

Simmons, B. I., Cirtwill, A. R., Baker, N. J., Wauchope, H. S., Dicks, L. V., Stouffer, D. B. and Sutherland, W. J. 2018. Motifs in bipartite ecological networks: uncovering indirect interactions. – Oikos doi: 10.1111/oik.05670

Appendix 1

Null model version of ‘Comparing indices and motifs’ analysis

Many network properties, and motif counts, can vary with network size and connectance. We therefore repeated our ‘Comparing indices and motifs’ analysis, using values for nestedness, modularity and motif counts that were standardised relative to a null expectation. Specifically, we used a null model previously used to study nestedness and modularity (Bascompte et al. 2003, Thébault and Fontaine 2010). In the null model, the probability of two species interacting is the average of the normalised degree of both species (Bascompte et al. 2003, Thébault and Fontaine 2010). This means that the probability of an interaction is proportional to the generalisation of the two species.

For each of the 20,000 networks generated by the bipartite cooperation model, we generated 1000 null networks. We then expressed each structural measure (nestedness, modularity and motif counts) as a relative measure: $M^* = (M - \overline{M_R}) / \overline{M_R}$, where M^* is the relative value of a given measure, M is the value of the measure in the original network, and M_R is the mean value of the measure across the 1000 null networks (Bascompte et al. 2003, Thébault and Fontaine 2010).

We found that our results were qualitatively identical to those found when structural measures were not standardised: at all values of connectance, standardised nestedness and standardised modularity, meso-scale variation was greater than macro-scale variation (Supplementary material Fig. A1).

The median paired differences in variation between macro- and meso-scale subsets were 0.14 when ranked by connectance (Wilcoxon: $p < 0.0001$), 0.15 when ranked by nestedness (Wilcoxon: $p < 0.0001$), and 0.15 when ranked by modularity (Wilcoxon: $p < 0.0001$). For connectance, nestedness and modularity as the ranking variable respectively, the motif framework captured 69%, 65% and 70% more variation in indirect interactions than traditional whole-network indices.

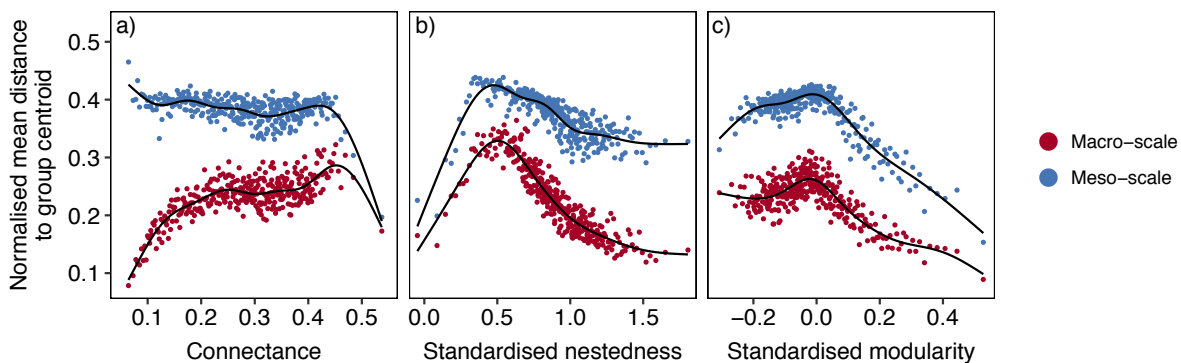


Figure A1. Network variation (normalised mean distance to group centroid) against mean connectance (a), nestedness (b) and modularity (c) for all networks. Points represent subsets of networks.

Appendix 2

Comparing indices to motifs from one size class

Motifs can be nested within each other. For example motif 3 is in motif 4, motif 4 is in motif 8, and motif 8 is in motif 18. Motifs nested in other motifs may mean that the same type of information on indirect interactions is described multiple times in a network's motif structural signature. To ensure this effect did not inflate the importance of indirect interactions, we repeated our 'Comparing indices to motifs' analysis, but only used motifs of a given size. Specifically, we compared macro-scale indices to 5-species motifs only (Supplementary material Fig. A2) and 6-species motifs only (Supplementary material Fig. A3), in two separate analyses. We found that our results were qualitatively unchanged, and our conclusions identical, by only considering motifs of a single size class, and we therefore conclude that any inflation of the importance of indirect interactions that may have occurred by considering motifs nested within larger motifs does not affect our conclusions.

