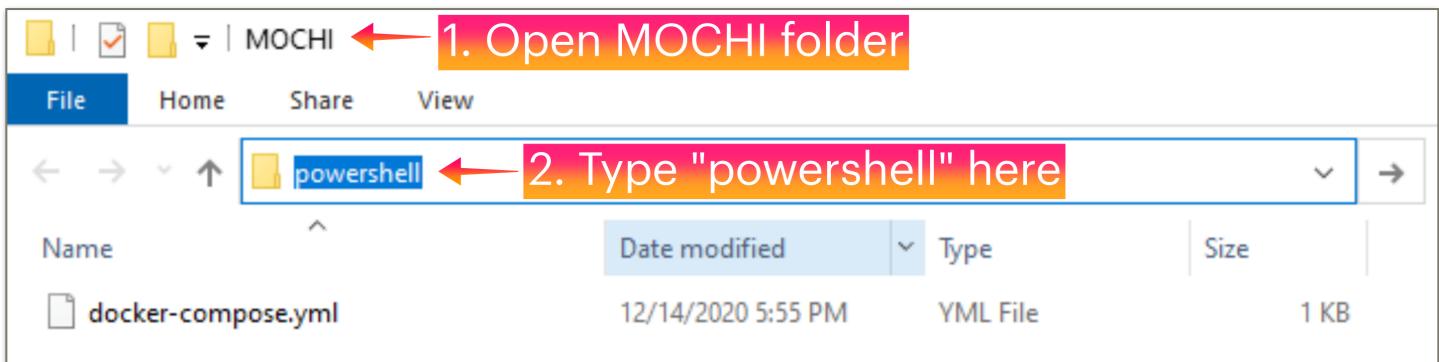


(B) Start MOCHI service

1. Download “**docker-compose.yml**” from the NCTU website, and place it in a folder named “**MOCHI**”.



2. Open **MOCHI** folder, type “**powershell**” in the address bar, and press enter. This will open a command-line shell under MOCHI directory.



3. In Powershell, run **docker-compose up -d** to download and start the MOCHI image from Docker Hub. (The download process will only run at the first setup. The size of the MOCHI image is about 10 GB, and the running time depends on the download speed.)

```
PS C:\Users\dodolab\Desktop\MOCHI> docker-compose up -d
Creating network "mochi_default" with the default driver
Pulling mochi_server (dockerjjz/mochi_local_version:...)...
latest: Pulling from dockerjjz/mochi_local_version
f15005b0235f: Pull complete
1901fd813023: Pull complete
a92940affedf: Pull complete
dbebda29cb22: Pull complete
3c63b26b92fd: Pull complete
e4191a297544: Pull complete
Digest: sha256:794909d921df9cc55edba44a3fe66701e43845c5c5578bf1e194064e071cbe
Status: Downloaded newer image for dockerjjz/mochi_local_version:latest
Creating mochi_server_version ... done
```

4. Open a browser, and type **127.0.0.1:3811** in the address bar. A MOCHI interactive webpage is now available to begin your analysis.

The screenshot shows the MOCHI web application interface. At the top, there's a navigation bar with links for Home, Sequence Preprocessing, Taxonomy Analysis, Function Analysis, and Tutorial. Below the navigation bar, a main title says "Welcome to MOCHI! (Microbiota amplicon CHaracterization Implement)". A brief description follows: "MOCHI is a 16S or 18S microbiota amplicon rRNA analytical tool for microbiota based primarily on QIIME2 with a friendly web interface powered by the R package Shiny. MOCHI may also be downloaded and operated locally." The central part of the page is titled "Overview of MOCHI". It illustrates the workflow from sequence data and metadata to taxonomy classification and function analysis. On the left, three input types are shown: "Sequence data" (represented by a document icon), "Metadata for samples" (also a document icon), and "Taxonomy database" (represented by a database icon). These inputs feed into three sequential steps: Step 1. Sequence summary (read counts, read quality), Step 2. Sequence denoising (DADA2) (sequence table, alpha rarefaction), and Step 3. Taxonomy classification (taxonomy prediction table). The output of Step 3 is FAPROTAX. From FAPROTAX, the process moves to the "Taxonomy Analysis" section, which includes a taxonomy table, bar plot, heatmap, PCoA plot, Krone, box plot, (ANCOM), comparison between groups, and post hoc analysis. Finally, it moves to the "Function Analysis" section, which includes a functional annotation table and a bar plot.

The advantages of MOCHI

- Friendly user interface: point-and-click and fill-in inputs, no programming required.
- Cross-platform: simple set-up with Docker containers on Linux, Windows, or MacOS.
- Local computing resource: runs on your premise with privacy, not subject to network reliability and limitation.
- Compatible with other downstream analytical tools
- Publishable plots and charts generated with chosen parameters

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Linux

(A) Install Docker

- ▶ Please follow the [official guidance](#) for setup and start Docker Engine on Ubuntu.

(B) Start MOCHI service

1. Download “**docker-compose.yml**” from [NCTU website](#), and place it in a folder named “**MOCHI**”.



2. Navigate to the MOCHI directory.

```
$ cd /path/to/place/MOCHI
```

3. Download and start the MOCHI image from Docker Hub. (The download process will only run during the first setup. The size of the MOCHI image is about 10 GB, and the running time depends on the download speed.)

```
$ docker-compose up -d
```

4. Open a browser, and type **127.0.0.1:3811** in the address bar. A MOCHI interactive webpage is now available to begin your analysis.

Additional information

* Stop, Restore or Remove MOCHI service

- ▶ To temporarily pause MOCHI service, please run **docker-compose stop**. This will create a paused MOCHI container, and can be restored with command **docker-compose start**.

NOTE: Please be aware that interrupting the MOCHI service when an analysis is running will not save the running process. The MOCHI container is automatically paused once you restart your computer or docker service.

- ▶ To permanently close MOCHI service, please run **docker-compose down**. This will remove all the data generated by MOCHI. Please save the results in advance. If you wish to open the service again, please run **docker-compose up -d**.
- ▶ To uninstall MOCHI image from your computer, please run **docker images**:

REPOSITORY	TAG	IMAGE ID	CREATED	SIZE
dockerjjz/mochi_local	latest	441fe987dce8	2 weeks ago	9.05GB

and look for “IMAGE ID” of the repository named “**dockerjjz/mochi_local**”. Then, run **docker rmi [IMAGE ID]** (e.g., **docker rmi 441**; type partial or complete image ID are both acceptable.)

* Remember to navigate under the MOCHI folder (where “**docker-compose.yml**” is located) before starting, stopping or restoring MOCHI service.

- ▶ For MacOS, Please see [MacOS / step B-3](#).
- ▶ For Windows 10, Please see [Windows 10 / step B-2](#).
- ▶ For Linux, Please see [Linux / step B-2](#).

* After installing MOCHI, two folders are created under the MOCHI folder:

1. **seqs_folder**

- ▶ This folder is used to store the user’s sequence data which will be loaded in “Sequence preprocessing - Sequence summary”.
- ▶ The file type of sequence data needs to be **fastq.gz** or **fq.gz**.
- ▶ The filename of sequence data needs to satisfy Casava 1.8 demultiplexed format or the following example format **[SampleID]_[direction of reads]**:
 - ✓ Forward read: LS105_R1 or LS105_1
 - ✓ Reverse read: LS105_R2 or LS105_2

2. **taxa_database**

► This folder is used to store the taxonomy database, such as Greengenes, Silva and PR2. Please see "Sequence preprocessing - Taxonomy classification".

- * If you wish to change the default path to the sequence data and the taxonomic database, open the "**docker-compose.yml**" file, replace the texts "**./seqs_folder**" and "**./taxa_database**" with new paths to the sequence data and the taxonomic database, respectively. Relative path is allowed.
- * The default maximum memory used by MOCHI is 16GB. To increase, please modify the resource limit in the "**docker-compose.yml**" file.

```
version: '3.7'

services:

  mochi_server:
    # build: .
    image: dockerjjz/mochi_local
    ports:
      - "3811:3838"
      - "8011:80"
    volumes:
      - ./seqs_folder:/home/imuser/raw_data/:rw
      - ./taxa_database/greengenes:/home/imuser/taxa_database/greengenes:rw
      - ./taxa_database/silva:/home/imuser/taxa_database/silva:rw
      - ./taxa_database/PR2/18S/seqs:/home/imuser/taxa_database/PR2/18S/seqs:rw
      - ./taxa_database/PR2/18S/taxonomy:/home/imuser/taxa_database/PR2/18S/taxonomy:rw
    container_name: mochi_server

    deploy:
      resources:
        limits:
          #cpus: '8'
          memory: 16G

      environment:
        - shiny_port=3811
        - nginx_port=8011
```

CHAPTER 2: ANALYSIS

Sequence preprocessing

(A) Sequence summary

1. Select “**Sequence Preprocessing**” in the top bar, and then choose “**Step 1. Sequence summary**”.

The screenshot shows the MOCHI web interface. At the top, there is a navigation bar with links for Home, Sequence Preprocessing (which is currently selected), Taxonomy Analysis, Function Analysis, and Tutorial. Below the navigation bar, a large blue header says "Welcome to MOCHI". Underneath the header, there are three steps listed: Step 1. Sequence summary (highlighted with a red arrow), Step 2. Sequence denoising, and Step 3. Taxonomy classification. A note at the bottom right states: "Run analysis on QIIME2 with a friendly web interface powered by the R package of Shiny. MOCHI may also be downloaded and operated locally."

2. Press the “**Select the directory**” button to open the selection window. Alternatively, you can press the “**Example sequences**” button to first download all the example files. The parameters for example analysis are set once you have pressed the “**Example sequences**” button.

! Important: The sequence files should be placed under “**seqs_folder**” where MOCHI was installed.

This screenshot shows the "Sequence files" section of the MOCHI interface. It includes a message asking to choose a directory containing sequence files (*.fastq.gz or *.fq.gz). Two buttons are present: "Select the directory" (highlighted with a red box) and "Example sequences". To the right, a large blue box titled "1. Sequences summary (for single end)" contains the sub-instruction "(1) Summarize the single-end sequences." and a "Start!" button.

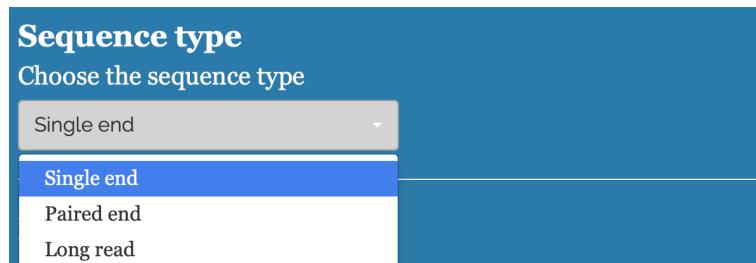
3. Select the directory containing the sequence files.

This screenshot shows a file selection dialog box titled "Please select a directory". It displays a list of directories and files under a path named "raw_data". A folder named "single_seqs_demo" is highlighted with a red box and labeled "Select folder". At the bottom of the dialog, there are two buttons: "Confirm selection" (highlighted with a red box) and "Select".

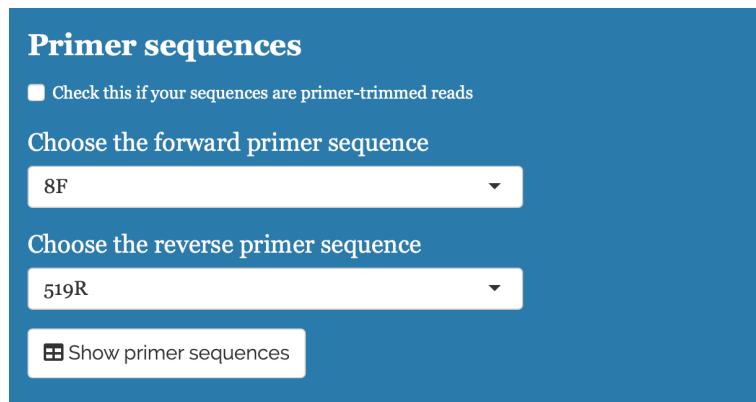
4. **Sequence type:** The settings for “**Step 1. Sequence summary**” and “**Step 2. Sequence denoising**” are different based on the sequence type chosen.

