Intraspecific variation in terrestrial invertebrate predator diets revealed by diet DNA metabarcoding

More of an commentary/critique on how we build food webs?

Body size questions

1. After convo with Elizabeth: Did we capture all the interactions?
   1. Saturation curves
2. In these interactions, is there a relationship between individual predator-prey body sizes?
   1. No – but it looks like predators that are smaller and/or use tools can relax predator-prey body size constraints
   2. Subsetting for that size range, this relationship seems to persist.
3. Is there a relationship between interaction frequency (a proxy for interaction strength) and predator-prey body size?
   1. It seems like most interactions are clustered around body sizes that are really similar to each other (1:1 ratio), and that the use of webs (both with all individuals and subsetting only those in the overlapping size range) relaxes the body size constraints such that more interactions with species that are web-users are with prey as big or larger than predators.
4. Modelling networks with different predator-prey body size ratios and the consequences for web structure (and function?).
   1. Using full dataset of possible prey and predators in our food web what does network look like if:
      1. Prey MUST be smaller than predators?
      2. Pred-prey sizes look similar to those of predators without tools?
      3. Pred-prey sizes mimic those we have based on tool use?
   2. Could do either an unweighted (based on distribution of individual pred-prey interaction ratios) OR weighted (based on the frequency of interactions based on different predator-prey interaction ratios).
5. Do larger individuals/species eat higher trophic position prey?
   1. No? but it looks like there are some interesting things to explore here, especially related to the hunting mode trends of above
6. Is there a relationship between interaction frequency (a proxy for interaction strength) and prey trophic position?
7. Is there ontogeny revealed by metabarcoding data?
   1. Is there nestedness (look at bitartite package)
   2. If not, is it sampling noise or ecological effect (sampling effort curves)
8. Ontogeny explorations
   1. Species part of analysis:
      1. Neoscona
      2. Heteropoda
      3. Pantala
      4. Phisis
      5. Scytodes
      6. SME
   2. Species not part of analysis for different reasons
      1. CEN (pretty low diet family diversity, and seems to be dominated by those predator IDs shared on the run – Tettigoniidae))
      2. EUB (low diet family diversity, and seems to be dominated by those predator IDs shared on the run – Tettigoniidae))
      3. LRS (low diet family diversity and low number of smaples)