

Group meeting [January 28th 2026]

Parties present:

Ryan
Howard
Soroush
Alex
Claire
David (on Zoom)

Agenda made by:

Alex

Minutes taken by:

Ryan

Agenda:

- Decide how we will be breaking our data into groups (HA, NA, or HA & NA).
 - Biological rationale for choosing a specific split?
 - Refer to QIIME2 processed data for group sizes + sample quality by group (i.e., sequencing depths)
- Formalize a research question based on the decision from above.
- Discuss the state of group assignment 1 & assign tasks for the remainder of it.
- Sign up for GitHub accounts & add everyone to the project repo.
- Questions for Claire:
 - How to deal with paired-end reads? Are there standards on allowances for differential trimming of forward and reverse reads?
 - How to deal with the use of multiple forward primers ("7-fold-degenerate primer 27f-YM+3") in general and specifically with regards to training the taxonomy classifier? What primer do I input as the forward primer? Can I input multiple?

Meeting minutes:

Do we need to trim evenly?

- No, reverse and forward reads do not need to be trimmed evenly. Reverse reads are shorter. We want 10-20 base pairs of overlap for the forward and reverse reads.
- Use the 515 and 806 primers. The max length of read for Illumina is 250.

How should we break up our data into groups?

- HA or/and NA. Look into which one has more influence on the microbiome if we do need to choose between the two.

- Current subtypes with greater than 5 samples:
- H5N5, H5N2, H5N1, H4N6 H3N8, H2N3.

Start Analysis by HA & NA

- If no clusters, we can try combining subtypes of similar HAs or NAs.

Outputs we need: table, taxonomy, phylogeny, and metadata file from Qiime to input into R for beta diversity analysis.

Figure out the rarefaction depth

Demux.qzv for 1C.

Photos form white board

How influenza affects the gut microbiome

IN R [Neg ant]

TSS

1500 bases,

[H5N5]
[H5N2]
[H5N1]
[H4N6]
[H3N8]
[H1N3]

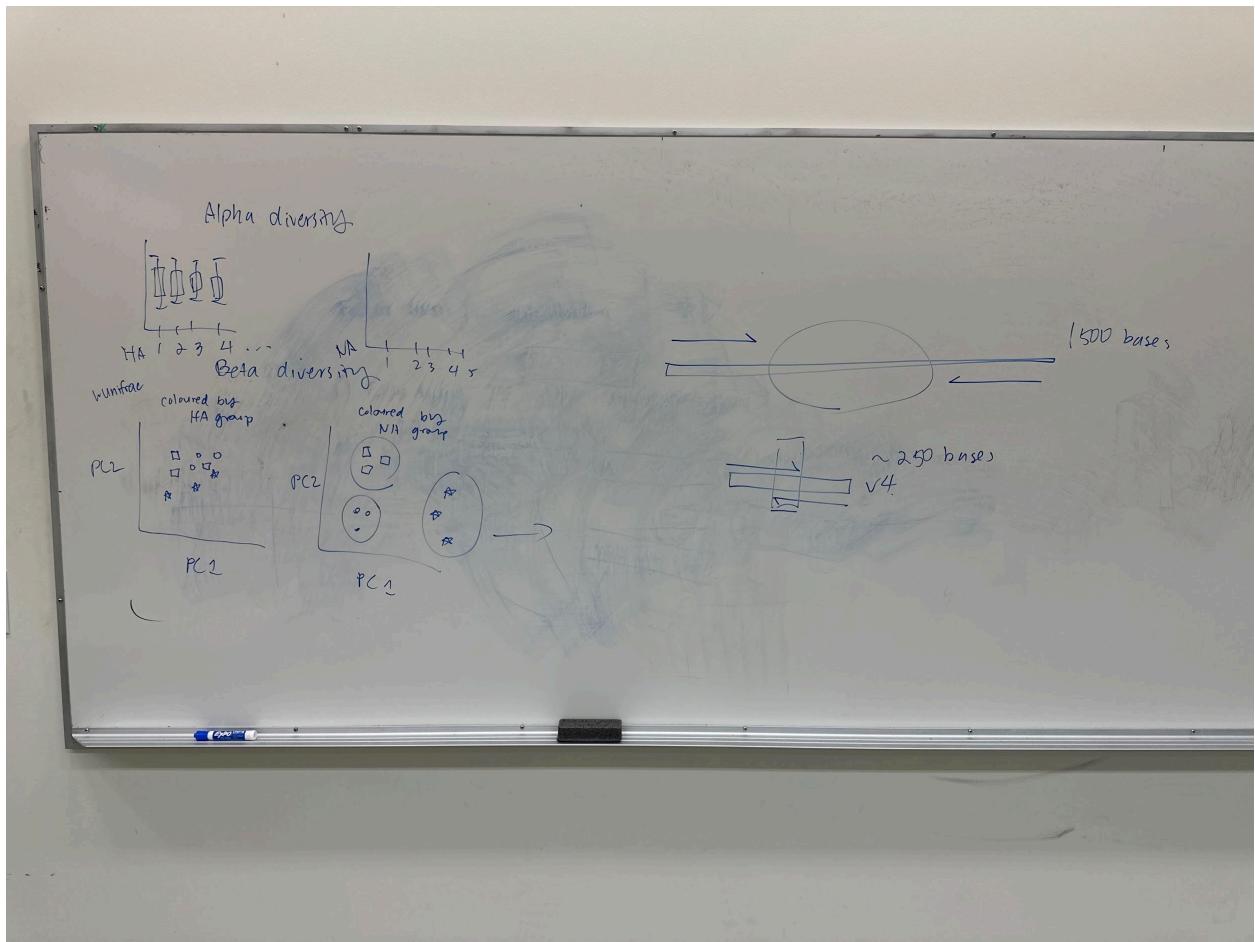
ST

Start analyses by HA & NA
If no clusters seen go general.

by sample

outputs
1) Table.g24
2) Taxon.g24
3) Phylo.g24
Repseq.g24 → maybe.
4) metadata.

Do β & δ div in R.



Action Items:

- Generate a rarefaction curve
- Figure out the rarefaction depth
- Figure out the taxonomy file
- Adjust the trimming?
- Do some reading on how other papers have presented and analyzed data?
- Look at how the different influenza subtypes influence the gut microbiome
- Sign up for GitHub and send it to Alex.
- Finish the group project
- Define the functions of HA and NA for the assignment (Ryan + anyone who took MICB 306)