4.a. **Single-end or Paired-end**

- 4.a.1. The **sequence type** is automatically detected. If not correct, please choose it manually.



- 4.a.2. Choose the **primers** or check the box when using **primer-trimmed reads**.



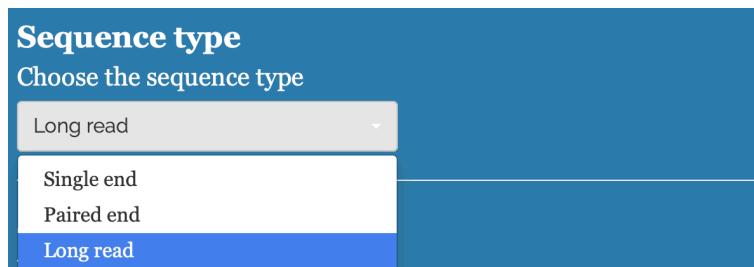
- 4.a.3. Set the **number of threads** for running the analysis. If zero, all available cores will be used. If you do not know the number to enter, leave it at the default number (all threads - 2).



- 4.a.4. Click the “**Start!**” button.

4.b. Long-read

- 4.b.1. The sequence type will not automatically be detected. **Please select it manually.**



- 4.b.2. Set the **number of threads** for running the analysis. If zero, all available cores will be used. If you do not know the number to enter, leave it at the default number (all threads - 2).



- 4.b.3. Click the “**Start!**” button.

5. Please wait while the process is running. When complete, a popup window will be displayed.

* Running status

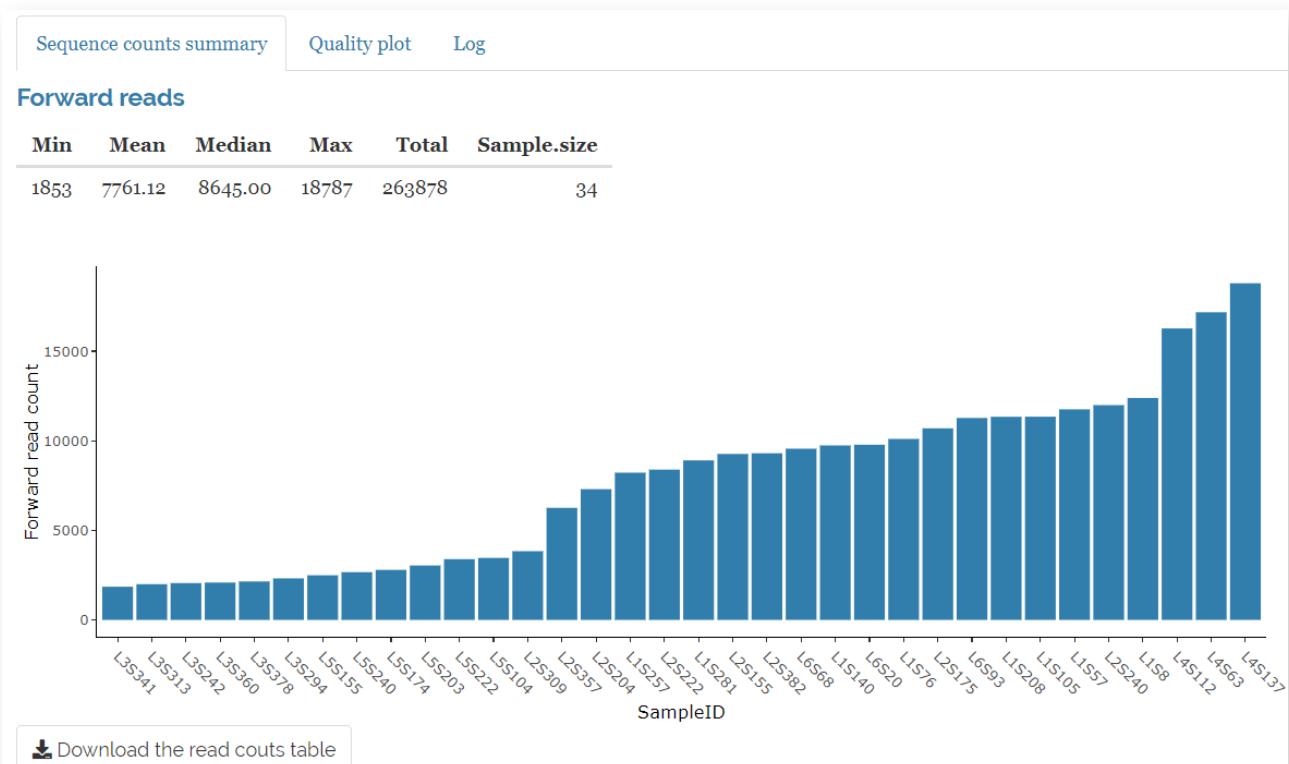


* Complete status

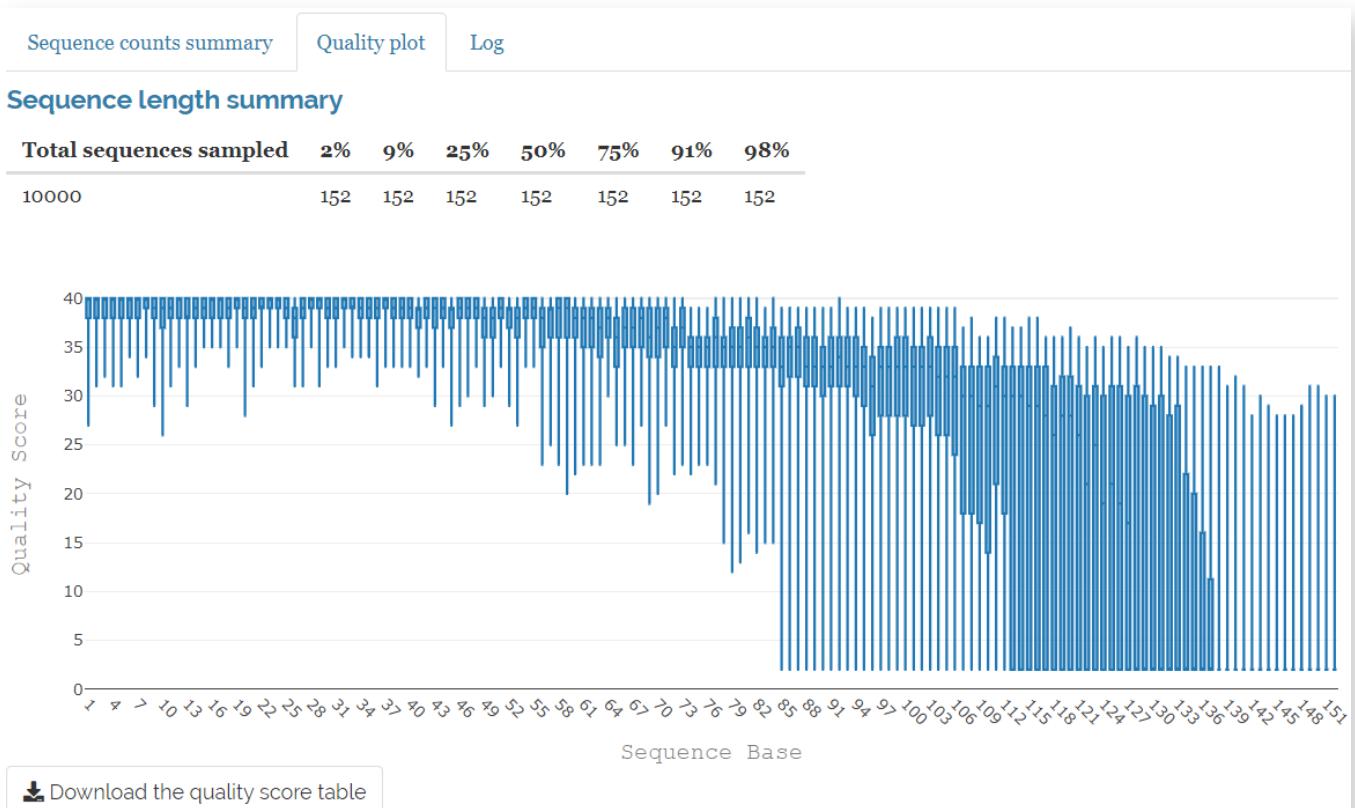
Successful!

This analysis took 11.5 secs. You can inspect the results now.

5.1. Demo results — “**Sequence counts summary**” summarizes the read counts for all the samples.



5.2. Demo results — “**Quality plot**” summarizes the sequence length and shows the distribution of the quality score for each sequence base.



5.3.Demo results — "Log" records the parameters used and provides a button for downloading the table.

Record	Value
time	2021-05-31 01:44:22
duration	11.16 secs
sequence_type	Single end
sample_size	34
primer_trimmed	TRUE
forward_primer	515F
reverse_primer	806R
computing_setting	6

 Download

(B) Sequence denoising

1. Select “**Sequence Preprocessing**” in the top bar, and then choose “**Step 2. Sequence denoising**”.

The screenshot shows the MOCHI web interface. At the top, there is a blue header bar with the MOCHI logo and links for Home, Sequence Preprocessing (which is currently selected), Taxonomy Analysis, Function Analysis, and Tutorial. Below the header, a large blue banner says "Welcome to MOCHI". On the right side of the banner, there is a dropdown menu with three options: Step 1. Sequence summary, Step 2. Sequence denoising (which has a red arrow pointing to it), and Step 3. Taxonomy classification. A small note below the dropdown says "Currently on QIIME2 with a friendly web interface powered by the R package Shiny. MOCHI may also be downloaded and operated locally."

2. Depending on the sequence type selected in “**Step 1. Sequence summary**”, the settings for denoising will be different.

2.a. Single-end or Paired-end

- 2.a.1. Set the **start and end positions** and the **quality score** for trimming the sequences.

The screenshot shows the "Sequence trimming" and "Quality score filtering" sections of the MOCHI interface. In the "Sequence trimming" section, there are two input fields: "The start position" (set to 0) and "The end position" (set to 0). Below these fields are two buttons: "learn more" and "Example". In the "Quality score filtering" section, there is one input field: "Quality score threshold" (set to 0). Below this field is a "learn more" button.

* Start and end position:

Base pairs below the start position and above the end position will be trimmed off. For instance, setting the start position to 5 and the end position to 120 will yield sequences from 5 to 120 bp.

In addition, reads shorter than the end position will be discarded. In the above example, sequences less than 120 bp will be discarded. If the end position is set to 0, no truncation or length trimming will be performed.

*** Quality score:**

Nucleotides with quality score less than or equal to the specified value will be trimmed off. The truncated reads shorter than the end position will be discarded.

- 2.a.2. Set the parameters of the **chimera and computing setting** and upload the **metadata**.

The screenshot shows two configuration sections. The first section, titled "Chimeric reads filtering", contains a label "The minimum fold-change value" and a text input field containing the value "1". Below the input field is a "learn more" button. The second section, titled "Computing setting", contains a label "Number of threads MOCHI can use" and a text input field containing the value "2".

*** Chimeric reads filter:**

A chimeric read is a sequence originating from multiple parent sequences. Chimeric reads are generally considered as contaminants. Whereas a chimeric read can be interpreted as a novel sequence, it is in fact an artifact. The higher this value is, the more chimeric reads will be used in the analysis. For most cases, 1 is the default value.

*** Computing setting:**

Specify the number of threads to optimize the computational process. Increasing the number of threads will decrease the running time. When zero is specified, all available cores will be used. If you do not know the number to enter, leave it at the default number.

