Step2_RNA_Analysis

Shashank Gupta

2023-01-18

Contents

Load all the packages used in the analysis

```
library("ranacapa")
library("phyloseq")
library("ggplot2")
library("stringr")
library("plyr")
library("reshape2")
library("reshape")
library("dplyr")
library("tidyr")
library("doBy")
library("plyr")
library("microbiome")
library("ggpubr")
library("vegan")
library("tidyverse")
library("magrittr")
library("cowplot")
library("dendextend")
library("WGCNA")
library("metagenomeSeq")
library("decontam")
library("RColorBrewer")
library("ampvis2")
library("ggpubr")
library("formatR")
```

Load data

```
raw <- import_biom("/Users/shashankgupta/Desktop/ImprovAFish/exported-feature-table/feature-table_taxon
tree <- read_tree("/Users/shashankgupta/Desktop/ImprovAFish/exported-feature-table/tree.nwk")
refseq <- Biostrings::readDNAStringSet("/Users/shashankgupta/Desktop/ImprovAFish/exported-feature-table/
dat <- read.table("/Users/shashankgupta/Desktop/ImprovAFish/metadata.txt", header = TRUE,row.names = 1,
# Merge into one complete phyloseq object
all <- merge_phyloseq(raw, sample_data(dat), tree, refseq)
```