The little things network paper – summary of results

(Using only the two taxa for which there are networks, using only the pollinators caught on flowers)

**First question: Does body size affect the network role of species, and does this effect, or body size itself, differ between pollinators and herbivores?**

Does body size affect network role? For a suite of metrics, there seems to be a quadratic relatinship, such that intermediate body sizes have lower values for roles pertaining to the number of connections with others in the network (Fig. 1).



Figure 1: Response of different network metrics to body size of pollinators and herbivores. In case of participation (connectivity among modules), relationship was non-significant for herbivores and only quadratic term was significant for pollinators. Only quadratic term for closeness was significant for pollinators. All other models had negative first order and positive 2nd order polynomial terms, and polynomial provided better fit than linear model.

Body size itself not significantly different between herbivores and pollinators:

ks.test(herbsizes,polsizes) # D = 0.080642, p-value = 0.8268

wilcox.test(herbsizes,polsizes) # W = 10800, p-value = 0.6224

Can also include your Bayesian stuff here.

**Second question: Does body size affect ubiquity among patches?**

There was a negative effect of body size (i.e. smaller species are more ubiquitous) on all species, herbivores, predators and detritivores. Body size had no effect however on either parasitoids or pollinators.

> modher = glm(fher ~ size, family=binomial, data=zher)

> modpol = glm(fpol ~ size, family=binomial, data=zpol)

> sumher = summary(modher); sumher **# Herbivores**

Call:

glm(formula = fher ~ size, family = binomial, data = zher)

Deviance Residuals:

Min 1Q Median 3Q Max

-1.2096 -0.9755 -0.5602 0.1058 7.2638

Coefficients:

Estimate Std. Error z value Pr(>|z|)

(Intercept) -1.50305 0.07593 -19.794 < 2e-16 \*\*\*

size -0.06666 0.01407 -4.739 2.14e-06 \*\*\*

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 608.16 on 294 degrees of freedom

Residual deviance: 583.15 on 293 degrees of freedom

AIC: 1243.7

Number of Fisher Scoring iterations: 4

> sumpol = summary(modpol); sumpol **# Pollinators**

Call:

glm(formula = fpol ~ size, family = binomial, data = zpol)

Deviance Residuals:

Min 1Q Median 3Q Max

-0.8533 -0.8388 -0.8226 0.0064 5.7460

Coefficients:

Estimate Std. Error z value Pr(>|z|)

(Intercept) -1.594622 0.159481 -9.999 <2e-16 \*\*\*

size -0.006087 0.026328 -0.231 0.817

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 179.17 on 75 degrees of freedom

Residual deviance: 179.12 on 74 degrees of freedom

AIC: 342.38

Number of Fisher Scoring iterations: 4

**Third question: If body size affects network role in both herbivores and pollinators, but occupancy only in herbivores, then is there a distance-decay in similarity of herbivore networks but not pollinators? What is the relative importance of habitat composition within a patch, patch area and distance between patches for determining their interaction similarity?** For this, I measured Poisot et al’s measure of species and interaction turnover. This can be partitioned into turnover driven by changing interactions among species that are present in two sites vs. Changing interactions due to turnover of species. I couldn’t do this partitioning with the pollinator dataset, I think because too many sites had no species in common. So all I looked at was species turnover and interaction turnover. These tests were all done using MRMs, after first testing which set of predictors (out of spatial distance, patch size and habitat types) provided best fit. Coefficients table of best fitting model is presented, with the appropriate p value being the Monte Carlo one.

Pollinators:

Species composition turnover

Coefficients:

Estimate Std. Error t value Pr(>|t|) P(MC)

(Intercept) 7.291e-01 1.886e-02 38.647 <2e-16

Habitat 6.326e-08 3.702e-08 1.709 0.0923 0.458

Interaction turnover (all sources)

Coefficients:

Estimate Std. Error t value Pr(>|t|) P(MC)

(Intercept) 9.470e-01 1.087e-02 87.141 < 2e-16

Habitat 3.190e-02 1.187e-02 2.688 0.00917 0.006

Patch size 2.273e-08 1.494e-08 1.521 0.13314 0.279

Herbivores:

Species composition turnover

Coefficients:

Estimate Std. Error t value Pr(>|t|) P(MC)

