

Mar 18, 2024 - Agenda

1:15 - 1:35 - DESeq2 presentation (Cayden) and discussion to interpret results

1:35 - 1:45 - Core microbiome presentation (Alicia)

1:45 - end - Discuss next steps, figures for paper and presentation

DESeq used more to comment on up/down regulation of bacteria that may be health/disease associated.

- Need to compare with core microbiome analysis

***Presenting order

- **Alpha beta diversity showed no significant differences → changes are more minute than compositional**
- **Core microbiome trends with one getting rescued**
- **Indicator species different lists with 3 and 6**
 - **Differences between treatment 3 vs treatment 6**

***Barchart with actual abundance values for *Prevotella* see abundance across different groups.**

Different naming schemes show different genus, but may be part of the same family. Definitely different species. E.g. *Bacteroides*.2 is distinct compared to *Bacteroides*.1

Genus with .1 are distinct enough to be categorized differently. Treat them as separate. Uncultured -> don't know what the genus is

Each result should have a conclusion. Could be simple but want to go into detail

- E.g. **Drug 3 influences/downregs PD associated bacteria**

Major result from DESeq: *prevotella* downregulation.

- Despite all drugs downregulating *prevotella*, actually these drugs have different effects. For example: core microbiome, indic species results

April 8 meeting: finalize presentation and present it to Chris for feedback

Change graph titles to be more informative

Core Microbiome stick with 2% but look at *g_Faecalibacterium*. Don't mention other %s

Core - which of these bacteria are the same in all the indiv

DESeq - shows effect of change

Conclusion:

- Treatment 4&6 may be effective in terms of bringing microbiome back to normal

- Show how the drugs bring g_Faecalibacterium back to normal levels compared to PD patients and healthy individuals
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Furhter analysis:

- Abundance of specific bacteria