

Hands on training sessions:  
Analyses of metagenomics data using R

**Requirements**

1. **Hardware & Operating System:**

A laptop with 4 GB RAM or more & Windows operating system (Preferable)

2. **Download R:**

Download R for windows

<https://cran.r-project.org/bin/windows/base/R-4.4.1-win.exe>

Download RStudio for windows

<https://download1.rstudio.org/electron/windows/RStudio-2024.04.2-764.exe>

**Tutorial for the installation help for R and R studio:**

<https://www.youtube.com/watch?v=YrEe2TLr3MI>

3. **R packages:**

install the following R packages within R studio using the given commands.

Package Names	Command
Bioconductor/BiocManager	if (!requireNamespace("BiocManager", quietly = TRUE)) install.packages("BiocManager")
DADA2	BiocManager::install("dada2")
phyloseq	BiocManager::install("phyloseq")
microeco	install.packages("microeco")
file2meco	install.packages("file2meco")
ggplot2	install.packages("ggplot2")
ggpubr	install.packages("ggpubr")
ggdendro	install.packages("ggdendro")
magrittr	install.packages("magrittr ")

4. **Download amplicon sequencing raw data (.zip) files for analyses, following this link:**

<https://github.com/RoyDibakar/National-Workshop-Microbiome-Informatics/archive/refs/heads/main.zip>

5. **Download the reference taxonomy file using the following link**

[https://zenodo.org/records/4587955/files/silva\\_nr99\\_v138.1\\_train\\_set.fa.gz](https://zenodo.org/records/4587955/files/silva_nr99_v138.1_train_set.fa.gz)

**Unzip the folder; keep the reference taxonomy file and the FASTQ files in the same folder.**