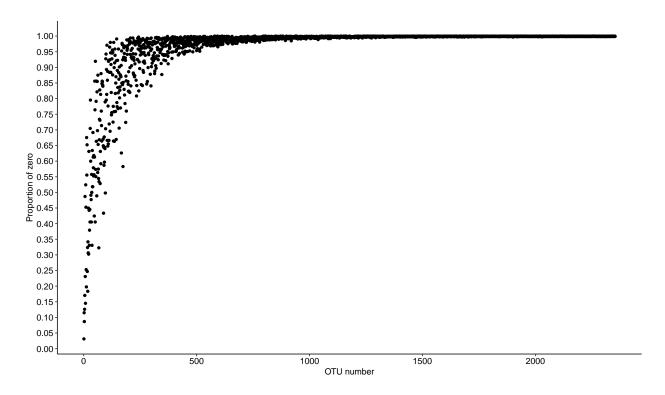
Microbiome Analysis

Olajumoke Evangelina Owokotomo 4/30/2019

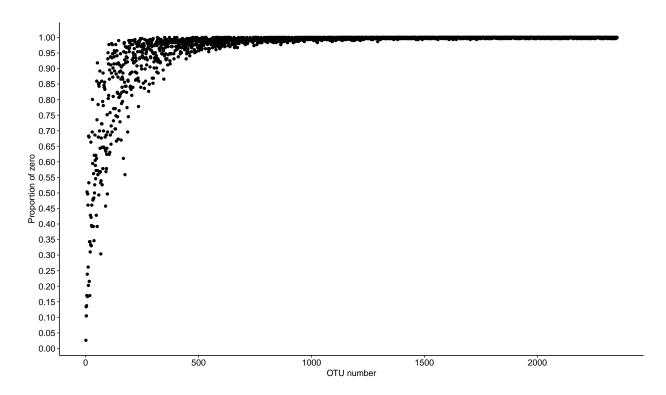
General information

- The dataset is a large phyloseq object saved as R datafile.
- The metadata has been converted to phyloseq format.
- The sample are Crohn's disease patients.
- The CDAI is the standard instrument for evaluating clinical symptoms and disease activity in Crohn's disease.
- Samples are randomized to take PlaceboIV or UstekinumabIV ni the trial.
- Taxonomic assignment of the OTU into 6 taxonomic ranks (Tax data) which are; "Kingdom" "Phylum" "Class" "Order" "Family" "Genus".
- OTU Table contains 2353 taxa and 992 samples for all time point (OTU table).
- 83 information was obtained about the samples which includes their age, sex, race , country, treatment information, CDAI etc.
- 306 samples information was obtained by baseline, 236 at week 4, 261 at week 6 and 189 at week 22. No information about week 8.
- Difference in a subject's initial Crohn's disease activity index (CDAI) at baseline and other time point $\Delta_4 \Delta_0$, $\Delta_6 \Delta_0$, $\Delta_8 \Delta_0$, $\Delta_{22} \Delta_0$.
- Placebo samples were coded as 0 while treated samples were coded as 1.

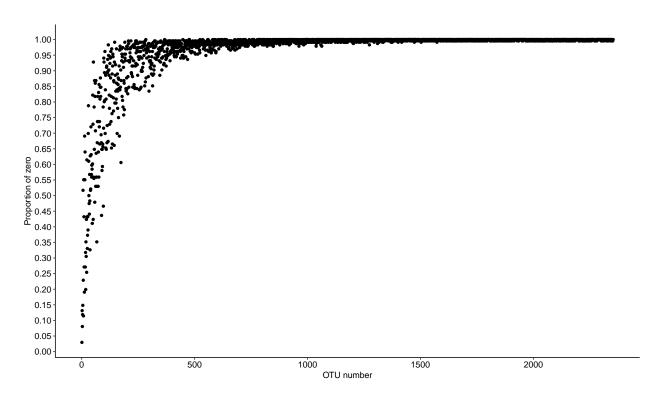
Proportion of zero samples per OTU At all timepoints



