



MRC microbiome analysis toolbox-A singularity container version

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Due to complex dependency and version conflicts, bioinformaticians are struggling about installation of different tools and solving their dependence relationship and debugging while version conflicts happens. To solve this problem and establish a comprehensive, mobile and easy to use framework for microbiome analysis to beginners, we build this MRC microbiome singularity image. This document describe the interface for different aspects of analysis using a demo example and the mrcmicrobiome.sif singularity image.

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cladoplot presenting of signatures

LEfSe signatures barchart

16S amplicon data analysis

In this tutorial, we use singularity version of the pipeline ***mrcmicrobiome.sif*** to run a high fat diet mouse model stool microbiome analysis. The demo dataset includes stools samples from mice on divergent diets: high fat diet v normal chow. Using this demo dataset, users will learn:

1. How to prepare data for analysis
2. Quality control of amplicon sequences
3. Taxonomic annotation of 16S rRNA sequences
4. Alpha and beta diversity analysis
5. Differential abundant analysis using Linear discriminant analysis Effect Size [LEfSe](#)

Prerequisites

You'll need a laptop with a web browser and a terminal. See also the [Setup](#) page.

You'll need a katana account for the training/have the the singularity file [***mrcmicrobiome.sif***](#) (This file is already on katana)

You might want to brush up on the fundamentals of the [Linux Shell for HPC](#).

Structure

This tutorial has been designed in a modular way. Modules are categorised as follows:

- Basic linux and setup prerequisite environment
- 16S microbiome analysis: taxonomy, alpha, beta diversity analysis and basic statistical analysis
- Microbial signatures identification with LEfSe

Once you've gone through this tutorial, you will be able to analyze 16S amplicon sequences microbiome data. You can refer to [QIIME2](#), [DADA2](#), [Mothur](#), [UPARSE](#) and [Phyloseq](#) for more information.

Schedule

	Setup	
10:00 - 10:30 am	1. Linux and HPC setup and data transfer	
10:40 - 12:00 am	2. Introduce of demo data set and quality control	
13:30 - 14:30 Pm	3. Taxonomy, phylogenetic tree, alpha and beta diversity analysis	
14:50 - 15:30 Pm	4. LEfSe to identify microbial signatures	

The actual schedule may vary slightly depending on the topics and exercises chosen by the instructor.

1. Linux and HPC setup

Overview

Teaching: 30 min **Exercises:** 0 min

Objectives

- Learn basic linux commands and HPC
- Learn how to transfer data from HPC to local computers

High Performance Cluster Basics

You can find a nice introduction to HPC [here](#). Below are some basic introductions.

What is a High Performance Cluster (HPC)

A High Performance Cluster refers to a cluster of computers used to tackle large scale analytical problems. Essentially it's a large collection of computing resources which can be utilised for scientific research.

Compute Nodes

Compute nodes can be thought of as powerful computers/servers, which carry out the majority of the work on a HPC. Each computer node has it's own, Operating System (OS), Central Processing Unit (CPU), Memory (RAM) and Hard Drive (HD).

Head Node

The Head node is essentially the brains behind the HPC. It is responsible for tracking and allocating computing resources to users.

Login Node

This is the node which controls user access and logon

Scheduling System

At the heart of the HPC is the software which manages the workload. Essentially it's a program that attempts to balance utilisation across the resource available.

Queue

All jobs run on queues. Queues have differing attributes which match the jobs which run on them. These attributes can relate to things like: job run time length, number of slots, amount of memory.

Job

A job is essentially your task, the code which you ask the HPC to execute.

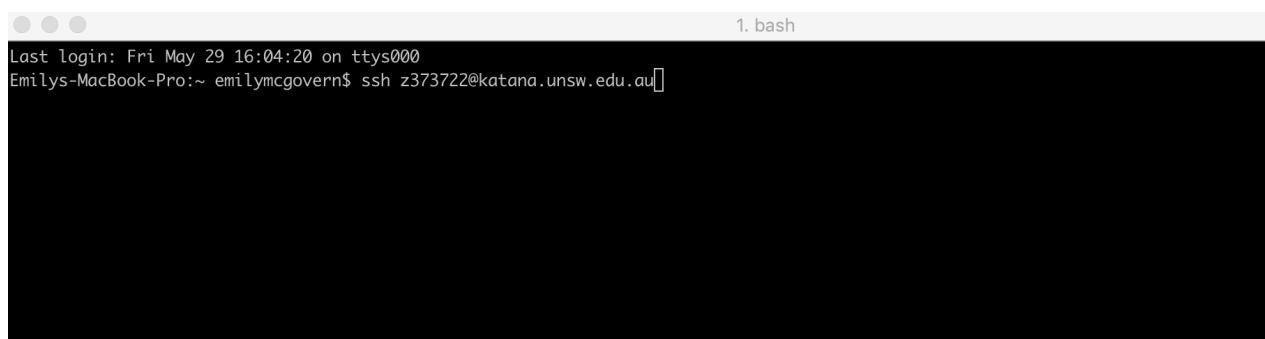
Katana | UNSW Research

Katana is a shared computational cluster located on campus at UNSW that has been designed to provide easy access to computational resources for groups working with non-sensitive data. Katana will be used for your next generation sequencing analysis.

Log on to Katana

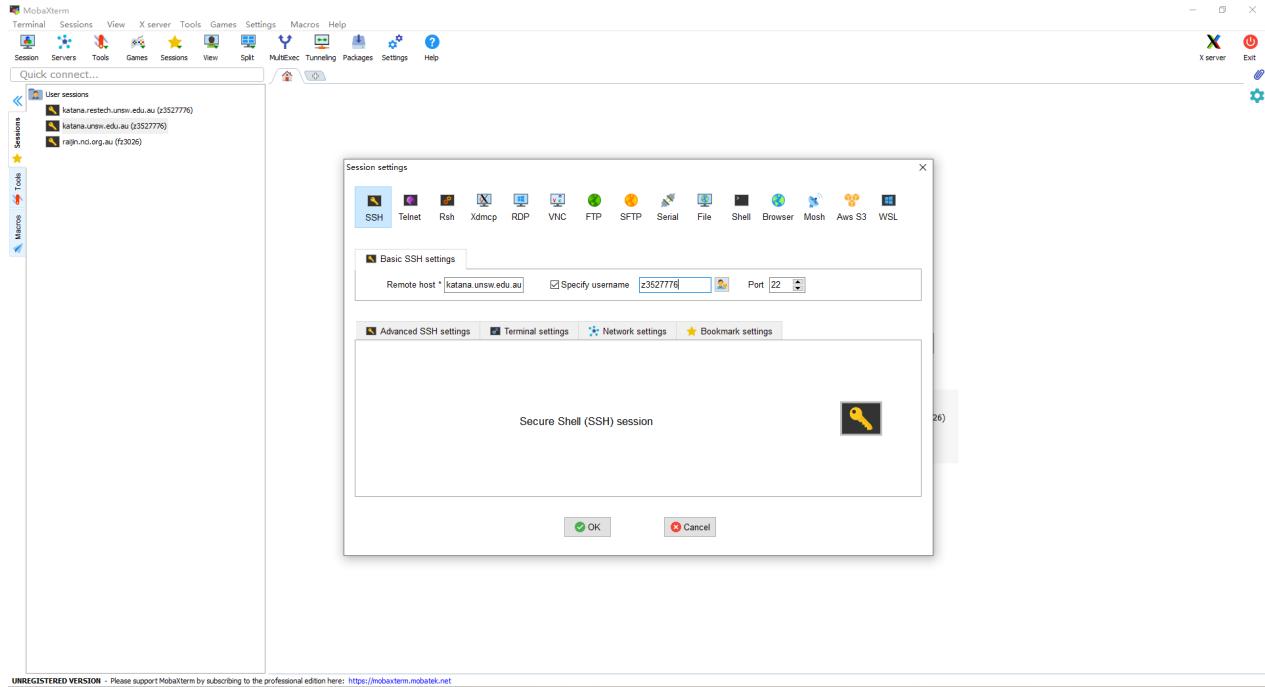
Download a terminal in order to log on to a remote terminal e.g. [Iterm](#) (Mac) or [mobaxterm](#) (Windows)

```
ssh zID@katana.unsw.edu.au
```



The screenshot shows a terminal window with a black background and white text. At the top left, there are three small circular icons. To the right of them, the text "1. bash" is displayed. Below this, the terminal prompt "Emilys-MacBook-Pro:~ emilymcgovern\$" is shown, followed by the command "ssh z373722@katana.unsw.edu.au". The response "Last login: Fri May 29 16:04:20 on ttys000" is visible, along with the user's name "Emilys". The rest of the screen is mostly blank black space.

Log on from Mobaxterm (Windows Computer)



UNREGISTERED VERSION - Please support MobatTerm by subscribing to the professional edition here: <https://mobatterm.mobatek.net>

Working on Katana

Always create an [interactive job](#) to work on Katana - Do not run jobs on head node

```
qsub -I -l nodes=1:ppn=1,mem=10gb,walltime=10:00:00
```

```
(base) [z3527776@katana1 ~]$ qsub -I -l nodes=1:ppn=1,mem=10gb,walltime=10:00:00
qsub: waiting for job 375480.kman.restech.unsw.edu.au to start
qsub: job 375480.kman.restech.unsw.edu.au ready

(base) [z3527776@k003 ~]$ qstat -u z3527776

kman.restech.unsw.edu.au:
Job ID          Username Queue    Jobname      SessID NDS TSK  Req'd  Req'd   Elap
-----          -----  -----    -----      -----  ---  ---  Memory Time   S Time
-----          -----  -----    -----      -----  ---  ---  -----  -----
375480.kman.res z3527776 mrcbio12 STDIN      26604   1   1   10gb 10:00 R 00:06
(base) [z3527776@k003 ~]$ █
```

Always work in your scratch drive, this directory has a lot more space than your home

```
cd /srv/scratch/zID
```

A lot of programs are pre-installed on Katana, to view:

```
module avail
```

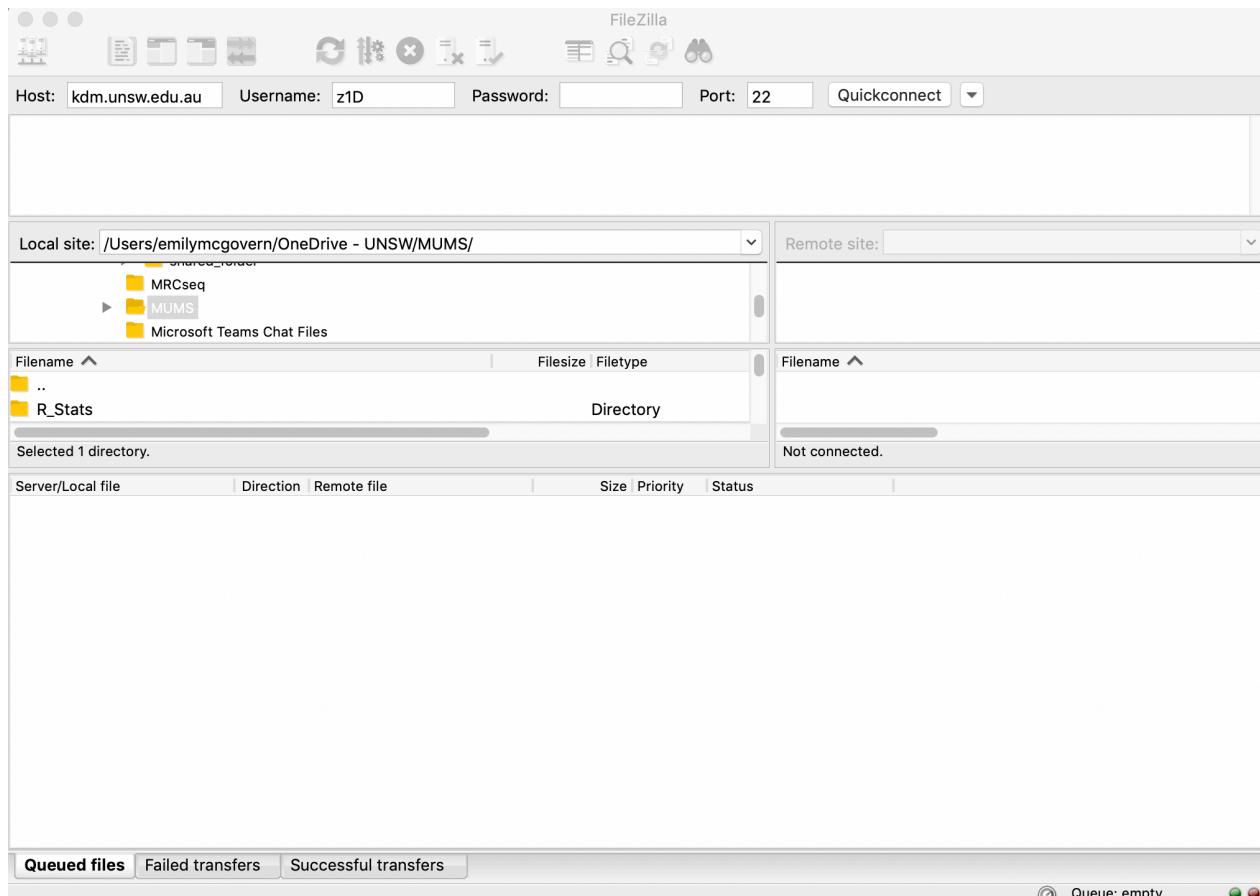
To load a program

```
module load program
```

Katana data Mover

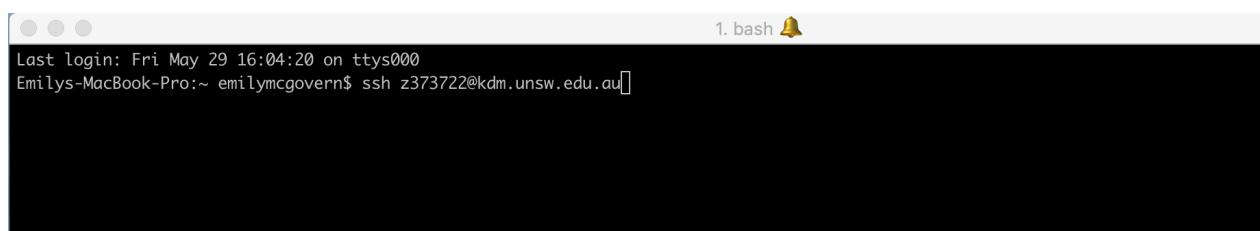
Use [Katana data mover \(kdm\)](#) to move data. Data can be moved from desktop to remote server using a SFTP client [FileZilla](#). Use this to upload data (e.g. study metadata) and download your results.

