

Microbiota amplicOn
CHaracterization Implement

MOCHI

User Guide

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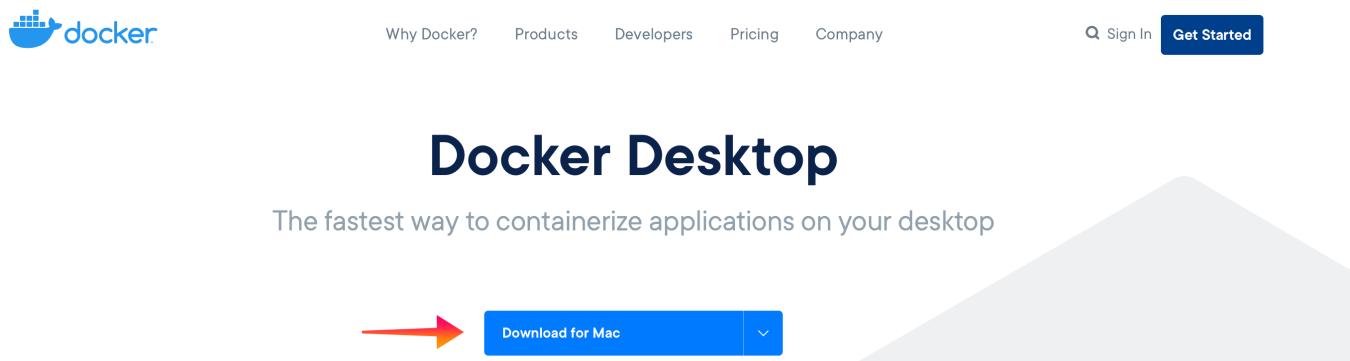
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CHAPTER 1: INSTALLATION OF LOCAL SERVICE

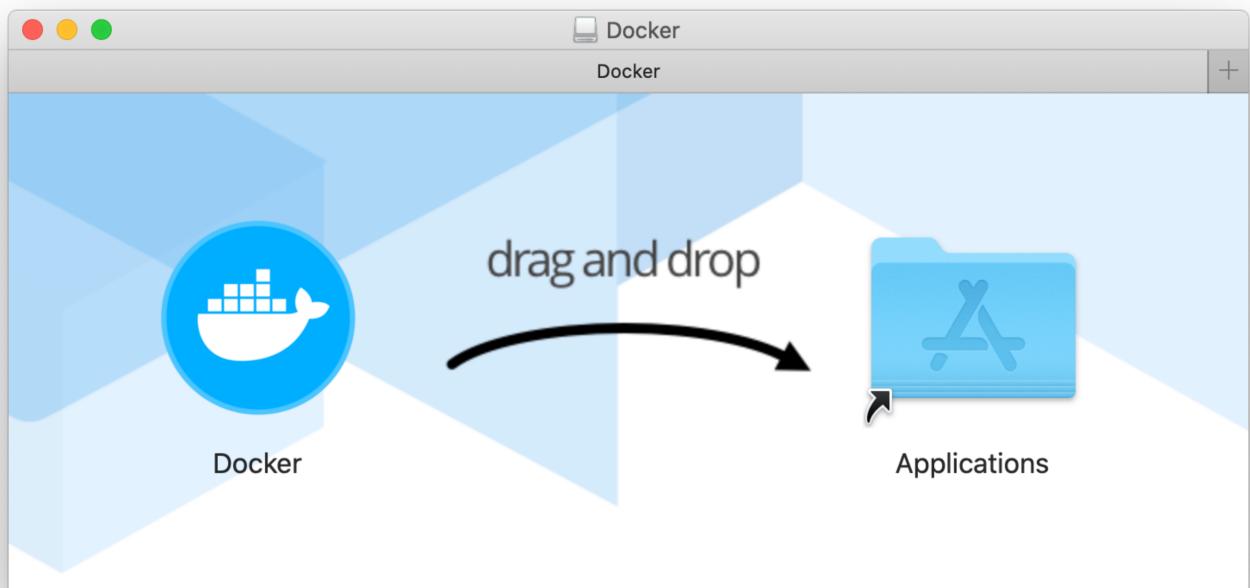
MacOS

(A) Install Docker

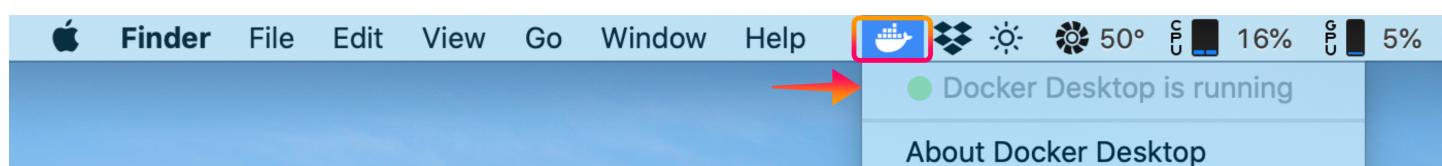
1. Download [Docker Desktop](#).



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



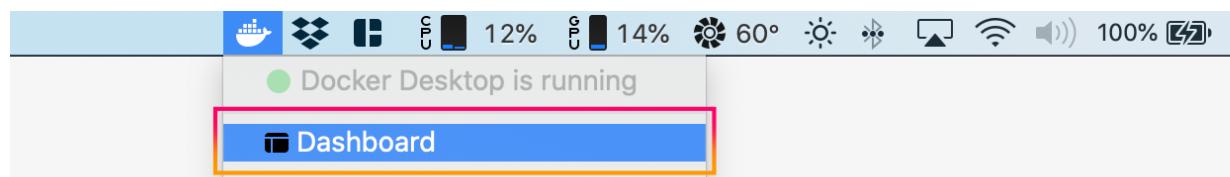
3. Start the Docker service by double clicking the Docker app. Wait for a few seconds to load, the docker icon should appear in the status bar.



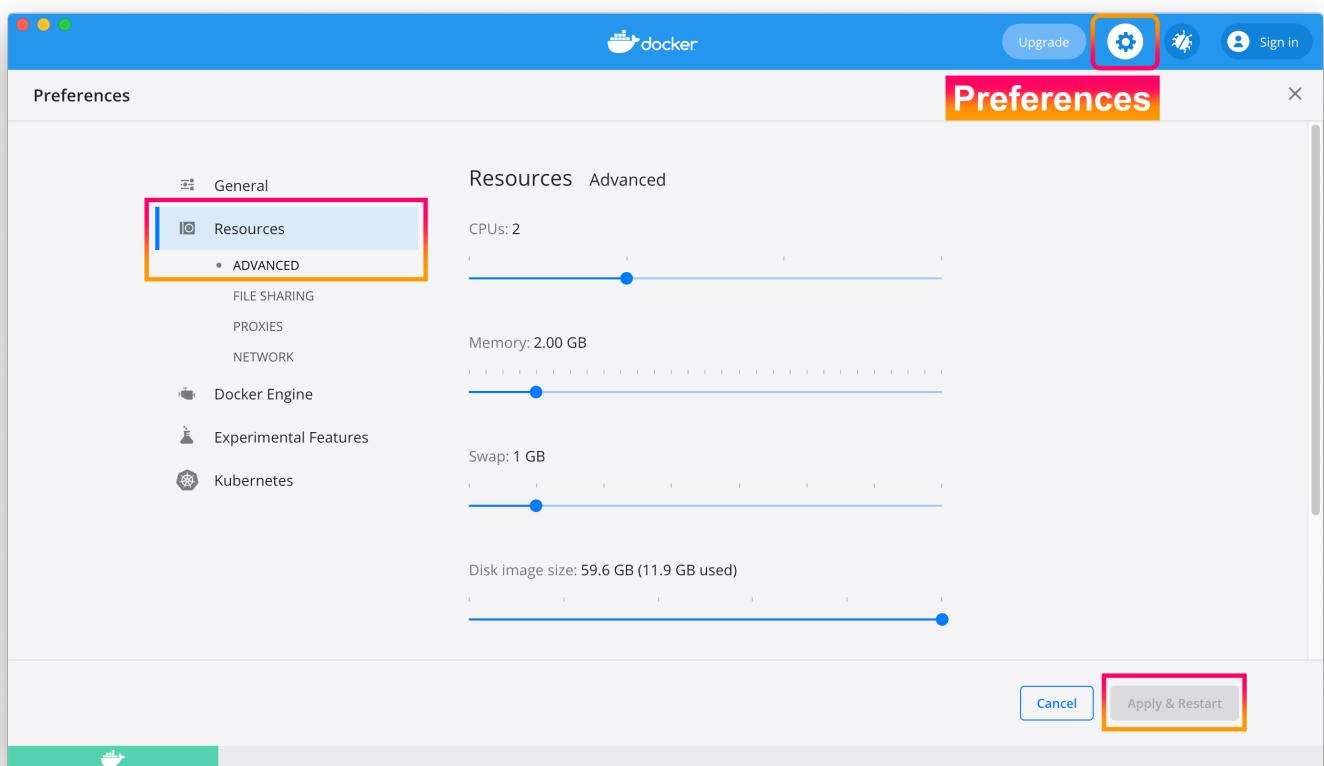
4. (Optional) In MacOS, the computational resources are preset in docker app. To optimize the efficiency of analysis, user can adjust the settings with following instruction. We recommend settings **above 4 CPUs** and **8-16 GB memory** (by default, MOCHI only use maximum 16GB memory).

⚠ Assign 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 with rolling bar. Press "Apply & Restart". Waiting for the Docker to restart.



(B) Start MOCHI service

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



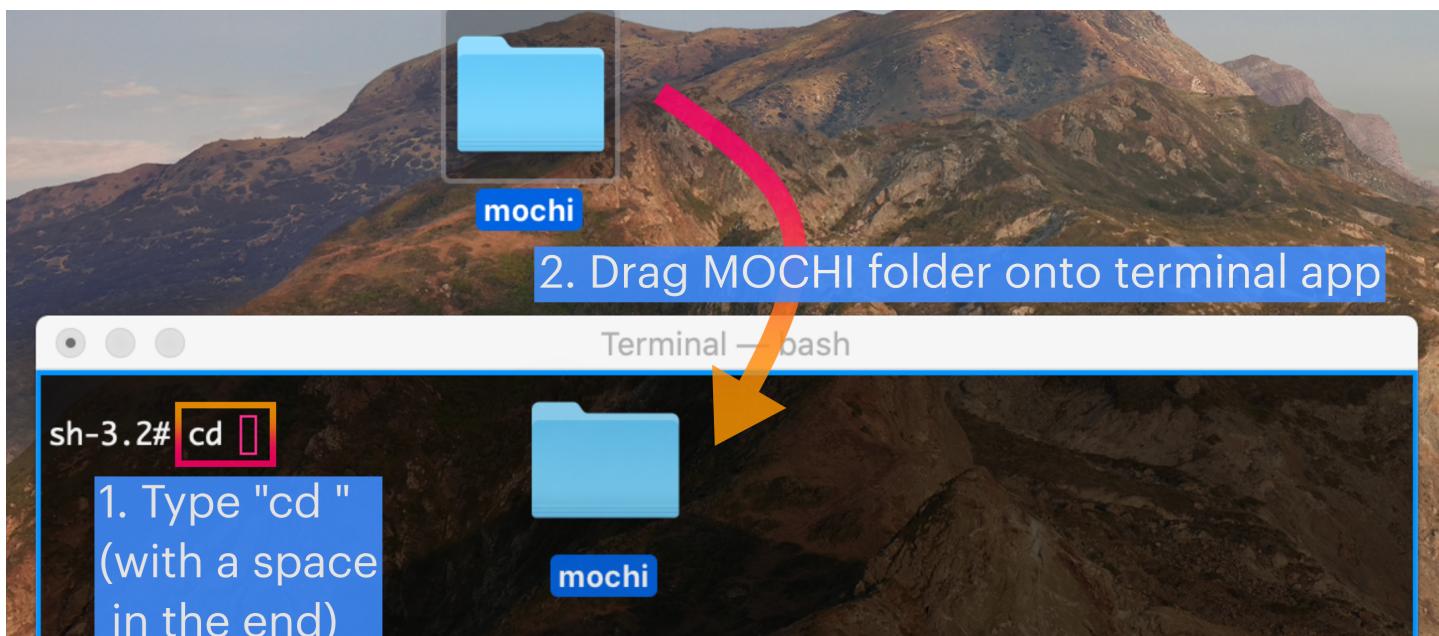
2. Open **Terminal** app. (Press “Command + Space” to open spotlight and type “terminal”.)



