Project overview and exploratory plots for GMPD group

How do host and parasite traits predict parasite species richness across host threat levels?

Overall, we predict parasite species richness will decrease when hosts are classified as more threatened.

However, we predict this general pattern might not be the same across all host and parasite traits.

Host traits we are interested in studying include:

- host threat status (either binary or grouped IUCN levels)
- group size
- population decline

Parasite traits we're interested in include:

- type (bacteria, virus, protozoa, etc.)
- transmission mode (close, non-close, vector)
- host breadth (mpd)

Data

Host-parasite pairs: Records of parasitic organisms reported from free-living mammals were obtained from GMPD.

Parasite traits: Host specificity (whether present in one or more hosts), transmission mode (close, non-close, VBD), and type (virus, protozoan, fungus, arthropod, helminth, or bacterium) were taken from GMPD. Host breadth (mpd across host spp) was taken from Park et al. (2018?) but TBD.

Host traits: Host traits were obtained from Pantheria and Phylacine.

Data were joined by host species names and filtered by hosts with records in GMPD.

```
##    hostName         dietBreadth     habitatBreadth    maxLongevity
## Length:19587      Min.   :1.000    Min.   :1.000    Min.   : 60.0
## Class :character  1st Qu.:1.000    1st Qu.:1.000    1st Qu.:204.0
## Mode  :character  Median :2.000    Median :1.000    Median :262.0
##                   Mean   :2.891    Mean   :1.197    Mean   :293.2
##                   3rd Qu.:5.000    3rd Qu.:1.000    3rd Qu.:354.0
##                   Max.   :7.000    Max.   :3.000    Max.   :744.0
##                   NA's   :2409     NA's   :3304     NA's   :2254
##    popGrpSize        socGrpSize       popDenChange       Order.1.2
## Min.   :     1.0   Min.   :  1.00   Min.   :-999.000   Length:19587
## 1st Qu.:     5.5   1st Qu.:  2.25   1st Qu.:   0.040   Class :character
## Median :    30.0   Median : 12.00   Median :   0.060   Mode  :character
## Mean   :  8029.4   Mean   : 14.37   Mean   :  -4.293
## 3rd Qu.:   500.0   3rd Qu.: 17.50   3rd Qu.:   0.110
## Max.   :100000.0   Max.   :110.00   Max.   :   0.440
## NA's   :16457      NA's   :11752    NA's   :2891
##   Family.1.2        Genus.1.2         IUCN.Status.1.2
## Length:19587      Length:19587      Length:19587
## Class :character  Class :character  Class :character
## Mode  :character  Mode  :character  Mode  :character
##
```

```
##
##
##
##       Mass.g              Group            parasiteName
## Min.   :      42.5   Length:19587       Length:19587
## 1st Qu.:   6000.0   Class :character   Class :character
## Median :  27939.1   Mode  :character   Mode  :character
## Mean   :  90973.8
## 3rd Qu.:  77874.4
## Max.   :2949986.3
## NA's   :789
##    ParType             ParPhylum          Prevalence        HostsSampled
## Length:19587       Length:19587       Min.   :  0.000   Min.   :    0.0
## Class :character   Class :character   1st Qu.:  0.100   1st Qu.:    9.0
## Mode  :character   Mode  :character   Median :  0.310   Median :   27.0
##                                       Mean   :  0.433   Mean   :  114.7
##                                       3rd Qu.:  0.714   3rd Qu.:   74.0
##                                       Max.   :100.000   Max.   :62650.0
##                                       NA's   :3164      NA's   :2683
##  SamplingType        HostEnvironment      Citation           parRich
## Length:19587       Length:19587       Length:19587       Min.   :   1.0
## Class :character   Class :character   Class :character   1st Qu.:  64.0
## Mode  :character   Mode  :character   Mode  :character   Median : 155.0
##                                                          Mean   : 362.8
##                                                          3rd Qu.: 531.0
##                                                          Max.   :1623.0
##
```

This left us with 19587 rows of data.

Statistical Analyses

Type of model/overall modeling scheme: TBD

- Because carnivores, primates, and ungulates have different life histories, ecologies, and predictors of exitinction risk, we will conduct models separately for each group, though the number of hosts per parasite (specialist/generalist variable) will be taken from merged host-parasite lists across all three groups.

Controling for uneven sampling: To control for uneven sampling of parasites among hosts, we will include as a covariate the number of unique citations per host (Altizer, Nunn & Lindenfors 2007). Note: could also try # of individuals sampled per host.

Details of model: * Variables will be checked for colinearity * Which packages used for which analyses: TBD * Whether to account for phylogenetic signal in residuals: TBD

Sensitivity analyses

- Reducing models by taking out predicts with p>0.1 and refitting with sampling/phylogenetic bias: TBD
- But threat status & citations will be forced into all models
- Could do bivariate model with threat status and citation count to explore effect of threat status in absence of ecological covratiates
- Others?

Results:

- Pattern of parasite spp richness across threat level (violin plot)
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