- Hostname = `ssh zID@kdm.unsw.edu.au`
- Username = zID
- Password = zID password
- Port = 22



You can also log on to the kdm on your ssh client in the same way you log on to katana.

Use this if you are downloading data or databases to Katana



```
ssh zID@kdm.unsw.edu.au
```

Training

UNSW research technology offer a range of training courses, that as of 2020 have been moved online. These are a great introduction to general programming and will help you improve the efficiency of your work. Explore them [here](#)

Basic Linux commands

Introduce yourself to basic linux command using an [online course](#)

Command	Meaning	Example
<code>ls</code>	list files in current directory, with -l, it also displays file permissions, sizes and last updated date/time	<code>ls -l</code> , <code>ls</code>
<code>pwd</code>	displays your current location in the file system	<code>pwd</code>
<code>env</code>	displays your user environment settings (e.g. search path, history size and home directory)	<code>env</code>
<code>cd</code>	change directory	<code>cd /file/path</code>
<code>mv</code>	move file, change file name - Careful with this, no undo!	<code>mv /path/file/ /newpath/file</code> , <code>mv oldname newname</code>
<code>cp</code>	copy files, -R copy directory	<code>cp /path/file/ /newpath/file</code> , <code>cp -R ./directory ./newdirectorylocation</code>
<code>head</code>	print top lines in file	<code>head filename</code> , <code>head -10 filename</code>
<code>tail</code>	print last lines in file	<code>tail filename</code> , <code>tail -10 filename</code>
<code>less</code>	view lines in file, use spacebar to go down file	<code>less filename</code>
<code>grep</code>	search file for pattern or string	<code>cat filename grep "aaatttcc"</code>
<code>*</code>	wildcard, use with other commands	<code>ls *.fastq</code> : list all files with suffix ".fastq"
<code>wc</code>	word count, with -l = linecount	<code>wc filename</code> , <code>wc -l filename</code>
<code>rm</code>	remove filename , with -R directory Again careful	<code>rm filename</code>
<code>exit</code>	exit remote server	<code>exit</code>
<code>.</code>	This represents the current directory	<code>pwd .</code> , <code>cd ./path/to/subdirectory/from/currentdir</code>
<code>..</code>	This represents the parent directory	<code>pwd ..</code> , <code>cd ../path/to/subdirectory/from/parentdir</code>

Table:Useful everyday commands

Text editing from the command line

When learning bioinformatics, you will most likely need to create or edit text files, shell scripts or Python scripts from the command line. Using a Unix-based text editor good practice for getting used to the environment if you are new to the command line.

There are multiple text editors available. Which one you use is based on user preference, beginners usually go for nano or vim.

Text Editors

- nano
- vim
- emacs

User Guides

- Simple [guide](#) from a beginners perspective
- More comprehensive [guide](#) to vim

Useful Tip

If using `vim` and you are stuck in a wrong mode etc, you can always escape using by pressing `Esc` followed by `:q!` and this will allow you exit without saving any changes.

2. Quality control

Understand the demo data set

Overview

Teaching: 10 min Exercises: 0 min

Objectives

- Download the demo data set
- Understand the meta data file and learn how to prepare it

Using the FTP software to upload the demo data set and the relevant meta data file to your HPC account

Singularity on katana

login to compute nodes to run jobs.

```
qsub -I -l nodes=1:ppn=1,mem=10gb,walltime=10:00:00
```

mrcmicrobiome singularity sif have conda, qiime2-2020.8 and lefse installed, all the relevant dependence are resolved. Copy the demo data set to your own work directory

Check the singularity image file /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif

Using the following command to create the wrok directory and copy the demo data set to your directory

```
#create the hf diet working directory
mkdir /srv/scratch/yourzID/hfdiet

#enter into the directory
cd /srv/scratch/yourzID/hfdiet

#copy the demo data set into your work directory
cp -r /srv/scratch/mrcbio/workshop/demo /srv/scratch/yourzID/hfdiet
```

Check the demo and database db directory

There are in total 16 samples in the demo, check the **meta_data.txt** file, you can find the samples information

```
[z3524677@katana2 hf diet]$ tree demo/
#output
demo/
|-- all_r1.fq
|-- all_r2.fq
|-- meta_data.txt
`-- rawfq
    |-- 5821_S50_L001_R1.fastq.gz
    |-- 5821_S50_L001_R2.fastq.gz
    |-- 5822_S34_L001_R1.fastq.gz
    |-- 5822_S34_L001_R2.fastq.gz
    |-- 5824_S96_L001_R1.fastq.gz
    |-- 5824_S96_L001_R2.fastq.gz
    |-- 5825_S7_L001_R1.fastq.gz
    |-- 5825_S7_L001_R2.fastq.gz
    |-- 5832_S8_L001_R1.fastq.gz
    |-- 5832_S8_L001_R2.fastq.gz
    |-- 5833_S78_L001_R1.fastq.gz
    |-- 5833_S78_L001_R2.fastq.gz
    |-- 5859_S27_L001_R1.fastq.gz
    |-- 5859_S27_L001_R2.fastq.gz
    |-- 5860_S122_L001_R1.fastq.gz
    |-- 5860_S122_L001_R2.fastq.gz
    |-- 5862_S51_L001_R1.fastq.gz
    |-- 5862_S51_L001_R2.fastq.gz
    |-- 5863_S30_L001_R1.fastq.gz
    |-- 5863_S30_L001_R2.fastq.gz
    |-- 6319_S128_L001_R1.fastq.gz
    |-- 6319_S128_L001_R2.fastq.gz
    |-- 6320_S67_L001_R1.fastq.gz
```

```
|-- 6320_S67_L001_R2.fastq.gz
|-- 6321_S20_L001_R1.fastq.gz
|-- 6321_S20_L001_R2.fastq.gz
|-- 6322_S131_L001_R1.fastq.gz
|-- 6322_S131_L001_R2.fastq.gz
|-- 6328_S93_L001_R1.fastq.gz
|-- 6328_S93_L001_R2.fastq.gz
|-- 6329_S37_L001_R1.fastq.gz
`-- 6329_S37_L001_R2.fastq.gz
```

Check meta data file

```
#enter into your own directory
cd demo/

#show the contents of the meta data file
[z3524677@katana2 demo]$ cat meta_data.txt
#SampleID LANID Diet
6319_S128_L001 fvb-a Normal
6320_S67_L001 fvb-a Normal
6321_S20_L001 fvb-b Normal
6322_S131_L001 fvb-b Normal
6328_S93_L001 fvb-c Normal
6329_S37_L001 fvb-c Normal
5821_S50_L001 181-1 HFD
5822_S34_L001 181-1 HFD
5824_S96_L001 181-2 HFD
5825_S7_L001 181-2 HFD
5832_S8_L001 181-3 HFD
5833_S78_L001 181-3 HFD
5859_S27_L001 181-4 HFD
5860_S122_L001 181-4 HFD
5862_S51_L001 181-5 HFD
5863_S30_L001 181-5 HFD
```

Check the database folder

```
[z3524677@katana2 workshop]$ tree /srv/scratch/mrcbio/workshop/db
```

```
#output
/srv/scratch/mrcbio/workshop/db
|-- gg-v3v4-classifier.qza
|-- gg-v4-classifier.qza
|-- mouse.genome.bowtie2.1.bt2
|-- mouse.genome.bowtie2.2.bt2
|-- mouse.genome.bowtie2.3.bt2
|-- mouse.genome.bowtie2.4.bt2
|-- mouse.genome.bowtie2.rev.1.bt2
`-- mouse.genome.bowtie2.rev.2.bt2
```

QIIME2 manifest file preparation, example below

```
[z3524677@katana2 demo]$ cat hf_d.manifest
```

```
#output
sample-id,absolute-filepath,direction
5821_S50_L001,/srv/scratch/z3524677/hfdiet/demo/rawfq//5821_S50_L001_R1.fastq.gz,forward
5821_S50_L001,/srv/scratch/z3524677/hfdiet/demo/rawfq//5821_S50_L001_R2.fastq.gz,reverse
5822_S34_L001,/srv/scratch/z3524677/hfdiet/demo/rawfq//5822_S34_L001_R1.fastq.gz,forward
5822_S34_L001,/srv/scratch/z3524677/hfdiet/demo/rawfq//5822_S34_L001_R2.fastq.gz,reverse
5824_S96_L001,/srv/scratch/z3524677/hfdiet/demo/rawfq//5824_S96_L001_R1.fastq.gz,forward
5824_S96_L001,/srv/scratch/z3524677/hfdiet/demo/rawfq//5824_S96_L001_R2.fastq.gz,reverse
5825_S7_L001,/srv/scratch/z3524677/hfdiet/demo/rawfq//5825_S7_L001_R1.fastq.gz,forward
5825_S7_L001,/srv/scratch/z3524677/hfdiet/demo/rawfq//5825_S7_L001_R2.fastq.gz,reverse
5832_S8_L001,/srv/scratch/z3524677/hfdiet/demo/rawfq//5832_S8_L001_R1.fastq.gz,forward
5832_S8_L001,/srv/scratch/z3524677/hfdiet/demo/rawfq//5832_S8_L001_R2.fastq.gz,reverse
```

Prepare manifest and run dada2

Overview

Teaching: 10 min Exercises: 0 min

Objectives

- Generate quality control shell scripts with ***mima_prepare_manifest_and_qc.pl***
- Understand how to perform quality control with dada2

```
[z3524677@katana2 demo]$ singularity exec --cleanenv
/srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c 'perl
/home/applications/mima/mima_prepare_manifest_and_qc.pl'

perl /home/applications/mima/mima_prepare_manifest_and_qc.pl <Absolute path to
store fastq files> <output.manifest> <total_1.fq> <total_2.fq> <outputdir> <#
of threads> <Singularity_sif>
<inputdir_abs_path> The absolute directory to store the pair-end fastq
files
<output.manifest> The manifest file that qiime needed when running dada2
<Merged_1.fq> The overall fastq file pair 1
<Merged_2.fq> The overall fastq file pair 2
<Output_dir> Output directory store all the QC files and dada2
output
<#ofthreads> Deafault 1
<Singularity sif img> the singualrity image to use
```

Run the one command pipeline to generate all the necessary scripts. This one command will generate all the necessary scripts for the QC analysis. You can submit this as a job or run each command individually in an interactive job. As QC can take time, it's advisable to submit all the commands as a job `qsub qc.pbs`. For learning purposes today we will go through each command and its output in an interactive model as the demo small

```
#run the command to generate commands for quality control
#Absolute path should be used input and output directory
[z3524677@katana2 demo]$ singularity exec --cleanenv
/srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c 'perl
/home/applications/mima/mima_prepare_manifest_and_qc.pl
/srv/scratch/z3527776/hfdiet/demo/rawfq/
/srv/scratch/z3527776/hfdiet/demo/hf_d.manifest all_r1.fq all_r2.fq
/srv/scratch/z3527776/hfdiet/demo/hf_qc 1
/srv/scratch/mrcbio/workshop/mrcmicrobiome.sif'
```

```
[z3524677@katana2 demo]$ tree hf_qc/
hf_qc/
|-- hf_d.manifest
`-- qc.pbs
```

Check the commands generated

```
[z3524677@katana2 demo]$ cat hf_qc/qc.pbs
#!/bin/bash
#PBS -l nodes=1:ppn=1
```

```

#PBS -l mem=80gb
#PBS -l walltime=100:00:00
export LC_ALL=en_AU.utf8
export LANG=en_AU.utf8
cd /srv/scratch/z3524677/hfdiet/demo/hf_qc

singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '
fastp -i all_r1.fq -I all_r2.fq -o
/srv/scratch/z3524677/hfdiet/demo/hf_qc/ALL_R1.fq -O
/srv/scratch/z3524677/hfdiet/demo/hf_qc/ALL_R2.fq -H
/srv/scratch/z3524677/hfdiet/demo/hf_qc/fastp.outreport.html'

singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.
activate qiime2-2020.8 && qiime tools import --type
'SampleData[PairedEndSequencesWithQuality]' --input-path
/srv/scratch/z3524677/hfdiet/demo/hf_d.manifest --output-path demux.qza --
input-format PairedEndFastqManifestPhred33'

singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.
activate qiime2-2020.8 && qiime dada2 denoise-paired --i-demultiplexed-seqs
demux.qza --p-trunc-len-f 295 --p-trunc-len-r 220 --p-trim-left-f 17 --p-
trim-left-r 21 --p-n-threads 1 --o-representative-sequences rep-seqs.qza --o-
table table.qza --o-denoising-stats stats-dada2.qza'

