Supplemental Analysis

ANONYMIZED

Phylogenetic Specialism

Here we quantify the phylogenetic specialism of frugivores. To do this, we'll employ the `ses.mpd()` from the `picante` library. This function allows us to use a null model of our choice to find the standard effect size of pairwise distance in communities. In our case, we're interested in pairwise mean phylogenetic distance, and our "communities" are the total sets of plants that each frugivore interactions with. We employ an independent swap null model, where the tip labels of the underlying phylogenetic tree are effectively swapped a given number of times (Gotelli, 2000).

```r
set.seed(1)
load("../Data.nosync/DataSources/BIEN_subtree.Rda")
# Create cophenetic distance matrix
dmatrix <- stats::cophenetic(BIEN_subtree)
# Standardize by the maximum value
dmatrix <- dmatrix/max(dmatrix)

# String manipulation so tree tip names match
birds$plant_Tips <- gsub(pattern = " ", replace = "_", x = birds$Plant_Species)
# Only include plant species for which phylogenetic info is
# available
birds_phylo <- dplyr::filter(birds, plant_Tips %in% BIEN_subtree$tip.label)

comm <- as.data.frame.matrix(table(birds_phylo$Frugivore_Species,
    birds_phylo$plant_Tips))  #Binary, unweighted intraction matrix
# The main function. Randomly swap tip labels 999 times and
# see whether the observed sets of plant interactors for
# each species is more phylogenetically clustered than this
# assumed distribution
test_mpd <- picante::ses.mpd(comm, dmatrix, null.model = "independentswap",
    abundance.weighted = FALSE, runs = 999, iterations = 1000)
# Remove singleton species (can't compute a phylogenetic
# distance)
phylospec <- dplyr::filter(test_mpd, ntaxa > 1)
# Remove singleton species (can't compute a phylogenetic
# distance)
sig <- nrow(dplyr::filter(phylospec, mpd.obs.p < 0.05))
print(sig)
```

```
## [1] 9
```

We see that the number of frugivores whose plant partners are more significantly related than expected compared to a random draw is equal to 9 (The exact value may change slightly when the seed is changed due to the stochastic nature of the model, but the results should be qualitatively similar each time)

Calculating the number of unqiue species in the dataset

In our dataset, we observe interactions between 242 unique frugivore species and 458 unique plant species.

Degree Distributions of Mutualistic Partners
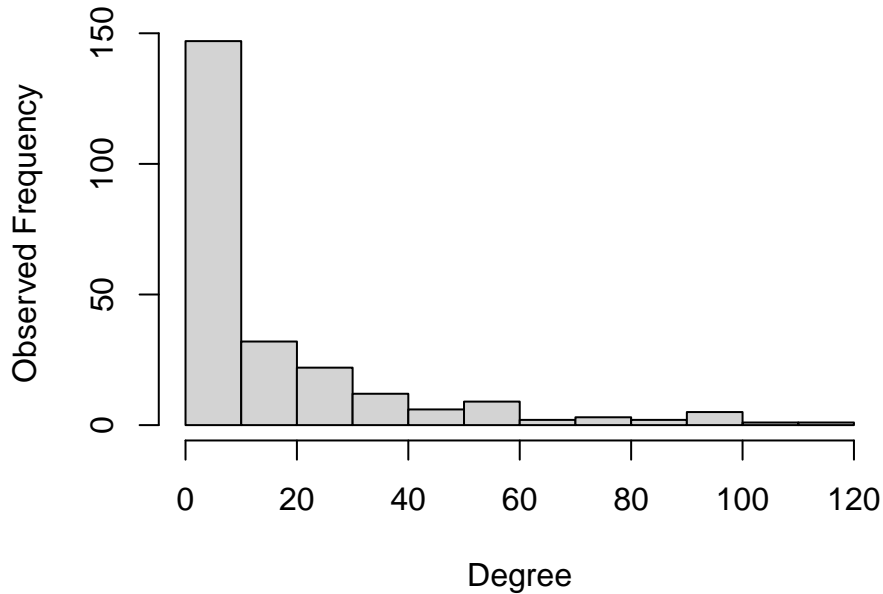
Figure S1: Observed degree distribution of avian frugivore species included in our analyses. X-axis represents node degree, or number of unique partners. Degree for frugivores ranged from 1 (53 species) to 120 unique plant interactions recorded for *Turdus rufiventris*; median frugivore degree was 5.
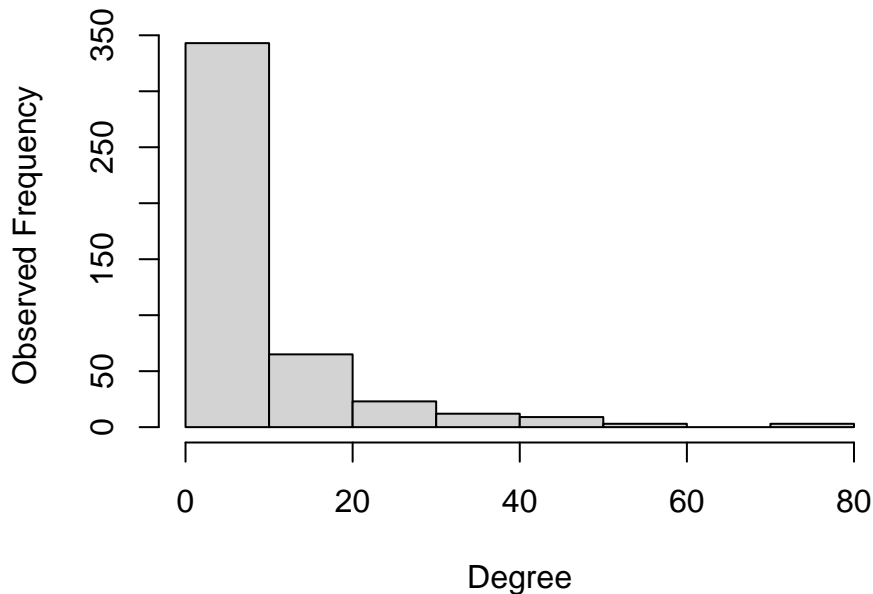
Figure S2: Observed degree distribution of avian frugivore species included in our analyses. X-axis represents node degree, or number of unique partners. Degree on average tended to be lower for plants than frugivores; plant node degre ranged from 1 (128 species) to 80 unique frugivorous interactions recorded for *Myrsine coriacea*; median plant degree was 5.

References

Gotelli N.J. (2000) Null model analysis of species co-occurrence patterns. Ecology, 81, 2606-2621