When comparing indices to 5-species motifs only (Supplementary material Fig. A2), the median paired differences in variation between macro- and meso-scale subsets were 0.10 when ranked by connectance (Wilcoxon: $p < 0.0001$), 0.09 when ranked by nestedness (Wilcoxon: $p < 0.0001$), and 0.10 when ranked by modularity (Wilcoxon: $p < 0.0001$). For connectance, nestedness and modularity as the ranking variable respectively, the motif framework captured 47%, 41% and 47% more variation in indirect interactions than traditional whole-network indices.

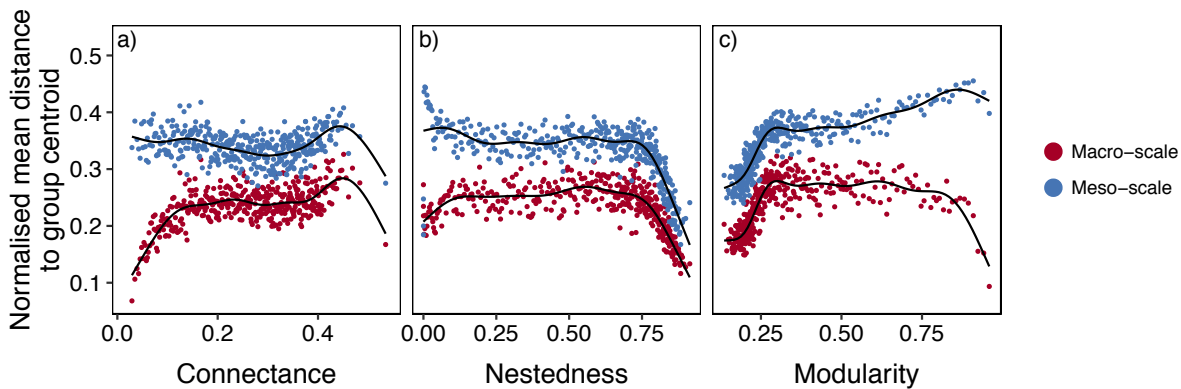


Figure A2. Network variation (normalised mean distance to group centroid) against mean connectance (a), nestedness (b) and modularity (c) for all networks. Points represent subsets of networks. Meso-scale vectors comprised 5-species motifs only.

When comparing indices to 6-species motifs only (Supplementary material Fig. A3), the median paired differences in variation between macro- and meso-scale subsets were 0.14 when ranked by connectance (Wilcoxon: $p < 0.0001$), 0.14 when ranked by nestedness (Wilcoxon: $p < 0.0001$), and 0.15 when ranked by modularity (Wilcoxon: $p < 0.0001$). For connectance, nestedness and modularity as the ranking variable respectively, the motif framework captured 69%, 60% and 69% more variation in indirect interactions than traditional whole-network indices.

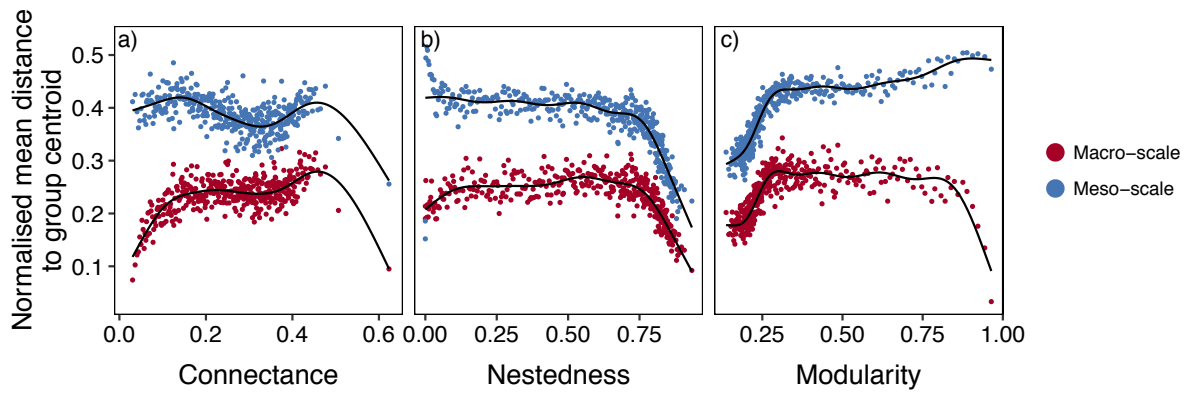


Figure A3. Network variation (normalised mean distance to group centroid) against mean connectance (a), nestedness (b) and modularity (c) for all networks. Points represent subsets of networks. Meso-scale vectors comprised 6-species motifs only.