```

Files in the folder after running the ***mima_prepare_manifest_and_qc.pl*** script. Now a file 'hf_d.manifest' and a folder 'hf_qc' are newly created.

```
(base) [z3527776@k212 demo]$ ll
total 52740
-rwx----- 1 z3527776 MRCBIO 27015199 Sep 10 18:45 all_r1.fq
-rwx----- 1 z3527776 MRCBIO 26974109 Sep 10 18:45 all_r2.fq
-rw-r--r-- 1 z3527776 MRCBIO      2890 Sep 14 12:43 hf_d.manifest
drwxr-xr-x 2 z3527776 MRCBIO       53 Sep 14 12:43 hf_qc
-rwx----- 1 z3527776 MRCBIO      322 Sep 10 18:45 meta_data.txt
drwx----- 2 z3527776 MRCBIO     4096 Sep 10 18:45 rawfq
(base) [z3527776@k212 demo]$
```

Overall assessment of quality of sequences with fastp

Prior to importing data into QIIME, the data will be assessed with Fastp. This step functions to assess overall sequence quality. Output information will be in a html format and will include: Run [Fastp](#) to assess the overall quality of the sequences.

```
[z3524677@katana2 demo]$ singularity exec
/srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c 'fastp -i all_r1.fq -I
all_r2.fq -o hf_qc/ALL_R1.fq -O hf_qc/ALL_R2.fq -h hf_qc/fastp.outreport.html'
bash: warning: setlocale: LC_ALL: cannot change locale (en_AU.utf8)
```

```

Read1 before filtering:
total reads: 40000
total bases: 12022031
Q20 bases: 10726471(89.2235%)
Q30 bases: 9355072(77.8161%)

Read2 before filtering:
total reads: 40000
total bases: 12001486
Q20 bases: 9746062(81.2071%)
Q30 bases: 8306044(69.2085%)

Read1 after filtering:
total reads: 38912
total bases: 11695532
Q20 bases: 10522964(89.9742%)
Q30 bases: 9202096(78.6804%)

Read2 after filtering:
total reads: 38912
total bases: 11674221
Q20 bases: 9568399(81.9618%)
Q30 bases: 8182633(70.0915%)

Filtering result:
reads passed filter: 77824
reads failed due to low quality: 1952
reads failed due to too many N: 224
reads failed due to too short: 0
reads with adapter trimmed: 24
bases trimmed due to adapters: 1575

Duplication rate: 22.3048%

Insert size peak (evaluated by paired-end reads): 460

JSON report: fastp.json
HTML report: /srv/scratch/z3524677/hfdiet/demo/hf_qc/fastp.outreport.html

```

Check the output directory

```

[z3524677@katana2 demo]$ ls -lh hf_qc/
total 51M
-rw-r--r--. 1 z3524677 unsw 26M Sep  9 12:09 ALL_R1.fq
-rw-r--r--. 1 z3524677 unsw 26M Sep  9 12:09 ALL_R2.fq
-rw-r--r--. 1 z3524677 unsw 436K Sep  9 12:09 fastp.outreport.html
-rw-r--r--. 1 z3524677 unsw 2.9K Sep  9 12:02 hf_d.manifest
-rw-r--r--. 1 z3524677 unsw 1.1K Sep  9 12:02 qc.pbs

```

Fastp Output explained:

- Insert size is the length of DNA that you want to sequence and that is inserted between the adapters (adapters excluded).
- Total reads refer to the total number of reads generated by the sequencing run
- Total bases refer to the total number of nucleotide bases sequenced during the sequencing run
- Quality Scores for Next-Generation Sequencing (NGS) assessing sequencing accuracy using Phred quality scoring (Q score). Low Q scores can increase false-positive variant calls, which can result in inaccurate conclusions and higher costs for validation experiments.

Phred Quality	Score Probability of incorrect bases call	Base call accuracy
10	1 in 10	90%
20	1 in 100	99%
30	1 in 1000	99.9%

Table: Phred Quality table

Check the quality of the overall sequences in the ***fastp.outreport.html*** after downloading to local computer

fastp.outreport.html open on local browser

fastp report

Summary

General

fastp version:	0.20.1 (https://github.com/OpenGene/fastp)
sequencing:	paired end (301 cycles + 301 cycles)
mean length before filtering:	300bp, 300bp
mean length after filtering:	300bp, 300bp
duplication rate:	22.304833%
Insert size peak:	460

Before filtering

total reads:	80.000000 K
total bases:	24.023517 M
Q20 bases:	20.472533 M (85.218717%)
Q30 bases:	17.661116 M (73.515947%)
GC content:	55.948049%

After filtering

total reads:	77.824000 K
total bases:	23.369753 M
Q20 bases:	20.091363 M (85.971653%)
Q30 bases:	17.384729 M (74.389871%)
GC content:	55.963411%

Filtering result

reads passed filters:	77.824000 K (97.280000%)
reads with low quality:	1.952000 K (2.440000%)
reads with too many N:	224 (0.280000%)
reads too short:	0 (0.000000%)

Import fasta sequences into demux.qza

```
[z3524677@katana2 demo]$ singularity exec
/srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '. activate qiime2-
2020.8 && \
qiime tools import \
--type 'SampleData[PairedEndSequencesWithQuality]' \
--input-path hf_d.manifest \
--output-path demux.qza \
--input-format PairedEndFastqManifestPhred33'

Imported /srv/scratch/z3524677/hfdiet/demo/hf_d.manifest as
PairedEndFastqManifestPhred33 to demux.qza
```

Pay attention to the PATH of the input and output files in the command, make sure it is your PATH, e.g., /srv/scratch/'yourzID'/hfdiet/demo/hf_d.manifest. A file 'demux.qza' is newly generated.

```
(base) [z3527776@k212 demo]$ ll
total 65484
-rwx----- 1 z3527776 MRCBIO 27015199 Sep 10 18:45 all_r1.fq
-rwx----- 1 z3527776 MRCBIO 26974109 Sep 10 18:45 all_r2.fq
-rw-r--r-- 1 z3527776 MRCBIO 13049747 Sep 14 12:53 demux.qza
-rw-r--r-- 1 z3527776 MRCBIO 2890 Sep 14 12:43 hf_d.manifest
drwxr-xr-x 2 z3527776 MRCBIO 53 Sep 14 12:43 hf_qc
-rwx----- 1 z3527776 MRCBIO 322 Sep 10 18:45 meta_data.txt
drwx----- 2 z3527776 MRCBIO 4096 Sep 10 18:45 rawfq
(base) [z3527776@k212 demo]$
```

Running dada2 within qiime2 to perform quality control, this takes about 1 minute

Run dada2 to trim end low quality bases, remove chimera sequencing and merge pair-end sequences, generate feature tables and statistics output of the results

```
[z3524677@katana2 demo]$ singularity exec
/srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '. activate qiime2-
2020.8 && \
qiime dada2 denoise-paired \
--i-demultiplexed-seqs demux.qza \
--p-trunc-len-f 295 \
--p-trunc-len-r 220 \
--p-trim-left-f 17 \
--p-trim-left-r 21 \
--p-n-threads 1 \
--o-representative-sequences rep-seqs.qza \
--o-table table.qza --o-denoising-stats stats-dada2.qza'

Saved FeatureTable[Frequency] to: table.qza
Saved FeatureData[Sequence] to: rep-seqs.qza
Saved SampleData[DADA2Stats] to: stats-dada2.qza
```

Three files: 'table.qza', 'rep-seqs.qza' and 'stats-dada2.qza' are newly generated.

```
(base) [z3527776@k212 demo]$ ll
total 65552
-rwx----- 1 z3527776 MRCBIO 27015199 Sep 10 18:45 all_r1.fq
-rwx----- 1 z3527776 MRCBIO 26974109 Sep 10 18:45 all_r2.fq
-rw-r--r-- 1 z3527776 MRCBIO 13049747 Sep 14 12:53 demux.qza
-rw-r--r-- 1 z3527776 MRCBIO 2890 Sep 14 12:43 hf_d.manifest
drwxr-xr-x 2 z3527776 MRCBIO 53 Sep 14 12:43 hf_qc
-rwx----- 1 z3527776 MRCBIO 322 Sep 10 18:45 meta_data.txt
drwx----- 2 z3527776 MRCBIO 4096 Sep 10 18:45 rawfq
-rw-r--r-- 1 z3527776 MRCBIO 28860 Sep 14 13:03 rep-seqs.qza
-rw-r--r-- 1 z3527776 MRCBIO 10706 Sep 14 13:03 stats-dada2.qza
-rw-r--r-- 1 z3527776 MRCBIO 22922 Sep 14 13:03 table.qza
(base) [z3527776@k212 demo]$
```

Decompress **stats-dada2.qza** and check the quality details:

```
singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.
activate qiime2-2020.8 && \
qiime tools export \
--input-path stats-dada2.qza \
--output-path stats-dada2'
```

Dada2 stats

- The **input column** refers to the sequence reads imported into QIIME2 from the initial QC filtration.
- Sequence reads are then filtered/denoised using parameters set by user. These are determined based on sequence 16SrRNA gene region amplified and quality assessment from the fastp report.
- The **merge column** (only present for paired end samples) refers to the number of the forward and reverse reads which were successfully merged together to obtain the full denoised sequences. Merging is performed by aligning the denoised forward reads with the reverse-complement of the corresponding denoised reverse reads, and then constructing the merged “contig” sequences. By default, merged sequences are only output if the forward and reverse reads overlap by at least 12 bases, and are identical to each other in the overlap region.
- The **non-chimeric column** refers to the number of sequences remaining after chimera removal. Chimeras are artifactual PCR product/amplicon generated erroneously from more than one DNA template. It is well-known that chimeras are inevitable when preparing amplicon sequencing libraries for NGS. It is therefore important to detect and filter them out before any types of microbiome analyses.

Look into the quality details:

```
cat stats-dada2/stats.tsv

#output:

sample-id input filtered percentage of input passed filter denoised merged
percentage of input merged non-chimeric percentage of input non-chimeric
#q2:types numeric numeric numeric numeric numeric numeric numeric
5821_S50_L001 2500 1337 53.48 1215 1089 43.56 1073 42.92
5822_S34_L001 2500 1467 58.68 1364 1256 50.24 1243 49.72
5824_S96_L001 2500 1312 52.48 1203 1100 44 1098 43.92
5825_S7_L001 2500 1365 54.6 1268 1131 45.24 1116 44.64
5832_S8_L001 2500 1350 54 1229 1069 42.76 1058 42.32
5833_S78_L001 2500 1218 48.72 1092 881 35.24 877 35.08
5859_S27_L001 2500 1279 51.16 1138 994 39.76 987 39.48
5860_S122_L001 2500 1449 57.96 1344 1229 49.16 1225 49
5862_S51_L001 2500 1232 49.28 1121 1000 40 998 39.92
5863_S30_L001 2500 1371 54.84 1263 1140 45.6 1133 45.32
```

```

6319_S128_L001 2500 1248 49.92 1176 1025 41 987 39.48
6320_S67_L001 2500 1283 51.32 1180 985 39.4 951 38.04
6321_S20_L001 2500 1339 53.56 1190 973 38.92 932 37.28
6322_S131_L001 2500 1466 58.64 1339 1116 44.64 1045 41.8
6328_S93_L001 2500 1531 61.24 1420 1256 50.24 1146 45.84
6329_S37_L001 2500 1327 53.08 1217 1012 40.48 1000 40

```

Contents of two important files **rep-seqs.qza** and **table.qza**

rep-seqs.qza

```

singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.
activate qiime2-2020.8 && \
qiime tools export \
--input-path rep-seqs.qza \
--output-path rep-seqs'

#Exported rep-seqs.qza as DNASequencesDirectoryFormat to directory rep-seqs

```

Look the feature sequences

```

head -4 rep-seqs/dna-sequences.fasta

#output:
>dfa833b266bd2993b86feab3617b34c3
TCGAGAATCATTACAATGGGGAAACCCCTGATGGTGCACGCCCGTGGGGATGAAGGTCTCGGATTGTAAACC
CCTGTCATGTGGGAGCAAATTAAAAAGATAGTACCAAGAGGAAGAGACGGCTAACCTGTGCCAGCAGCCGGTA
ATACAGAGGTCTCAAGCGTTTCGAATCACTGGCGTAAAGCGTGCCTAGGCTGTTCTGAAGTCGTGTGAAAG
GCGCGGGCTAACCCGCGGACGGCACATGATACTGCGAGACTAGAGTAATGGAGGGGAACCGGAATTCTCGGTGTAG
CAGTGAAATGCGTAGATATCGAGAGGAACACTCGTGGCGAAGGCAGGTTCTGGACATTAACTGACGCTGAGGCACGA
AGGCCAGGGAGCGAAAG
>f67a6d5da8c0b71206955aeae1505a74
TGAGGAATATTGGTCAATGGCGGGAGACTGAACCAGCCAAGCCCGTGAGGGAAAGAAGGTACAGCGTATCGTAAACC
TCTTTGCCGGGAACAAGAGCTTCCACGAGTGGAGTGTGAGCGTACCCGGAGAAAAGCATGGCTAACCTCGTGC
CAGCAGCCCGGTAATACGGAGGATGCGAGCGTTATCCGGATTATTGGGTTAAAGGGTGCCTAGGGCGAGTTAA
GTCAGCGGTAAGGCCGGGCTAACCCGCCCGCCGTGAAACTGGCTGGCTTGAGTTGGGAAAGGCAGGCCGA
ATGCGCGGTGTAGCGGTGAAATGCATAGATATCGCGCAGAACCCGATTGCGAAGGCAGCCTGCCGGCCCACACTGA
CGCTGAGGCACGAAAGCGTGGGTATCGAAC