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

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

Hint: If you do not know the folder path of MOCHI, type **cd** with a space, and drag MOCHI folder onto the terminal window. The folder path should appear on 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 MOCHI image is around 8 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** on the address bar. A MOCHI interactive webpage is now available 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:
 - Step 1. Sequence summary:** Read counts and read quality.
 - Step 2. Sequence denoising (DADA2):** Sequence table and alpha rarefaction.
 - Step 3. Taxonomy classification:** Taxonomy prediction table.
- Taxonomy Analysis:** This step includes various plots and analyses:
 - Krona chart.
 - Bar plot.
 - Heatmap.
 - (alpha diversity) plot.
 - Box plot.
 - PCoA plot.
 - ANCOM (comparison between groups).
 - Post hoc analysis table.
- Function Analysis:** This step includes:
 - FAPROTAX table.
 - Functional annotation table.
 - 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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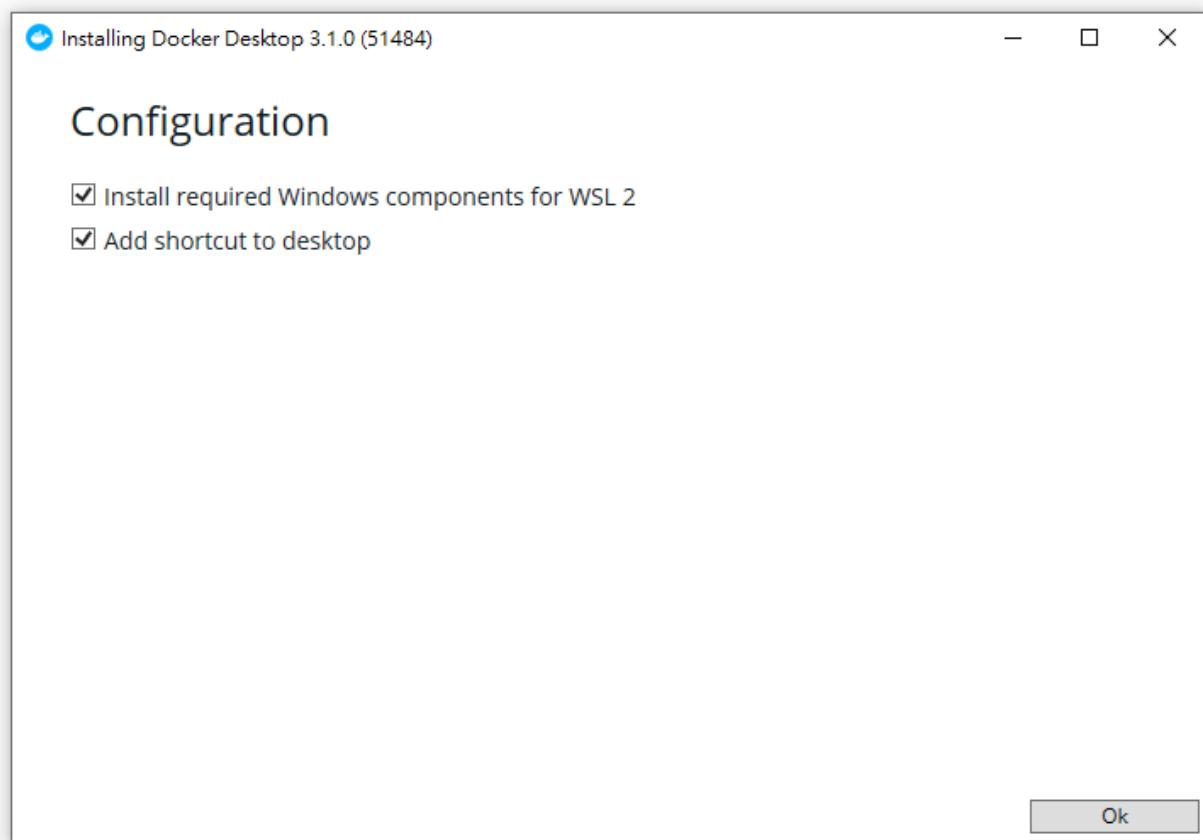
Window 10

(A) Install Docker

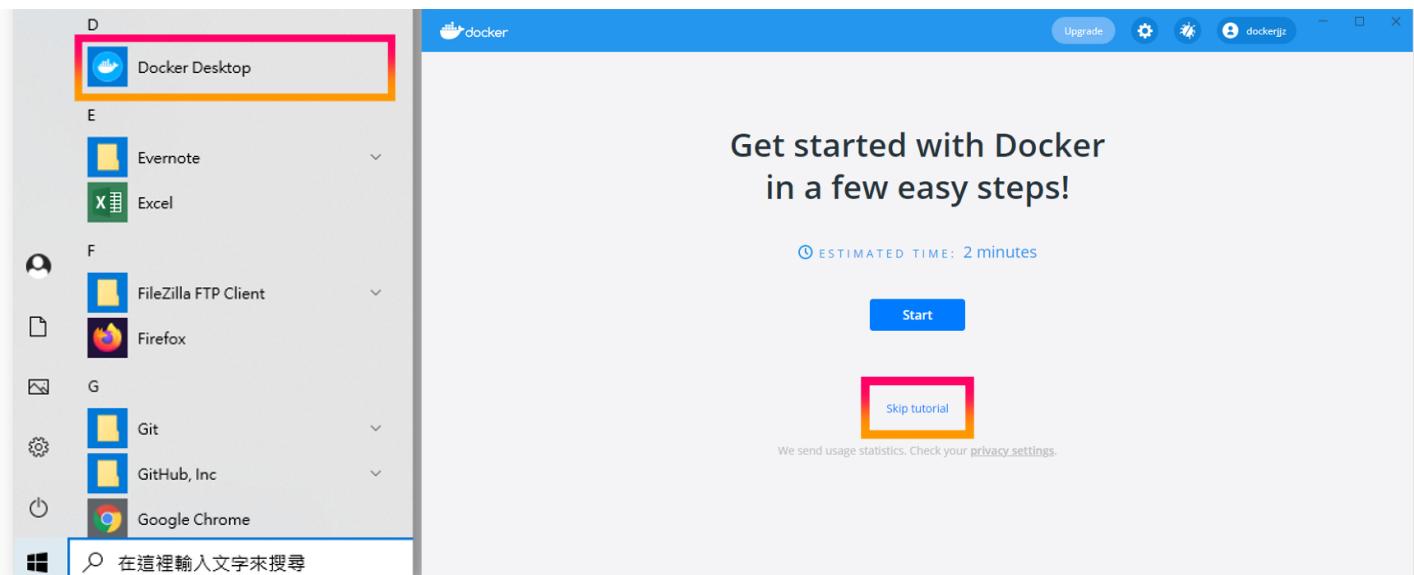
6. Download Docker Desktop.



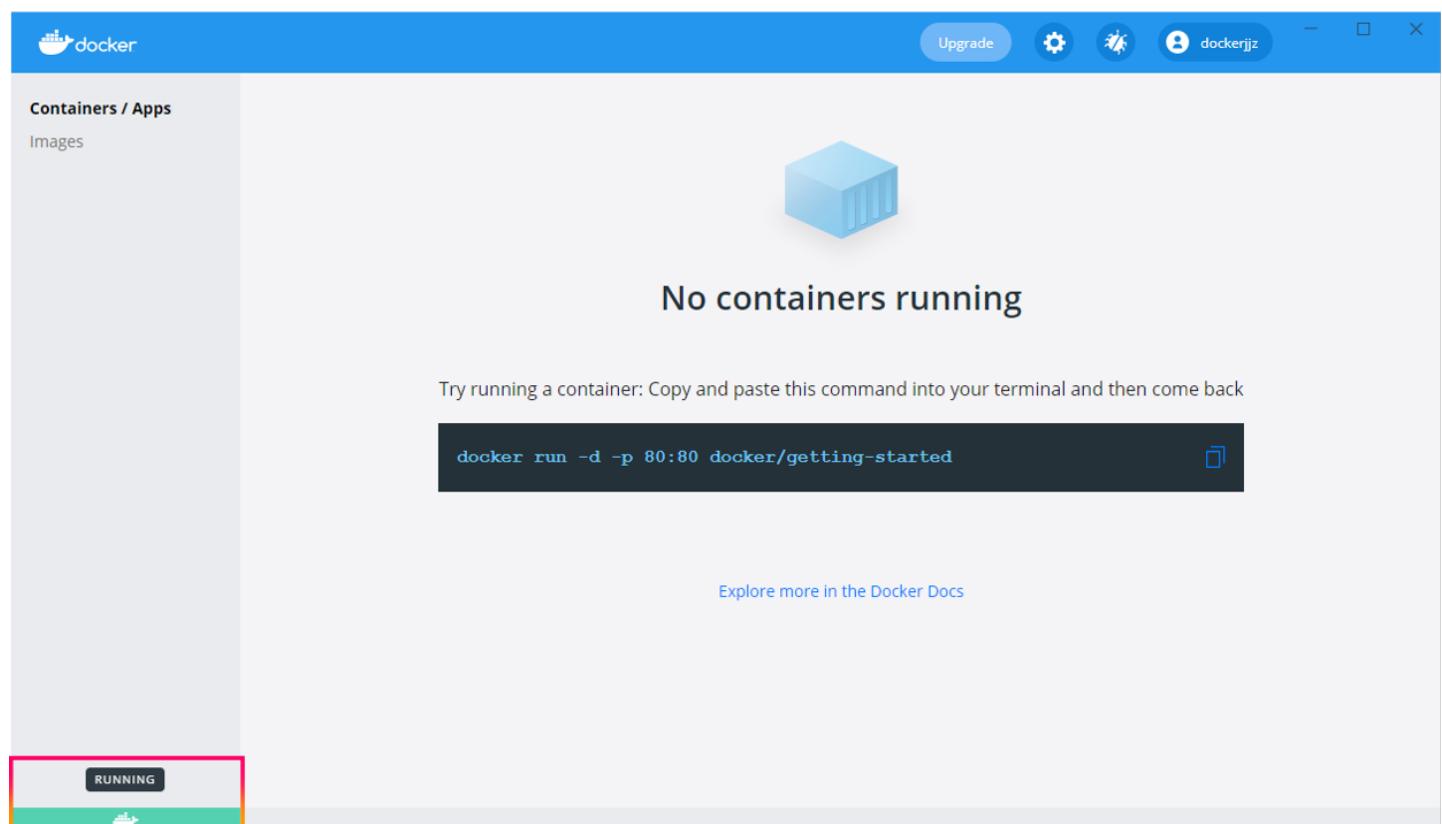
7. Open "**Docker Desktop Installer.exe**" and follow the instruction to setup. (You may be asked whether or not to install WSL2 engine. By default, it is installed along with the docker package to speed up the performance but not required for running MOCHI service. Please leave it to default setting if you don't know what to choose.)



