**Introduction to Data Analysis of Microbial Sequencing in R**

Wednesday, October, 9th, 2019

Florida State University

Instructor: Brian Piccolo, Ph.D., Arkansas Children’s Nutrition Center

**Materials Required:**

1. Computer/Laptop with R installed. R contains a basic text editor that can read the coding script for the workshop, but many people prefer to use RStudio instead. RStudio is an “integrated development environment” that packages both console and script editor in a single window. RStudio has many more features and is widely used by novice and advanced R users. It can be downloaded [here](https://rstudio.com/products/rstudio/download/#download).
   1. Best if [R version ≥ 3.6.0](https://cran.r-project.org/).
2. “FSU 10-9-2019 MicrobSeq Workshop Script.r” file
3. Data files: (can be downloaded at [Github site](https://github.com/bdpiccolo/FSU-Microbial-Data-Analysis/tree/master/Data))
   1. UCDT2DM16SExcel.xlsx
   2. UCDT2DMmetadata.xlsx

**Prerequisite:**

1. Review chapters 1-3 in [accompanied web-book](https://bdpiccolo.github.io/FSU-Microbial-Data-Analysis/index.html).

**Schedule:**

9:00 – 9:15 Opening remarks & introduction

9:15 – 9:30 Installing necessary R libraries and setting working directory

* Script lines 41-72

9:30 – 10:00 Importing data and creating phyloseq object

* Import: Script lines 74-175
* phyloseq: 177-346

10:00 – 10:30 Pre-processing data

* Script lines 348-471

10:30 – 10:50 Alpha-Diversity

* Script lines 473-562

10:50 – 11:20 Beta-Diversity

* Script lines 564-833

11:20 – 11:50 Differential Abundance

* Script lines 836-1175

11:50 – 12:00 Closing remarks

Adjourn by 12:00