```

table.qza

```

singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.
activate qiime2-2020.8 && \
qiime tools export \
--input-path table.qza \
--output-path table'
#Exported table.qza as BIOMV210DirFmt to directory table

#convert biom file to tsv file
singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.
activate qiime2-2020.8 && \
biom convert -i table/feature-table.biom -o table/feature-table.txt --to-tsv'

```

Look into the table matrix file, the numbers in the table are abundance of that feature sequences in different samples

```

head -4 table/feature-table.txt

#output:

# Constructed from biom file
#OTU ID 5821_S50_L001 5822_S34_L001 5824_S96_L001 5825_S7_L001 5832_S8_L001
5833_S78_L001 5859_S27_L001 5860_S122_L001 5862_S51_L001 5863_S30_L001
6319_S128_L001 6320_S67_L001 6321_S20_L001 6322_S131_L001 6328_S93_L001
6329_S37_L001
dfa833b266bd2993b86feab3617b34c3 193.0 186.0 271.0 290.0 208.0 176.0 210.0
322.0 223.0 230.0 140.0 63.0 54.0 117.0 0.0 0.0
f67a6d5da8c0b71206955aeae1505a74 55.0 126.0 72.0 85.0 57.0 39.0 46.0
51.0 48.0 36.0 131.0 35.0 38.0 0.0 109.0 14.0

```

Host contamination removal if necessary when processing mucosal samples

Overview

Teaching: 10 min **Exercises:** 0 min

Objectives

- Understand why there are contamination in the amplicons data
- Finish the commands to decontamination

Although the sequencing target is the 16S hyper variable region PCR products, the data generated by Ramaciotti sometimes includes host contaminations. Hence, we need to remove the host sequences in the **table.qza** and **rep-seq.qza**, and update the stats-dada2.qza again to check the percentage of host contamination.

Check the help information for **mima_decontaminate_host.pl**

```
[z3524677@katana2 demo]$ singularity exec
/srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '. activate qiime2-
2020.8 && perl /home/applications/mima/mima_decontaminate_host.pl '
perl /home/applications/mima/mima_decontaminate_host.pl <rep_seqs.qza>
<table.qza> <outputdir> <host_genome.fa_bowtie2_index> <threads>

<rep_seqs.qza> qiime format representative sequences output from dada2
<table.qza> qimme format features table
<outputdir> output directory to store the decontaminated updated
rep_seqs.qza and table.qza
<host_genome.fa_bowtie2_index> bowtie2 index of the host genome
<threads> number of threads used in bowtie2 mapping
```

This script uses bowtie2 to map the rep_seqs.qza against host genome to identify the contaminated sequences and update the sequences and table with qiime2. The updated files can be used for downstream analysis.

Run the decontamination script to generate the bash file and run the analysis with singularity

```
[z3524677@katana2 demo]$ singularity exec
/srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '. activate qiime2-
2020.8 && perl /home/applications/mima/mima_decontaminate_host.pl rep-
seqs.qza table.qza hf_host_decontamination
/srv/scratch/mrcbio/workshop/db/mouse.genome 1'

[z3524677@katana2 demo]$ ls hf_host_decontamination/
decontaminationhost.sh
```

A folder 'hf_host_decontamination/' is newly created, with one file 'decontaminationhost.sh' in it.

```
(base) [z3527776@k212 demo]$ ll
total 65552
-rwx----- 1 z3527776 MRCBIO 27015199 Sep 10 18:45 all_r1.fq
-rwx----- 1 z3527776 MRCBIO 26974109 Sep 10 18:45 all_r2.fq
-rw-r--r-- 1 z3527776 MRCBIO 13049747 Sep 14 12:53 demux.qza
-rw-r--r-- 1 z3527776 MRCBIO 2890 Sep 14 12:43 hf_d.manifest
drwxr-xr-x 2 z3527776 MRCBIO 44 Sep 14 13:29 hf_host_decontamination
drwxr-xr-x 2 z3527776 MRCBIO 53 Sep 14 12:43 hf_qc
-rwx----- 1 z3527776 MRCBIO 322 Sep 10 18:45 meta_data.txt
drwx----- 2 z3527776 MRCBIO 4096 Sep 10 18:45 rawfq
-rw-r--r-- 1 z3527776 MRCBIO 28860 Sep 14 13:03 rep-seqs.qza
drwxr-xr-x 2 z3527776 MRCBIO 31 Sep 14 13:05 stats-dada2
-rw-r--r-- 1 z3527776 MRCBIO 10706 Sep 14 13:03 stats-dada2.qza
-rw-r--r-- 1 z3527776 MRCBIO 22922 Sep 14 13:03 table.qza
(base) [z3527776@k212 demo]$ tree hf_host_decontamination
hf_host_decontamination
└── decontaminationhost.sh

0 directories, 1 file
(base) [z3527776@k212 demo]$
```

Execute the shell commands

```
singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.  
activate qiime2-2020.8 && sh hf_host_decontamination/decontaminationhost.sh'
```

After running the decontamination pipeline, we get an updated **rep-seqs.qza** and **table.qza**

Explain of the output folder

- The file 'align-hostgenome.sam.txt' in folder 'rep-seqsold' holds the mapping info of the fasta sequences in 'dna-sequences.fasta'. Due to the small size of the demo data, there is no host reads detected therefore no record in 'align-hostgenome.sam.txt'.
- The file 'metadata.table.txt' holds the IDs of the fasta sequences that are mapped to host reference, therefore there is no record in this file, either.
- The file 'filtered_dnaseqs.fasta' has the fasta sequences that are not mapped to host reference, therefore we shall focus on this file in the downstream analysis.

```
(base) [z3527776@k212 demo]$ tree hf_host_decontamination  
hf_host_decontamination  
├── decontaminationhost.sh  
├── filtered_dnaseqs.fasta  
├── metadata.table.txt  
└── rep-seqsold  
    ├── align-hostgenome.sam.txt  
    └── dna-sequences.fasta  
rep-seqs.qza  
  
1 directory, 6 files  
(base) [z3527776@k212 demo]$
```

3. Taxonomy annotation and diversity analysis

Overview

Teaching: 60 min Exercises: 0 min

Objectives

- Running diversity analysis pipeline and taxonomy annotation, alpha and beta diversity analysis
- Understand how to interpret the output

Taxonomy annotation of **rep-seqs.qza** with naive bayesian classifier, for this part analysis, we have a comprehensive pipeline script, it can generate a series of commands that can finish different analysis, we firstly run this pipeline and then go to details of each part of the flow.

Create a directory **hf_diver** under the demo directory and copy the updated rep-seqs.qza and table.qza into this folder

```

#make the diversity output directory
mkdir hf_diver

#move the two files feature table and features sequences into the hf_diver
directory
cp rep-seqs.qza hf_diver/
cp table.qza hf_diver/

```

Execute taxonomy annotation and diversity analysis pipeline command

```

singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.
activate qiime2-2020.8 && \
perl /home/applications/mima/mima_diversity-basic-statistic.pl \
-m meta_data.txt \
-c /srv/scratch/mrcbio/workshop/db/gg-v3v4-classifier.qza \
-n 1 \
-d 800 \
-o hf_diver'

```

The **mama_diversity-basic-statistic.pl** pipeline will generate a shell file *beta-diversity-commands.sh*, which includes all the taxonomical, alpha, beta diversity analysis . A file *beta-diversity-commands.sh* and a folder **hf_diver** are newly generated.

```

(base) [z3527776@k212 demo]$ ll
total 65560
-rwx----- 1 z3527776 MRCBIO 27015199 Sep 10 18:45 all_r1.fq
-rwx----- 1 z3527776 MRCBIO 26974109 Sep 10 18:45 all_r2.fq
-rw-r--r-- 1 z3527776 MRCBIO      4103 Sep 14 13:44 beta-diversity-commands.sh
-rw-r--r-- 1 z3527776 MRCBIO 13049747 Sep 14 12:53 demux.qza
drwx----- 4 z3527776 MRCBIO      100 Sep 14 13:44 hf_diver
-rw-r--r-- 1 z3527776 MRCBIO     2890 Sep 14 12:43 hf_d.manifest
drwxr-xr-x 3 z3527776 MRCBIO      155 Sep 14 13:31 hf_host_decontamination
drwxr-xr-x 2 z3527776 MRCBIO      53 Sep 14 12:43 hf_qc
-rwx----- 1 z3527776 MRCBIO     322 Sep 10 18:45 meta_data.txt
drwx----- 2 z3527776 MRCBIO      10 Sep 14 13:43 mkdir
drwx----- 2 z3527776 MRCBIO    4096 Sep 10 18:45 rawfq
-rw-r--r-- 1 z3527776 MRCBIO   28860 Sep 14 13:03 rep-seqs.qza
drwxr-xr-x 2 z3527776 MRCBIO      31 Sep 14 13:05 stats-dada2
-rw-r--r-- 1 z3527776 MRCBIO   10706 Sep 14 13:03 stats-dada2.qza
-rw-r--r-- 1 z3527776 MRCBIO   22922 Sep 14 13:03 table.qza
(base) [z3527776@k212 demo]$ tree hf_diver
hf_diver
├── alpha-group
└── beta-group
└── rep-seqs.qza
└── table.qza

2 directories, 2 files
(base) [z3527776@k212 demo]$

```

Run the above diversity analysis in batch model (This command run the pipeline)

```
#Run the analysis in batch model, the /scratch should be bind for this
function, the database directory should be bind as well to get access to
classifier database
singularity exec -B /srv/scratch/mrcbio/workshop/db/,/scratch
/srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '. activate qiime2-
2020.8 && sh beta-diversity-commands.sh '
```

Taxonomy assignment of feature sequences

Overview

Teaching: 10 min Exercises: 0 min

Objectives

- Understand what is a phylogenetic tree and the purpose of why we need this
- Finish the commands to generate rooted tree

```
#taxonomy assignment of feature representative sequences
singularity exec -B /srv/scratch/mrcbio/workshop/db/
/srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '. activate qiime2-
2020.8 && \
qiime feature-classifier classify-sklearn \
--i-classifier /srv/scratch/mrcbio/workshop/db/gg-v3v4-classifier.qza \
--i-reads hf_diver/rep-seqs.qza \
--o-classification hf_diver/taxonomy.qza'
```

Check the contents of the taxonomy.qza by decompress it and view it

Decompress *hf_diver/taxonomy.qza*

```
singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.
activate qiime2-2020.8 && \
qiime tools export \
--input-path hf_diver/taxonomy.qza \
--output-path hf_diver/taxonomy'

#output meassage
#Exported hf_diver/taxonomy.qza as TSVTaxonomyDirectoryFormat to directory
hf_diver/taxonomy
```

Check the taxonomic annotation of represent sequences

```

head -4 hf_diver/taxonomy/taxonomy.tsv

#output
Feature ID  Taxon Confidence
dfa833b266bd2993b86feab3617b34c3  k__Bacteria; p__Verrucomicrobia;
c__Verrucomicrobiae; o__Verrucomicroiales; f__Verrucomicrobiaceae;
g__Akkermansia; s__muciniphila 0.9999999999999716
f67a6d5da8c0b71206955aeae1505a74  k__Bacteria; p__Bacteroidetes;
c__Bacteroidia; o__Bacteroidales; f__S24-7; g__; s__ 0.9999839589828744
d272bf25781448dde9031a24679a9012  k__Bacteria; p__Bacteroidetes;
c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides;
s__acidifaciens 0.9995083080422182

```

Normalize the feature table to a uniform depth

Note: The decision of how deep should be selected is based on **stats-dada2/stats.tsv** clean reads in all samples, you should keep as much samples as possible, and should keep a good enough depth, usually for stool samples over 10000 sequences should be fine. Here, as this is a demo, the raw sequences are 2500 and the final clean reads are all over 800, we chose 800 reads as the cut off.

```

singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.
activate qiime2-2020.8 && \
qiime feature-table rarefy \
--i-table hf_diver/table.qza \
--p-sampling-depth 800 \
--o-rarefied-table hf_diver/rarefy.table.qza'

```

Generate stack barchart

```

singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.
activate qiime2-2020.8 && \
qiime taxa barplot \
--i-table hf_diver/rarefy.table.qza \
--i-taxonomy hf_diver/taxonomy.qza \
--m-metadata-file meta_data.txt \
--o-visualization hf_diver/normalized.taxa-bar-plots.qzv'