Appendix 3

Supplementary methods for sampling effort analysis

We used simulations to assess the effect of sampling effort on network structural signatures and species role signatures. Sampling simulations were divided into two stages. In the first stage, a proportion, p , of plant species were sampled, with higher degree plant species having a higher probability of being sampled (a supplementary analysis was also conducted where plant species were chosen randomly; see Supplementary Figure 4). The number of sampled plant species was equal to pf where f is the number of plant species. If pf was not an integer, it was rounded to the nearest integer. For the analysis of species roles, it was necessary to ensure that the focal species, s , remained in the network (i.e. that it interacted with one or more partners). If s was a plant, we included it in the sample, then sampled $pf - 1$ plants from all remaining plant species. If s was an animal, we sampled one of s 's plant partners either in proportion to their degree for the main analysis, or randomly for the supplementary analysis. We then sampled $pf - 1$ plants from all remaining plant species.

In the second stage, a proportion, q , of each plant species' interactions were sampled with higher strength interactions having a higher probability of being sampled. The number of sampled interactions for a given plant species, w , was equal to ql_w where l_w is the degree of species w . If ql_w was not an integer, it was rounded to the nearest integer. If ql_w was 0, it was set to 1 to ensure all sampled plant species were present in the network. Again, for the analysis of species roles, it was necessary to ensure that s had at least one interaction with another species. If s was a plant species, the above process already ensured this. If s was an animal species, we randomly chose one of its plant partners, a , to have a minimum of one interaction with s . For a , we then sampled $ql_a - 1$ interactions from all remaining animal species. For all other plant species, we sampled ql_w of their interactions as described above.

We performed simulations on 40 empirical pollination and seed dispersal networks (Supplementary material Table A1) for different values of p and q between 0.5 and 1. We carried out 1000 randomisations for each p and q combination. We measured R^2 between the network structural signature or species role signatures of the sampled network and the network structural signature or species role signatures of the corresponding 'true' network which contained all species and interactions. Network structural signatures were normalised as a proportion of the maximum number of species combinations that could occur in each motif (Poisot and Stouffer 2016), while species role signatures were normalised within each motif size class (Baker et al. 2015).

Other supplementary figures and tables

a)



b)

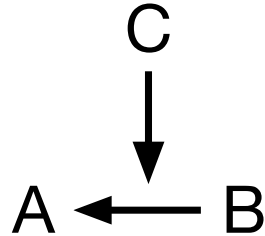


Figure A4. Two mechanisms through which species can indirectly influence each other. (a) An interaction chain, where species Z influences species A through a series of direct interactions involving changes in abundance of one or more intermediary species, such as B. (b) An interaction modification, where species C influences species A by changing the interaction between species A and B. Adapted from Wootton (1994).