8. Start docker service 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 app.

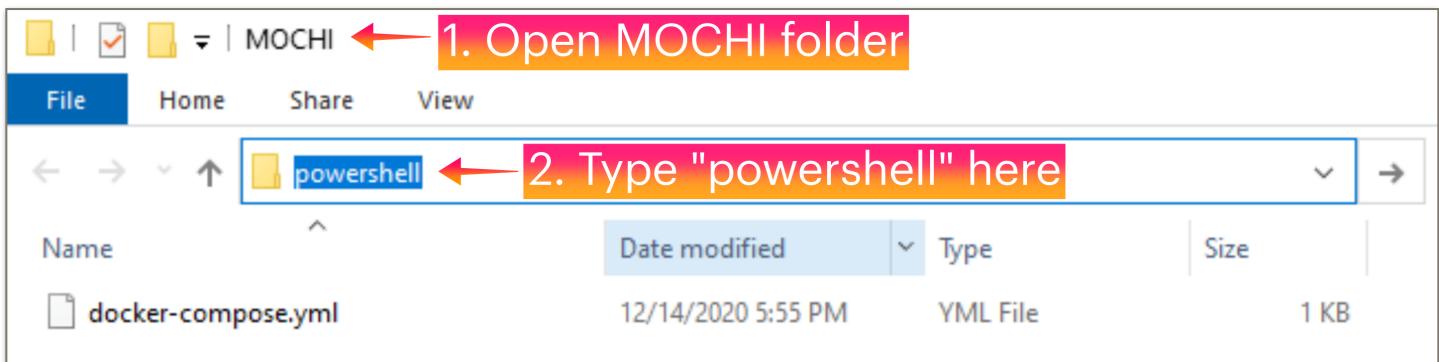


(B) Start MOCHI service

1. Download “**docker-compose.yml**” from [NCTU website](#), and place it under 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 MOCHI image is around 8 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: sha256:794909d921dfe9cc55edba44a3fe66701e43845c5c5578bf1e194064e071cbe
Status: Downloaded newer image for dockerjjz/mochi_local_version:latest
Creating mochi_server_version ... done
```

4. Open the browser, and type **127.0.0.1:3811** on 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 (a database icon). These feed into three main processing steps: Step 1. Sequence summary (read counts, read quality), Step 2. Sequence denoising (DADA2) (sequence table, alpha rarefaction), and Step 3. Taxonomy classification (FAPROTAX, taxonomy prediction table). Arrows point from these steps to a large central panel containing various analytical plots: taxonomy table, bar plot, heatmap, (alpha diversity) box plot, PCoA plot, Krone, (ANCOM), comparison between groups, post hoc analysis, functional annotation table, and bar plot. The bottom of the page has a footer with the text "The advantages of MOCHI" and a bulleted list of its benefits, followed by "Molecular Bioinformatics Lab, National Yang Ming Chiao Tung University, Taiwan 300, R.O.C. Last updated on 03/23/2021".

Linux

(A) Install Docker

- ▶ Please follow the [official guidance](#) to setup and start docker engine on Ubuntu.

(B) Start MOCHI service

1. Download “**docker-compose.yml**” from [NCTU website](#), and place it under 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 MOCHI image is around 8 GB, and the running time depends on the download speed.)

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

4. Open the browser, and type **127.0.0.1:3811** on 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 cautious 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 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 Window 10, Please see [Window 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 user’s sequence data which will be loaded in “Sequence preprocessing - Sequence summary”.
- ▶ The file type of sequence data need to be **fastq.gz** or **fq.gz**.
- ▶ The filename of sequence data need 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 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 modified 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**” on the top bar, choose “**Step 1. Sequence summary**”.

Welcome to MOCHI

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

Step 1. Sequence summary

Step 2. Sequence denoising

Step 3. Taxonomy classification

Characterization Implement

Home Sequence Preprocessing Taxonomy Analysis Function Analysis Tutorial

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

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

Sequence files

Please choose the directory containing sequence files (*.fastq.gz or *.fq.gz)

Select the directory

Example sequences

1. Sequences summary (for single end)

(1) Summarize the single-end sequences.

Start!

3. Select a directory containing sequence files.

Please select a directory

Create new folder Sort content

raw_data

Directories Content

single_seqs_demo

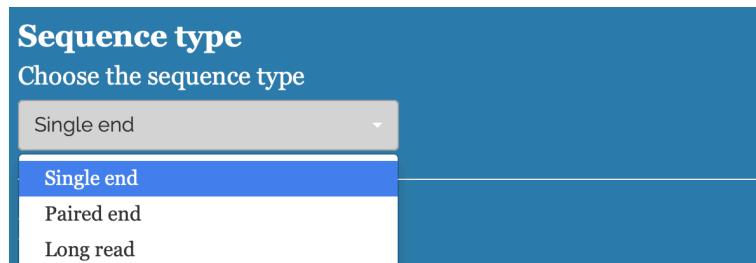
1	L1S105_9_L001_R1_001.fastq.gz	889.1 kB
1	L1S140_6_L001_R1_001.fastq.gz	675.3 kB
1	L1S208_10_L001_R1_001.fastq.gz	861.9 kB
1	L1S257_11_L001_R1_001.fastq.gz	633.7 kB
1	L1S281_5_L001_R1_001.fastq.gz	685.7 kB
1	L1S57_13_L001_R1_001.fastq.gz	896.4 kB
1	L1S76_12_L001_R1_001.fastq.gz	767.0 kB
1	L1S88_8_L001_R1_001.fastq.gz	887.4 kB
1	L2S155_25_L001_R1_001.fastq.gz	770.0 kB
1	L2S175_27_L001_R1_001.fastq.gz	873.6 kB
1	L2S204_1_L001_R1_001.fastq.gz	615.1 kB
1	L2S222_23_L001_R1_001.fastq.gz	736.1 kB
1	L2S240_7_L001_R1_001.fastq.gz	929.2 kB
1	L2S309_33_L001_R1_001.fastq.gz	314.7 kB
1	L2S357_15_L001_R1_001.fastq.gz	502.5 kB
1	L2S382_34_L001_R1_001.fastq.gz	792.2 kB
1	L3S242_19_L001_R1_001.fastq.gz	149.3 kB

Confirm selection Cancel Select

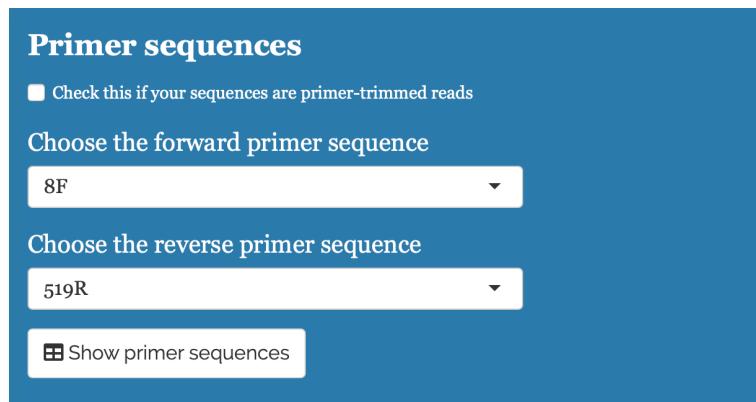
4. Sequence type: The settings for “**Step 1. Sequence summary**” and “**Step 2. Sequence denoising**” are different based on the sequence type chosen.

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

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



