One Health Workshop: mOTUs

# Session 1: 9:00 – 10:00

*Shini to write*

# Session 2: 10:30 – 12:00

Hans will lead this session. The first aim is to get everybody connected to a virtual machine and to euler. The second is for the students to be able to navigate Unix and understand the requirements for and how to install mOTUs.

### Introduction (5 mins)

Overview of the session. Demonstrate how to connect to a virtual machine and show the software available there (Moba and R).

### Students Connect (15 mins)

This should give enough time to troubleshoot the inevitable problems there will be connecting to the virtual machines.

### Connect to Euler (10 mins)

Demonstrate connecting to the server when most students have been able to connect to a virtual machine and then they can proceed to do the same. By the end of the first half hour we hope to have everyone connected to the resources they require.

### Unix Introduction (30 mins)

*Hans to write*

### Installation of mOTUs (30 mins)

*Hans to write*

# Session 3: 14:00 – 15:30

Hans will begin this session, covering read quality filtering. Chris will then take over for the use of mOTUs. The aim is for the students to understand how to go from their raw data through to a mOTUs output table, and which parameters can be changed to modify this output.

### Introduction (15 mins)

Overview of the session. Discuss the motivation behind read quality filtering and demonstrate bbduk. Students then follow.

### Basic Use of mOTUs (30 mins)

Show that mOTUs can be run on a single sample without any difficulty. Then repeat, but breaking down the process into steps. Show and explain the output file. Follow up with multiple samples and look at the new output. Show that different runs can also be merged. Students will follow via exercise.

### Advanced Use (30 mins)

Discuss each of the optional output parameters, particularly explaining the difference between relative abundance and counts, and the different taxonomy levels. Then move onto the effects of modifying the sensitivity parameters and have students produce output for both extremes, giving three sets for later comparison.

### Comparing Output in R (15 mins but running into the next session)

Introduce the prewritten script and explain how to move the data to the virtual desktop for use in R-Studio. The script will read in the data and produce some simple table/graph that shows the differences between outputs. Students should be able to see the effects of modifying the sensitivity parameters.

# Session 4: 16:00 – 17:30

Chris will continue into this session, with Hans finishing with a demonstration of database extension and showing the students where they can put the data they want to be able to access after the workshop is over. Shini gives closing remarks at the end of the Q&A.

### Analysing the Output (60 mins)

The output comparison will run over into this session as necessary. The students will then be shown where the pre-computed mOTUs data is, and the exercise will take them through some very basic analysis such as computing a distance matrix, hierarchically clustering samples to highlight how clusters correspond with metadata, and a comparison between metaT and metaG followed by looking into some of the interesting rare overexpressed OTUs.

### Database Extension (20 mins)

Since this is complex, Hans will just demonstrate how this can be done and show how the output from mOTUs changes as a result. The students will have the opportunity to move any data they wish to look at after the workshop to a public space.

### Q & A (10 mins)

We finish with a question and answer session (though they are encouraged throughout the day) to cover any topics not already discussed, with closing remarks by Shini.