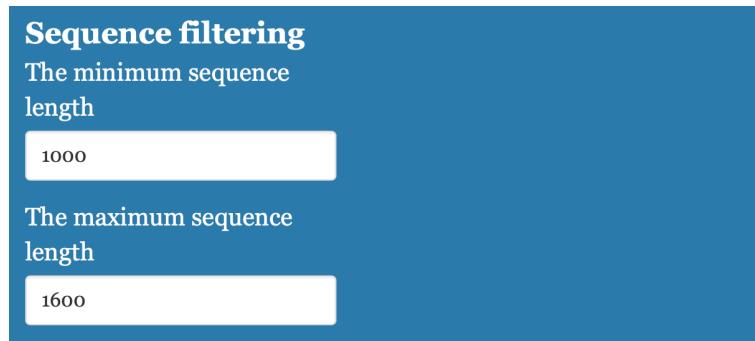
2.b. Long-read

- 2.b.1. Set the minimum and maximum sequence lengths allowed for analysis. Sequences below the minimum length and above the maximum length will be discarded.

Sequence filtering

The minimum sequence length
1000

The maximum sequence length
1600



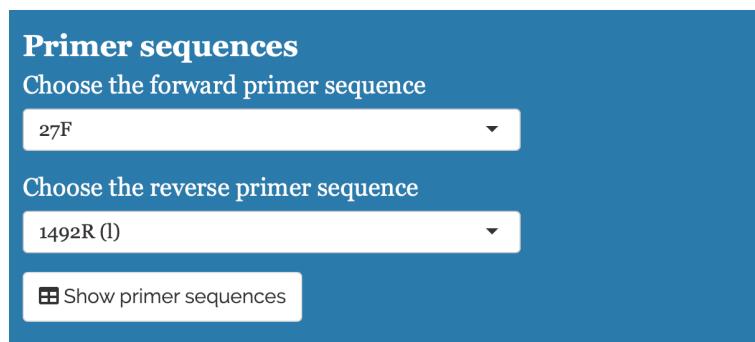
- 2.b.2. Choose the primers.

Primer sequences

Choose the forward primer sequence
27F

Choose the reverse primer sequence
1492R (l)

Show primer sequences



- 2.b.3. Assign the number of threads permitted for denoising.

Computing setting

Number of threads MOCHI can use
2



3. Click the “**Start!**” button.

2. Sequence denoising (DADA2) for Single end

(1) Start to denoise.

 Start!

4. Please wait while it is running. When complete, a popup window will be displayed.

Denoising successfully!

This analysis took 1.25 mins. You can inspect the results!

(C) Taxonomy classification

1. Select “**Sequence Preprocessing**” in the top bar, choose “**Step 3. Taxonomy classification**”.

The screenshot shows the MOCHI web interface. At the top, there is a navigation bar with links for Home, Sequence Preprocessing (which is currently selected), Taxonomy Analysis, Function Analysis, and Tutorial. Below the navigation bar, a blue header bar says "Welcome to MOCHI". Underneath the header, there is a sub-menu for "Step 3. Taxonomy classification" which includes "Step 1. Sequence summary", "Step 2. Sequence denoising", and "Step 3. Taxonomy classification". A red arrow points to the "Step 3. Taxonomy classification" link. To the right of the sub-menu, there is a note: "MOCHI is a 16S or 18S microbiota amplicon rRNA characterization implemented with QIIME2 with a friendly web interface powered by the R package of Shiny. MOCHI may also be downloaded and operated locally...".

2. Download and select **database** (Silva, Greengene, or PR2) to predict taxa.

The screenshot shows a "Database" selection page. It has a title "Database" and a subtitle "Select the reference database for taxonomy classification." Below this, there is a section titled "Choose the database" with a dropdown menu set to "Silva (Not detected)". There is also a button labeled "Auto download database" and a "Example" button.

2.1. Automatically download database:

- * Select a database from the drop-down menu “**Choose the database**”. Press “**Auto download database**”. The latest database will be pulled from the server. The download process may take a while depending on the file size and the network speed.

2.2. Manually download the database:

- * Silva: Follow [this link](#). Choose a version to download. Decompress the downloaded file. Copy the two folders “**rep_set**” and “**taxonomy**” to the folder “**taxa_database/silva**”.
- * Greengene: Follow the [this link](#). Choose a version and download the corresponding compressed file “**otus.tar.gz**”. Decompress this file. Copy the two folders “**rep_set**” and “**taxonomy**” into the folder “**taxa_database/greengenes**”.
- * PR2: Follow the [this link](#). Choose a version and download the corresponding compressed files “**pr2_version_X.XX.X_16S_mothur.fasta.gz**” and “**pr2_version_X.XX.X_16S_mothur.tax.gz**”. Decompress these files. Copy the file “**pr2_version_X.XX.X_16S_mothur.fasta**” into the folder “**taxa_database/PR2/18S/seqs**” and the file “**pr2_version_X.XX.X_16S_mothur.tax**” into the folder “**taxa_database/PR2/18S/taxonomy**”.

3. Check if your **primers** are correct.

Reference sequence filtering

1. Check primers
If incorrect, go to 'Step 1. Sequence summary' to select the correct primer.

Your forward primer is **8F** now.

Your reverse primer is **519R** now.

4. Set the **minimum and maximum lengths** for filtering the **reference sequence**.

2. Filter the reference sequence by length

Minimum length

Maximum length

[learn more](#)

*** Minimum and maximum lengths:**

Reference sequences outside the range of the specified values will be discarded. The default values are minimum and the maximum lengths of the denoised sequences. To disable length filtering, set the values to zero.

5. Set the **number of threads** for running the analysis. If zero is specified, all available cores will be used. If you do not know the number to enter, leave it at the default number (all threads - 2).

Computing setting

Number of threads MOCHI can use

6. Click the “**Start!**” button.

3. Taxonomy classification

(1) Classify taxonomy

 Start!

7. Please wait while the process is running. When complete, a popup window will be displayed.

Taxonomy classification has been finished!

This analysis took 55.92 secs. You can inspect the results!

8. Demo results — “**Taxonomy results**” shows the ASVs and assigned taxonomies. The three buttons at the bottom are for downloading the files required for subsequent analyses.

Inspect the taxonomy classification result.

Taxonomy result	Log	
Show 10 entries		Search:
ASV	Taxon	Confidence
1 4b5eeb300368260019cfbc7a3c718fc	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides; s__	0.99340978592142
2 fe30ff0f1a38a39cf1717ec2be3a2fc	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Neisseriales; f__Neisseriaceae; g__Neisseria; s__	0.839490583340447
3 868528ca947bc57b69ffd83e6b73bae	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides; s__	0.983868032171919
4 154709e160e8ada6bf21115acc80f5	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides; s__	0.980528382140841
5 d29fe3c70564fec0f69f2e03e0d1e5561	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus; s__	0.999999998690498
6 1d2e5f3444ca750e85302ceee2473331	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae; g__Haemophilus; s__parainfluenzae	0.968380683630633
7 0305a4993ecfd2d8ef4149fdfe7592603	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides; s__uniformis	0.996031457767898
8 997056ba80681bbbdd5d09aa591eadco	k__Bacteria; p__Fusobacteria; c__Fusobacteriia; o__Fusobacteriales; f__Fusobacteriaceae; g__Fusobacterium; s__	0.907315818016303
9 3c9c437f27aca05f8db167do8off1ec	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotella; s__melaninogenica	0.999998818423878
10 bfbcd36e63b69fec4627424163d20118	k__Bacteria; p__Firmicutes; c__Clostridia; o__Clostridiales; f__Ruminococcaceae; g__Faecalibacterium; s__prausnitzii	0.999996821028142

Showing 1 to 10 of 501 entries

Previous 1 2 3 4 5 ... 51 Next

[Download](#)

(3) Download the files for the next step.

[The taxonomic table](#) [The ASVs table](#) [The seqs data](#)

9. Demo results — "Log" records the parameters used and provides a button for downloading the table.

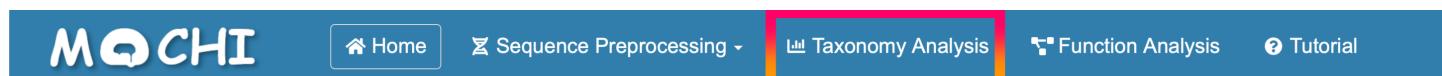
Taxonomy result	Log
Record	Value
time	2021-03-18 05:53:21
duration	1.39 mins
sequence_type	Single end
database	Greengenes_16S_88
forward_primer	515F
reverse_primer	806R
min_length	100
max_length	400
computing_setting	6

 Download

Taxonomy Analysis

(A) Upload files

1. Select “**Taxonomy analysis**” in the top bar.



Welcome to MOCHI! (Microbiota amplicOn CHaracterization Implement)

MOCHI is a 16S or 18S microbiota amplicon rRNA analytical tool for microbiota based primarily on QIIME2 with a friendly web interface powered by the R package of Shiny. MOCHI may also be downloaded and operated locally.

2. In the left panel, press the “**Browse**” button to upload the **metadata, taxonomic table** and **ASVs table** files. These files can be downloaded from the “Sequence Preprocessing - Taxonomic classification” section. Please see [Sequence preprocessing / Taxonomic classification / step 8](#). Alternatively, you can press the “Demo” button to download the example files first and then upload the files. If sequences are 18S rRNA, please check the “18S rRNA” box.

The image shows the left panel of the MOCHI web interface. It has three main sections for file uploads: "Upload the metadata file", "Upload the taxonomic table file", and "Upload the ASV table file". Each section has a "Browse" button and a "No file selected" message. Below the ASV table section are buttons for "Start!", "Reset", and "Example files". A yellow box highlights the "Upload the ASV table file" section.

* Metadata (.tsv):

The first column name must be **SampleID**.

* Taxonomic table file (.qza):

You can upload self-derived taxonomic table file from QIIME2.

* ASVs table (.qza):

An “amplicon sequence variant” table is a higher-resolution analogue of the traditional OTU table.

* ASV table (.txt):

The table should include ASV in the first column and Taxon in the last column.

- Click the “**Start!**” button to run the analysis. (Or, click the “**reset**” button to re-upload the files.)
- The results will be displayed in the right panel once the files are uploaded.

Upload the metadata file

Browse... Metadata_example.tsv
Upload complete

Upload the taxonomic table file

Browse... Taxonomic_table_example_from_MOCHI.qza
Upload complete

Upload the ASV table file

Browse... ASV_table_example_from_MOCHI.qza
Upload complete

■ 18S rRNA

Start! Reset Example files

Taxonomic table Taxonomic barplot Taxonomic heatmap Krona Alpha diversity Beta diversity Phylogenetic diversity ANCOM

Choose the group
 SampleID barcode.sequence body.site year month day subject reported.antibiotic.usage days.since.experiment.start

Show 10 entries Search:

Kingdom (K=3)	Phylum (K=20)	Class (K=45)	Order (K=72)	Family (K=126)	Genus (K=190)	Species (K=198)	L1S8	L1S57	L1S76	L1S105	L2S155	L2S175	L2S204
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Unassigned	4217	3887	4238	2977	10	10	3
Bacteria	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	Unassigned	Unassigned	0	0	0	5	51	109	43
Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus	Unassigned	30	5	0	0	377	929	126
Bacteria	Proteobacteria	Gammaproteobacteria	Pasteurellales	Pasteurellaceae	Gallibacterium	Unassigned	5	0	0	0	27	51	0
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	uniformis	260	553	530	1439	0	0	0
Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Unassigned	Unassigned	0	0	0	0	82	227	96
Bacteria	Fusobacteria	Fusobacteriia	Fusobacteriales	Fusobacteriaceae	Fusobacterium	Unassigned	3	0	0	31	31	53	0
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella	Unassigned	0	0	0	80	16	88	10
Bacteria	Proteobacteria	Gammaproteobacteria	Unassigned	Unassigned	Unassigned	Unassigned	0	0	0	0	97	41	1376
Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium	prausnitzii	129	693	906	910	0	6	15

Showing 1 to 10 of 229 entries Previous 1 2 3 4 5 ... 23 Next

Download Taxonomic table

(B) Inspect results

- MOCHI displays the results in eight parts: (1) Taxonomic table, (2) Taxonomic barplot, (3) Taxonomic heatmap, (4) Krona, (5) Alpha diversity, (6) Beta diversity, (7) Phylogenetic diversity, and (8) ANCOM:

1. Taxonomic table

This table describes taxonomy information and read counts.

