Table 1: species body size summaries

Table 2: samples on sequencing runs

Table 3: Species and traits

Table 4: Prey identity

Table 5: supp model of number of individuals per sample vs. interactions

Table 6: ASVs with highest reads for positive conrols

Table 7: Size model output

Table 8: Trait use model output

Figure 1: preliminary nano run for sequencing depth

Figure 2: Run to run variation in ASV number/family number

Figure 3: Sequencing depth dada2 vs unoise3

Figure 4: DADA2 cross-run errors

Figure 5: Sequencing depth across samples

Figure 6: Sequencing depth cutoff for low sequenced samples

Figure 7: hist of number of individuals per sample

Figure 8: Number of individuals per sample vs. number of interactions

Figure 9: Positive and negative control ASV numbers

Figure 10: Predator mass-length model by species

Figure 11: Prey phylogenetic tree

Figure 12: Prey size distribution