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



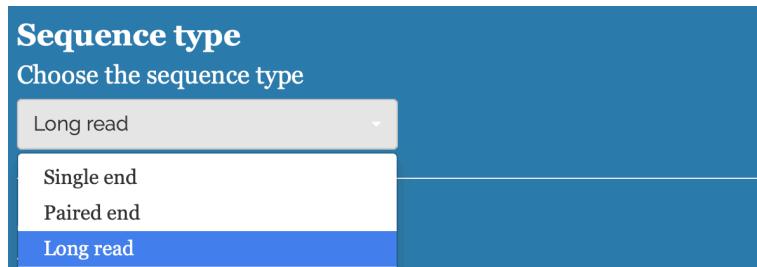
- 4.a.3. Set the number of threads to run the analysis. If zero, all available cores will be used. If you do not know the number to enter, leave it to the default number (all threads - 2).



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

4.b. **Long-read**

- 4.b.1. the sequence type will not automatically detected. **Please select manually.**



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



- 4.b.3. Click on the "**Start!**" button.

5. Please wait while it 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.

(B) Sequence denoising

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

The screenshot shows the MOCHI web interface. At the top is a blue navigation bar with links for Home, Sequence Preprocessing (which is currently selected), Taxonomy Analysis, Function Analysis, and Tutorial. Below the navigation bar is a section titled "Welcome to MOCHI". On the right side of this section, there is a dropdown menu with three options: "Step 1. Sequence summary", "Step 2. Sequence denoising", and "Step 3. Taxonomy classification". A red arrow points from the text "depending on sequence type selected in 'Step 1. Sequence summary'" in the following list item to the "Step 2. Sequence denoising" option in the dropdown menu. To the right of the dropdown menu, a note states: "Denoising is based on QIIME2 with a friendly web interface powered by the R package of Shiny. MOCHI may also be downloaded and operated locally."

2. Depending on 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 position and the quality score to trim 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 button: "learn more".

* Starting and ending position:

Base pairs below starting position and above ending position will be trimmed off. For instance, setting the starting position to 5 and the ending position to 120 will obtain sequences from 5 to 120 bp with 115 bp long.

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

* Quality score:

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

2.a.2. Set the parameter of **chimera**, **computing setting** and upload the **metadata**.

The screenshot shows two configuration sections. The first section, "Chimeric reads filtering", has a sub-section "The minimum fold-change value" with a value of "1" in a text input field. Below it is a "learn more" button. The second section, "Computing setting", has a sub-section "Number of threads MOCHI can use" with a value of "2" in a text input field.

*** Chimeric reads filter:**

A chimeric read is a sequence originated from multiple parent sequences. Chimeric reads are generally considered contaminant. 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 speed up the analytical process. Increasing the number of threads will decrease the running time. When zero is provided, all available cores will be used. If you do not know the number to enter, leave it to the default number.

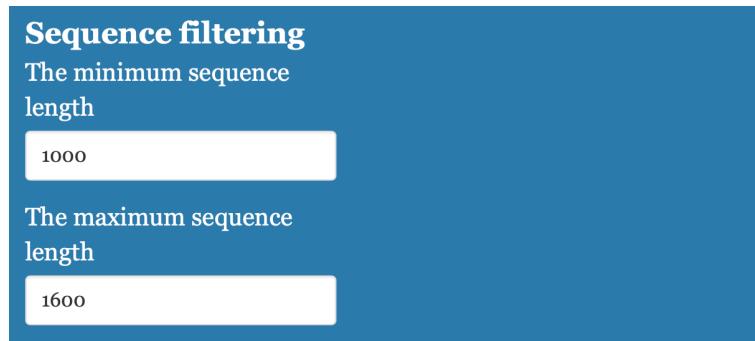
2.b. Long-read

- 2.b.1. Set the minimum and maximum sequence length 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



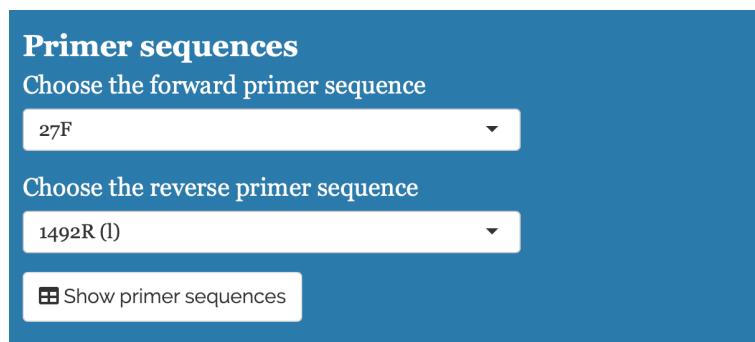
- 2.b.2. Choose the primers.

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 on 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**” on the top bar, choose “**Step 3. Taxonomy classification**”.

The screenshot shows the MOCHI web interface. At the top, there is a blue header bar with the MOCHI logo, a Home button, a Sequence Preprocessing dropdown, a Taxonomy Analysis button, a Function Analysis button, and a Tutorial button. Below the header, the main content area has a blue background. On the left, it says "Welcome to MOCHI". In the center, there is a dropdown menu with four options: "Step 1. Sequence summary", "Step 2. Sequence denoising", "Step 3. Taxonomy classification", and "Characterization Implement". A red arrow points to the "Step 3. Taxonomy classification" option. To the right of the dropdown, there is some descriptive text about MOCHI being a 16S or 18S microbiota amplicon rRNA analysis tool developed with QIIME2 and Shiny, and mentioning that 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. The title is "Database" and the subtitle is "Select the reference database for taxonomy classification." There is a "Choose the database" section with a dropdown menu set to "Silva (Not detected)". Below the dropdown is a "Auto download database" button. At the bottom is an "Example" button.