Kingdom (K=3)	Phylum (K=20)	Class (K=45)	Order (K=72)	Family (K=126)	Genus (K=190)	Species (K=198)	L1S8	L1S57	L1S76	L1S105	L2S155
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Unassigned	4217	3887	4238	2977	10
Bacteria	Proteobacteria	Betaproteobacteria	Neisseriales	Neisseriaceae	Unassigned	Unassigned	0	0	0	5	51
Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus	Unassigned	30	5	0	0	377
Bacteria	Proteobacteria	Gammaproteobacteria	Enterobacterales	Enterobacteriaceae	Gallibacterium	Unassigned	5	5	0	0	27
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	uniformis	260	0	0	0	0
Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Unassigned	Unassigned	0	0	0	0	82
Bacteria	Fusobacteria	Fusobacteria	Fusobacteriales	Fusobacteriaceae	Fusobacterium	Unassigned	3	0	0	31	31
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae	Prevotella	Unassigned	0	0	0	80	16
Bacteria	Proteobacteria	Gammaproteobacteria	Unassigned	Unassigned	Unassigned	Unassigned	0	0	0	0	97
Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	Faecalibacterium	prausnitzii	129	693	906	910	0

* Choose the group:

Select a group provided in the metadata to categorize the read counts (see below).

* Taxonomy information:

The left part of the table (the first 7 columns) represents taxonomy information. The column names indicate taxonomy levels. K denotes the number of taxa at a given level.

* Read counts:

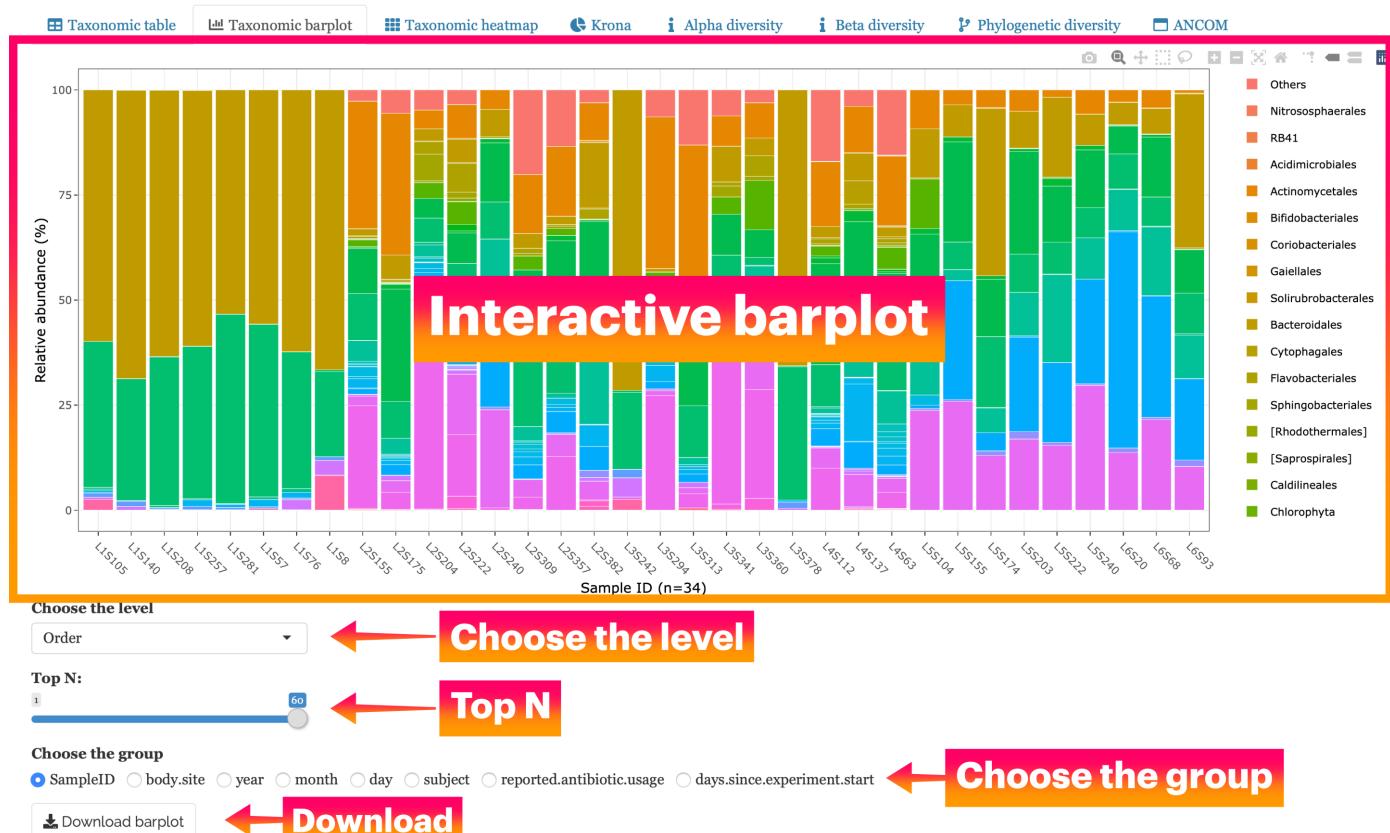
The right part of the table displays read counts. These are categorized by the selected group. Each column name indicates the variables in the selected group.

* Download the taxonomic table:

Click the “**Download Taxonomic table**” button to download the displayed table.

2. Taxonomic barplot

This is an interactive barplot showing the percentages of taxa for all the samples. Each taxon is represented by a sub-bar with different colors.



* Interactive barplot:

When the cursor hovers over the bar region, the information for species will be presented. Click and drag on the plot to zoom in and out. Double click on the plot to zoom back.

* Choose the level:

The taxa in the plot will be presented at the selected taxonomic level.

* Top N:

Control the numbers of taxa displayed in the plot. When you specify a value of N, the plot will show the union of the top N relatively abundant taxa in each sample. For example, if N = 2 results for and the top two abundant taxa in Sample A and Sample B are “taxa_1 and taxa_2” and “taxa_1 and taxa_3”, respectively, the plot will show the relative abundance of taxa_1, taxa_2 and taxa_3.

* Choose the group:

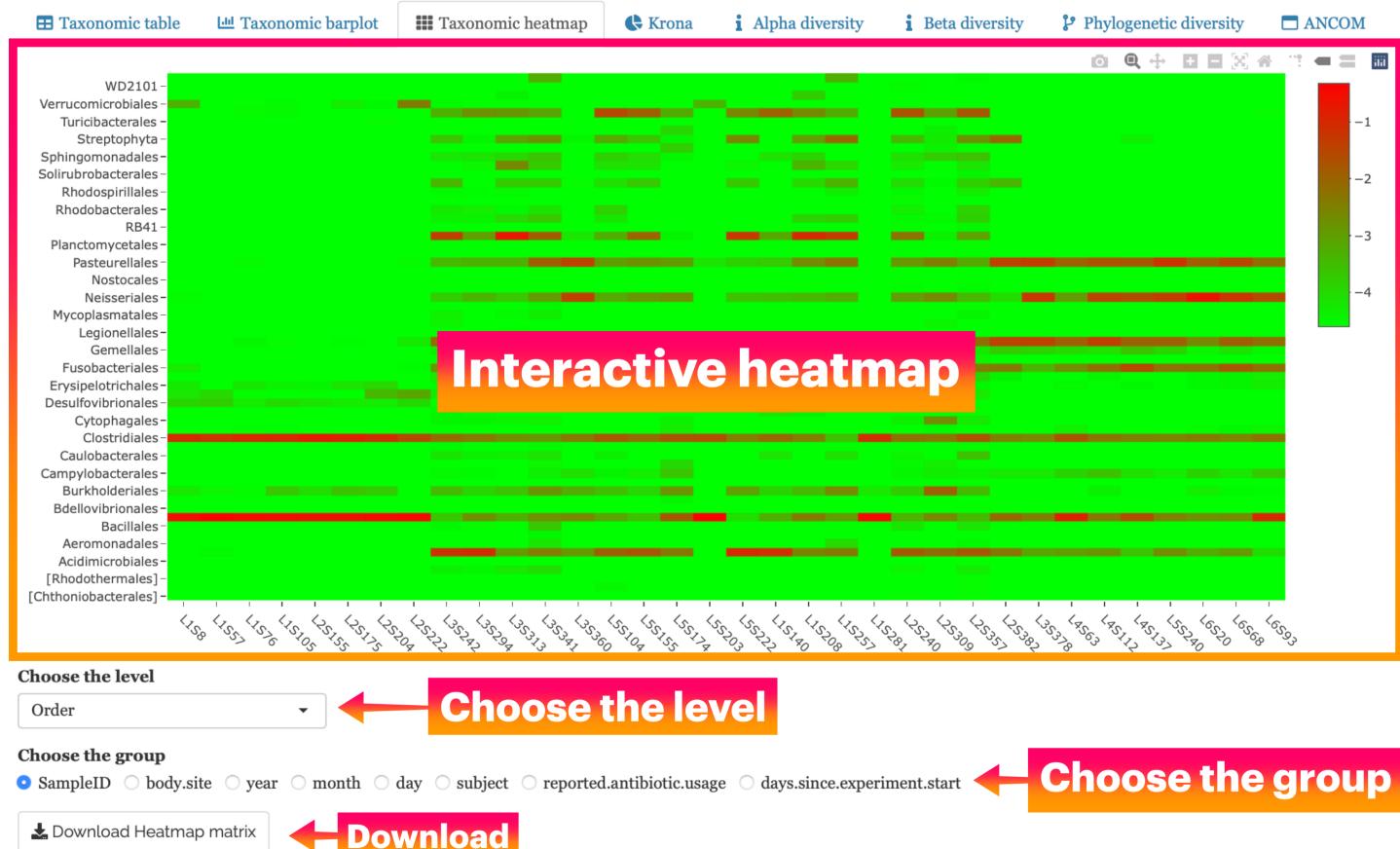
The barplot will be grouped based on the selected metadata.

* Download the barplot:

Click the “**Download barplot**” button to download the barplot. Alternatively, click on the camera icon in the top-right region of the barplot.

3. Taxonomic heatmap

This is an interactive heatmap showing the log10-transformed percentages of taxa for all samples. To prevent taking logarithms of zero, a small value of 0.01 is added to all percentage values before transformation. The transformed values are shown in color gradients.



* Interactive heatmap:

When the cursor hovers over the heatmap, the information for a transformed value will be presented. Click and drag on the plot to zoom in and out. Double click on the plot to zoom back. Click on the camera icon in the top-right region of the heatmap to download the plot.

* Choose the level:

The taxa in the plot will be presented at the selected taxonomic level.