```

Decompress qzv file and download to local to browse the file

```

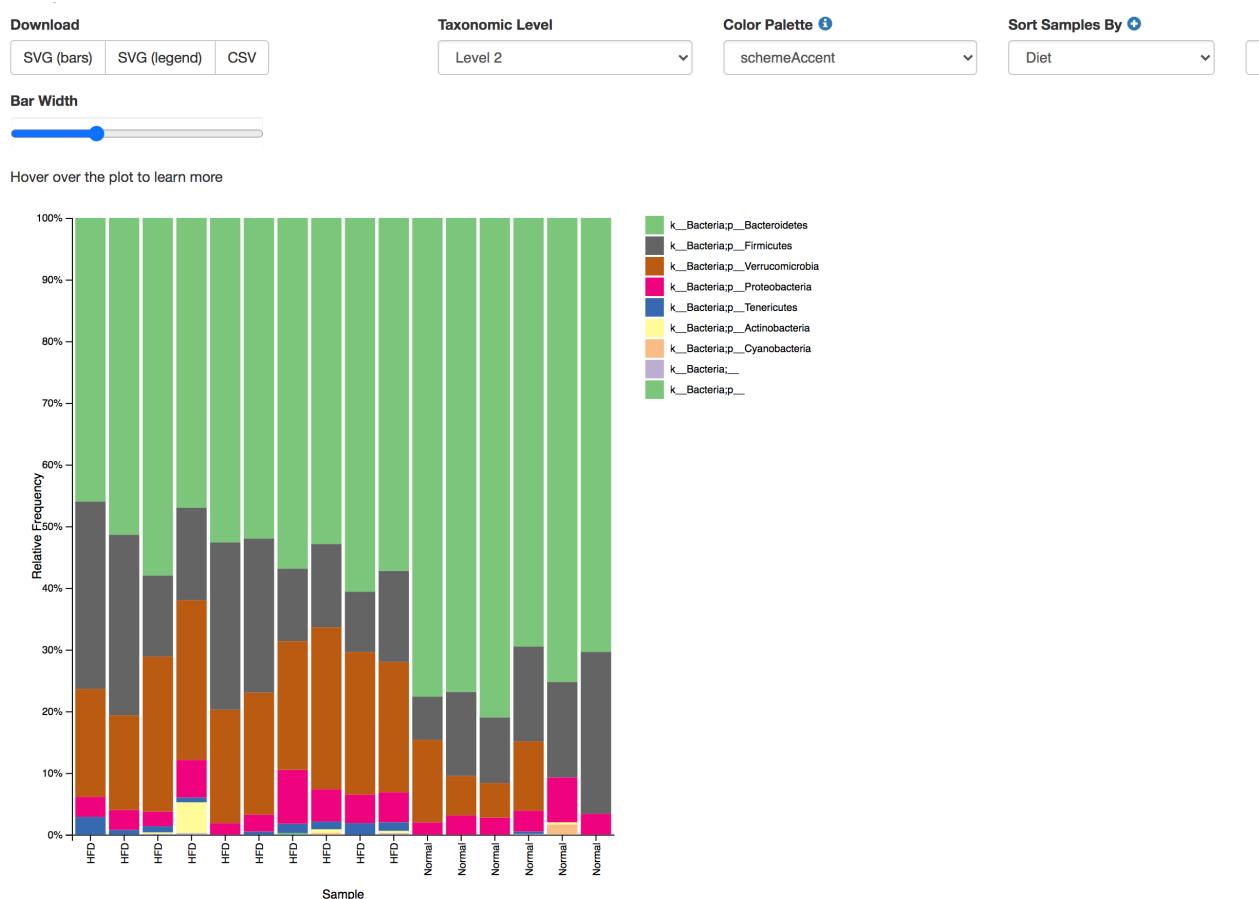
singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.
activate qiime2-2020.8 && \
qiime tools export \
--input-path hf_diver/normalized.taxa-bar-plots.qzv \
--output-path hf_diver/normalized.taxa-bar-plots'

```

Three files 'taxonomy.qza', 'rarefy.table.qza', 'normalized.taxa-bar-plots.qzv' and one folder 'normalized.taxa-bar-plots' are generated sequentially.

```
(qiime2-2020.2) [z3527776@k212 demo]$ ll hf_diver/
total 884
drwxr-xr-x 2 z3527776 MRCBIO      10 Sep 14 13:44 alpha-group
drwxr-xr-x 2 z3527776 MRCBIO      10 Sep 14 13:44 beta-group
drwxr-xr-x 4 z3527776 MRCBIO    4096 Sep 14 13:59 normalized.taxa-bar-plots
-rw-r--r-- 1 z3527776 MRCBIO 348445 Sep 14 13:58 normalized.taxa-bar-plots.qzv
-rw-r--r-- 1 z3527776 MRCBIO 27779 Sep 14 13:58 rarefy.table.qza
-rw----- 1 z3527776 MRCBIO 28860 Sep 14 13:43 rep-seqs.qza
-rw----- 1 z3527776 MRCBIO 22922 Sep 14 13:43 table.qza
-rw----- 1 z3527776 MRCBIO 420230 Sep 14 13:48 table-summarize.qzv
-rw-r--r-- 1 z3527776 MRCBIO 40406 Sep 14 13:49 taxonomy.qza
```

If you download file 'normalized.taxa-bar-plots.qzv' locally then upload to qiime2 view, the visualization should look like this. 'Taxonomic Level', 'Color Palette' and 'Sort Samples By' all can be manually modified.



Phylogenetic tree construction

Overview

Teaching: 10 min **Exercises:** 0 min

Objectives

- Understand what is a phylogenetic tree and the purpose of why we need this
- Finish the commands to generate rooted tree

In order to generate the UniFrac distance, a phylogenetic tree should be build for all the representative feature sequences

```
#constructing phylogenetic tree
singularity exec -B /scratch /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif
bash -c '. activate qiime2-2020.8 && \
qiime alignment mafft \
--i-sequences hf_diver/rep-seqs.qza \
--o-alignment hf_diver/aligned-rep-seqs.qza'

singularity exec -B /scratch /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif
bash -c '. activate qiime2-2020.8 && \
qiime alignment mask \
--i-alignment hf_diver/aligned-rep-seqs.qza \
--o-masked-alignment hf_diver/masked-aligned-rep-seqs.qza'

singularity exec -B /scratch /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif
bash -c '. activate qiime2-2020.8 && \
qiime phylogeny fasttree \
--i-alignment hf_diver/masked-aligned-rep-seqs.qza \
--o-tree hf_diver/unrooted-tree.qza --p-n-threads 1'

singularity exec -B /scratch /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif
bash -c '. activate qiime2-2020.8 && \
qiime phylogeny midpoint-root \
--i-tree hf_diver/unrooted-tree.qza \
--o-rooted-tree hf_diver/rooted-tree.qza'
```

Four files 'aligned-rep-seqs.qza', 'masked-aligned-rep-seqs.qza', 'unrooted-tree.qza' and 'rooted-tree.qza' are generated sequentially. The **rooted-tree.qza** will be used in the core diversity analysis

```
(qiime2-2020.2) [z3527776@k212 demo]$ ll -t hf_diver/
total 1036
-rw-r--r-- 1 z3527776 MRCBIO 37356 Sep 14 14:09 rooted-tree.qza
-rw-r--r-- 1 z3527776 MRCBIO 32900 Sep 14 14:08 unrooted-tree.qza
-rw-r--r-- 1 z3527776 MRCBIO 38095 Sep 14 14:07 masked-aligned-rep-seqs.qza
-rw-r--r-- 1 z3527776 MRCBIO 34835 Sep 14 14:07 aligned-rep-seqs.qza
drwxr-xr-x 4 z3527776 MRCBIO 4096 Sep 14 13:59 normalized.taxa-bar-plots
-rw-r--r-- 1 z3527776 MRCBIO 348445 Sep 14 13:58 normalized.taxa-bar-plots.qzv
-rw-r--r-- 1 z3527776 MRCBIO 27779 Sep 14 13:58 rarefy.table.qza
-rw-r--r-- 1 z3527776 MRCBIO 40406 Sep 14 13:49 taxonomy.qza
-rw----- 1 z3527776 MRCBIO 420230 Sep 14 13:48 table-summarize.qzv
drwxr-xr-x 2 z3527776 MRCBIO 10 Sep 14 13:44 beta-group
drwxr-xr-x 2 z3527776 MRCBIO 10 Sep 14 13:44 alpha-group
-rw----- 1 z3527776 MRCBIO 22922 Sep 14 13:43 table.qza
-rw----- 1 z3527776 MRCBIO 28860 Sep 14 13:43 rep-seqs.qza
(qiime2-2020.2) [z3527776@k212 demo]$
```

Run the core diversity analysis

Overview

Teaching: 10 min Exercises: 0 min

Objectives

- Understand the output for the core diversity analysis
- Checking the results for PcoA with different beta diversity distance

Sometimes we need to filter samples by the meta data to select part of the samples for analysis

```
singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.  
activate qiime2-2020.8 && \  
qiime feature-table filter-samples \  
--i-table hf_diver/table.qza \  
--m-metadata-file meta_data.txt \  
--o-filtered-table hf_diver/core.table.qza'
```

core diversity with phylogenetic information

```
singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.  
activate qiime2-2020.8 && \  
qiime diversity core-metrics-phylogenetic \  
--i-phylogeny hf_diver/rooted-tree.qza \  
--i-table hf_diver/core.table.qza \  
--p-sampling-depth 800 \  
--m-metadata-file meta_data.txt \  
--output-dir hf_diver/core-metrics-results'
```

One files 'core.table.qza' and one folder 'core-metrics-results', which has the core diversity analysis outputs, are generated sequentially. This step generate alpha diversity indexes such a Shannon, observed features, jaccard, evenness, and faith phylogenetic distance data and plot. The beta diversity of PcoA such as bray-curtis distance, weighted and unweighted UniFrac distance.

```
(qiime2-2020.2) [z3527776@k212 demo]$ ll -t hf_diver/
total 1068
drwxr-xr-x 2 z3527776 MRCBIO 4096 Sep 14 14:11 core-metrics-results
-rw-r--r-- 1 z3527776 MRCBIO 28304 Sep 14 14:11 core.table.qza
-rw-r--r-- 1 z3527776 MRCBIO 37356 Sep 14 14:09 rooted-tree.qza
-rw-r--r-- 1 z3527776 MRCBIO 32900 Sep 14 14:08 unrooted-tree.qza
-rw-r--r-- 1 z3527776 MRCBIO 38095 Sep 14 14:07 masked-aligned-rep-seqs.qza
-rw-r--r-- 1 z3527776 MRCBIO 34835 Sep 14 14:07 aligned-rep-seqs.qza
drwxr-xr-x 4 z3527776 MRCBIO 4096 Sep 14 13:59 normalized.taxa-bar-plots
-rw-r--r-- 1 z3527776 MRCBIO 348445 Sep 14 13:58 normalized.taxa-bar-plots.qzv
-rw-r--r-- 1 z3527776 MRCBIO 27779 Sep 14 13:58 rarefy.table.qza
-rw-r--r-- 1 z3527776 MRCBIO 40406 Sep 14 13:49 taxonomy.qza
-rw----- 1 z3527776 MRCBIO 420230 Sep 14 13:48 table-summarize.qzv
drwxr-xr-x 2 z3527776 MRCBIO 10 Sep 14 13:44 beta-group
drwxr-xr-x 2 z3527776 MRCBIO 10 Sep 14 13:44 alpha-group
-rw----- 1 z3527776 MRCBIO 22922 Sep 14 13:43 table.qza
-rw----- 1 z3527776 MRCBIO 28860 Sep 14 13:43 rep-seqs.qza
(qiime2-2020.2) [z3527776@k212 demo]$ tree hf_diver/core-metrics-results
hf_diver/core-metrics-results
├── bray_curtis_distance_matrix.qza
├── bray_curtis_emperor.qzv
├── bray_curtis_pcoa_results.qza
├── evenness_vector.qza
├── faith_pd_vector.qza
├── jaccard_distance_matrix.qza
├── jaccard_emperor.qzv
├── jaccard_pcoa_results.qza
├── observed_features_vector.qza
├── rarefied_table.qza
├── shannon_vector.qza
├── unweighted_unifrac_distance_matrix.qza
├── unweighted_unifrac_emperor.qzv
├── unweighted_unifrac_pcoa_results.qza
├── weighted_unifrac_distance_matrix.qza
├── weighted_unifrac_emperor.qzv
└── weighted_unifrac_pcoa_results.qza

0 directories, 17 files
(qiime2-2020.2) [z3527776@k212 demo]$
```

d

Check alpha diversity contents, shannon vector for example

```
singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '
activate qiime2-2020.8 && \
qiime tools export \
--input-path hf_diver/core-metrics-results/shannon_vector.qza \
--output-path hf_diver/core-metrics-results/shannon_vector'
```

