**NATIONAL WORKSHOP ON MICROBIOME INFORMATICS AT BOSE INSTITUTE**

**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)

1. ***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>

1. ***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>

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