Feb 5, 2024 - Agenda

1:15-1:25 - finalize research question
1:25-1:45 - discussion of next steps: project proposal planning, literature review and types of downstream analysis
1:45-1:55 - Github and project documentation review
1:55-end - remaining questions for Chris about assignments, R, etc

Parkinsons - what are the effects of dopamine agonists pramipexole and amantadine, and monoamine oxidase-B inhibitor rasagiline on PD patients?

Idea: Look to see if treatments brings microbiome back to what normal person would have. Some microbes associated with health vs disease.

Idea: look at different BMI groups or different alcohol consumption categories. Do these factors affect response to treatment?

Aim 1: getting people with multi-treatments into their own group
First do α β diversity: control, PD untreated, PD treated (1, 2, 3, 4), PD combo

- Min sample size = 5 individuals

Move forward with only interesting group(s)
Aims 3-5: do all taxonomic analyses: core microbiome, indicator taxa, differential abundance

Aim 6 (optional): confounding factors. What other variables could affect efficacy of treatments

Data needs to be processed before proposal → aka complete aim 1

- Add 1 column: treatment = healthy, PD_untreated, drug1, drug2, drug3, drug4, drug5(combo)

Look at efficiency on how these treatments are recovering the microbiota of PD patients

Make another folder for R script.

- Follow the same process as qiime.

Documenting qiime process: make a .sh script

- Another folder in the qiime folder for qza files etc…

6+ combinational →

- We can keep a low sample size and keep it as a limitation of the study
- May end up being a supplementary figure

Only have ¾ drugs → no need for MVA

1. Processing/filtering
    a. Stratifying by treatment/multi-drug treatment
2. Basic alpha and beta alpha diversity analysis in these
    a. 5 groups: healthy, PD untreated, 4 drug groups
    b. From the alpha/beta → see what groups are interesting and move forward with those
3. Do ALL the taxonomic analyses
    a. Core microbiome, indicator taxa, differential abundance
4. Explore confounding factors

End presentation " we looked at how diff treatment plans → found only 1 was interesting → went deeper to see what bacteria are actually changing in these patients

- Must have QIIME processing done before proposal submission because part of the proposal is an overview of the dataset
    - Need to complete aim 1 before it
    - Generate diversity metrics in QIIME and R
    - Create a single column with our 7 categories already labeled

<u>Github</u>

- For QIIME processing
    - Have a folder for QIIME and folder for R
        - Have a .sh script for QIIME where it has all of our commands
        - Have another folder within QIIME for .qza, .qzv files
        - **You can edit the .sh file on github**
- No specifics for how to interface it
- Within R folder
    - Have different folders for the different aims/R analyses
- Stay on main branch?
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