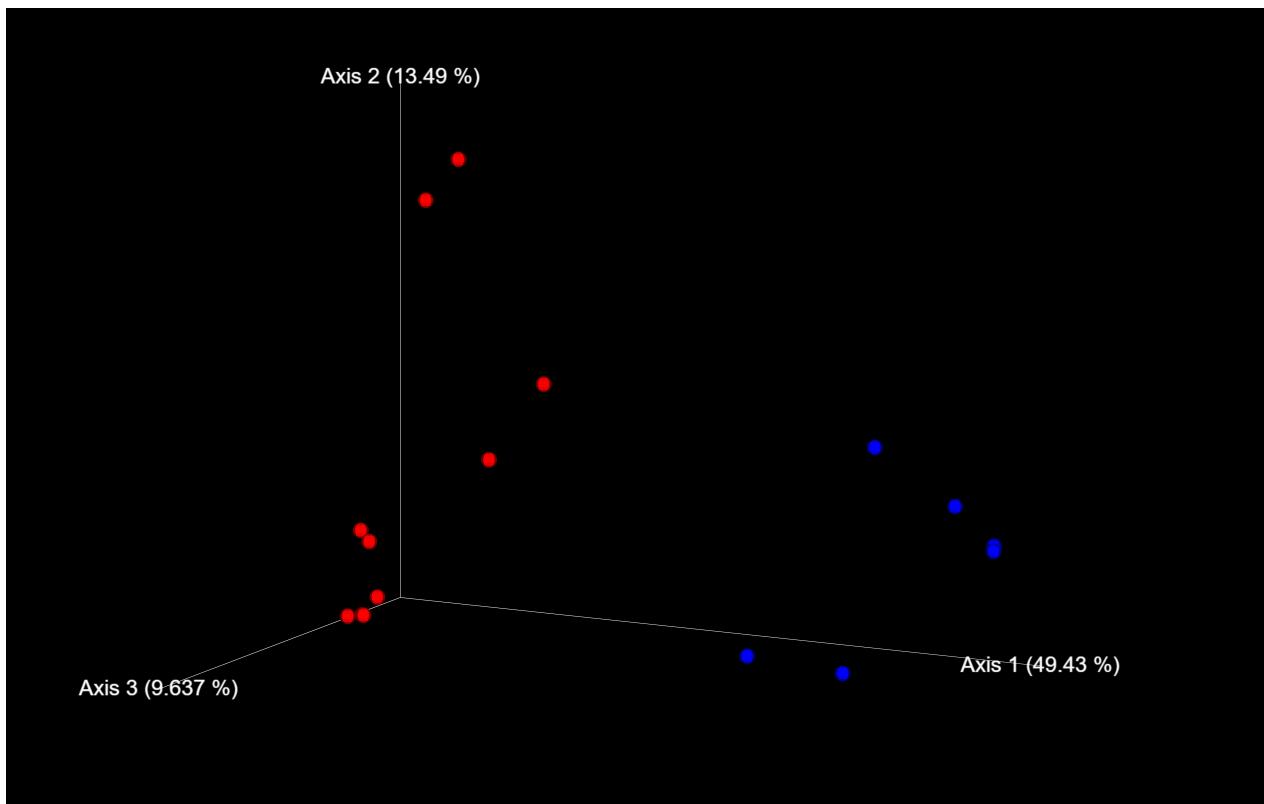
Look into the output file

```
head -4 hf_diver/core-metrics-results/shannon_vector/alpha-diversity.tsv

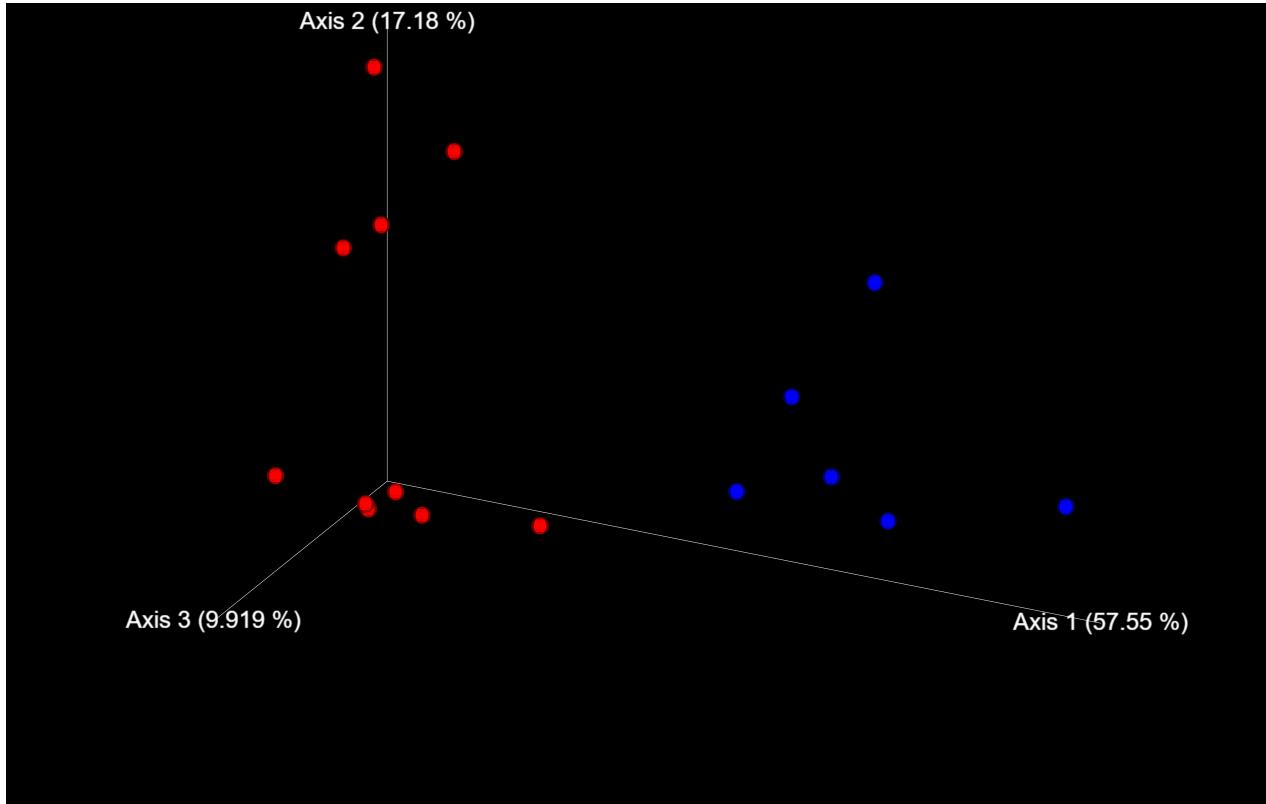
#output:
shannon_entropy
5821_S50_L001 4.284775238361043
5822_S34_L001 4.492180841533424
5824_S96_L001 4.474363582402979
```

Check PcoA plot for bray-curtis distance and weighted unifrac distance

If you download file 'bray_curtis_emperor.qzv' locally then upload to qiime2 view, the visualization should be look like this. (Red is high fat diet samples and blue are healthy)



If you download file 'weighted_unifrac_emperor.qzv' locally then upload to qiime2 view, the visualization should be look like this.



Alpha diversity rarefaction curve

Overview

Teaching: 5 min Exercises: 0 min

Objectives

- Understand the meaning of rarefaction curve
- Generating rarefaction curve with qiime diversity plugin

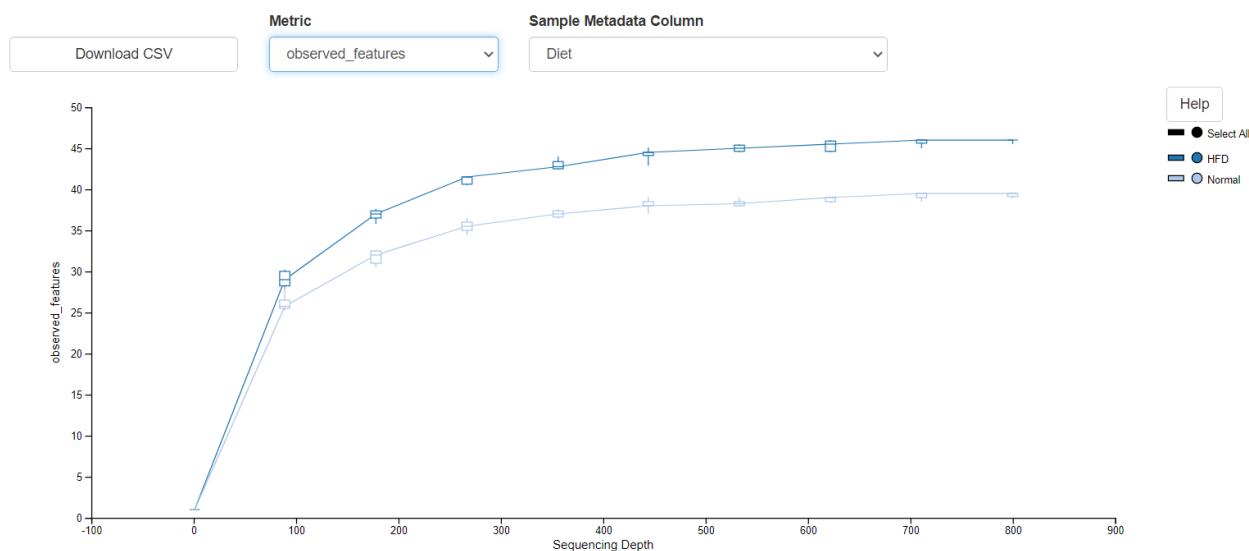
```
singularity exec /srv/scratch/mrcbio/workshop/mrcmbio.sif bash -c '.
activate qiime2-2020.8 && \
qiime diversity alpha-rarefaction \
--i-table hf_diver/table.qza \
--i-phylogeny hf_diver/rooted-tree.qza \
--p-max-depth 800 \
--m-metadata-file meta_data.txt \
--o-visualization hf_diver/alpha-rarefaction.qzv'
```

A file 'alpha-rarefaction.qzv' is created.

```
(qiime2-2020.2) [z3527776@k212 demo]$ ll -t hf_diver/
total 1396
-rw-r--r-- 1 z3527776 MRCBIO 332060 Sep 14 14:24 alpha-rarefaction.qzv
drwxr-xr-x 2 z3527776 MRCBIO 4096 Sep 14 14:11 core-metrics-results
-rw-r--r-- 1 z3527776 MRCBIO 28304 Sep 14 14:11 core.table.qza
-rw-r--r-- 1 z3527776 MRCBIO 37356 Sep 14 14:09 rooted-tree.qza
-rw-r--r-- 1 z3527776 MRCBIO 32900 Sep 14 14:08 unrooted-tree.qza
```

If you download file 'alpha-rarefaction.qzv' locally then upload to qiime2 view, the visualization should be look like this. 'Metric' has options (1) observed_features, (2) shannon and (3) faith_pd.

Alpha rarefaction



PERMANOVA statistical testing of alpha and beta diversity with meta data

Overview

Teaching: 10 min Exercises: 0 min

Objectives

- Understand PERMANOVA testing for group significance
- Identifying the most significant influential meta data that associated with microbial alpha and beta diversity

PERMANOVA statistical testing of alpha diversity for groups

Faith_ph

```
singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.
activate qiime2-2020.8 && \
qiime diversity alpha-group-significance \
--i-alpha-diversity hf_diver/core-metrics-results/faith_pd_vector.qza \
--m-metadata-file meta_data.txt \
--o-visualization hf_diver/alpha-group/faith-pd-group-significance.qzv'
```

A file 'faith-pd-group-significance.qzv' is newly generated.

```
(qiime2-2020.2) [z3527776@k212 demo]$ ll -t hf_diver/alpha-group/
total 324
-rw-r--r-- 1 z3527776 MRCBIO 328428 Sep 14 14:28 faith-pd-group-significance.qzv
(qiime2-2020.2) [z3527776@k212 demo]$
```

If you download file 'faith-pd-group-significance.qzv' locally then upload to qiime2 view, the visualization should be look like this.



evenness

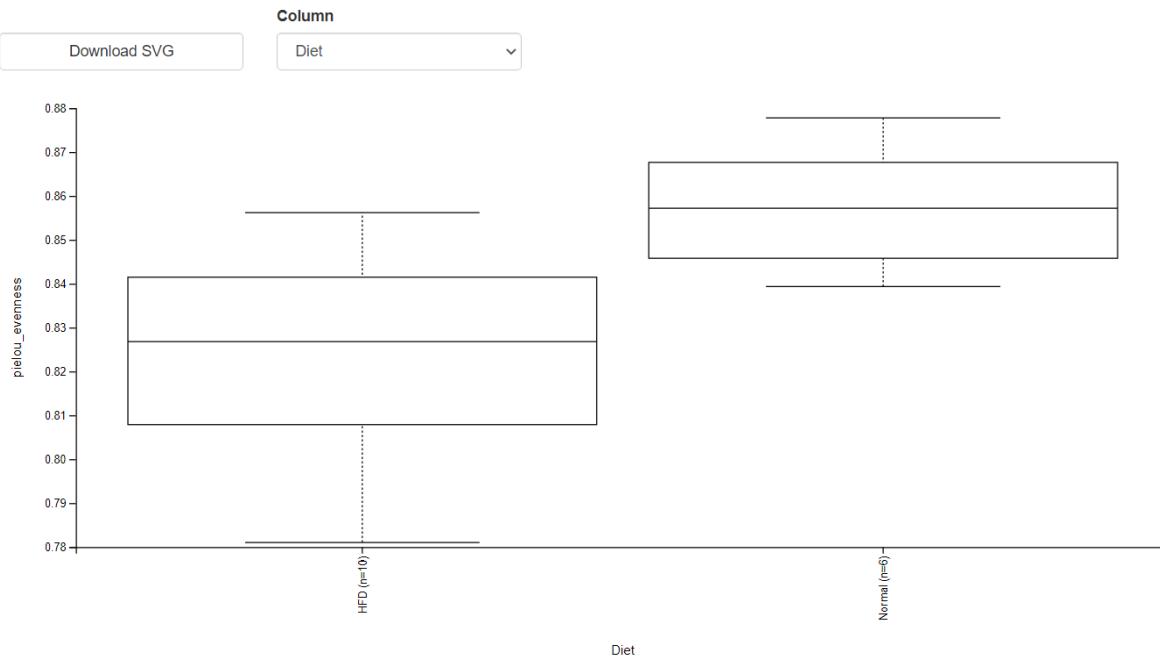
```
singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.
activate qiime2-2020.8 && \
qiime diversity alpha-group-significance \
--i-alpha-diversity hf_diver/core-metrics-results/evenness_vector.qza \
--m-metadata-file meta_data.txt \
--o-visualization hf_diver/alpha-group/evenness-group-significance.qzv'
```

A file 'evenness-group-significance.qzv' is newly generated.

```
(qiime2-2020.2) [z3527776@k212 demo]$ ll -t hf_diver/alpha-group/
total 648
-rw-r--r-- 1 z3527776 MRCBIO 328463 Sep 14 14:33 evenness-group-significance.qzv
-rw-r--r-- 1 z3527776 MRCBIO 328428 Sep 14 14:28 faith-pd-group-significance.qzv
(qiime2-2020.2) [z3527776@k212 demo]$
```

If you download file 'evenness-group-significance.qzv' locally then upload to qiime2 view, the visualization should be look like this.

