Feb 26 meeting notes

- Set deliverables for next week?
- Each meeting someone different presents what they did
- Put timeline chart on github readme
- Next immediate thing: look at stats for alpha diversity for aim 2
    - Some may be significant/interesting
    - Will give idea of which drugs are more or less important → follow up with core microbiome and indicator taxa analyses
    - Plot richness function to make the graphs (part of phyloseq package)

- Try to do aim 3 as well
- Use rarefied final phyloseq object for core, indicator, deseq??? → CHRIS WILL GET BACK ON THIS. **ASSUME WE DONT REFY FOR NOW**
- For α stats, use kruskal-wallis
    - Do kruskal wallis + tukey/hsd post-hoc test
- For β diversity, run with all the distance matrices (brae curtis, jacquard, weighted and unweighted)
    - PERMANOVA → 4 different stats total
    - If including one, weighted unifrac would be best → but probably not including any

<u>Microbiome</u>

- Run core microbiome for all 7 groups
    - Decide on detection and prevalence limit
    - Good way to decide: use a package (CHRIS WILL EMAIL TO US, WITH SCRIPT) to generate heatmap. Has different prevalence and detections, can see how core microbiome changes as you adjust parameters
    - Create venn diagram and UpSet plot for next week
        - Ali can create UpSet plot once code is completed

<u>Indicator species</u>

- David will lead → leave for next week
- Looking at the indicator taxa table from group 2 (PD) vs all the other groups
    - Looking at if any species that are missing/present in drug treatment groups vs PD group
    - Indicator taxa table tells us which species are missing
- Table 2 vs 3, 4, 5,
    - Which bacterias present in 3, missing in 2, or other way