Hypotheses

* Do fungal taxa appear predictably with bacterial taxa?
  + Are these patterns in line/connected to prediction of antifungal function?
* Are co-occurrences species specific or do they vary by geographic regions?
* Maybe – do these patterns correlate with pathogen-caused mortality rates?

The Data

Skin swabs were collected from *Notophthalmus viridescens* from 20 sites across the Eastern United States. Sites range from Pennsylvania and New York to Virginia. DNA extracted from swabs was sequenced for the ITS or 16S rRNA marker gene regions for fungal and bacterial identification, respectively.

Types of Analysis

**MAIN:** Co-occurrence networks based on presence absence

* Compare looking at network parameters (do we have more spread out or tightly clustered networks in some places vs others?)
* Look at strength of co-occurrence for specific taxa (not entirely sure how to do this yet, still looking into methods)

Also look at things like alpha and beta diversity and how that changes by location

Depending on what I can dig up, may be interesting to also throw in some factors like soil characteristics/type, av temperatures/seasonal ranges, precipitation, etc.