Alpha Diversity Boxplots



observed features

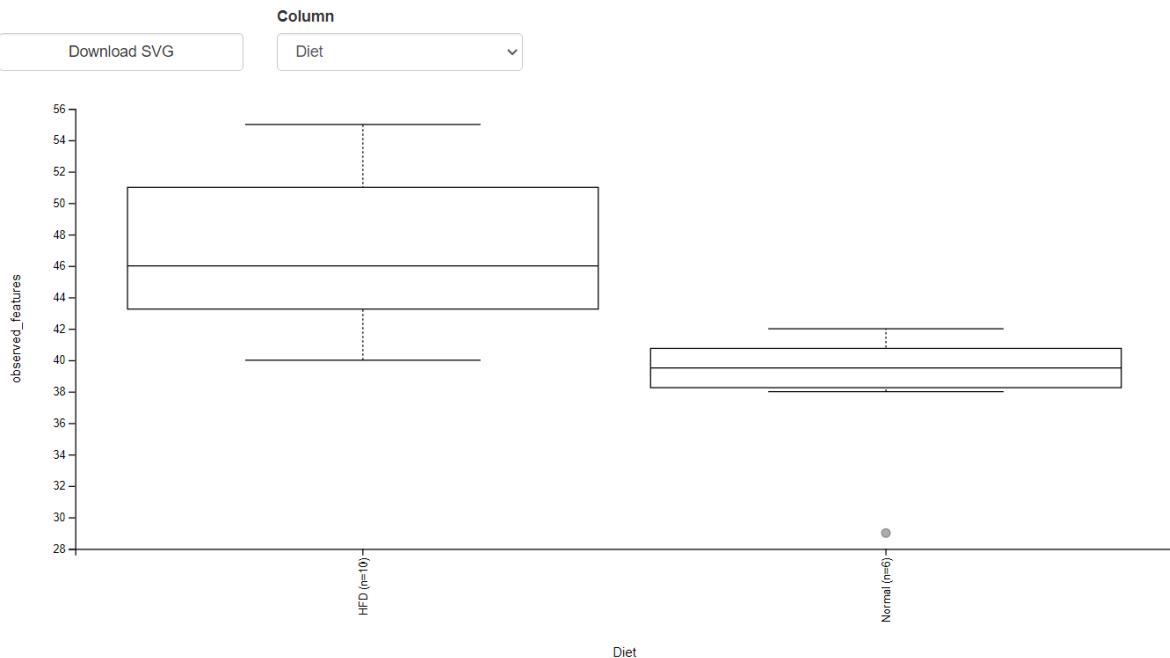
```
singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.
activate qiime2-2020.8 && \
qiime diversity alpha-group-significance \
--i-alpha-diversity hf_diver/core-metrics-
results/observed_features_vector.qza \
--m-metadata-file meta_data.txt \
--o-visualization hf_diver/alpha-group/observed_features_vector.qzv'
```

A file 'observed_features_vector.qzv' is newly generated.

```
(qiime2-2020.2) [z3527776@k212 demo]$ ll -t hf_diver/alpha-group/
total 972
-rw-r--r-- 1 z3527776 MRCBIO 328061 Sep 14 14:35 observed_features_vector.qzv
-rw-r--r-- 1 z3527776 MRCBIO 328463 Sep 14 14:33 evenness-group-significance.qzv
-rw-r--r-- 1 z3527776 MRCBIO 328428 Sep 14 14:28 faith-pd-group-significance.qzv
(qiime2-2020.2) [z3527776@k212 demo]$
```

If you download file 'observed_features_vector.qzv' locally then upload to qiime2 view, the visualization should be look like this.

Alpha Diversity Boxplots



shannon index

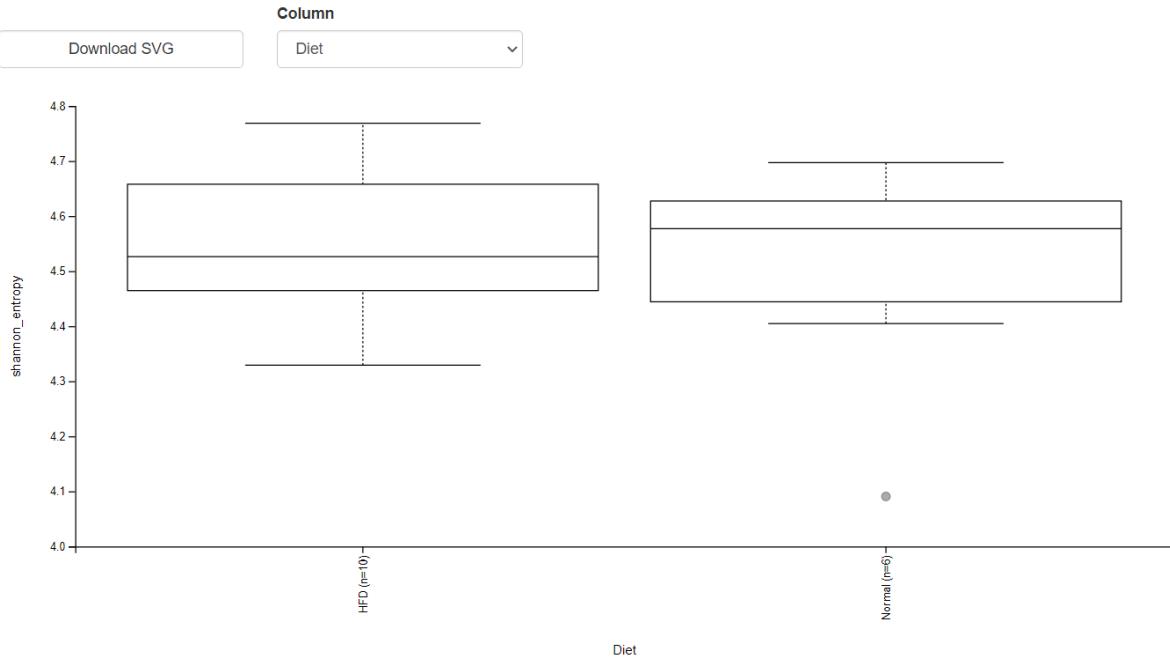
```
singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.
activate qiime2-2020.8 && \
qiime diversity alpha-group-significance \
--i-alpha-diversity hf_diver/core-metrics-results/shannon_vector.qza \
--m-metadata-file meta_data.txt \
--o-visualization hf_diver/alpha-group/shannon_vector.qzv'
```

A file 'shannon_vector.qzv' is newly generated.

```
(qiime2-2020.2) [z3527776@k212 demo]$ ll -t hf_diver/alpha-group/
total 1296
-rw-r--r-- 1 z3527776 MRCBIO 328483 Sep 14 14:36 shannon_vector.qzv
-rw-r--r-- 1 z3527776 MRCBIO 328061 Sep 14 14:35 observed_features_vector.qzv
-rw-r--r-- 1 z3527776 MRCBIO 328463 Sep 14 14:33 evenness-group-significance.qzv
-rw-r--r-- 1 z3527776 MRCBIO 328428 Sep 14 14:28 faith-pd-group-significance.qzv
(qiime2-2020.2) [z3527776@k212 demo]$
```

If you download file 'shannon_vector.qzv' locally then upload to qiime2 view, the visualization should be look like this.

Alpha Diversity Boxplots



Output alpha diversity values from qiime2 output

```
singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.
activate qiime2-2020.8 && \
qiime tools export \
--input-path hf_diver/alpha-group/shannon_vector.qzv \
--output-path hf_diver/alpha-group/shannon_vector'
```

A folder 'shannon_vector' is newly generated. You can download the whole directory to your local pc or laptop and open the file 'index.html' to visualize.

```
(qiime2-2020.2) [z3527776@k212 demo]$ ll -t hf_diver/alpha-group/
total 1296
drwxr-xr-x 4 z3527776 MRCBIO 173 Sep 14 14:37 shannon_vector
-rw-r--r-- 1 z3527776 MRCBIO 328483 Sep 14 14:36 shannon_vector.qzv
-rw-r--r-- 1 z3527776 MRCBIO 328061 Sep 14 14:35 observed_features_vector.qzv
-rw-r--r-- 1 z3527776 MRCBIO 328463 Sep 14 14:33 evenness-group-significance.qzv
-rw-r--r-- 1 z3527776 MRCBIO 328428 Sep 14 14:28 faith-pd-group-significance.qzv
(qiime2-2020.2) [z3527776@k212 demo]$ ll -t hf_diver/alpha-group/shannon_vector
total 16
drwxr-xr-x 2 z3527776 MRCBIO 85 Sep 14 14:37 dist
drwxr-xr-x 6 z3527776 MRCBIO 71 Sep 14 14:37 q2templateassets
-rw-r--r-- 1 z3527776 MRCBIO 924 Sep 14 14:37 column-Diet.jsonp
-rw-r--r-- 1 z3527776 MRCBIO 2502 Sep 14 14:37 index.html
-rw-r--r-- 1 z3527776 MRCBIO 117 Sep 14 14:37 kruskal-wallis-pairwise-Diet.csv
-rw-r--r-- 1 z3527776 MRCBIO 647 Sep 14 14:37 metadata.tsv
(qiime2-2020.2) [z3527776@k212 demo]$
```

PERMANOVA statistical testing of beta diversity for groups

Bray curtis distance on diet

```

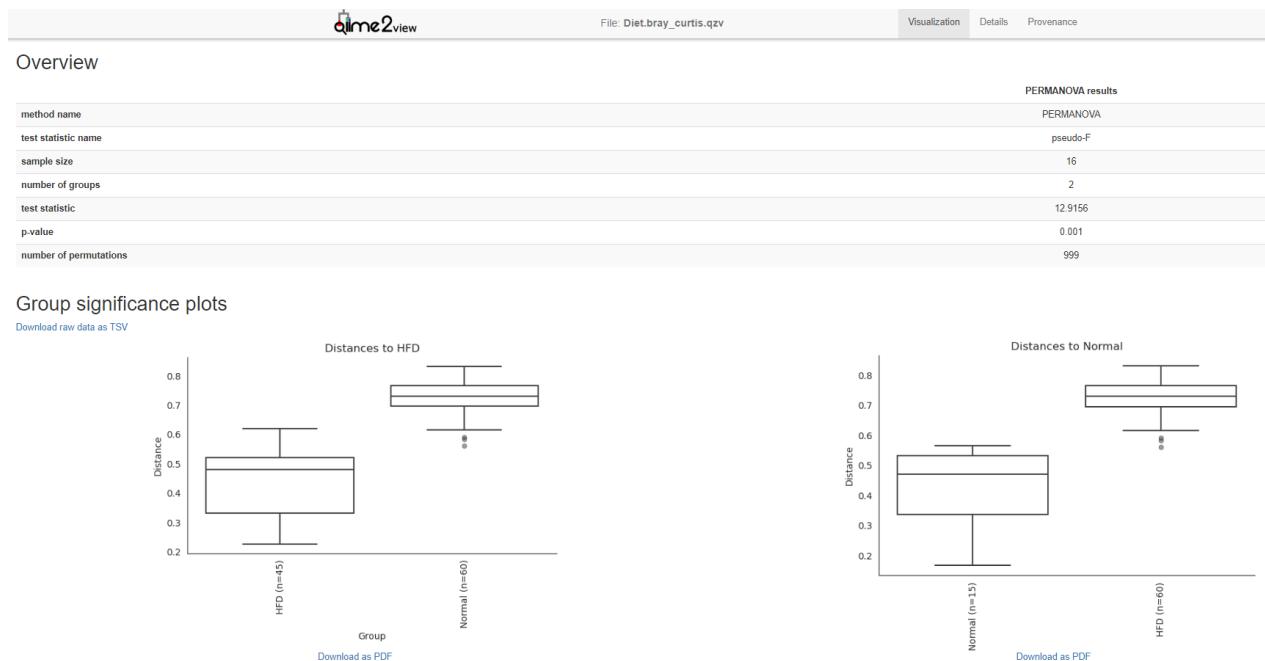
singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.
activate qiime2-2020.8 && \
qiime diversity beta-group-significance \
--i-distance-matrix hf_diver/core-metrics-
results/bray_curtis_distance_matrix.qza \
--m-metadata-file meta_data.txt \
--m-metadata-column "Diet" \
--o-visualization hf_diver/beta-group/Diet.bray_curtis.qzv --p-pairwise'

```

A file 'Diet.bray_curtis.qzv' is newly generated.

```
(qiime2-2020.2) [z3527776@k212 demo]$ ll -t hf_diver/beta-group/
total 288
-rw-r--r-- 1 z3527776 MRCBIO 294459 Sep 14 14:40 Diet.bray_curtis.qzv
(qiime2-2020.2) [z3527776@k212 demo]$
```

If you download file 'Diet.bray_curtis.qzv' locally then upload to qiime2 view, the visualization should be look like this.