2.1. Automatically download database:

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

2.2. Manually download database:

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

2. Filter the reference sequence by length

Minimum length

Maximum length

[learn more](#)

*** Minimum and maximum length:**

Reference sequences not in range of the specified values will be discarded. The default values are the minimum and the maximum length of denoised sequences. To disable length filtering, set the values to zero.

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

Computing setting

Number of threads MOCHI can use

6. Click on the "**Start!**" button.

3. Taxonomy classification

(1) Classify taxonomy

 Start!

7. Please wait while it 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!

Taxonomy analysis

(A) Upload files

8. Select “**Taxonomy analysis**” on 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.

9. In the left panel, press the “Browse” button to upload **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 could press the “Demo” button to download the example files first and then upload them. If sequences are 18S rRNA, please check the “18S rRNA” box.

* Metadata (.tsv):

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

* Taxonomic table file (.qza):

You could 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.

The image shows the left panel of the MOCHI web interface, which contains three main input fields for file uploads. 1. "Upload the metadata file" with a "Browse..." button and a "No file selected" message. 2. "Upload the taxonomic table file" with a "Browse..." button and a "No file selected" message. 3. "Upload the ASVs table file" with a "Browse..." button and a "No file selected" message. Below these fields is a checkbox for "18S rRNA" with an information icon. At the bottom are two buttons: "Start!" and "reset", and a "Demo" button.

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

11. The results will be displayed on the right panel once the files are uploaded.

Upload the metadata file i

Browse... demo_metadata_single.tsv
Upload complete

Upload the taxonomic table file i

Browse... Taxonomic_table_example.qza
Upload complete

Upload the ASVs table file i

Browse... ASVs_table_example.qza
Upload complete

■ 18S rRNA i

Start! reset

Demo

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

ANCOM

Choose the group

SampleID body.site year month day subject reported.antibiotic.usage days.since.experiment.start

Show 10 entries Search:

Kingdom (K=3)	Phylum (K=21)	Class (K=42)	Order (K=69)	Family (K=134)	Genus (K=281)	Species (K=356)	L1S8	L1S57	L1S76	L1S105
Unassigned	Unassigned	Unassigned	Unassigned	Unassigned	Unassigned	Unassigned	0	0	0	0
Archaea	Crenarchaeota	Thaumarchaeota	Nitrosphaerales	Nitrosphaeraceae	Candidatus Nitrosphaera	Unassigned	0	0	0	0
Archaea	Crenarchaeota	Thaumarchaeota	Nitrosphaerales	Nitrosphaeraceae	Candidatus Nitrosphaera	SCA1145	0	0	0	0
Bacteria	Unassigned	Unassigned	Unassigned	Unassigned	Unassigned	Unassigned	0	0	0	0
Bacteria	Acidobacteria	[Chloracidobacteria] RB41	Ellin6075	Unassigned	Unassigned	Unassigned	0	0	0	0
Bacteria	Actinobacteria	Acidimicrobia	Acidimicrobiales	Unassigned	Unassigned	Unassigned	0	0	0	0
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unassigned	Unassigned	Unassigned	0	0	0	0
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces	Unassigned	0	0	0	0
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces	Unassigned	0	0	0	0

Showing 1 to 10 of 385 entries Previous 1 2 3 4 5 ... 39 Next

Download Taxonomic table

(B) Inspect results

- MOCHI displays the results in eight approaches: (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

A table describes taxonomy information and read count.

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=21)	Class (K=42)	Order (K=69)	Family (K=134)	Genus (K=281)	Species (K=356)	L1S8	L1S57	L1S76	L1S105	L2S155	L2S175
Unassigned	Unassigned	Unassigned	Unassigned	Unassigned	Unassigned	Unassigned	0	0	0	0	0	0
Archaea	Crenarchaeota	Thaumarchaeota	Nitrosphaerales	Nitrosphaeraceae	Candidatus Nitrosphaera	Unassigned	0	0	0	0	0	0
Archaea	Crenarchaeota	Thaumarchaeota	Nitrosphaerales	Nitrosphaeraceae	Candidatus Nitrosphaera	SCA1145	0	0	0	0	0	0
Bacteria	Unassigned	Unassigned	Unassigned	Unassigned	Unassigned	Unassigned	0	0	0	0	25	13