(Intercept) 3.697e-01 7.646e-02 4.835 4.77e-06

logDistance 3.639e-02 9.971e-03 3.650 0.000418 0.04

Habitat 5.589e-02 1.658e-02 3.370 0.001065 0.021

Patch size 1.635e-07 2.273e-08 7.193 1.13e-10 0.001

Interaction turnover (all sources)

Coefficients:

Estimate Std. Error t value Pr(>|t|) P(MC)

(Intercept) 7.204e-01 5.996e-02 12.015 < 2e-16

logDistance 2.119e-02 7.818e-03 2.711 0.007887 0.073

Habitat 2.745e-02 1.300e-02 2.111 0.037249 0.041

Patch size 6.375e-08 1.782e-08 3.577 0.000536 0.042

# compare slopes of species and interaction responses to log distance for herbivores

3.639e-02-2.119e-02/sqrt((9.971e-03^2)+(7.818e-03^2))

[1] -1.635997  # T statistic Not significant

Overall it appears that herbivores are more influenced by spatial processes; their composition and turnover are affected by isolation and patch size, as well as habitat differences. In contrast, pollinators are only influenced by habitat distances. This is because network roles are affected by body size for both taxa, but spatial distribution is only affected by body size for herbivores.

The idea from here would be to make the argument that plants benefit from being far away (spatially) from those species with which they share herbivores, because they can still benefit from sharing pollinators, but don’t pay the cost of negative indirect effects (apparent competition) via shared herbivores. This would only be the case if plants that share herbivores also share pollinators

**Fourth question: Do plants that share herbivores also share pollinators?**

Then maybe test whether that is explained by phylogenetic distance?

Calculated the potential for apparent competition (using PAC() function in bipartite) among plant species via shared herbivores and shared pollinators. For this analysis, I only used plants that were present in both the pollinator and herbivore dataset. This analysis tests whether the extent of sharing of pollinators is correlated with the extent of sharing of plants.

> mantel.rtest(dist(herbPAC,diag=F,upper=T),dist(pollPAC,diag=F,upper=T))

Monte-Carlo test

Call: mantel.rtest(m1 = dist(herbPAC, diag = F, upper = T), m2 = dist(pollPAC,

diag = F, upper = T))

Observation: 0.7159745

Based on 99 replicates

Simulated **p-value: 0.01**

Alternative hypothesis: greater

Std.Obs Expectation Variance

8.10968667 0.01163524 0.00754320

Need to repeat this on per-site basis, to account for fact that species more likely to share things if they occur spatially together.:

Pearson's product-moment correlation

data: m1 and m2

t = 115.36, df = 11879, p-value < 2.2e-16

alternative hypothesis: true correlation is not equal to 0

95 percent confidence interval:

0.7182876 0.7352523

sample estimates:

cor

0.7268808

Monte-Carlo test

Call: as.randtest(sim = randomcoefs$randomcoefs, obs = test$estimate,

alter = "two-sided")

Observation: 0.7268808

Based on 999 replicates

Simulated p-value: 0.001

Alternative hypothesis: two-sided

Std.Obs.cor Expectation Variance

6.726442e+01 8.538908e-05 1.167491e-04

Std.Obs.cor Expectation Variance

6.726442e+01 8.538908e-05 1.167491e-04

Pearson's product-moment correlation

data: m1 and m2

t = 108.98, df = 11879, p-value < 2.2e-16

alternative hypothesis: true correlation is not equal to 0

95 percent confidence interval:

0.6979696 0.7159557

sample estimates:

cor

0.707077

Monte-Carlo test

Call: as.randtest(sim = randomcoefs$randomcoefs, obs = test$estimate,

alter = "two-sided")

Observation: 0.707077

Based on 999 replicates

Simulated p-value: 0.001

Alternative hypothesis: two-sided

Std.Obs.cor Expectation Variance

9.158246e+19 -1.190466e-04 5.962866e-41

Std.Obs.cor Expectation Variance

9.158246e+19 -1.190466e-04 5.962866e-41

Pearson's product-moment correlation

data: m1 and m2

t = 100.99, df = 11879, p-value < 2.2e-16

alternative hypothesis: true correlation is not equal to 0

95 percent confidence interval:

