Scripts and included analyses with outputs:

X Split by mesocosm and field and rarefy (might want to have a rarefied and non-rarefied version depending on feedback from austen)

* Outputs: rarefied meso, rarefied field, non-rarefied meso, non-rarefied read

X Assign taxonomies to ASVs

* Output: merged BOLD and NCBI taxonomies with corresponding larger categories of “predator”, “potential prey”, etc.

X Rarefied taxonomically sorted

* Read abundances of known prey, all prey, and predator DNA rarefied

X Raw taxonomically sorted

* Again, read abundances of known prey, all prey, and predator DNA of RAW data

Prey detection Analyses

* Outputs: graphs of prey detection in both environments and summaries of total detection in the population

Abundance analyses – these need to be reconsidered

Richness analyses

* Outputs: graphs of prey richness for field as well as prey composition heat map. Also supplementary figures of the prey dotplots