**Oct 29 meeting minutes**

1. **Review proposal feedback**
    1. How did we do? Any areas where we exceeded or could improve? Any urgent changes to be made to any methods/aims?
    2. Plan for revision and resubmission based on feedback
        - Make changes in the introduction
        - Be more intentional about each aims to connect with the broad question
        - Methodology – add indicator taxa in the first aim
        - Set a meeting: divide workload to make edits (preferably different section compared to what we worked on)
2. **Present Figures**
    1. Preliminary findings/trends
        - **Aim 1 alpha diversity**: no sig differences, but do stats on Chao1, Shannon and InvSimpson to confirm
            - Maker the graphs look nicer
            - For manuscript include: observed, shannon, chow1
            - Use colours to make it look visually appealing
        - **Aim2 alpha diversity**
            - Differences between certain groups
            - Can say smoking has an impact on microbiome
            - Smoking does not impact old people
            - Do stats on: Observed, Chao1, Shannon
                - Shannon: PMS/smoker/old start to decrease
                    - Shannon: richness and evenness
                    - Chao1: richness
                    - Observed: richness
        - **Beta diversity**: do Permanova analysis
        - **Aim 3: Core microbiome analysis:**
            - Maybe change 0 to 0.01 in case there are rare species
            - 80 is okay but can go as low as 50
                - Chris said try 50% as another option
            - There are at least 2 core species in all
            - Young MS nonsmokers have a lot more distinct species compared to other groups
            - Old MS: look into literature that relates age to decrease in microbiome diversity
            - Check the list of species between Young MS smoker vs nonsmoker
            - Smoking still influences the core microbiome when you're older
            - Asha can include all the 8 groups in the vein diagram but figure will be produced as an UpSet bar chart
                - From there, discuss 2-3 core microbes and why they may be abundant
    2. Which diversity metrics should we narrow down to?
    3. Plans for moving forward
        - Can start on literature (esp. Aim2 alpha diversity/beta diversity) and interpret why the data is shown like that

Continue with the aims we are working on? Is it best to start on write ups for each section after all analyses are done? We are here ↓

## Action Items For next meeting

1. **Remake Aim1/2 alpha diversity figures to only include the selected parameters (look in notes above)**
   a. **Aim1 beta diversity add ellipsoids for where clusters are present**
   b. **Aim1 add indicator taxa**
2. **Do stats on alpha diversity figures**
3. **Redo core microbiome analysis with 0.01 and 50%**
   a. **Use the UpSet function in R**
4. **Interpret the data (learning what the ASVs are) for the manuscript**
5. **Revise proposal**
6. **DeSeq for next week if time, but focus on completing Aim1 and Aim2**