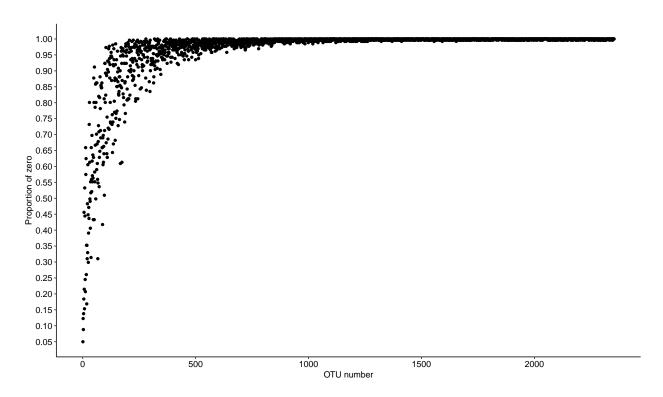
At week 0



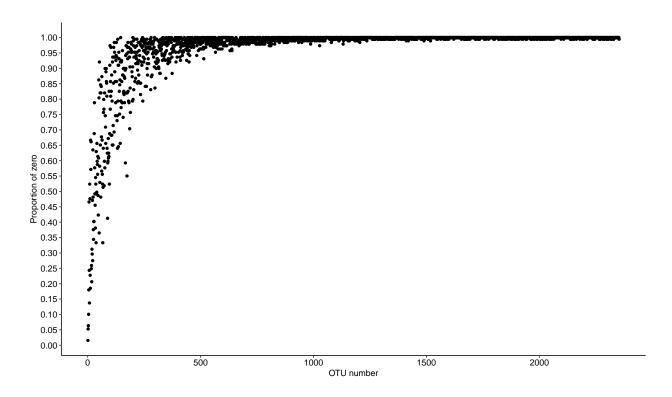
At week 4



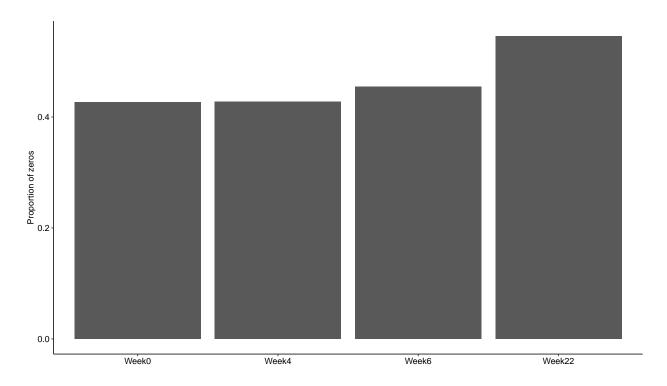
At week 6



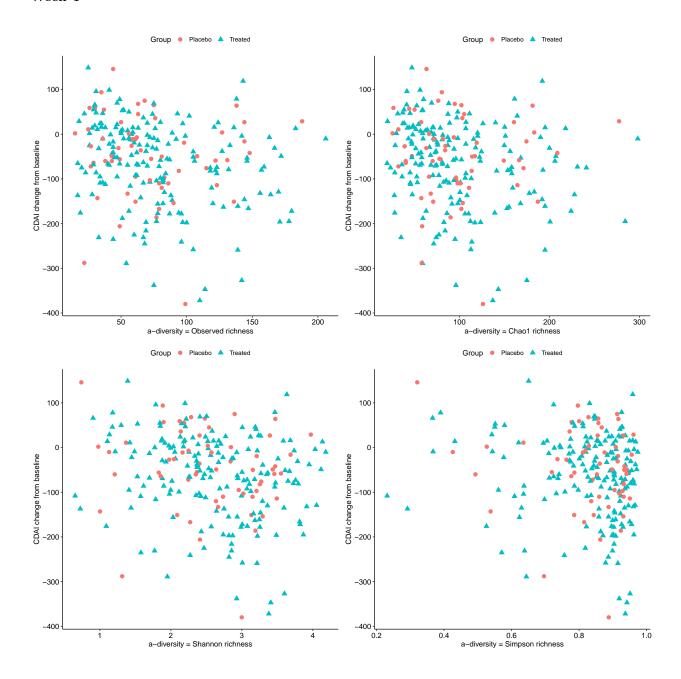
At week 22

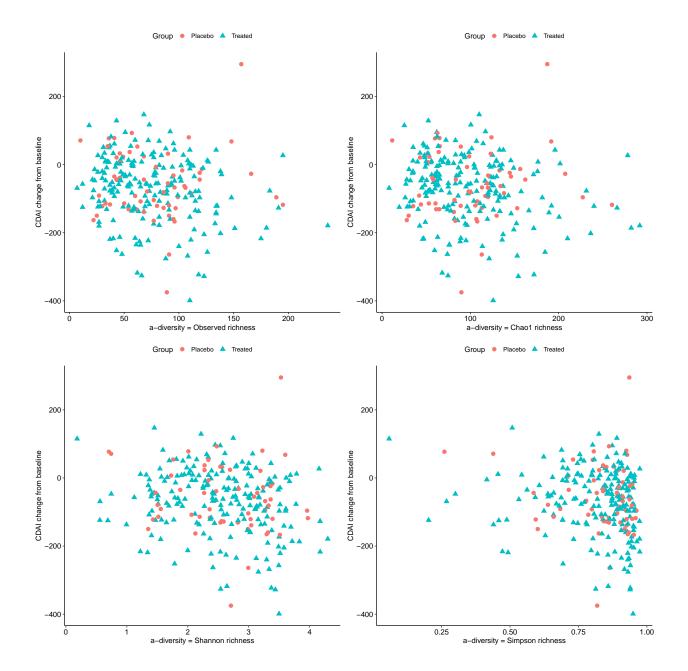


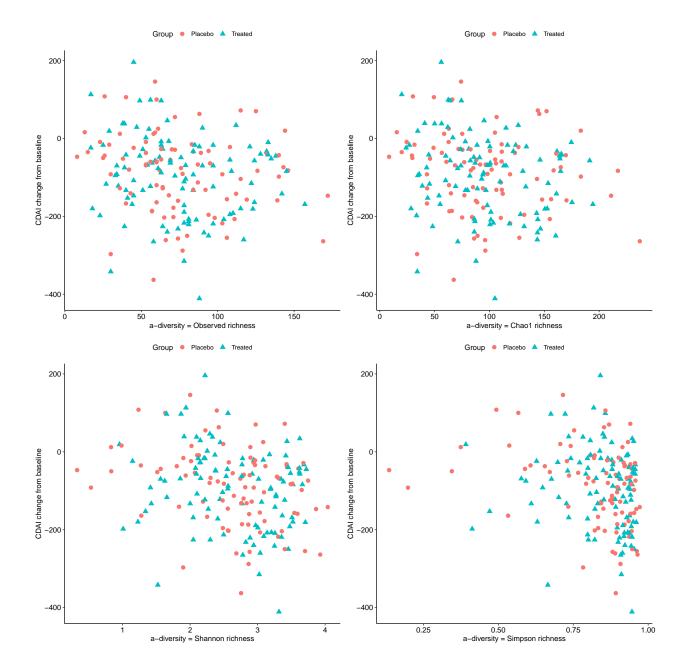
Proportion of OTU per week with zero values for all sample All timepoints



Alpha-diversity plot







Adjusted association from Joint modelling (Response is CDAI change from baseline) $\,$

