

Preparation for dada2 workflow workshop

To make sure we can actually run through the entire script with plenty of time for any explanations of the code and possibly extensions into downstream analysis, having the key programs and packages downloaded would be beneficial. Here is a list of things it would be useful to have done before the workshop (or whatever it is):

1. Install R. I am using the latest version (v3.4.2) which can be downloaded [here](#)
2. Install RStudio. I will be using RStudio to demonstrate things and as such will be useful if we are all using the same things. RStudio can be downloaded [here](#)
3. Install the packages we will be using. I have attached a script that will hopefully make this straightforward. You will want to install the most up to date versions of the packages hosted on Bioconductor (version 3.6). For people who have never used Bioconductor, I imagine this will happen automatically. For others, at the end of the script there is code to update Bioconductor. Press y whenever asked.
4. Take a look at the GitHub repository [AB_dada2_pipeline_R](#). Download the folder and place somewhere on your laptop. The folder layout is needed
5. If you want to run the code on your own data, place your data in `data/raw_fastq`
6. Bring biscuits or cake. This is the most important prerequisite.

Disclaimer: I have only ran this a few times so I am likely know not much more than you! But lets see how we get on...