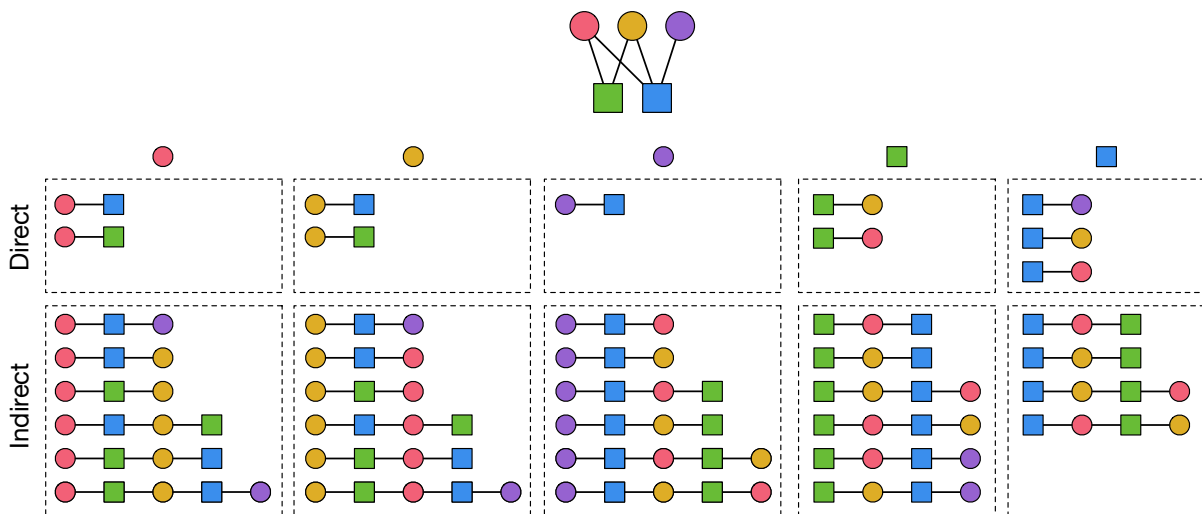


Figure A5. A small five-species motif and all the possible direct and indirect interaction chains embedded within it. Each column indicates the donor species.

Table A1. Properties of the 40 networks used to assess the effects of sampling on network structural signatures and species role signatures. Networks were obtained from the Web of Life repository (<www.web-of-life.es>). Nestedness was calculated as NODF (Almeida-Neto et al. 2008)

Network	Interaction	Species	Links	Connectance	Nestedness
M_PL_004	Pollination	114	167	0.14	28.15
M_PL_006	Pollination	78	146	0.14	44.58
M_PL_007	Pollination	52	85	0.15	31.54
M_PL_013	Pollination	65	103	0.2	34.25
M_PL_017	Pollination	104	299	0.15	40.37
M_PL_019	Pollination	125	264	0.08	17.51
M_PL_024	Pollination	29	38	0.19	29.02
M_PL_025	Pollination	57	143	0.25	46.02
M_PL_033	Pollination	47	141	0.32	29.5
M_PL_040	Pollination	72	114	0.09	15.18
M_PL_041	Pollination	74	145	0.11	25.3
M_PL_045	Pollination	43	63	0.14	30.77
M_PL_051	Pollination	104	164	0.13	26.96
M_PL_054	Pollination	431	773	0.02	8.08
M_PL_055	Pollination	259	431	0.03	8.71
M_PL_056	Pollination	456	871	0.03	6.86
M_PL_058	Pollination	113	319	0.12	26.64
M_PL_059	Pollination	26	71	0.42	76.88
M_PL_063	Pollination	59	155	0.38	45.73
M_PL_064	Pollination	22	32	0.29	41.32
M_PL_066	Pollination	37	104	0.56	50.3
M_PL_068	Pollination	40	83	0.3	45.69
M_PL_069_01	Pollination	20	22	0.26	19.18
M_PL_070	Pollination	16	41	0.64	62.23
M_PL_071	Pollination	52	89	0.25	38.53
M_SD_001	Seed dispersal	28	50	0.34	40.77
M_SD_002	Seed dispersal	40	119	0.43	62.16
M_SD_003	Seed dispersal	41	68	0.17	41.09
M_SD_004	Seed dispersal	54	95	0.14	39.82
M_SD_005	Seed dispersal	38	49	0.15	27.93
M_SD_006	Seed dispersal	36	51	0.16	32.79
M_SD_008	Seed dispersal	26	110	0.69	56.33
M_SD_009	Seed dispersal	25	38	0.3	33.02
M_SD_010	Seed dispersal	64	234	0.33	42.13
M_SD_012	Seed dispersal	64	146	0.14	33.04
M_SD_020	Seed dispersal	58	150	0.18	53.55
M_SD_023	Seed dispersal	23	38	0.32	66.8
M_SD_031	Seed dispersal	44	61	0.24	27.7
M_SD_033	Seed dispersal	24	53	0.37	67.45
M SD 034	Seed dispersal	121	419	0.14	32.35

Table A2. Properties of the monthly networks used to compare the roles of *Lassioglossum magense* and *Apis mellifera* in four mountaintop plant-pollinator communities sampled over eight consecutive months between September 2012 and April 2013 in the Seychelles (Kaiser-Bunbury et al. 2017). Nestedness was calculated as NODF (Almeida-Neto et al. 2008).

