**Microbial Diversity and Ecology Lab, Fall 2018**

**Lab 11: DADA2**

In this lab you will go through a tutorial dedicated to high throughput sequencing processing in DADA2. The goal of this exercise is to familiarize you with the basics of DADA2.

You are provided a working environment which contains the products of the some of the longer steps in this tutorial. This will allow you to work through this tutorial during class time.

**##Setting up your session**

Exercise 1 (Line 43-46):

Task 1: Copy the description from the DADA2 help page and record what version you have installed.

Answer:

**###Step 1: Filter and Trim**

Exercise 2 (Line 53):

Task 1: Copy the path you entered to both the forward and reverse reads.

Answer:

Exercise 3 (Line 60)

Question 1: Where would you cut your forward and reverse reads?

Answer:

Question 2: What is the main difference between 16S and ITS reads?

Answer:

Exercise 4 (Lines 87-92): Copy your code for the filterAndTrim function with all of your customizations.

Answer:

Exercise 5 (Lines 101 &102): Copy and paste the pathways to the forward and reverse folders.

Answer:

Exercise 6 (Line 163): View the first 10 columns of your sequence table. Copy the code you used to do so here.

Exercise 7 (Lines 171 – 178): Record the number of reads retained through the entire pipeline. What function did you use to get this number?

Answer:

Exercise 8 (Lines 184-188): Download the Sliva 128 database and move it to your desktop folder. Change the pathway in line 187 to the correct location. You will need to include the name of the database in your pathway here.

Answer:

Exercise 9 (Line 190): View the first 10 lines of your taxonomy table. Record your code and what families are represented.

Answer:

Exercise 10 (Line 216): Install the Phyloseq package. What code did you run to accomplish this?

Answer: