**November 5 meeting agenda**

1. Review proposal revisions
   1. Introduction
   2. Random forest
      1. Markers are input; telling us different things with different inputs so its telling us two ways
   3. Does intention for each aim connect better with the broad question
      1. Sentence that
   4. Research objectives
      1. Redundancy is ok because each part is marked individually. About 1 page is ok
   5. Overall comments & suggestions since last week
2. Revised figures
   1. Aim 1 alpha diversity
      1. Remade figures with revised parameters; addition of indicator taxa
      2. Theme.classic; geom\_points in box plot overlayed (looks nicer); increase Y-axis
      3. Take max value and \*0.5
   2. Aim 2 alpha diversity
   3. Aim 1 & 2 beta diversity
      1. Add ellipsoids for clusters
   4. Aim 3: core microbiome analysis
      1. Changed to 0.01 and 0.5 (prevalence); plot that was asked by chris
      2. Taxa barplot analysis: get good overview with rare species instead of core microbiome (unique microbes that are highly prevalent and shared between/different between groups); look at all the ASV’s but also could show bottom most rare species (top 80 and bottom 20 as separate plots)
      3. Save coremicrobiome as back up if nothing else works out
3. Moving forward
   1. DeSeq
   2. Literature interpretation for revised figures

**Action Items for next meeting**

1. Theme.classic; geom\_points in box plot overlayed (looks nicer); increase Y-axis
2. Dpi = 300
3. Figures
   1. Aim 1 alpha diversity + beta + indicator species (significance built in)
      1. Eli aesthetic fixes. Otherwise done.
      2. Eli Indicator species.
   2. Aim 2 beta diversity + indicator species (significance built in)
      1. Caro to send code to chris.
      2. Caro Indicator species.
   3. Core microbiome/taxa barplots
      1. Asha
      2. Highlight first 3 columns that are unique in old,PMS
   4. DeSEQ + PICRUSt2 (depending on data if it can be included together)
      1. Poppy + Eli + Burak
      2. LDEX2 : better for microbiome data
      3. Get list of microbes and log fold change; can order it and see which ones are similar from two algorithms to confirm that groups are different
      4. Old PMS NS + Old PMS smoker
         1. Justification of why we’re doing this; age related or more smoking related. Go off of data
   5. Project = niche markers that can be used for random forest