Bacteria	Acidobacteria	[Chloracidobacteria] KB41	Ellin6075	Unassigned	Unassigned	Unassigned	0	0	0	0	0	0
Bacteria	Actinobacteria	Acidimicrobia	Acidimicrobiales	Unassigned	Unassigned	Unassigned	0	0	0	0	0	0
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Unassigned	Unassigned	Unassigned	0	0	0	0	7	0
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Unassigned	Unassigned	0	0	0	0	0	0
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces	Unassigned	0	0	0	0	0	0
Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Actinomycetaceae	Actinomyces	Unassigned	0	0	0	0	0	0

Showing 1 to 10 of 385 entries

Previous 1 2 3 4 5 ... 39 Next

Download Taxonomic table

Download button

* Choose the group:

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

* Taxonomy information:

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

* Read count:

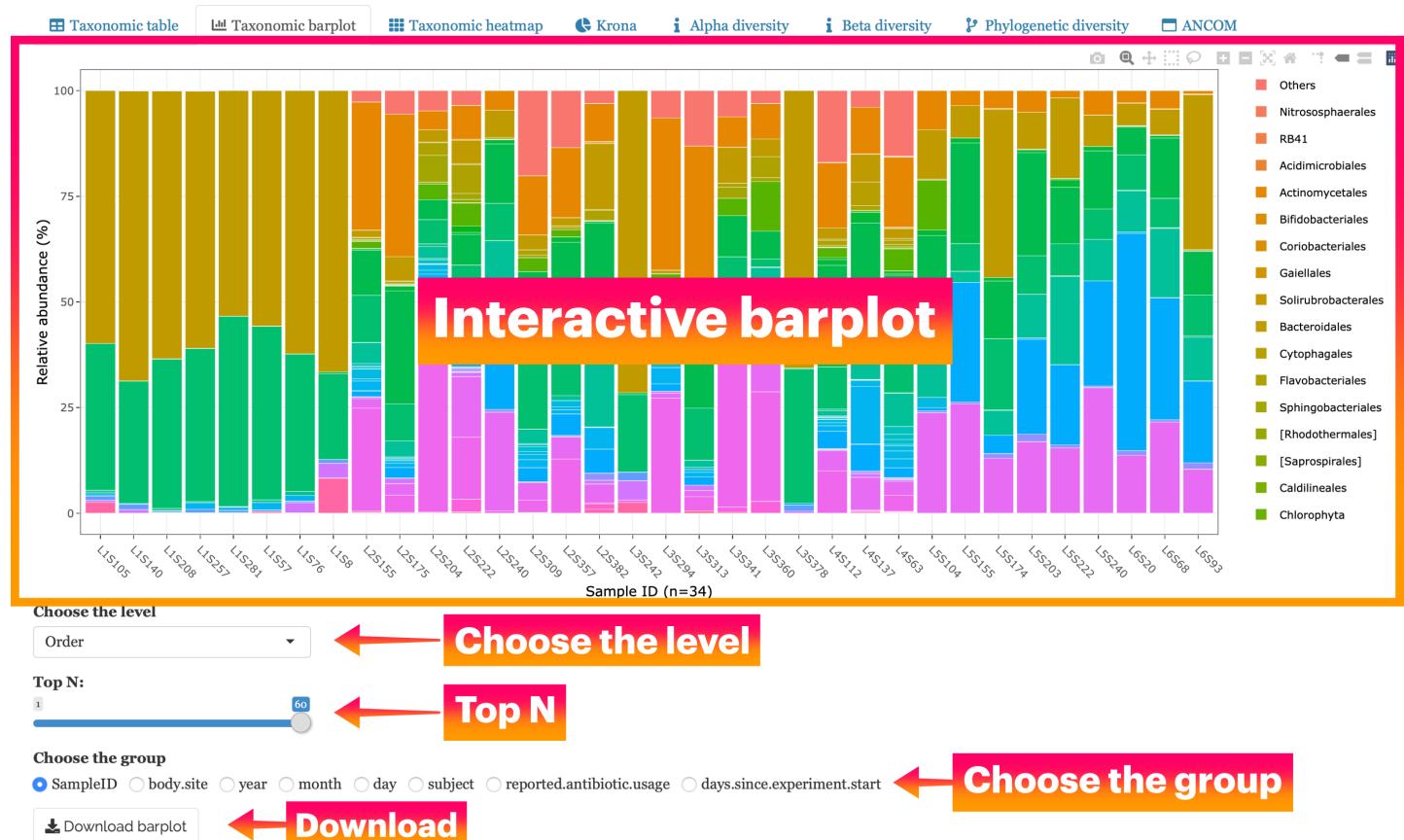
The right part of the table represents read count. The values of read count are categorized by the selected group. The column name indicates the variables of the selected group.

* Download taxonomic table:

Click on the "Download Taxonomic table" button to download the displayed table.

2. Taxonomic barplot

An interactive barplot showing the percentage of taxa in all sample. Each taxon is represented by a sub-bar with different colors.



* Interactive barplot:

When a cursor hovers over the bar region, the information of 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 on the plot. When you select value N, the plot will show the union of the top N relatively abundant taxa in each sample. For example, if N = 2 is selected and the top 2 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:

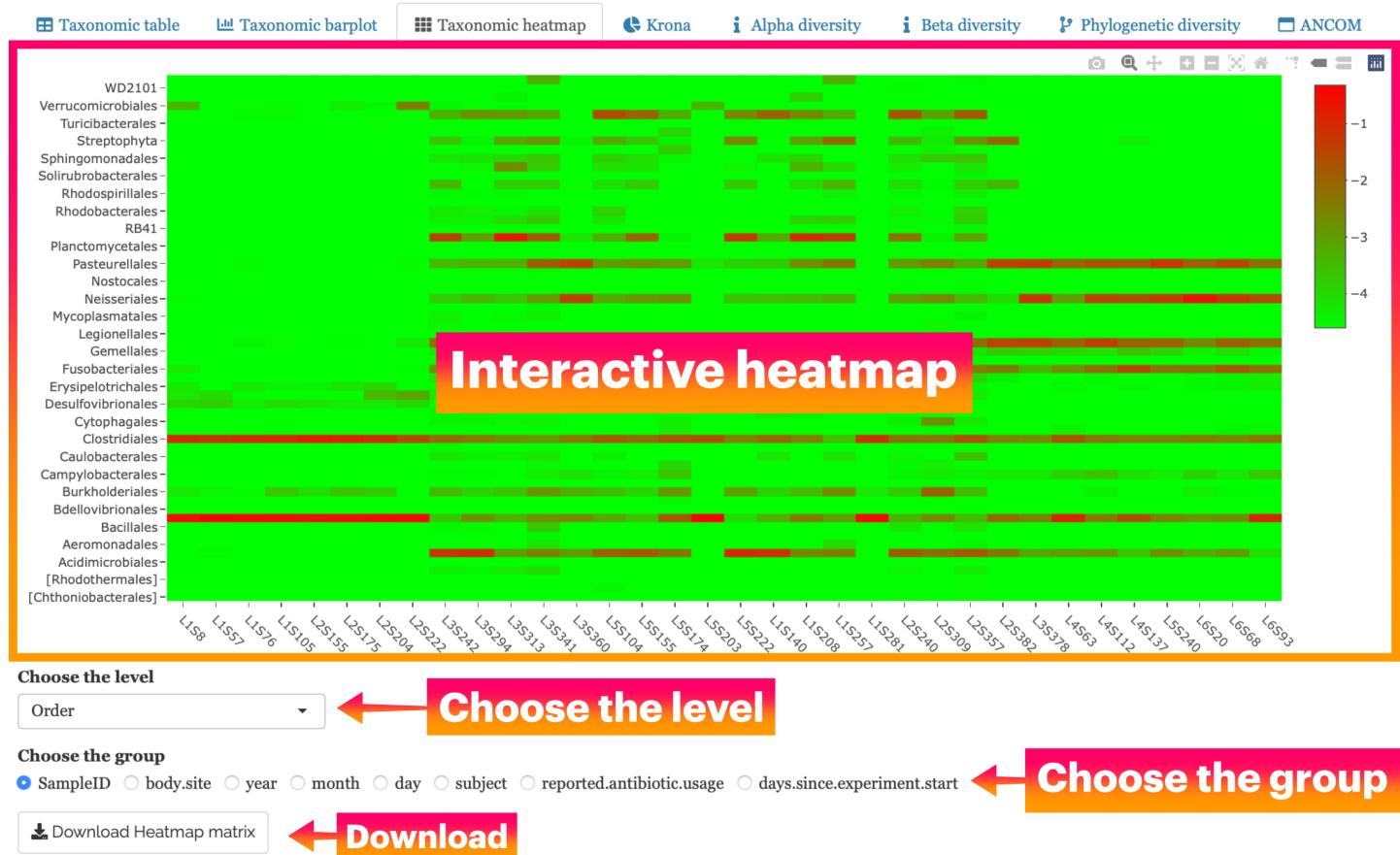
The barplot will be grouped based on the selected metadata.

* Download barplot:

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

3. Taxonomic heatmap

An interactive heatmap showing the log10-transformation percentage of taxa in all samples. To prevent taking logarithm of zero, a small value of 0.01 is added to all percentage values before the transformation. The transformed values are shown in color gradient.



* Interactive heatmap:

When a cursor hovers over the heatmap, the information of 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 on 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:

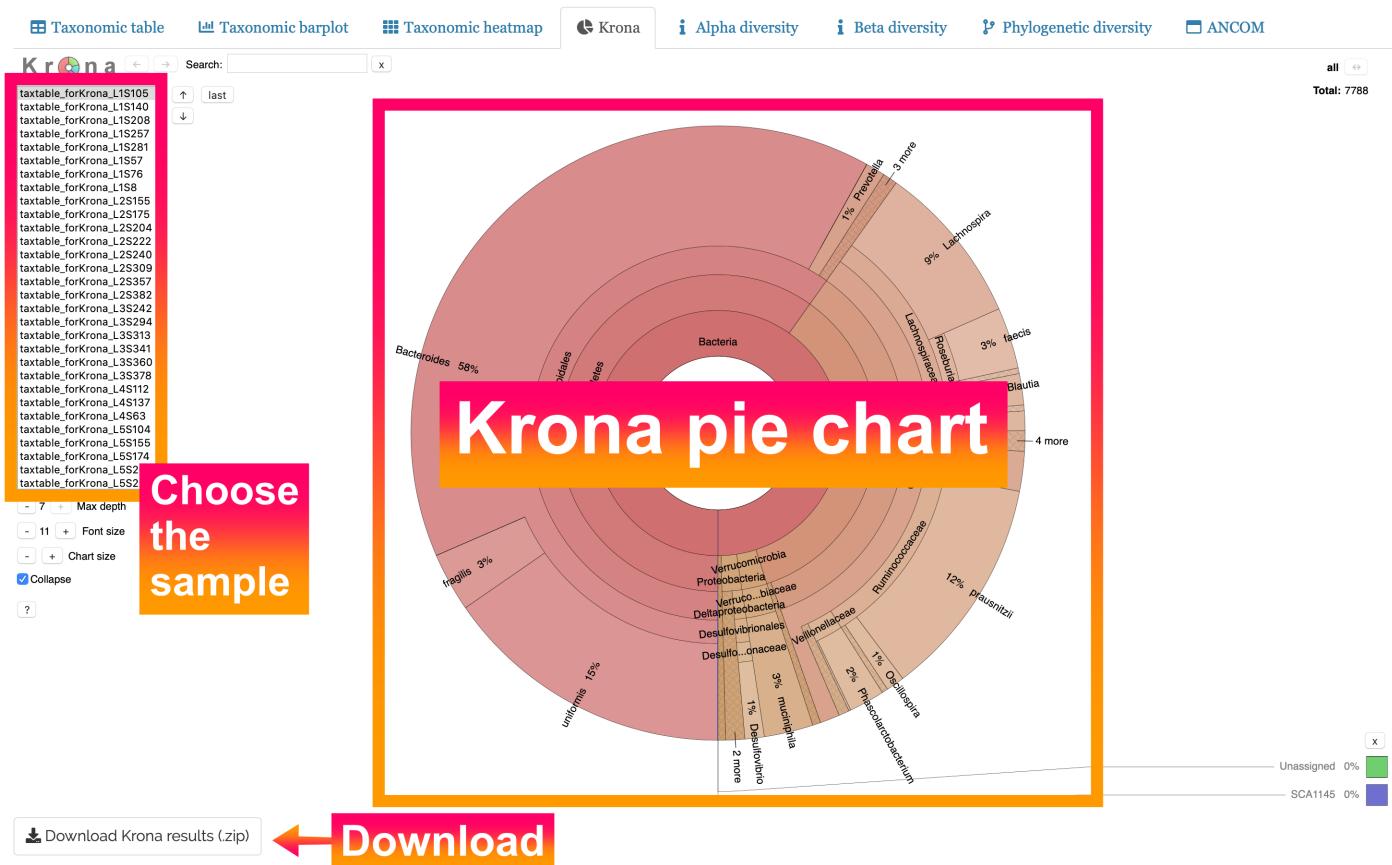
The heatmap will be grouped based on the selected metadata.

* Download heatmap matrix:

Click on the "Download Heatmap matrix" button to download the heatmap matrix data.

4. Krona

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



- * Kona pie chart:
An interactive pie plot. Single click a taxon will show the ratio of the selected taxon over different taxonomy level. Double click a taxon will zoom in the selected taxonomy level. To zoom back, click the backspace button on the top-left region.
 - * Choose the sample:
Select the sample to switch to the corresponding pie plot.
 - * Download Kona results:
Click on the “Download Kona results (.zip)” button to download the interactive pie plot (html files with Javascript).

5. Alpha diversity

Evaluation of species diversity within samples. In MOCHI, we adapt 8 indexes (richness, Chao1, ACE, Shannon diversity, InvSimpson diversity, Shannon evenness, Simpson evenness, and Goods coverage).

5.1. Table

Table

Show 10 entries

Search:

	Sample	Richness	Chao1	ACE	Shannon_diversty	Simspon_diversity	InvSimpson_diversity	Shannon_evenness	Simpson_evenness
1	L1S105	63	63	63	2.6808	0.8705	7.7201	0.4033	0.0015
2	L1S140	65	65	65	2.6609	0.8519	6.7499	0.4004	0.0015
3	L1S208	85	85	85	3.1189	0.8995	9.955	0.4693	0.0014
4	L1S257	81	81	81	3.259	0.9256	13.4455	0.4903	0.0014
5	L1S281	72	72	72			26	0.4792	0.0014
6	L1S57	70	70	70			67	0.4368	0.0015
7	L1S76	61	61	61	2.4883	0.7959	4.8999	0.3744	0.0016
8	L1S8	44	44	44	2.2026	0.7939	4.851	0.3314	0.0016
9	L2S155	109	109	109	3.5545	0.9388	16.3338	0.5348	0.0014
10	L2S175	104	104	104	3.4387	0.9221	12.8439	0.5174	0.0014

Showing 1 to 10 of 34 entries

Previous 1 2 3 4 Next

[!\[\]\(7c3d2608a7a555c07f6aa454ffa411df_img.jpg\) Download Alpha Diversity Table](#)

[Download](#)

Alpha diversity table

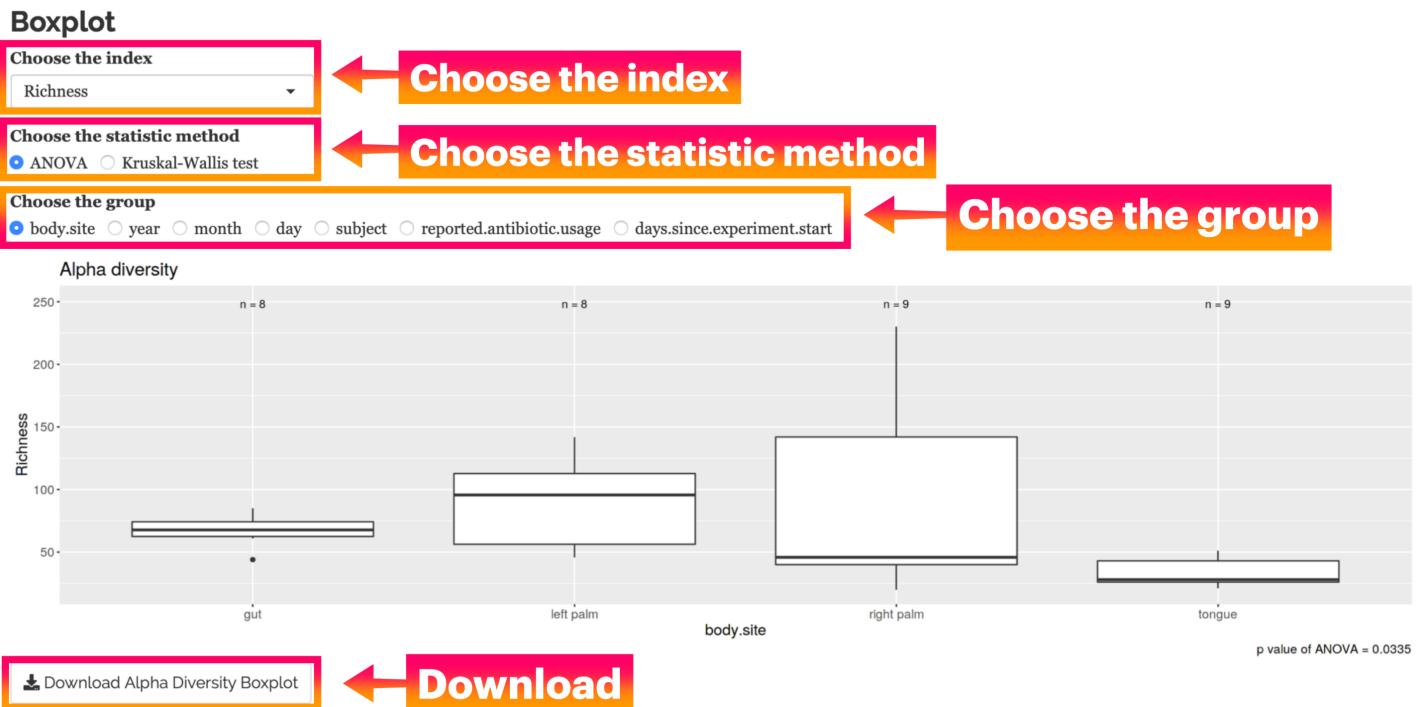
* Alpha diversity table:

This table shows the values of 8 alpha diversity indexes.

* Download alpha diversity table:

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

5.2. Boxplot



* Choose the index:

A boxplot will be presented with the selected index.