0.6698849 0.6892374

sample estimates:

cor

0.6796794

Monte-Carlo test

Call: as.randtest(sim = randomcoefs$randomcoefs, obs = test$estimate,

alter = "two-sided")

Observation: 0.6796794

Based on 999 replicates

Simulated p-value: 0.001

Alternative hypothesis: two-sided

Std.Obs.cor Expectation Variance

8.023748e+01 -2.388015e-04 7.180567e-05

Std.Obs.cor Expectation Variance

8.023748e+01 -2.388015e-04 7.180567e-05

Pearson's product-moment correlation

data: m1 and m2

t = 58.48, df = 11879, p-value < 2.2e-16

alternative hypothesis: true correlation is not equal to 0

95 percent confidence interval:

0.4587196 0.4866456

sample estimates:

cor

0.4728013

Monte-Carlo test

Call: as.randtest(sim = randomcoefs$randomcoefs, obs = test$estimate,

alter = "two-sided")

Observation: 0.4728013

Based on 999 replicates

Simulated p-value: 0.001

Alternative hypothesis: two-sided

Std.Obs.cor Expectation Variance

43.6295068174 -0.0002500621 0.0001175590

Std.Obs.cor Expectation Variance

43.6295068174 -0.0002500621 0.0001175590

Pearson's product-moment correlation

data: m1 and m2

t = 48.983, df = 11879, p-value < 2.2e-16

alternative hypothesis: true correlation is not equal to 0

95 percent confidence interval:

0.3948567 0.4247784

sample estimates:

cor

0.4099278

Monte-Carlo test

Call: as.randtest(sim = randomcoefs$randomcoefs, obs = test$estimate,

alter = "two-sided")

Observation: 0.4099278

Based on 999 replicates

Simulated p-value: 0.001

Alternative hypothesis: two-sided

Std.Obs.cor Expectation Variance

1.343811e+02 -1.905970e-04 9.314124e-06

Std.Obs.cor Expectation Variance

1.343811e+02 -1.905970e-04 9.314124e-06

[1] "Pollinator matrix empty"

Pearson's product-moment correlation

data: m1 and m2

t = 40.282, df = 11879, p-value < 2.2e-16

alternative hypothesis: true correlation is not equal to 0

95 percent confidence interval:

0.3307544 0.3623968

sample estimates:

cor

0.3466742

Monte-Carlo test

Call: as.randtest(sim = randomcoefs$randomcoefs, obs = test$estimate,

alter = "two-sided")

Observation: 0.3466742

Based on 999 replicates

Simulated p-value: 0.001

Alternative hypothesis: two-sided

Std.Obs.cor Expectation Variance

4.901030e+01 2.094944e-06 5.003375e-05

Std.Obs.cor Expectation Variance

4.901030e+01 2.094944e-06 5.003375e-05

[1] "Pollinator matrix empty"

Pearson's product-moment correlation

data: m1 and m2

t = 118.24, df = 11879, p-value < 2.2e-16

alternative hypothesis: true correlation is not equal to 0

95 percent confidence interval:

0.7268999 0.7434234

sample estimates:

cor

0.7352709

Monte-Carlo test

Call: as.randtest(sim = randomcoefs$randomcoefs, obs = test$estimate,

alter = "two-sided")

Observation: 0.7352709

Based on 999 replicates

Simulated p-value: 0.001

Alternative hypothesis: two-sided

Std.Obs.cor Expectation Variance

1.286905e+02 2.656356e-05 3.264153e-05

Std.Obs.cor Expectation Variance

1.286905e+02 2.656356e-05 3.264153e-05

Pearson's product-moment correlation

data: m1 and m2

t = 55.086, df = 11879, p-value < 2.2e-16

alternative hypothesis: true correlation is not equal to 0

95 percent confidence interval:

0.4366400 0.4652877

sample estimates:

cor

0.45108

Monte-Carlo test

Call: as.randtest(sim = randomcoefs$randomcoefs, obs = test$estimate,

alter = "two-sided")