* Choose the group:

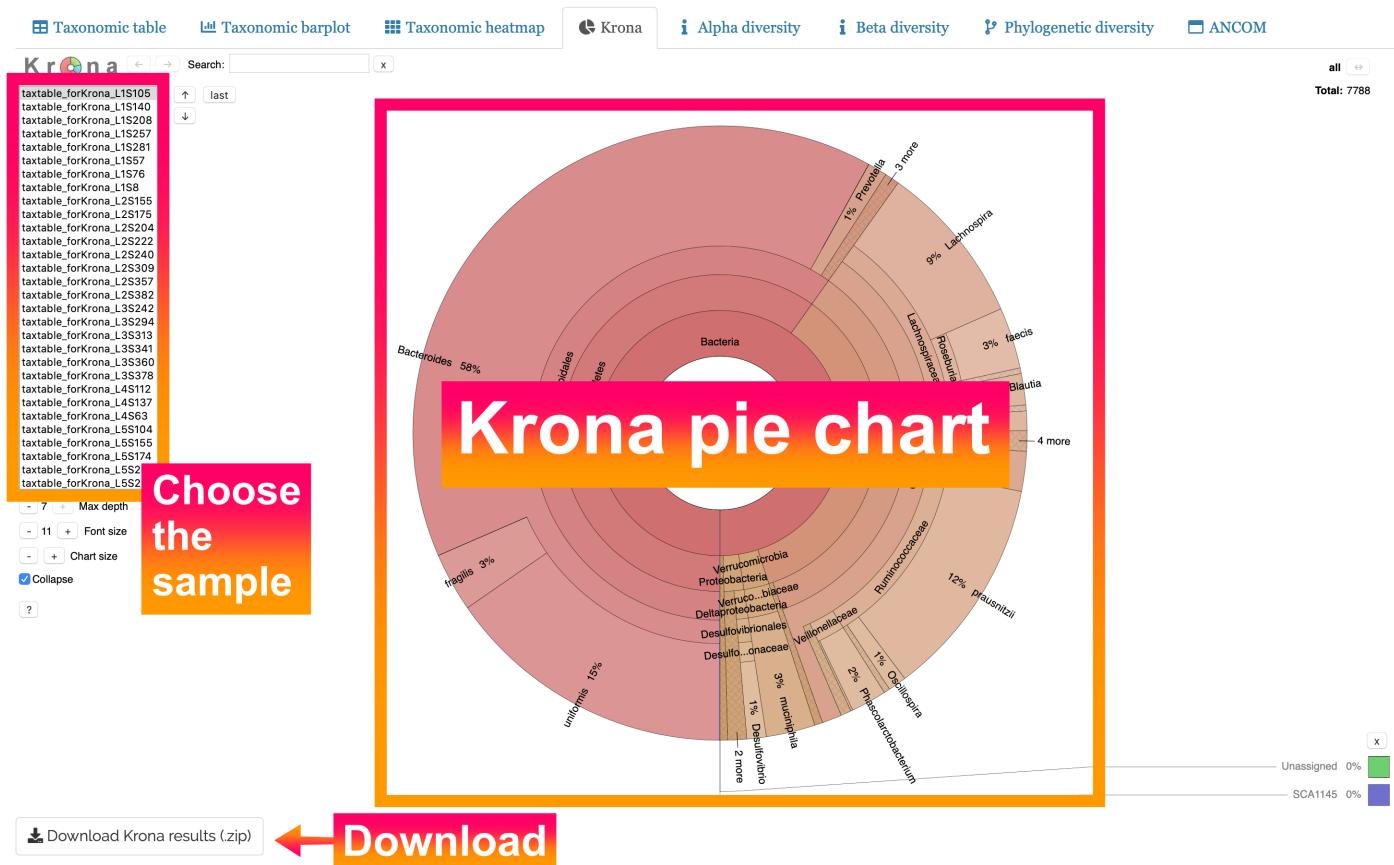
The heatmap will be grouped based on the selected metadata.

* Download the heatmap matrix:

Click the “**Download Heatmap matrix**” button to download the heatmap matrix data.

4. Krona

This is a visualization tool allowing hierarchical data to be explored with zooming, multi-layered pie charts. [Get more information.](#)



* Krona pie chart:

An interactive pie plot. Single click a taxon to show the ratio of that taxon over different taxonomy levels. Double click a taxon to zoom at the selected taxonomy level. To zoom back, click the backspace button in the top-left region.

* Choose the sample:

Select a sample to switch to the corresponding pie plot.

* Download Krona results:

Click the “**Download Krona results (.zip)**” button to download the interactive pie plot (html files with Javascript).

5. Alpha diversity

This is a measure for evaluating species diversity **within** samples. In MOCHI, we provide six indexes (ACE, Shannon diversity, InvSimpson diversity, Shannon evenness, and Simpson evenness).

5.1. Table

* Alpha diversity table:

This table shows the values of the six alpha diversity indexes.

Table							
Show 10 entries							
Sample	ACE	Shannon_diversity	Simpson_diversity	InvSimpson_diversity	Shannon_evenness	Simpson_evenness	
1	LiS105	63	2.6823	0.8708	7.7386	0.6474	0.1228
2	LiS140	65	2.6612	0.8519	6.7521	0.6375	0.1039
3	LiS208	84	3.1173	0.8998	9.979	0.7035	0.1188
4	LiS257	81	3.2625	0.9261	13.5372	0.7424	0.1671
5	LiS281	72	3.0339	0.9051	11.198	0.7458	0.1515
6	LiS57	70	2.9339	0.8998	11.198	0.684	0.1067
7	LiS76	61	2.4893	0.7962	4.9065	0.6055	0.0804
8	LiS8	44	2.2034	0.7941	4.8565	0.5823	0.1104
9	L2S155	109	3.5545	0.9388	16.3338	0.7577	0.1499
10	L2S175	104	3.4393	0.9222	12.86	0.7405	0.1237

Alpha diversity table

Showing 1 to 10 of 34 entries

Previous 1 2 3 4 Next

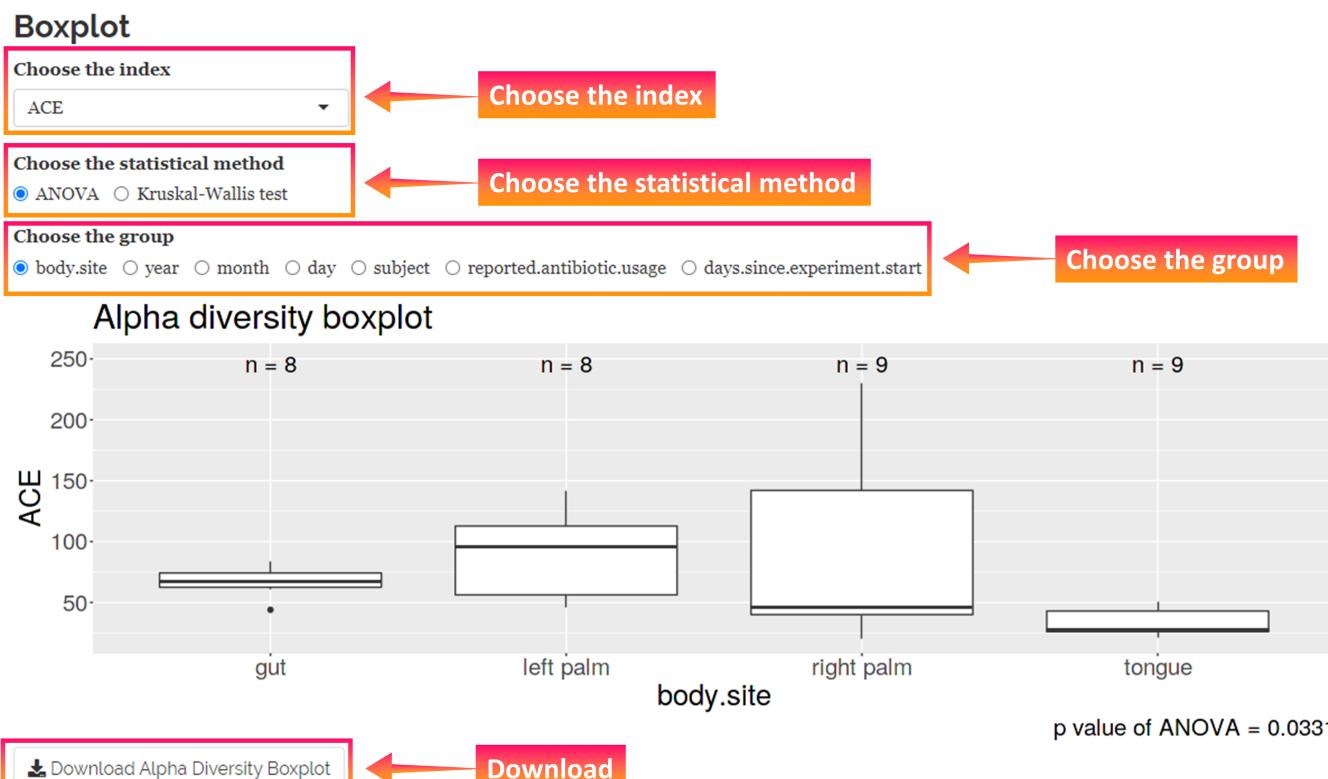
[!\[\]\(f47579369abb76577b982a41567f829d_img.jpg\) Download Alpha Diversity Table](#)

[Download](#)

* Download the Alpha diversity table:

Click the “**Download Alpha Diversity Table**” button to download the table.

5.2. Boxplot



* Choose the index:

A boxplot will be presented for the selected index.

* Choose the statistical method:

Select ANOVA (a parametric method) or Kruskal-Wallis (a nonparametric method) to test whether the distribution of the index is significantly different among the groups.

* Choose the group:

The values of the index in the boxplot will be grouped based on the selected metadata.

* Download the Alpha diversity boxplot:

Click the **“Download Alpha Diversity Boxplot”** button to download the boxplot.

5.3. Post hoc analysis

Post hoc analysis

Tukey test

Group A	Group B	Diff	P value
tongue	right palm	-52.78	0.06
tongue	left palm	-57.46	0.04
tongue	gut	-34.96	0.34
right palm	left palm	-4.68	1.00
right palm	gut	17.82	0.82
left palm	gut	22.50	0.72

 Download Alpha Diversity statistical result

Post hoc analysis

Dunn test

Group A	Group B	Z	P value
gut	left palm	-0.58	0.28
gut	right palm	0.76	0.22
gut	tongue	2.89	0.00
left palm	right palm	1.35	0.09
left palm	tongue	3.49	0.00
right palm	tongue	2.20	0.01

 Download Alpha Diversity statistical result

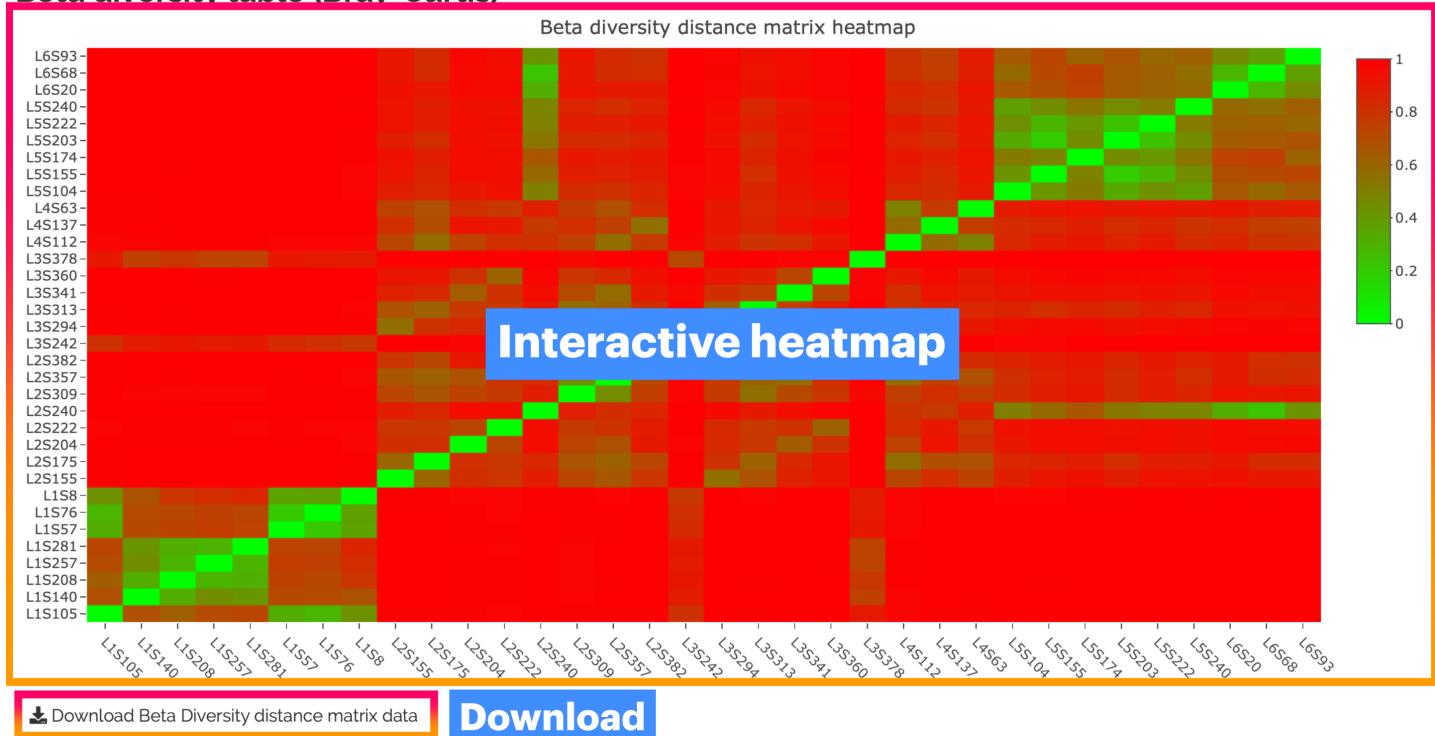
- * If ANOVA is selected when creating the boxplot, the Tukey test will be used for the post-hoc test. If Kruskal-Wallis is selected, then the Dunn test will be used.
- * Download the Alpha diversity post hoc test result:
Click the “**Download Alpha Diversity statistical result**” button to download the post-hoc test results.

