

Using DADA2 to analyze high-throughput amplicon sequencing data

April 3rd, 2019 2-4 pm [CIRES Rm. S274](#)

Fierer Lab PhD students Angela Oliverio and Hannah Holland-Moritz will lead a workshop for those who work with high-throughput amplicon sequencing data and are looking to implement DADA2 into their workflow. Come learn with us!

[DADA2](#) is a free, open-source, amplicon-processing pipeline implemented in R. DADA2 utilizes machine learning to identify exact sequence variants. It is easy to install and can be used to process entire MiSeq runs on a personal laptop. This 2-hour workshop will take you from installation to sequence table.

Workshop Schedule:

- 2:00 – 2:30 Install software
- 2:30 – 3:00 Pipeline overview
- 3:00 – 3:40 Run the pipeline
- 3:40 – 4:00 Questions and open discussion

To fully participate in this workshop:

- Please bring a laptop with Mac OS or a computer with access to a Unix-based terminal
- You must have the ability to install software on the computer you bring.
- If you are using a Mac OS and do not have Xcode installed, please follow the instructions [here](#) to install it before the workshop.

If you are interested in trying to install any of the software ahead of time or see a preview of the pipeline, please follow the links below.

[idemp](#)

[cutadapt](#)

[DADA2](#)

[Fierer Lab DADA2 Pipeline](#)

Questions/Comments?

Please contact Angela (angela.oliverio@colorado.edu) or Hannah (hannah.hollandmoritz@colorado.edu)