**Working title**

Can we use metabarcoding data for food web studies of invertebrate communities or

What is learned from these types of data that complements/revises/boosts other methods?

**Introduction**

Challenge: Invertebrate communities have many cryptic interactions, making it challenging to build interaction data based on real observations. Metabarcoding diet could be a solution in these systems to otherwise inferred or unknown data.

There is a dearth of terrestrial food webs in the literature, due to many historic limitations, one including lack of an ability to capture interactions for many consumers who are invertebrates. This also has the potential to re-evaluate and disaggregate data for aquatic food webs with invertebrate consumers.

Werewolf: If we use metabarcoding data to build interaction data, we want to know that it is giving us information comparable to or better than rule-based or ecology-based inferred or observation-based data.

Silver Bullet: We ask how high throughput sequencing (HTS) diet data of generalist predators compares to traditional link assignment methods for these groups of predators in other food webs (link assignment methods include: a) literature based inference, including feeding rules and interaction reports, b) field observations of feeding links, and c) a combination of these two methods). Specifically, we explore 1) how many links are assigned via HTS molecular diet data compared to these other link assignment methods and 2) the identity of links in terms of key species traits (trophic level and body size) in a HTS molecular diet dataset compared to the identities of links assigned by other methods.

**Questions**

1. Does molecular diet give you more diet resolution (links) than other approaches?
   1. Per species links comparison between published interactions and their collection methods and molecular
      1. Family Level (more data)
         1. Result: When only considering the total number of interactions per predator species without taking into account the total richness of the community, HTS produces more links per species
         2. Result: When considering the underlying family richness of the food web links, all methods perform equally well to each other.
            1. To Do: Supplement: number of diet families for each food web method (NOT sure what I meant by this?)
2. Does molecular diet give you different kinds of links (e.g. functional groups) than other approaches?
   1. Trophic levels and functional composition of links
      1. To Do: family level – a separate model by trophic group offset by the total number of species in that trophic group in the food web
         * 1. To Do: Supplement: bias in HTS? Look at families represented at Palmyra compared to families in HTS data (are we seeing more/fewer predators than would be expected by random chance?)
           2. To Do: Supplement: comparison of literature to isotopic trophic level
3. Does molecular diet give you a different picture of predator-prey body size ratios for a predator species?
   1. To Do: Body size ratios between average predator size and their prey at species level.

**Methods**

Sample collection methods:

How many predators of total predators in Palmyra food web?

Sample extraction, PCR, and sequencing methods:

Sample cleaning, denoising, taxonomic assignment, and rarefying methods:

Literature search:

Looking for datasets of terrestrial invertebrate interactions with the total species richness of the community specified. We used various sources that curate online food webs, including Mangal (through rmangal in R version), Dryad data, NCEAS InteractionWeb Database, and the Global Web Database. For rmangal (accessed July 20, 2020), 11 of 172 datasets included terrestrial invertebrate interactions, and these consisted of 19 individual food webs ranging from a species richness of 8 to 714 for each food web. For Dryad datasets, we searched using multiple search terms (all accessed between June 24-July 1, 2020: “food web” (463 papers), “interaction network” (553 papers), “predator prey interactions” (520 papers), “diet analysis insect” (42 datasets), “diet analysis spider” (16 datasets), “gut content analysis” (41 datasets), “diet analysis invertebrate” (24 datasets)). Of these datasets, 13 reported invertebrate predation interactions and two of these represented interaction data with diet resolution at the family level or lower and also specified species richness of the sampled community. (Laigle et al. 2017, Rohr et al.). Species richness was 878 (Laigle) and 55 (Rohr) species. There were no terrestrial food webs in the NCEAS InteractionWeb Database on our access date (June 2020), and no terrestrial food webs with family-level or lower resolution for invertebrate consumers in the Global Web Database.

Reporting stats:

Number of predators in each study. Number of prey items in each study.