6. Beta diversity

This is a measure for evaluating species diversity **between** samples. In MOCHI, we use the Bray-Curtis index.

6.1. Distance matrix

Beta diversity table (Bray-Curtis)



* Interactive heatmap:

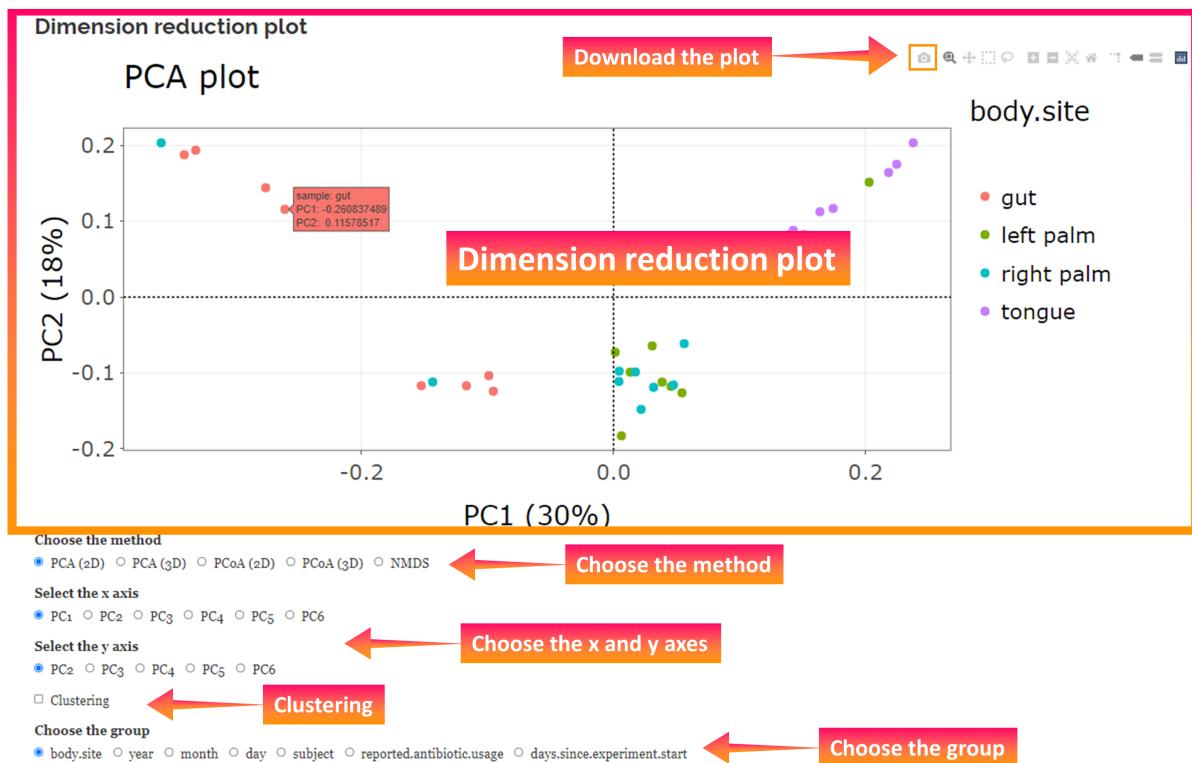
When the cursor hovers over the heatmap, the distance between species will be presented. Click and drag on the plot to zoom in and out. Double click on the plot to zoom back. Click on the camera icon in the top-right region of the heatmap to download the plot.

* Download the distance matrix:

Click on the button "**Download Beta Diversity distance matrix data**" to download the matrix data.

* The values shown in the heatmap are the natural logarithms of the original values first augmented by 0.01.

6.2. Dimension-reduction plot



* Choose the method:

Select a dimension reduction method. We provide three dimension-reduction methods for visualization of beta diversity: PCA (Principal Component Analysis, 2D & 3D), PCoA (Principal Co-ordinates Analysis, 2D & 3D) and NMDS (Non-metric Multidimensional Scaling).

* Choose the axes:

Individually select the PCs as x/y axes or x/y/z axes for 2D or 3D plots, respectively.

* Clustering:

When checking the box, samples in the same group will be surrounded by a circle.

* Choose the group:

Samples will be labeled in colors based on the selected metadata.

* Download the Beta diversity plot:

Click on the camera icon to download the plot.

6.3. Statistical analysis

Statistical analysis

PERMANOVA		ANOSIM		MRPP							
R ²	P value	R	P value	A	P value						
0.3999	0.001	0.6855	0.001	0.2085	0.001						
Download PERMANOVA table		Download ANOSIM table		Download MRPP table							
Pairwise PERMANOVA		Pairwise ANOSIM		Pairwise MRPP							
Comparisons	R ²	P value	Adjusted P value	Comparisons	R	P value	Adjusted P value	Comparisons	A	P value	Adjusted P value
gut - left palm	0.3983	0.001	0.0012	gut - left palm	1	0.001	0.0015	gut - left palm	0.2055	0.001	0.0012
gut - right palm	0.2834	0.001	0.0012	gut - right palm	0.6686	0.001	0.0015	gut - right palm	0.1456	0.001	0.0012
gut - tongue	0.5474	0.001	0.0012	gut - tongue	1	0.002	0.0024	gut - tongue	0.3046	0.001	0.0012
left palm - right palm	0.0585	0.544	0.544	left palm - right palm	-0.0538	0.78	0.78	left palm - right palm	-0.0018	0.543	0.543
left palm - tongue	0.2985	0.001	0.0012	left palm - tongue	0.6953	0.001	0.0015	left palm - tongue	0.1373	0.001	0.0012
right palm - tongue	0.276	0.001	0.0012	right palm - tongue	0.5343	0.001	0.0015	right palm - tongue	0.1412	0.001	0.0012
Download pairwise PERMANOVA table		Download pairwise ANOSIM table		Download pairwise MRPP table							

- * We provide three statistical methods: PerMANOVA (Permutational Multivariate Analysis of Variance), ANOSIM (Analysis of Similarities), and MRPP (Multiple Response Permutation Procedure), to test whether beta diversity is significantly different among groups or between pairs of groups. The adjusted p-values are multiple testing corrected using the Benjamini-Hochberg method.
- * Download the table of statistical results:
Click on the button below the table to download the statistical results.

7. Phylogenetic diversity

This is a measure of diversity for quantifying the genetic differences between species. In MOCHI, we use Faith PD (a kind of alpha diversity which considers the genetic distance) and Unifrac distance (a kind of beta diversity which considers the genetic distance).

Phylogenetic diversity is a measure of diversity that take the genetic distance between species into consideration.

Upload the sequence file ⓘ

Browse... No file selected

Sampling depth

898

learn more

Number of threads MOCHI can use

1

The default value is (number of threads on the system -2).

Start!

Start

Demo

* Upload the sequence file:

Upload the sequence file (.qza). If you have already finished the “Sequence Preprocessing” steps, download the file after the “Sequence Preprocessing - Taxonomic classification” stage and then upload it. See [Sequence preprocessing / Taxonomic classification / Step 8](#).

* Sampling depth:

Samples with total count smaller than the set value will be dropped from the diversity analysis. The default value is the smallest total count among samples where no sample will be dropped.

* Number of threads:

Specify the number of threads to use for multithreading. The default value is all threads minus two.

* Start:

Click the “**Start!**” button to execute the analysis after the above files and parameters have been uploaded and set.

- 7.1. Faith PD table: Faith PD (Faith's Phylogenetic Diversity) is a commonly used phylogenetic index. PD is a species diversity that considers genetic distance among species.

Faith PD table

Show **10** entries Search:

	SampleID	FaithPD
1	L1S105	7.03504527906064
2	L1S140	6.81348963332276
3	L1S208	7.56734619259508
4	L1S257	6.85786737645975
5	L1S281	6.75666778936291
6	L1S57	6.63365160132782
7	L1S76	6.33300452179527
8	L1S8	5.36655055450142
9	L2S155	18.3846874539932
10	L2S175	16.260657028738

Showing 1 to 10 of 34 entries

Previous Next

 Download Faith PD table

Download

* Faith PD table:

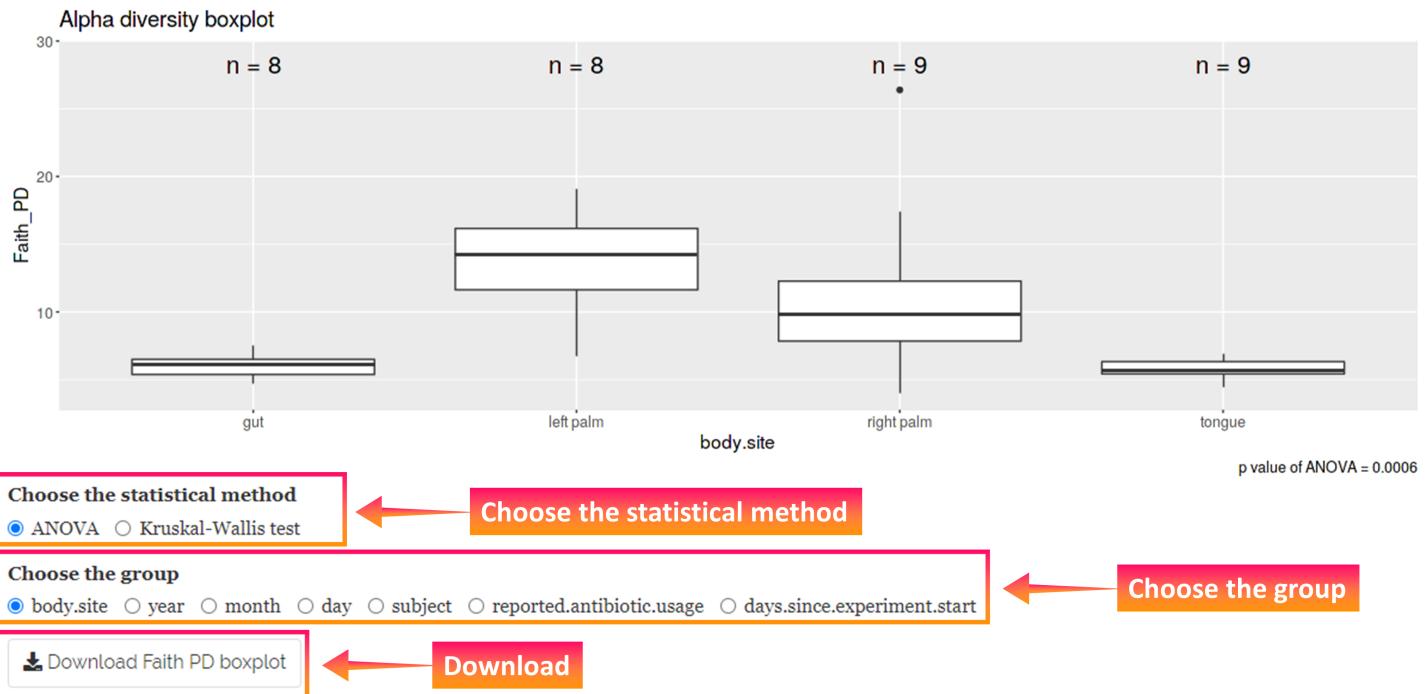
This table shows the Faith PD (phylogenetic diversity) for all the samples.