* Choose the statistic 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 Alpha diversity boxplot:

Click on 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

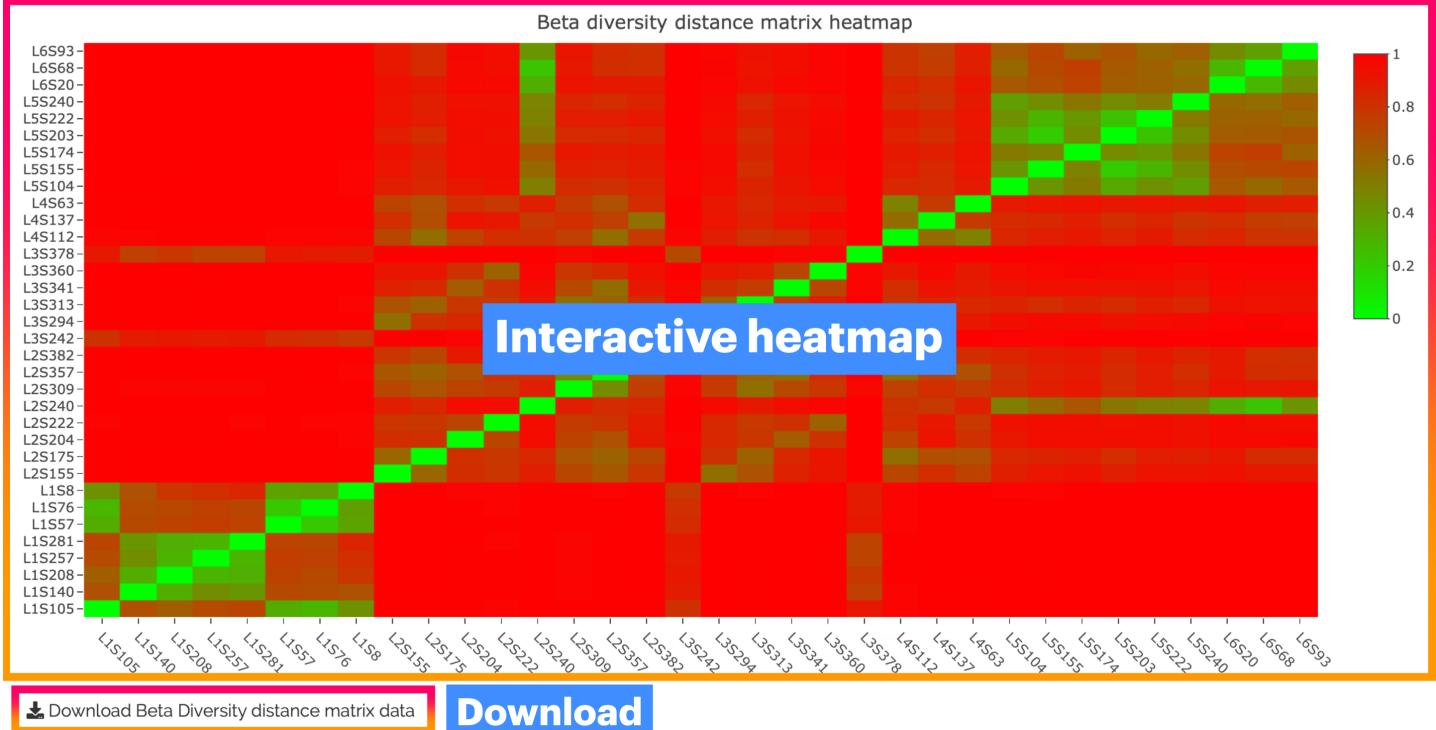
- * If ANOVA is selected when creating the boxplot, the Tukey test will be used for the post-hoc test. If Kruskal-Wallis is selected, then the Dunn test will be used.
- * Download Alpha diversity post-hoc test result:
Click on the “Download Alpha Diversity statistical result” button to download the post-hoc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

6. Beta diversity

Evaluation of species diversity between samples. In MOCHI, we use the Bray-Curtis index.

6.1. Distance matrix

Beta diversity table (Bray-Curtis)



* Interactive heatmap:

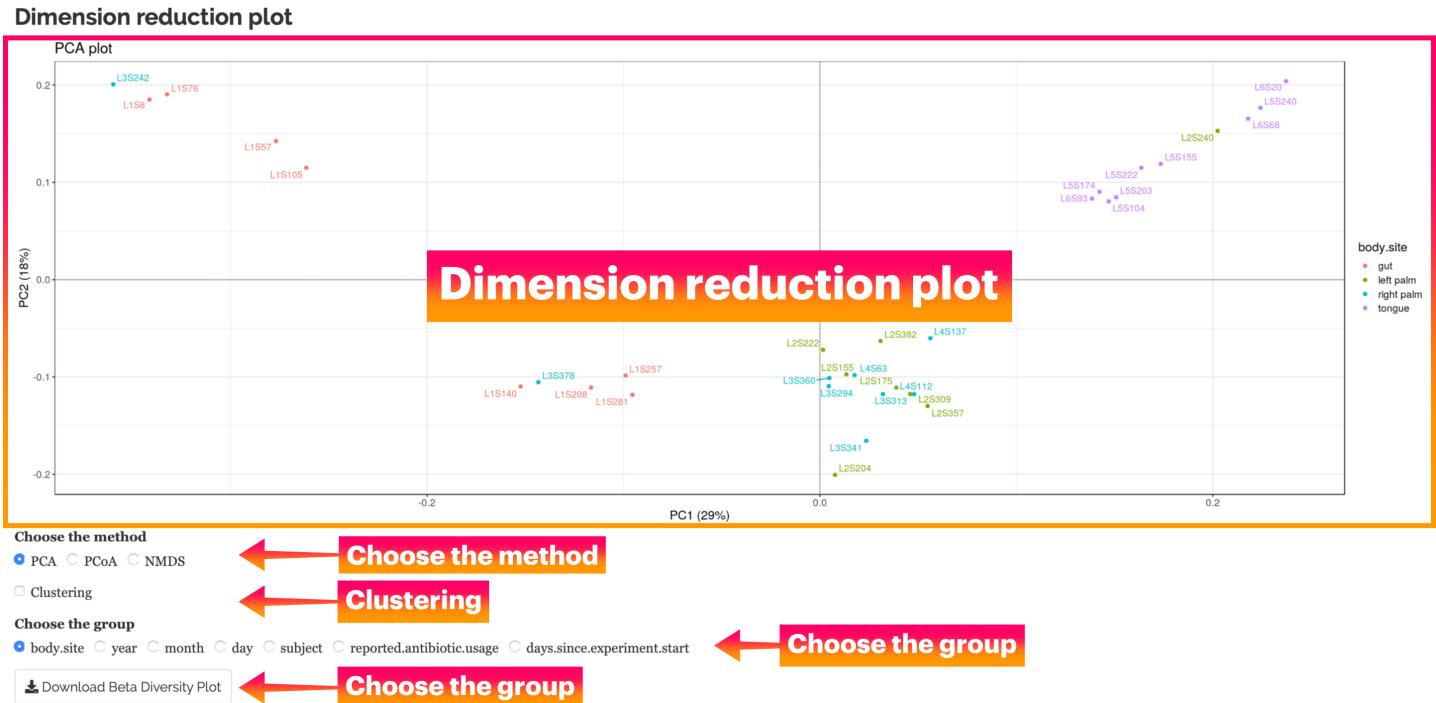
When a cursor hovers over the heatmap, the distance between species will be presented. Click and drag on the plot to zoom in and out. Double click on the plot to zoom back. Click on the camera icon on the top-right region of the heatmap to download the plot.

* Download 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 original values plus 0.01 and then natural log transformed.

6.2. Dimension-reduction plot



- * We provide three dimension-reduction methods, including PCA (Principal Component Analysis), PCoA (Principal Co-ordinates Analysis) and NMDS (Non-metric Multidimensional Scaling) for visualization of beta diversity.
- * Choose the method:
Select a dimension reduction method.
- * 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 beta diversity plot:
Click on the “Download Beta Diversity Plot” button 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		
Comparisons	R ²	P value	Comparisons	R	P value
gut - left palm	0.3983	0.001	gut - left palm	1	0.001
gut - right palm	0.2834	0.001	gut - right palm	0.6686	0.001
gut - tongue	0.5474	0.001	gut - tongue	1	0.002
left palm - right palm	0.0585	0.544	left palm - right palm	-0.0538	0.78
left palm - tongue	0.2985	0.001	left palm - tongue	0.6953	0.001
right palm - tongue	0.276	0.001	right palm - tongue	0.5343	0.001
Download pairwise PERMANOVA table			Download pairwise ANOSIM table		
Pairwise MRPP			Pairwise MRPP		
Comparisons	A	P value	Comparisons	A	P value
gut - left palm	0.2055	0.001	gut - left palm	0.2055	0.001
gut - right palm	0.1456	0.001	gut - right palm	0.1456	0.001
gut - tongue	0.3046	0.001	gut - tongue	0.3046	0.001
left palm - right palm	-0.0018	0.543	left palm - right palm	-0.0018	0.543
left palm - tongue	0.1373	0.001	left palm - tongue	0.1373	0.001
right palm - tongue	0.1412	0.001	right palm - tongue	0.1412	0.001
Download pairwise MRPP table					

- * We provide three statistical methods, including 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 with Benjamini-Hochberg method.
- * Download the table of statistical results:
Click on the button below the table to download the statistical results.

7. Phylogenetic diversity

A species diversity considers the genetic distance. 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).

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

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!

Demo

* Upload the sequence file:

Upload the sequence file (.qza). If you have already finished the “Sequence Preprocessing” steps, download the file from “Sequence Preprocessing - Taxonomic classification” section and upload. Please see [Sequence preprocessing / Taxonomic classification / step 8](#).

* Sampling depth:

Samples with total count smaller than 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:

The number of threads to use for multithreaded process. The default value is all threads minus two.

* Start:

Click on 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 2 3 4 Next

 Download Faith PD table

Download

* Faith PD table:

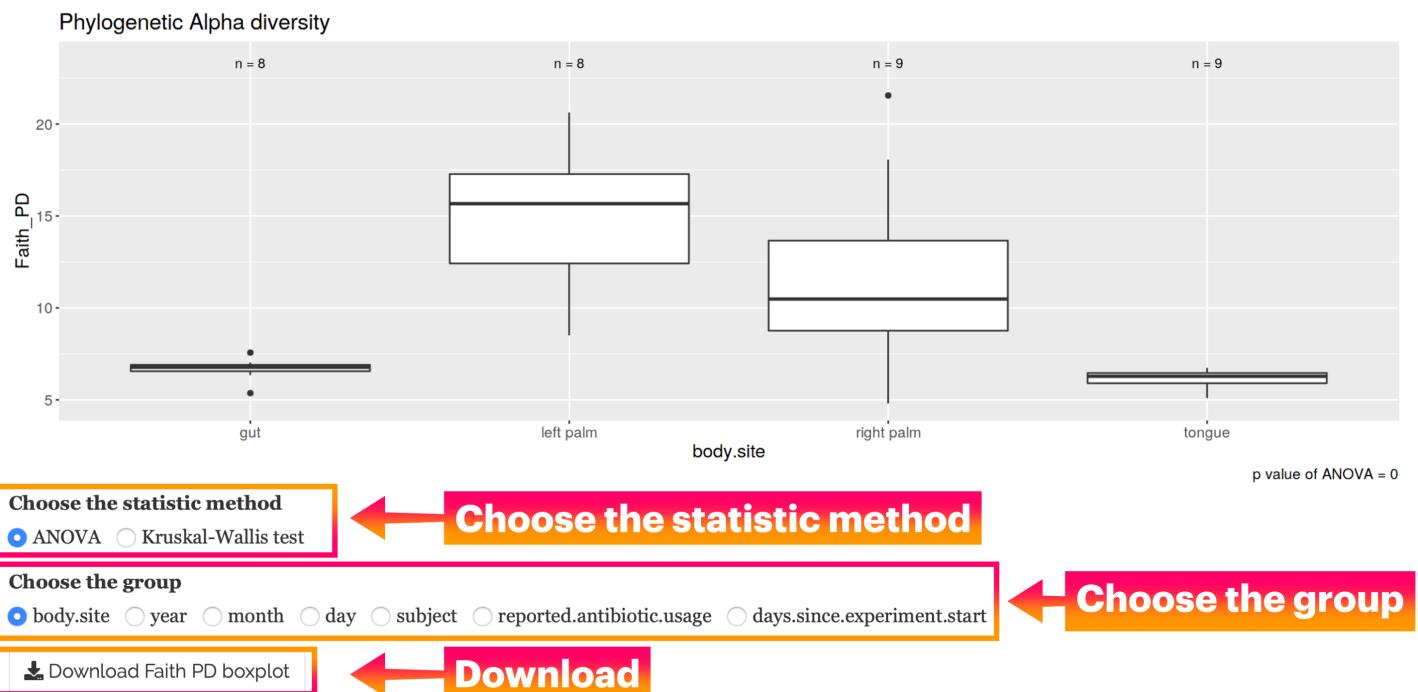
This table shows the Faith PD (phylogenetic diversity) of all samples.

* Download Faith PD table:

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

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

Faith PD boxplot



* Choose the statistic 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 Faith PD boxplot:

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

7.3. Post-hoc analysis

Post hoc analysis

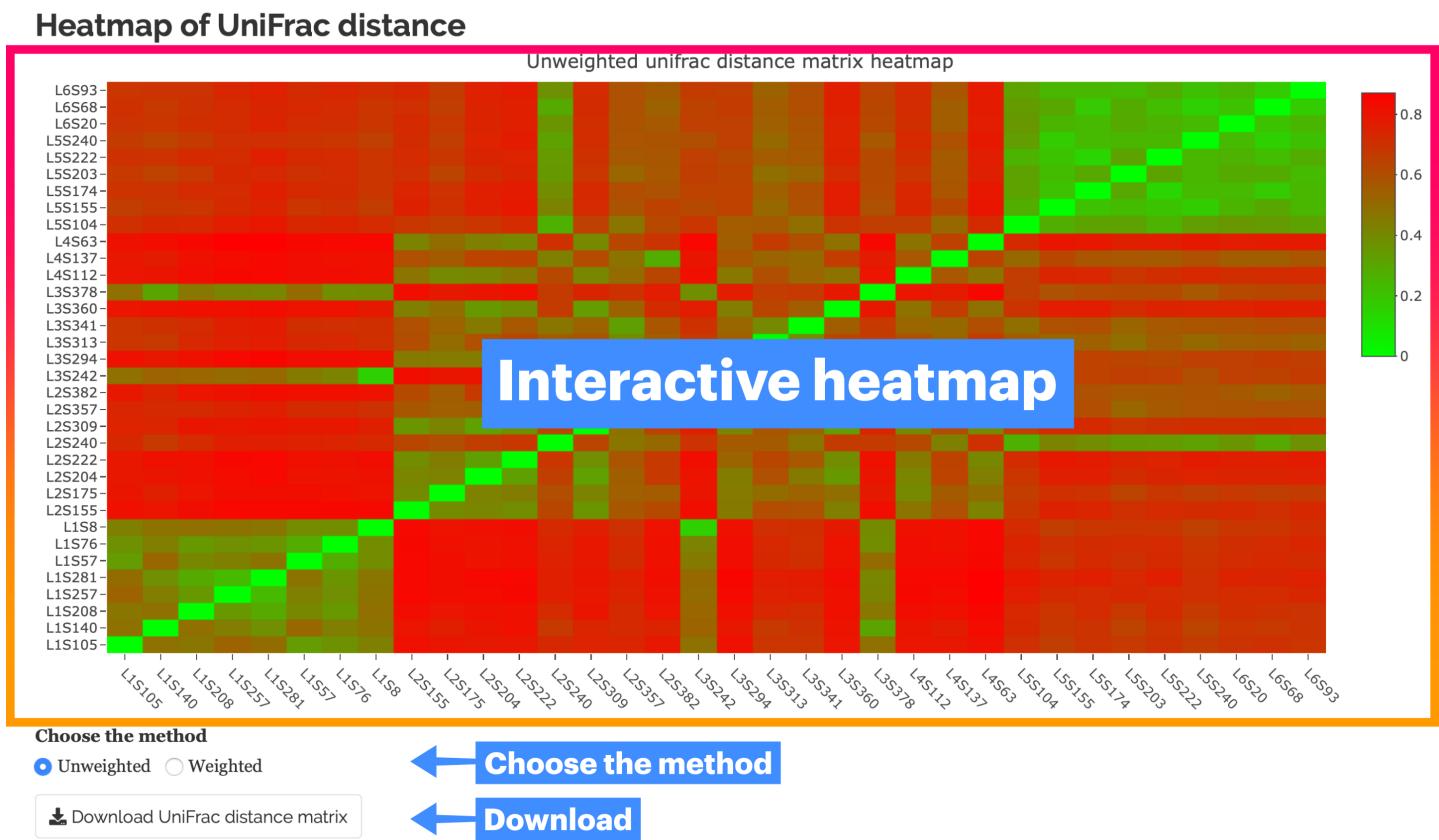
Tukey test

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 test. If Kruskal-Wallis is selected, then the Dunn test will be used.
