**Mar 18 Notes**

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

Further analysis:

* Abundance of specific bacteria