* Download the Faith PD table:

Click the “**Download Faith PD table**” button to download the table.

7.2. Faith PD boxplot: This shows the distribution of Faith PD values using a boxplot.

Faith PD boxplot



* Choose the statistical method:

Select ANOVA (parametric method) or Kruskal-Wallis (nonparametric method) to test whether the distribution of Faith PD is significantly different among the groups.

* Choose the group:

Faith PD will be grouped based on the selected metadata.

* Download the Faith PD boxplot:

Click the **“Download Faith PD Boxplot”** button to download the boxplot.

7.3. Post hoc analysis

Post hoc analysis

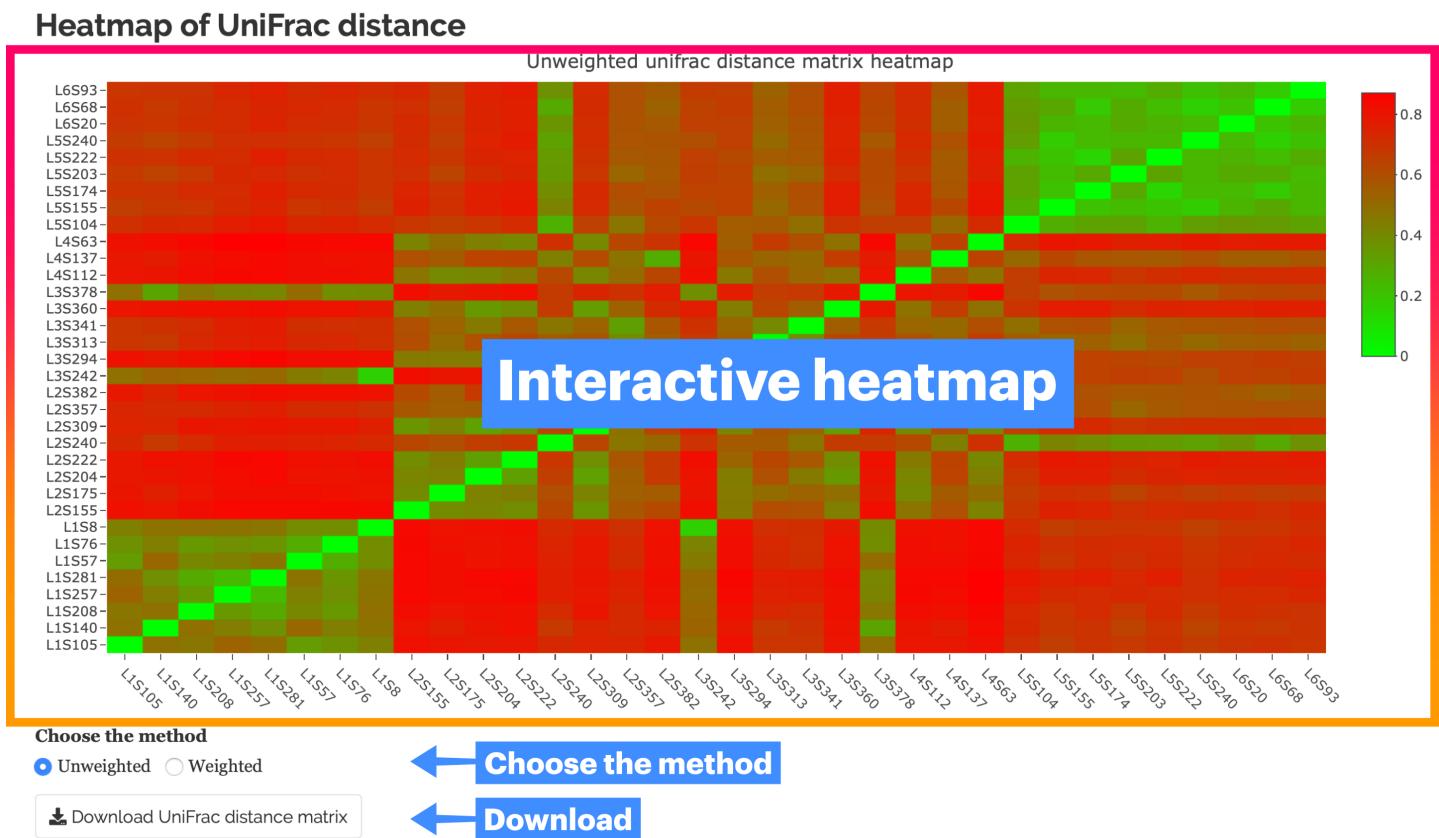
Tukey test

Group A	Group B	Diff	P value
tongue	right palm	-5.60	0.01
tongue	left palm	-8.65	0.00
tongue	gut	-0.50	0.99
right palm	left palm	-3.05	0.30
right palm	gut	5.10	0.03
left palm	gut	8.15	0.00

 Download Faith PD post hoc result

- * If ANOVA is selected when creating the Faith PD boxplot, the Tukey test will be used for the post-hoc tests. If Kruskal-Wallis is selected, then the Dunn test will be used.
 - * Download the Faith PD post hoc results:
Click the “**Download Faith PD post hoc results**” button to download the results.
-

7.4. Heatmap of UniFrac distance



* **Interactive heatmap:**

When the cursor hovers over the heatmap, the information for the corresponding species will be presented. Click and drag on the plot to zoom in and out. Double click on the plot to zoom back. Click on the camera icon in the top-right region of the heatmap to download the plot.

* **Choose the method:**

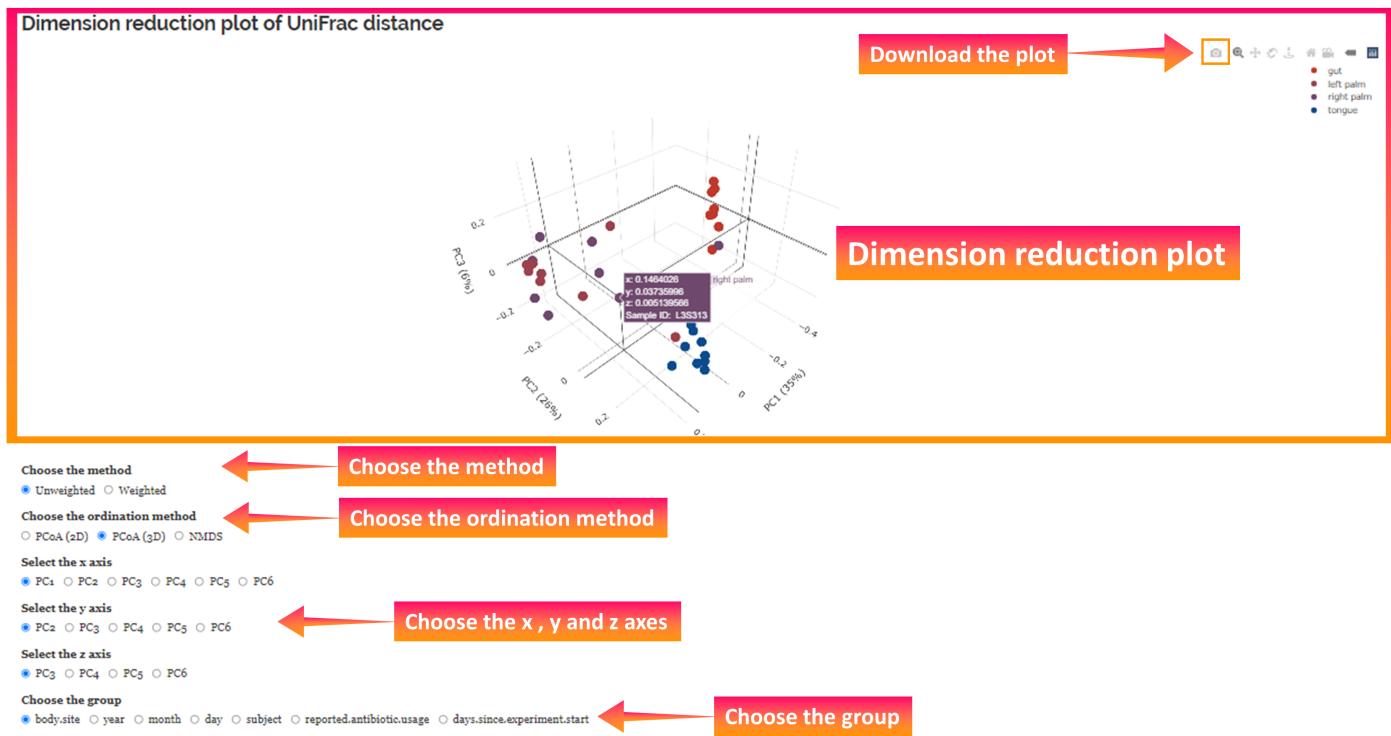
Select unweighted UniFrac (which does not consider the richness of taxa) or weighted UniFrac (which does consider the richness of taxa).

* **Download heatmap matrix:**

Click the “**Download UniFrac distance matrix**” button to download the matrix data.

* **The values shown in the heatmap are the natural logarithms of the original values first augmented by 0.01.**

7.5. Dimension-reduction plot of UniFrac distance



* **Choose the method:**

Select unweighted UniFrac (which does not consider the richness of taxa) or weighted UniFrac (which does consider the richness of taxa).

* **Choose the ordination method:**

Select a dimension reduction method. We provide two dimension-reduction methods for visualizing UniFrac distance: PCoA (Principal Co-ordinates Analysis, 2D & 3D) and NMDS (Non-metric Multidimensional Scaling).

* **Choose the axes:**

Individually select the PCs as x/y axes or x/y/z axes for 2D or 3D plots, respectively.

* **Clustering:**

When checking the box, samples in the same group will be surrounded by a circle.

* **Choose the group:**

The samples in the plot will be labeled using colors based on the selected metadata.

* **Download the UniFrac plot:**

Click on the camera icon to download the plot.

7.6. Statistical analysis

Statistical analysis

PERMANOVA

R ²	P value
0.1567	0.042

[Download PERMANOVA table](#)

ANOSIM

R	P value
0.1219	0.027

[Download ANOSIM table](#)

MRPP

A	P value
0.0488	0.02

[Download MRPP table](#)

Pairwise PERMANOVA

Comparisons	R ²	P value	Adjusted P value
gut - left palm	0.5049	0.001	0.0012
gut - right palm	0.3261	0.001	0.0012
gut - tongue	0.6587	0.001	0.0012
left palm - right palm	0.0649	0.394	0.394
left palm - tongue	0.4563	0.001	0.0012
right palm - tongue	0.3071	0.001	0.0012

[Download pairwise PERMANOVA table](#)

Pairwise ANOSIM

Comparisons	R	P value	Adjusted P value
gut - left palm	0.9933	0.002	0.0024
gut - right palm	0.5742	0.001	0.0015
gut - tongue	1	0.001	0.0015
left palm - right palm	-0.0191	0.504	0.504
left palm - tongue	0.7509	0.001	0.0015
right palm - tongue	0.4767	0.001	0.0015

[Download pairwise ANOSIM table](#)

Pairwise MRPP

Comparisons	A	P value	Adjusted P value
gut - left palm	0.2643	0.001	0.0012
gut - right palm	0.1556	0.001	0.0012
gut - tongue	0.3811	0.001	0.0012
left palm - right palm	0.0008	0.45	0.45
left palm - tongue	0.2476	0.001	0.0012
right palm - tongue	0.1856	0.001	0.0012

[Download pairwise MRPP table](#)

- * We provide three statistical methods: PerMANOVA (Permutational Multivariate Analysis of Variance), ANOSIM (Analysis of Similarities) and MRPP (Multiple Response Permutation Procedure), to test whether UniFrac distance is significantly different among groups or between pairs of groups. The adjusted p-values are multiple testing corrected using the Benjamini-Hochberg method.

