

Meeting #5 Agenda

Maddy to take minutes

1. Discuss the specifics about how to begin with the first steps of our project, what issues we might encounter, how to solve them, and general logistical questions.
 - a. By next week's meeting (Nov 1st) we intend to
 - i. Have added a mom BMI column to our filtered table using R
 - ii. Split that filtered table into two separate tables based on BMI categories (26 and under or over 26)
 - iii. Generate the relevant diversity metrics to complete experimental aim 1A in its entirety

Minutes

1. Pivot wire - program in the code he sent us a while ago - this is how we will add the BMI column
 - a. Save the table with the mom bmi column added as an object so you can easily use it going forward rather than re-generating it each time
2. One person works on alpha, one works on beta - get a rough skeleton of the code you want to use done right away
 - a. Get code for all experimental aims done asap and then actually run the stuff
 - b. Next three meetings data based, last two meetings about the manuscript itself
3. Could even use the mouse dataset as a test dataset to draft the script and then once it's done you can just swap out the variables for our actual data
4. One person on alpha, one person on beta, one person on DeSeq and one person on PieCrust
 - a. Maddy and Nicole on PieCrust and alpha
 - b. Hayley and Emily on beta and DeSeq

How you want to visualize your stuff - start thinking about this because it'll take more time than you think

Eg. text size, preventing text overlap, colours, shapes

Link Avril sent about ggplot formatting - go back through Canvas mail
Where he sent a bunch of cheatsheets

DeSeq - main output is a barplot

Generate a scatter plot as a supplementary figure to the barplot so you can visualize individual points

- Let him know once we get to this point b/c he can help make this go faster

Ggpiecrust2 - runs DeSeq and PieCrust simultaneously (?) in R

- Can maybe make plots with it?

DeSeq is not the only option for differential abundance in this package - make sure you actually check what it is your code is running b/c it might not be DeSeq by default

- You'll have to specify it to use DeSeq, otherwise you can use whatever other program it has by default but you need to know what it is and state that in the manuscript

A lot of packages like ggpiecrust2 might have sample datasets you can use - check this out to see

Try to run the vignette for the packages you are unfamiliar with to learn what the output looks like

- Most packages will have a github
- Google name of package and follow the github link that comes up to find vignette

Goal: Bare skeleton code for all the analyses by next meeting (Nov 3)