**Practical assignment**

**Module topic: 16S rRNA analysis ppeline**

**Contact session title: Taxonomic classification and alignment using the dada2 pipeline**

**Trainer: Imane Allali**

**Participant:** <*write your name here>*

**Date:** <*write today’s date here*>

**DADA2 workflow**

**Introduction**

The aim of this module is to give you a general understanding of the 16S rRNA analysis pipeline using the DADA2 pipeline and to be able to run the complete DADA2 workflow.

**Tools used in this session**

*The link of the tutorial:* [*https://iallali.github.io/DADA2\_pipeline/16SrRNA\_DADA2\_pipeline.html*](https://iallali.github.io/DADA2_pipeline/16SrRNA_DADA2_pipeline.html)

**Please note**

* **Hand-in information** please upload your completed assignment to the Vula ‘Assignments’ tab. Take note of the final hand-in date for each assignment, which will be indicated on Vula.

**Task 1: Construct Sequence Table**

**Task 1: instructions**

*Under the construct sequence tablesection. You need to create the ASV.*

1. *How many ASVs were identified?*
2. *What the minimum length and the maximum length of your sequences?*

**Task 1: participant’s answer**

<*start typing your answer here*>

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**Task 2: Chimera Checking and Removal**

**Task 2: instructions**

*Under the chimera removal section. You need to identify the number of chimeric sequences and removed them.*

1. *how many chimeric sequences were identified?*
2. *How many ASVs were left after chimera checking and removal?*
3. *What is the percentage of the non chimeric sequences out of the total?*

**Task 2: participant’s answer**

<*start typing your answer here*>

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**Task 3: Track your reads**

**Task 3: instructions**

*Under the track reads section. You need to know how many reads made it through the tutorial.*

1. *Could you list how many reads were in the input, filtered, denoisedF, denoisedR, merged and nonchim for Dog8, Dog17, Dog24, and Dog31.*

**Task 3: participant’s answer**

<*start typing your answer here*>

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**Task 4: Assign Taxonomy**

**Task 4: instructions**

*Under the assign taxonomy section. You use the results of the taxonomy assignment to have an overview of your different taxonomic classification.*

1. *Could you list the phylum that were identified in your sequences?*

**Task 4: participant’s answer**

<*start typing your answer here*>

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