 - * Download Faith PD post hoc result:
Click on the “Download Faith PD post hoc result” button to download the result.
-

7.4. Heatmap of UniFrac distance



* **Interactive heatmap:**

When a cursor hovers over the heatmap, the information of 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 on the top-right region of the heatmap to download the plot.

* **Choose the method:**

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

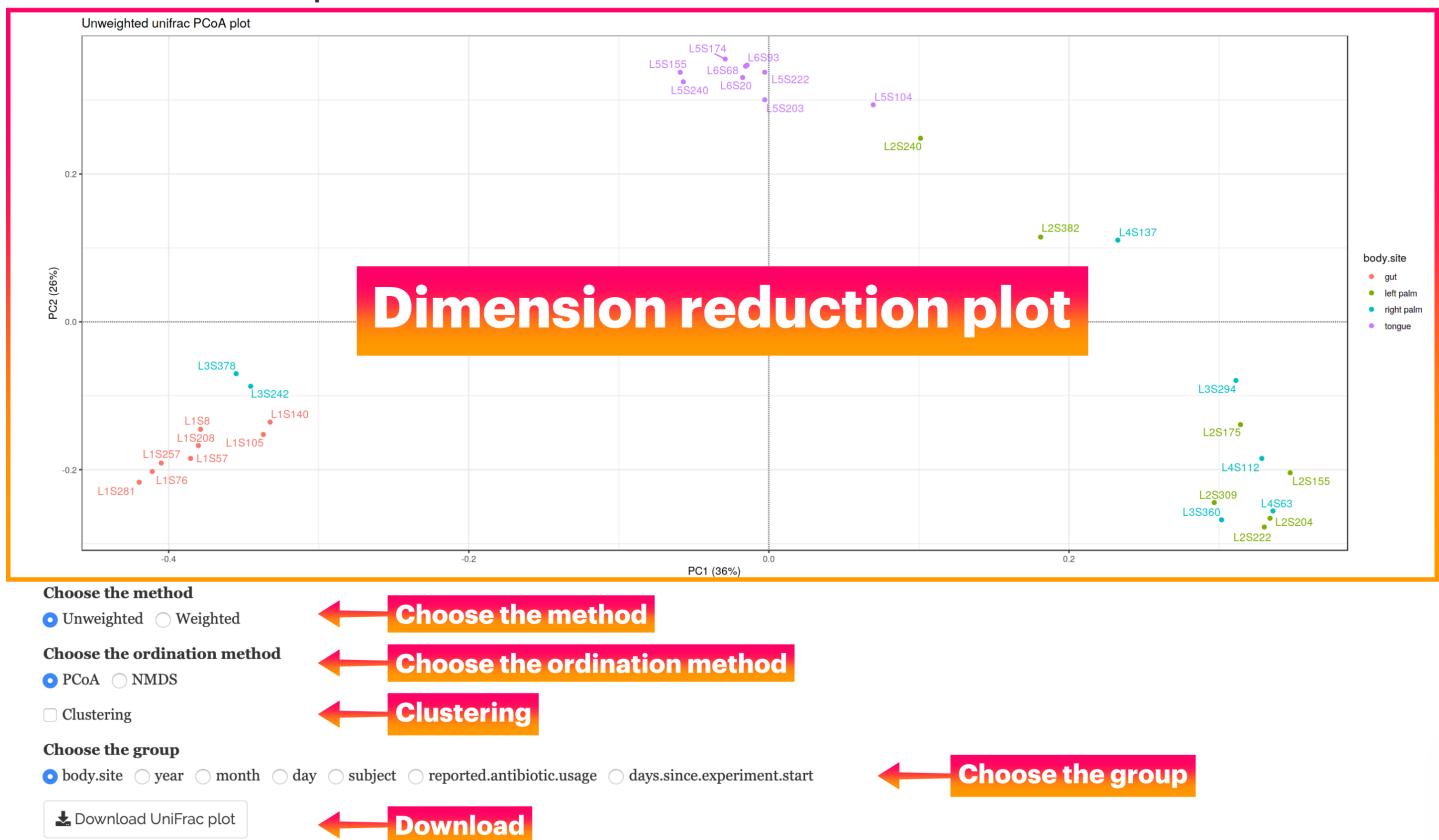
* **Download heatmap matrix:**

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

* **The values shown in the heatmap are the original values plus 0.01 and then natural log transformed.**

7.5. Dimension-reduction plot of UniFrac distance

Dimension reduction plot of UniFrac distance



- * We provide two dimension-reduction methods, including PCoA (Principal Co-ordinates Analysis) and NMDS (Non-metric Multidimensional Scaling) for visualizing UniFrac distance.
- * Choose the method:
Select unweighted UniFrac (not consider the richness of taxa) or weighted UniFrac (consider the richness of taxa).
- * Choose the ordination method:
Select a dimension reduction method.
- * 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 UniFrac plot:
Click on the “Download UniFrac Plot” button 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, including 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 with Benjamini-Hochberg method.

- * Download statistical result table:

Click on the button below the table to download the statistical results.

8. ANCOM

Analyze composition of microbiomes. Used for comparing the composition of microbiomes in two or more populations. [Get more information](#).

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

ANCOM (Analysis of composition of microbiomes) is used for comparing the composition of microbiomes in two or more populations.

Select an attribute comparison

Select an attribute comparison.

body.site year month day subject reported.antibiotic.usage days.since.experiment.start

Choose the level

Phylum

Choose the level

 Start!

Start

* Select an attribute comparison:

Select a group. ANCOM will then find significantly different abundant taxa among subgroups in that group.

* Choose the level:

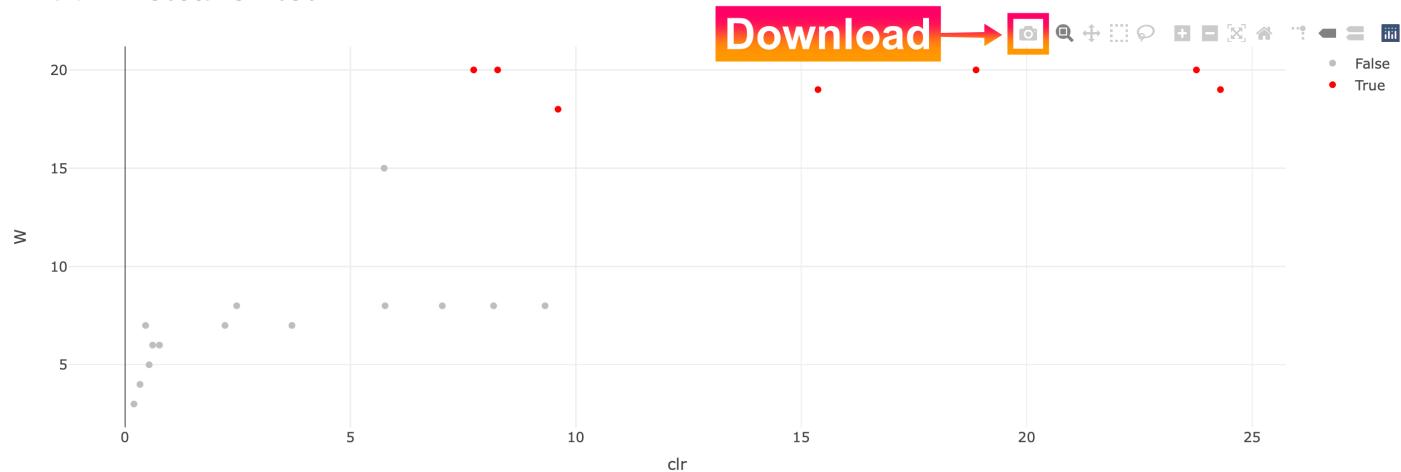
Select a taxonomic level for comparison.

* Start:

Click on the “Start!” button to execute the analysis.

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

ANCOM Volcano Plot



The W value is the number of sub-hypotheses that have rejected for a given taxon in ANCOM analysis.
The clr 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:						
	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

 Download the ANCOM result table (Contain all species)

* Download the ANCOM result table:

Click on the “Download the ANCOM result table” button to download the results. 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

2. Select “**Function analysis**” on 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.

3. In the left panel, press the “**Browse**” buttons to upload metadata and taxonomic table. Alternatively, you could press the “Demo” button to download the example files first and then upload.

The image shows the MOCHI upload interface. On the left, there are two sections for uploading files: "Upload the metadata file" and "Upload the taxonomic table file". Each section has a "Browse..." button and a "No file selected" placeholder. On the right, there are two buttons: "Function annotation table" and "Function barplot". At the bottom center is a large orange "Upload" button with a white arrow pointing left. To the left of the "Upload" button is a large blue "Start!" button with a play icon, which is highlighted with a red box. Below the "Start!" button are three smaller buttons: "reset", "learn more", and "Demo".

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

(B) Inspect result

1. Function annotation table

Display reads of the function types in every 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](#)

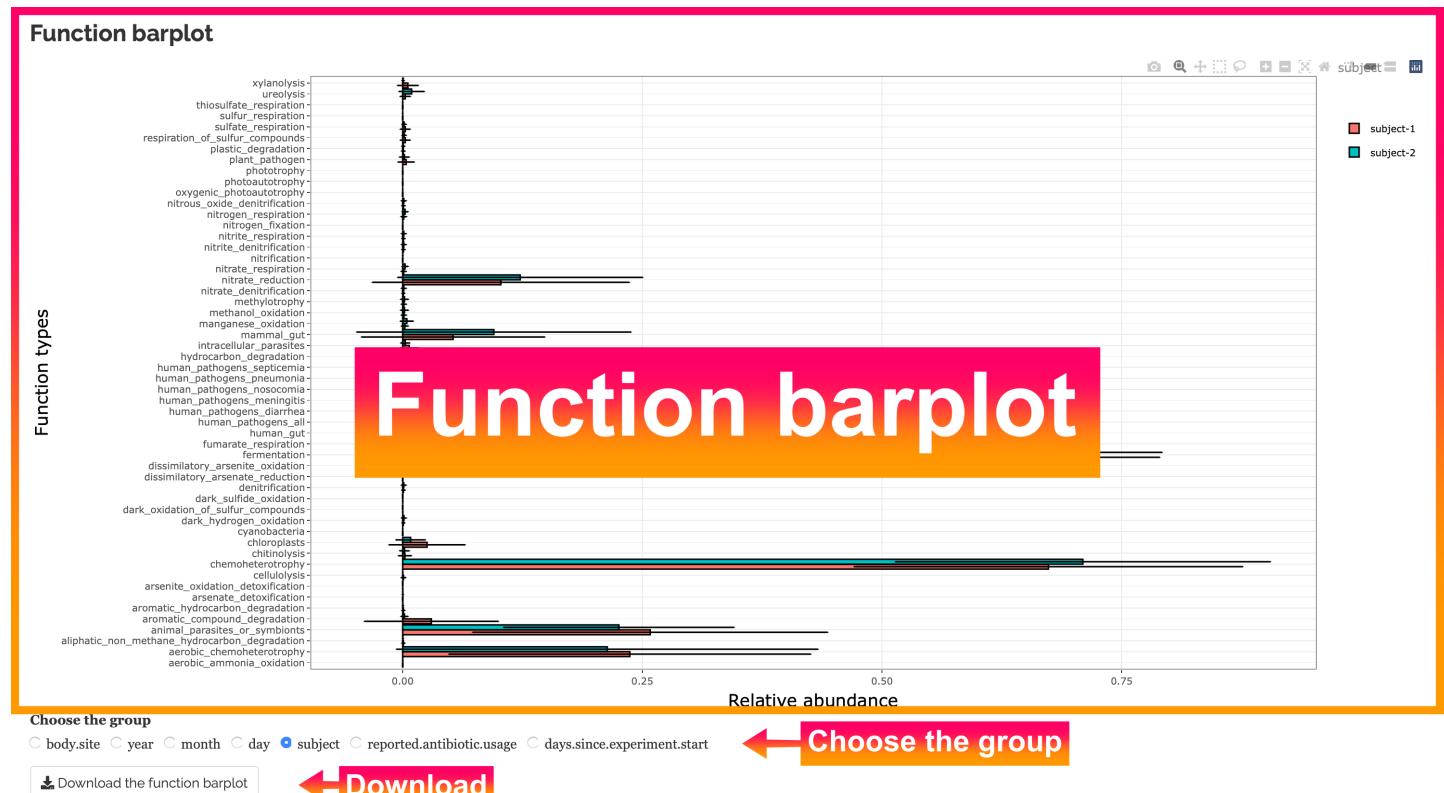
* Summary: Essential information regarding the function prediction.

* Download the function table:

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

2. Function barplot

The horizontal bars indicate reads of 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 on the “Download the function barplot” button to download the barplot.