Jaccard distance

```

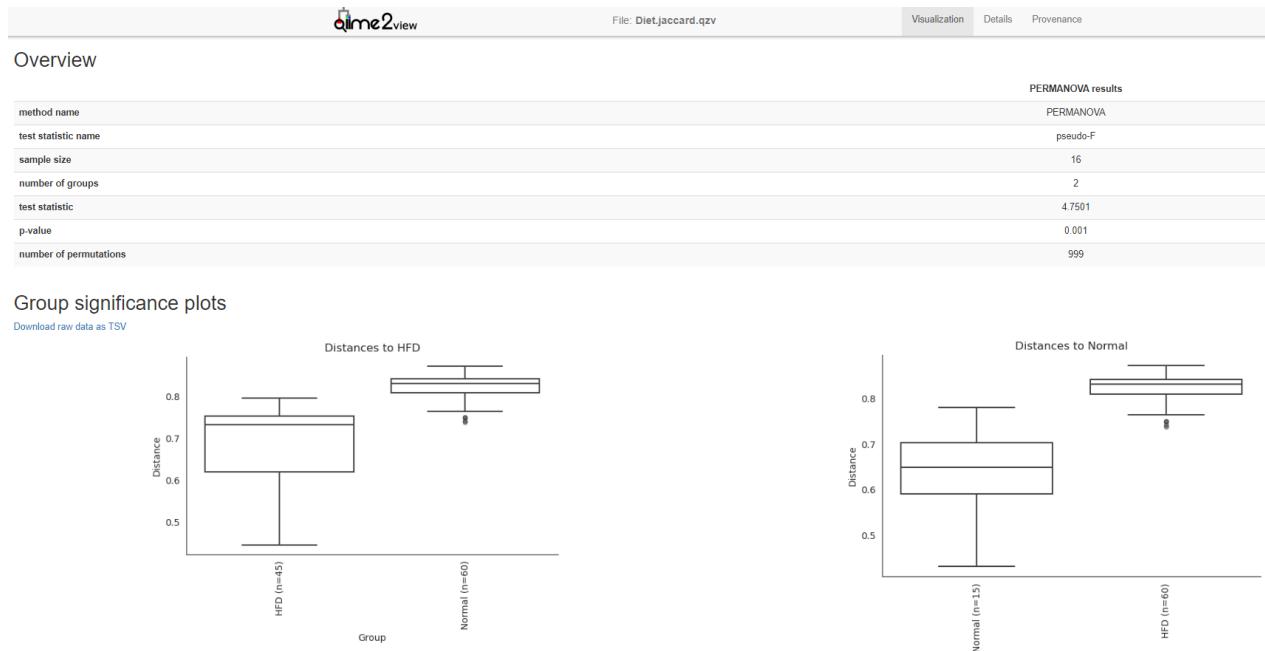
singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.
activate qiime2-2020.8 && \
qiime diversity beta-group-significance \
--i-distance-matrix hf_diver/core-metrics-
results/jaccard_distance_matrix.qza \
--m-metadata-file meta_data.txt \
--m-metadata-column "Diet" \
--o-visualization hf_diver/beta-group/Diet.jaccard.qzv --p-pairwise'

```

A file 'Diet.jaccard.qzv' is newly generated.

```
(qiime2-2020.2) [z3527776@k212 demo]$ ll -t hf_diver/beta-group/
total 576
-rw-r--r-- 1 z3527776 MRCBIO 291627 Sep 14 14:42 Diet.jaccard.qzv
-rw-r--r-- 1 z3527776 MRCBIO 294459 Sep 14 14:40 Diet.bray_curtis.qzv
(qiime2-2020.2) [z3527776@k212 demo]$
```

If you download file 'Diet.jaccard.qzv' locally then upload to qiime2 view, the visualization should be look like this.



Unweighted UniFrac distacne

```
singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.
activate qiime2-2020.8 && \
qiime diversity beta-group-significance \
--i-distance-matrix hf_diver/core-metrics-
results/unweighted_unifrac_distance_matrix.qza \
--m-metadata-file meta_data.txt \
--m-metadata-column "Diet" \
--o-visualization hf_diver/beta-group/Diet.unweighted_unifrac.qzv --p-
pairwise'
```

A file 'Diet.unweighted_unifrac.qzv' is newly generated.

```
(qiime2-2020.2) [z3527776@k212 demo]$ ll -t hf_diver/beta-group/
total 868
-rw-r--r-- 1 z3527776 MRCBIO 296326 Sep 14 14:45 Diet.unweighted_unifrac.qzv
-rw-r--r-- 1 z3527776 MRCBIO 291627 Sep 14 14:42 Diet.jaccard.qzv
-rw-r--r-- 1 z3527776 MRCBIO 294459 Sep 14 14:40 Diet.bray_curtis.qzv
(qiime2-2020.2) [z3527776@k212 demo]$
```

If you download file 'Diet.unweighted_unifrac.qzv' locally then upload to qiime2 view, the visualization should be look like this.

qiime2view		File: Diet.unweighted_unifrac.qzv	Visualization	Details	Provenance
Overview					
method name			PERMANOVA results		
test statistic name			PERMANOVA		
sample size			pseudo-F		
number of groups			16		
test statistic			2		
p-value			6.20919		
number of permutations			0.001		
			999		

Group significance plots

[Download raw data as TSV](#)



Weighted UniFrac distance

```
singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.
activate qiime2-2020.8 && \
qiime diversity beta-group-significance \
--i-distance-matrix hf_diver/core-metrics-
results/weighted_unifrac_distance_matrix.qza \
--m-metadata-file meta_data.txt \
--m-metadata-column "Diet" \
--o-visualization hf_diver/beta-group/Diet.weighted_unifrac.qzv --p-
pairwise'
```

A file 'Diet.weighted_unifrac.qzv' is newly generated.

```
(qiime2-2020.2) [z3527776@k212 demo]$ ll -t hf_diver/beta-group/
total 1156
-rw-r--r-- 1 z3527776 MRCBIO 293949 Sep 14 14:46 Diet.weighted_unifrac.qzv
-rw-r--r-- 1 z3527776 MRCBIO 296326 Sep 14 14:45 Diet.unweighted_unifrac.qzv
-rw-r--r-- 1 z3527776 MRCBIO 291627 Sep 14 14:42 Diet.jaccard.qzv
-rw-r--r-- 1 z3527776 MRCBIO 294459 Sep 14 14:40 Diet.bray_curtis.qzv
(qiime2-2020.2) [z3527776@k212 demo]$
```

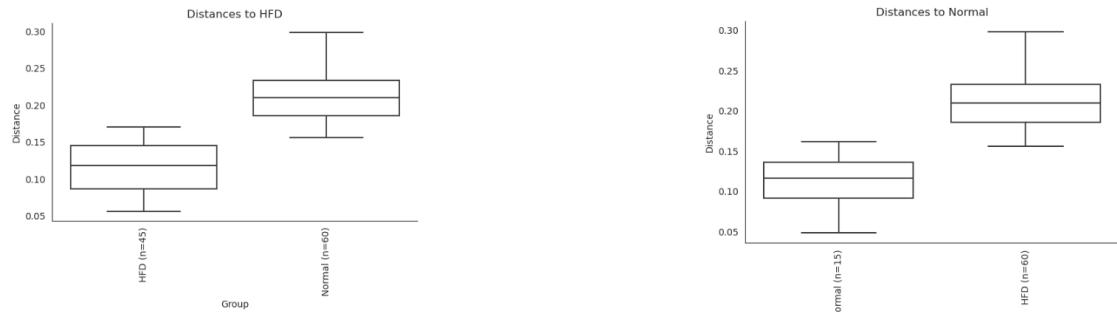
If you download file 'Diet.weighted_unifrac.qzv' locally then upload to qiime2 view, the visualization should be look like this.

Overview

method name	PERMANOVA results
test statistic name	PERMANOVA
sample size	pseudo-F
number of groups	16
test statistic	2
p-value	18.0095
number of permutations	0.001
	999

Group significance plots

[Download raw data as TSV](#)



Decompress visualization qzv file and download to local computer to check the results

```
singularity exec /srv/scratch/mrcbio/workshop/mrcmicromicrobiome.sif bash -c '.
activate qiime2-2020.8 && \
qiime tools export \
--input-path hf_diver/beta-group/Diet.weighted_unifrac.qzv \
--output-path hf_diver/beta-group/Diet.weighted_unifrac'
```

A folder 'Diet.weighted_unifrac' is newly generated. You can download the whole directory to your local pc or laptop and open the file 'index.html' to visualize.

```
(qiime2-2020.2) [z3527776@k212 demo]$ ll -t hf_diver/beta-group/
total 1156
drwxr-xr-x 3 z3527776 MRCBIO    236 Sep 14 14:46 Diet.weighted_unifrac
-rw-r--r-- 1 z3527776 MRCBIO 293949 Sep 14 14:46 Diet.weighted_unifrac.qzv
-rw-r--r-- 1 z3527776 MRCBIO 296326 Sep 14 14:45 Diet.unweighted_unifrac.qzv
-rw-r--r-- 1 z3527776 MRCBIO 291627 Sep 14 14:42 Diet.jaccard.qzv
-rw-r--r-- 1 z3527776 MRCBIO 294459 Sep 14 14:40 Diet.bray_curtis.qzv
(qiime2-2020.2) [z3527776@k212 demo]$
```

4. Using LEfSe to identify differential abundant taxa

Overview

Teaching: 20 min **Exercises:** 0 min

Objectives

- Understand how LEfSe identify microbial signatures
- Identify differential abundant taxa in the high fat diet mouse

Check the help information for the pipeline

```
singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.  
activate qiime2-2020.8 && perl /home/applications/mima/mima_lefsetable_16s.pl  
rarefy.table.qza taxonomy.qza Diet meta_data.txt hf_lefse_tables'
```

LEfSe outputs are in directory 'hf_lefse_tables', this step will generate input file of differnt ranks and merge all 7 ranks taxa into one file to be used in the following step to draw clade plot and bar plot of LDA scores.

For a regular tab seperated table to do LEfSe analysis, the following pipeline can be used

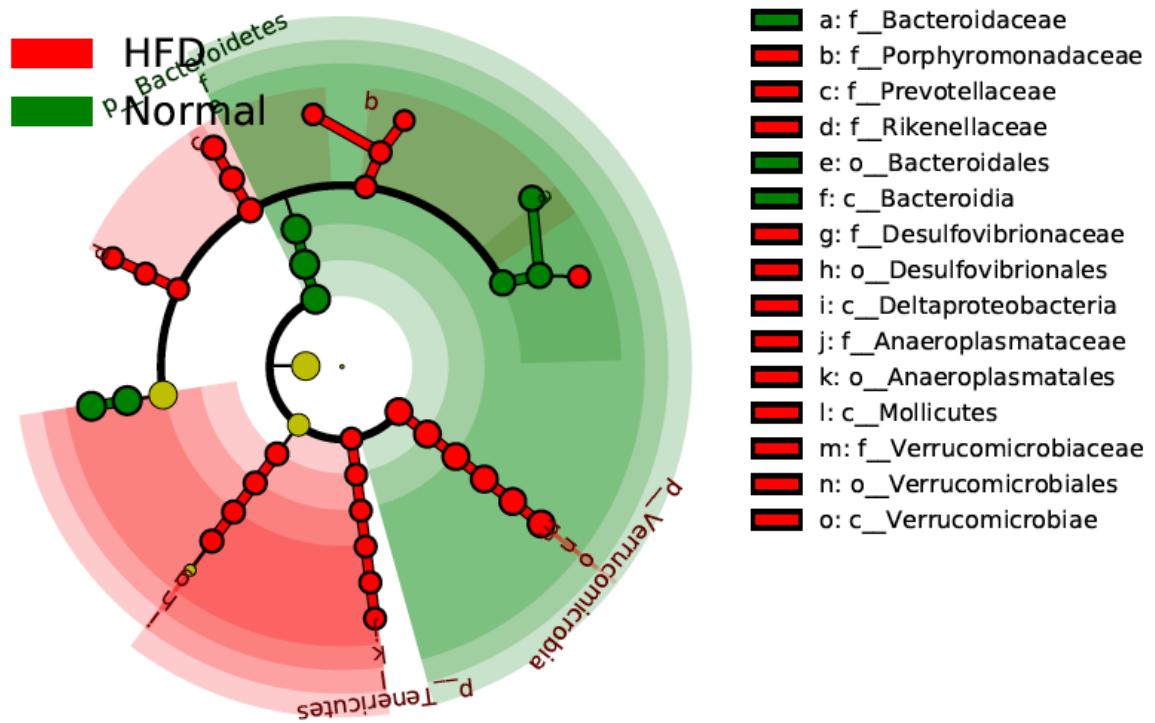
```
singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.  
activate lefse-conda && perl /home/applications/mima/mima_lefse_pipeline.pl '  
  
-i table.tsv, the rarefied feature table used to do LEfSe  
-m meta datafile, a table with rows as sample and column as differnt meta  
data  
-g group vector should be column_name:group1,group2,group3 #the detail  
groups in one column to compare  
-o output dir/ string  
-f prefix to the output file, string format  
-d LDA schore forcut off default 2  
-x width of figure default 8 inch  
-y height of figure default 8 inch  
-h print this help information
```

Here in this example, we would like to identify the differential abundant taxa that enriched in high fat diet mouse.

```
singularity exec /srv/scratch/mrcbio/workshop/mrcmicrobiome.sif bash -c '.  
activate lefse-conda && perl /home/applications/mima/mima_lefse_pipeline.pl -  
i hf_lefse_tables/lefse_allrank/merge_taxonomy.csv -m meta_data.txt -g  
Diet:Normal,HFD -o hf_lefsenew -f dietlefse -d 3'
```

cladoplot presenting of signatures

Cladogram



LEfSe signatures barchart

 HFD  Normal