- * Download the statistical results table:
Click on the button below the table to download the statistical results.

8. ANCOM

This stands for ANalysis of Composition of Microbiome and is used for comparing the composition of microbiomes in two or more populations. [Get more information.](#)

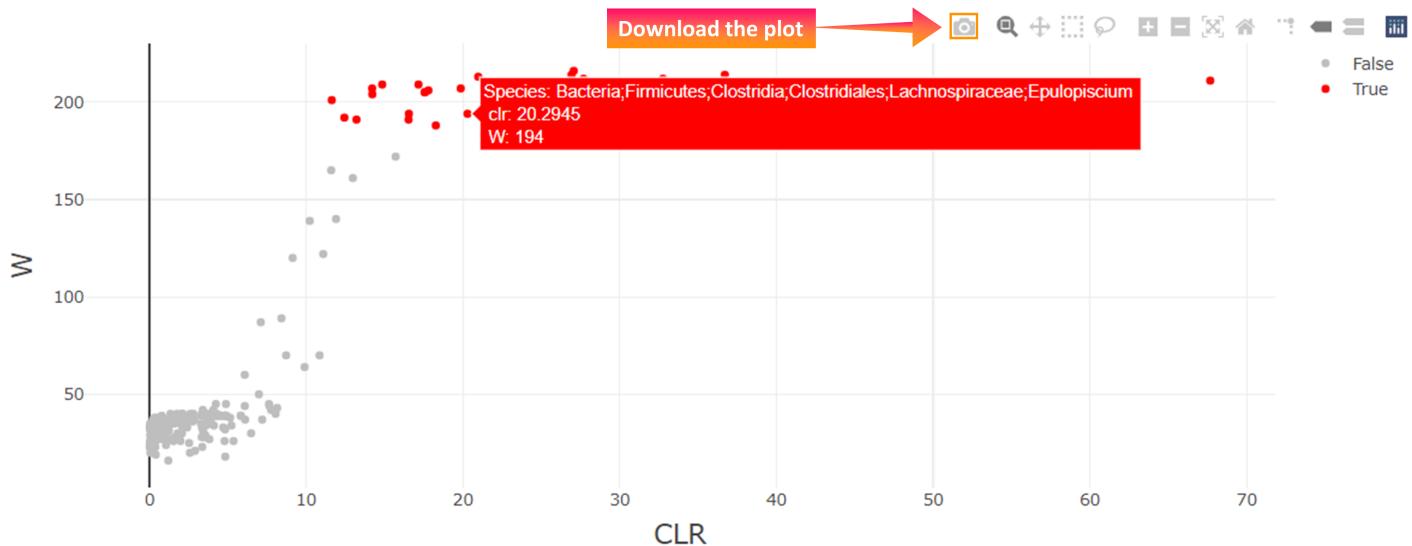
The screenshot shows the QIIME2 interface with the following elements:

- Top navigation bar: Taxonomic table, Taxonomic barplot, Taxonomic heatmap, Krona, Alpha diversity, Beta diversity, Phylogenetic diversity, and ANCOM (which is highlighted).
- Section title: ANCOM (Analysis of composition of microbiomes) is used for comparing the composition of microbiomes in two or more populations.
- Section header: Select an attribute comparison.
- Attribute selection: A list of options including body.site (selected), year, month, day, subject, reported.antibiotic.usage, and days.since.experiment.start.
- Level selection: Choose the level (Phylum selected).
- Action buttons: Start! (disabled) and Start.

- * Select an attribute comparison:
Select a group. ANCOM will then find significantly different abundant taxa among subgroups in that group.
- * Choose the level:
Select a taxonomic level for comparison.
- * Start:
Click the “**Start!**” button to perform the analysis.

- 8.1. ANCOM volcano plot: An interactive plot which shows the significantly different abundant taxa (in red). When the cursor hovers over a dot, the corresponding taxa information will be presented.

ANCOM Volcano Plot (Order)



The W value on the y axis is the number of sub-hypotheses that have been rejected for a given taxon in the ANCOM analysis.
The clr on the x axis represents log-fold change relative to the average microbe.

- * Download the ANCOM volcano plot:
Click on the camera icon to save the plot.
-

8.2. ANCOM statistical results: A table shows the W values for all taxa.

ANCOM results (Taxa with significant W value)

Show 10 entries		Search: <input type="text"/>						
	Kingdom	Phylum	Class	Order	Family	Genus	Species	W
1	Bacteria	Fusobacteria						20
2	Bacteria	Proteobacteria						20
3	Bacteria	Actinobacteria						20
4	Bacteria	Cyanobacteria						20
5	Bacteria	Firmicutes						19
6	Bacteria	Bacteroidetes						19
7	Bacteria	Verrucomicrobia						18

Showing 1 to 7 of 7 entries

Previous 1 Next

[!\[\]\(8185c5966122e049c676dbc6fb3c1f97_img.jpg\) Download the ANCOM result table \(Contain all species\)](#)

* Download the ANCOM result table:

Click the “**Download the ANCOM result table**” button to download the result. The table will contain the W values for all taxa.

Function Analysis

The database FAPROTAX is used to predict the function of microbiota.

(A) Upload files

1. Select “**Function Analysis**” in the top bar.



Welcome to MOCHI! (Microbiota amplicOn CHaracterization Implement)

MOCHI is a 16S or 18S microbiota amplicon rRNA analytical tool for microbiota based primarily on QIIME2 with a friendly web interface powered by the R package of Shiny. MOCHI may also be downloaded and operated locally.

2. In the left panel, press the “**Browse**” buttons to upload a metadata file and a taxonomic table. Alternatively, you can press the “**Example files**” button to download all the example files first and then upload the required files.

The image shows the MOCHI upload interface. On the left, there are two sections: "Upload the metadata file" and "Upload the taxonomic table file". Each section has a "Browse..." button and a "No file selected" placeholder. Below each section is a "Choose file format" dropdown with two options: "MOCHI/QIIME2 output (.qza)" (radio button) and "Plain text table (.txt)" (checkbox, which is checked). To the right of these sections is a sidebar with two buttons: "Function annotation table" and "Function barplot". At the bottom of the left panel are three buttons: "Start!" (highlighted with a red box), "Reset", and "learn more". A "example files" button is also present. A red arrow points from the "Upload" button in the sidebar to the "Start!" button in the main panel.

3. Click on the “**Start!**” button to conduct the analysis. (Or, click on the “**reset**” button to re-upload the files.)

(B) Inspect results

1. Function annotation table

This displays reads of the function types for each sample.

Function annotation table

Show 10 entries Search:

Type	L1S105	L1S140	L1S208	L1S257	L1S281	L1S57	L1S76	L1S8	L2S155	L2S175	L2S204
1 methanol_oxidation	0	0	0	0	0	0	0	0	34	12	6
2 methylotrophy	0	0	0	0	0	0	0	0	34	12	6
3 aerobic_ammonia_oxidation	0	0	0	0	0	0	0	0	0	0	0
4 nitrification	0	0	0	0	0	0	0	0	0	0	0
5 sulfate_respiration	79								0	0	2
6 sulfur_respiration	0								0	0	0
7 thiosulfate_respiration	0	0	0	0	0	0	0	0	0	0	0
8 respiration_of_sulfur_compounds	79	40	21	27	24	35	29	62	0	0	2
9 arsenate_detoxification	0	0	0	0	0	0	0	0	0	0	0
10 dissimilatory_arsenate_reduction	0	0	0	0	0	0	0	0	0	0	0

Showing 1 to 10 of 54 entries Previous [1](#) [2](#) [3](#) [4](#) [5](#) [6](#) Next

[Download the function annotation table](#) [Download](#)

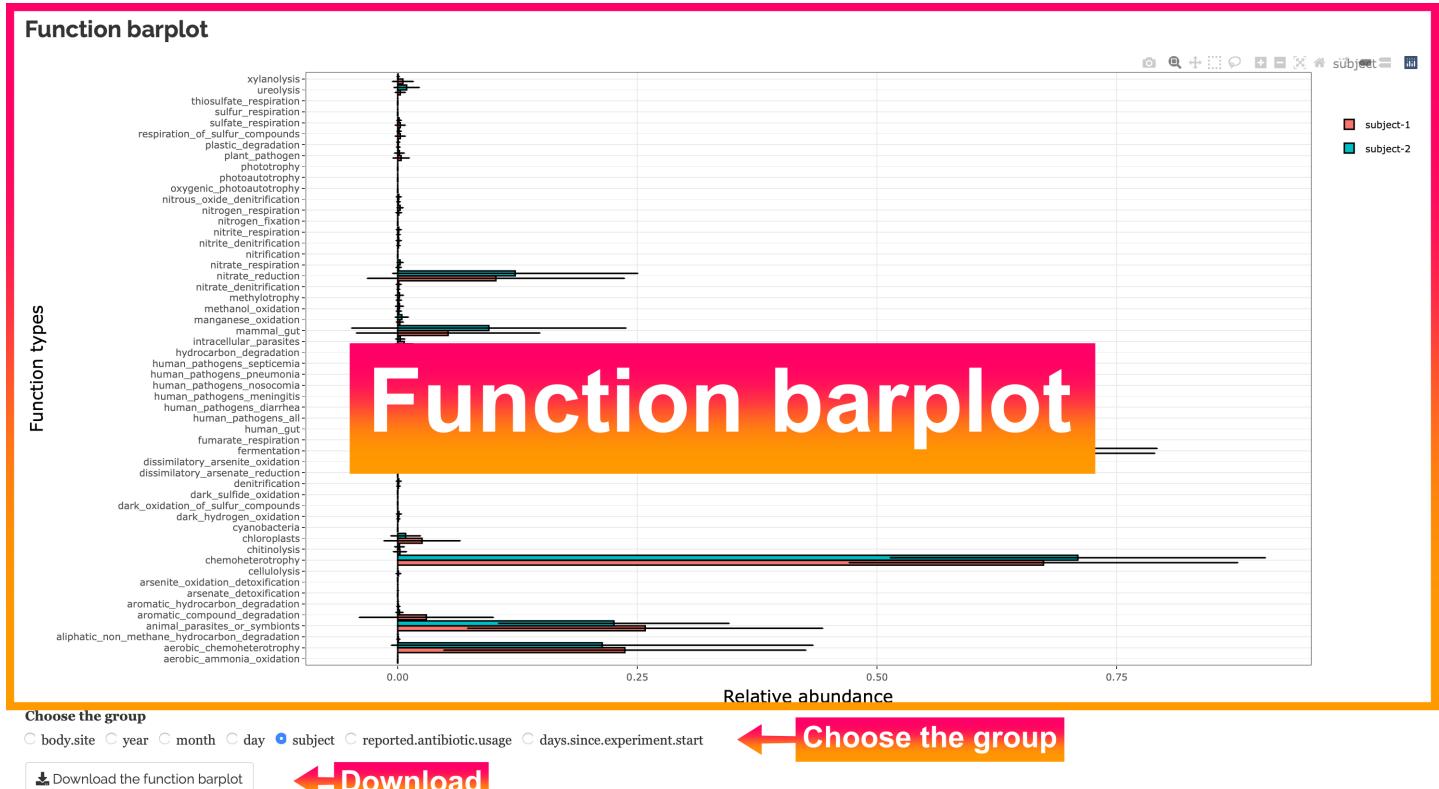
* Summary: Essential information regarding the function predictions.

* Download the function table:

Click the “**Download the function table**” button to download the table.

2. Function barplot

The horizontal bars indicate reads for each function and are grouped based on the metadata.



- * Choose the group: The bars will be categorized based on the selected metadata.
- * Download the function barplot:
Click the "**Download the function barplot**" button to download the barplot.