Observation: 0.45108

Based on 999 replicates

Simulated p-value: 0.001

Alternative hypothesis: two-sided

Std.Obs.cor Expectation Variance

4.434778e+01 8.826283e-05 1.034173e-04

Std.Obs.cor Expectation Variance

4.434778e+01 8.826283e-05 1.034173e-04

Pearson's product-moment correlation

data: m1 and m2

t = 59.576, df = 11879, p-value < 2.2e-16

alternative hypothesis: true correlation is not equal to 0

95 percent confidence interval:

0.4656694 0.4933615

sample estimates:

cor

0.4796349

Monte-Carlo test

Call: as.randtest(sim = randomcoefs$randomcoefs, obs = test$estimate,

alter = "two-sided")

Observation: 0.4796349

Based on 999 replicates

Simulated p-value: 0.001

Alternative hypothesis: two-sided

Std.Obs.cor Expectation Variance

4.934621e+01 -1.538331e-04 9.453496e-05

Std.Obs.cor Expectation Variance

4.934621e+01 -1.538331e-04 9.453496e-05

Pearson's product-moment correlation

data: m1 and m2

t = 66.467, df = 11879, p-value < 2.2e-16

alternative hypothesis: true correlation is not equal to 0

95 percent confidence interval:

0.5074291 0.5336455

sample estimates:

cor

0.52066

Monte-Carlo test

Call: as.randtest(sim = randomcoefs$randomcoefs, obs = test$estimate,

alter = "two-sided")

Observation: 0.52066

Based on 999 replicates

Simulated p-value: 0.001

Alternative hypothesis: two-sided

Std.Obs.cor Expectation Variance

6.981334e+01 -5.968749e-05 5.563284e-05

Std.Obs.cor Expectation Variance

6.981334e+01 -5.968749e-05 5.563284e-05

[1] "Pollinator matrix empty"

Pearson's product-moment correlation

data: m1 and m2

t = 46.555, df = 11879, p-value < 2.2e-16

alternative hypothesis: true correlation is not equal to 0

95 percent confidence interval:

0.3774961 0.4079118

sample estimates:

cor

0.3928114

Monte-Carlo test

Call: as.randtest(sim = randomcoefs$randomcoefs, obs = test$estimate,

alter = "two-sided")

Observation: 0.3928114

Based on 999 replicates

Simulated p-value: 0.001

Alternative hypothesis: two-sided

Std.Obs.cor Expectation Variance

4.270056e+01 -1.817379e-04 8.470378e-05

Std.Obs.cor Expectation Variance

4.270056e+01 -1.817379e-04 8.470378e-05

Pearson's product-moment correlation

data: m1 and m2

t = 133.41, df = 11879, p-value < 2.2e-16

alternative hypothesis: true correlation is not equal to 0

95 percent confidence interval:

0.7671236 0.7815214

sample estimates:

cor

0.7744228

Monte-Carlo test

Call: as.randtest(sim = randomcoefs$randomcoefs, obs = test$estimate,

alter = "two-sided")

Observation: 0.7744228

Based on 999 replicates

Simulated p-value: 0.001

Alternative hypothesis: two-sided

Std.Obs.cor Expectation Variance

7.422393e+01 3.246046e-04 1.087688e-04

Std.Obs.cor Expectation Variance

7.422393e+01 3.246046e-04 1.087688e-04

Also try testing how ratio of mutualism to antagonism changes with spatial distance. Maybe divide (cell by cell) PAC matrix for pollinators by PAC matrix for herbivores (assuming they are both standardised to be proportional – need to check PAC function). This will give ratio of mutualism to antagonism in each site. Then do pairwise comparison of each site matrix to see how different their ratios are (e.g. with distance matrix) and see how this changes with spatial distance. See if there’s a nonlinearity or threshold of distance at which you get maximal mutualism to antagonism ratio.

* This won’t work – need to use something like Carol’s within- vs. Between-site apparent competition, as it needs to be pairwise sharing rather than difference in within-site apparent comp.

Could relate to Janzen-Connell, benefits of being far from parent.

The phylogenetic side could give a good simple rule about e.g. don’t plant closely-related species near to each other.

Relationship plotted on log scale, indirect effects with self excluded: 

In summary, plants that share herbivores also significantly tend to share pollinators. However, the distance over which pollinator communities change is far greater than herbivore communities. So plants should benefit from being at large distances from those with which they share pollinators and herbivores, to maximise the ratio of apparent facilitation to apparent competition.