Notes from meeting with Austen:

Thinking about pipelines with sterilization as a fixed effect?

Would have to split field and lab spiders separately.

Factors bioinformatically that I should consider:

X ASVs per sample

Prey ASVs

Prey reads

Prey ASV %

Prey read %

Known Diet

Rather than bioinformatics and then sample processing more,

At two scales, how we treat our samples does it matter?

1. Large-scale, total prey and other composition changes
   1. By pipeline AND sterilization (split into field and lab experiments): Total ASVs per pipeline, Species richness, and phylogenetic diversity
   2. By pipeline AND sterilization (split into field and lab experiments): ASVs per sample, prey ASVs, Prey reads, Prey ASV %, Prey read %, Known diet detection (going to drop abundance analyses from PERMANOVA-type stuff, since that seems redundant to the prey ASVs and reads above).
2. Zooming in to the more species-specific analyses
   1. Presence-based Jaccard indicies (Split into field and lab experiments)
   2. Think about the range of things that could be prey based on how common they are in the diet? (looking at core prey/microbiome (ie things that occur across samples) and whether inference of sterilization changes)

Thinking about core microbiomes – is there a way to determine which are the most likely “core diet items” and whether they vary?

Anything that could be prey – literature or field work – any way that you can delimit a core microbiome?

Think about the range of sampling depth – where do we lose diet items? (ANOTHER PAPER)

Rarefaction curves for all pipelines rather than just UNOISE3

Rarefy first:

Then: per sample, what is the Is total number of predator:prey ratio constant across all samples? In which case could you use predator DNA to relativize prey reads based on prey reads?

For this amount of predator read abundance, we get this amount of grasshopper read abundance

New Outline of R Markdown:

Thinking about how we deal with samples, including how we collect them in the field and then how we treat HTS datasets after they are collected (sterilization and pipeline).

How do these change larger-scale interpretation of these datasets?

Including:

X ASVs per sample

Prey ASVs

Prey reads

Prey ASV %

Prey read %

Known Diet