Site	Month	Species	Interactions	Connectance	Nestedness
Bernica	1	25	31	0.27	22.31
Bernica	2	30	31	0.19	11.53
Bernica	3	18	22	0.29	19.3
Bernica	4	31	39	0.2	14.34
Bernica	5	29	41	0.24	20.06
Bernica	6	22	28	0.27	20.63
Bernica	7	27	37	0.24	21.23
Bernica	8	21	27	0.3	22.08
Salazie	1	29	33	0.24	21.3
Salazie	2	23	31	0.3	20.91
Salazie	3	24	29	0.27	20.93
Salazie	4	31	46	0.27	19.48
Salazie	5	33	42	0.21	15.49
Salazie	6	29	36	0.26	14.89
Salazie	7	27	32	0.21	20.7
Salazie	8	14	14	0.42	16.38
Tea Plantation	1	25	33	0.26	21.36
Tea Plantation	2	27	33	0.22	10.89
Tea Plantation	3	43	60	0.2	15.19
Tea Plantation	4	31	42	0.21	15.53
Tea Plantation	5	25	31	0.23	13.72
Tea Plantation	6	35	55	0.25	19.77
Tea Plantation	7	33	45	0.22	14.98
Tea Plantation	8	32	43	0.21	18.11
Trois Freres	1	18	18	0.23	16.12
Trois Freres	2	28	35	0.24	16.2
Trois Freres	3	30	37	0.2	14.02
Trois Freres	4	29	40	0.24	18.35
Trois Freres	5	45	71	0.19	13.6
Trois Freres	6	28	38	0.22	22.95
Trois Freres	7	34	46	0.2	14.27
Trois Freres	8	17	21	0.32	33.57

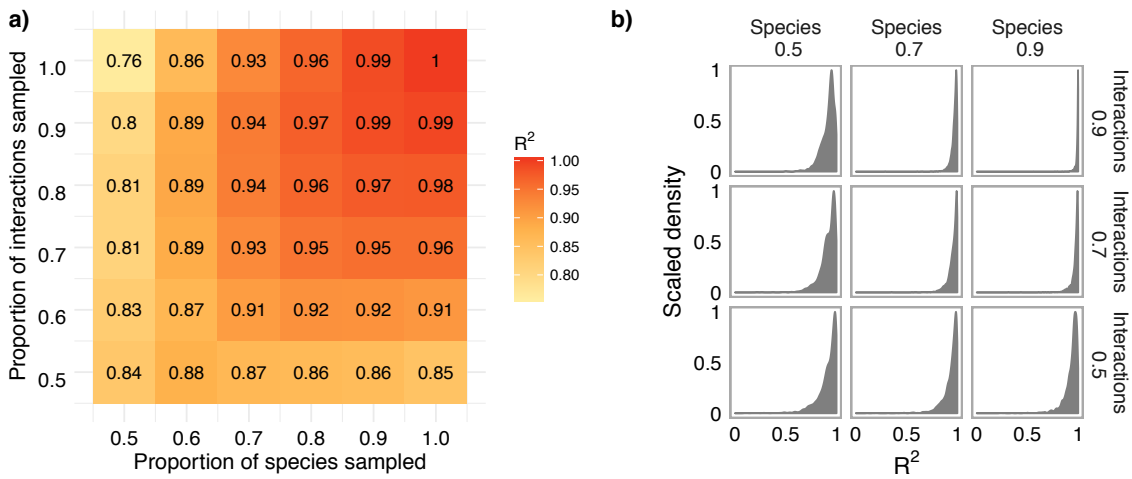


Figure A6. Results of simulations assessing the sensitivity of motifs to variation in sampling effort when plant species had a random probability of being sampled. (a) The mean R^2 between the structural signatures of the sampled networks and the structural signatures of their corresponding 'true' networks across all 40 networks for different levels of species and interaction removal. (b) Distribution of mean R^2 between species role signatures in sampled networks and species role signatures in their corresponding 'true' networks for all species across all 40 networks for different levels of species and interaction removal.

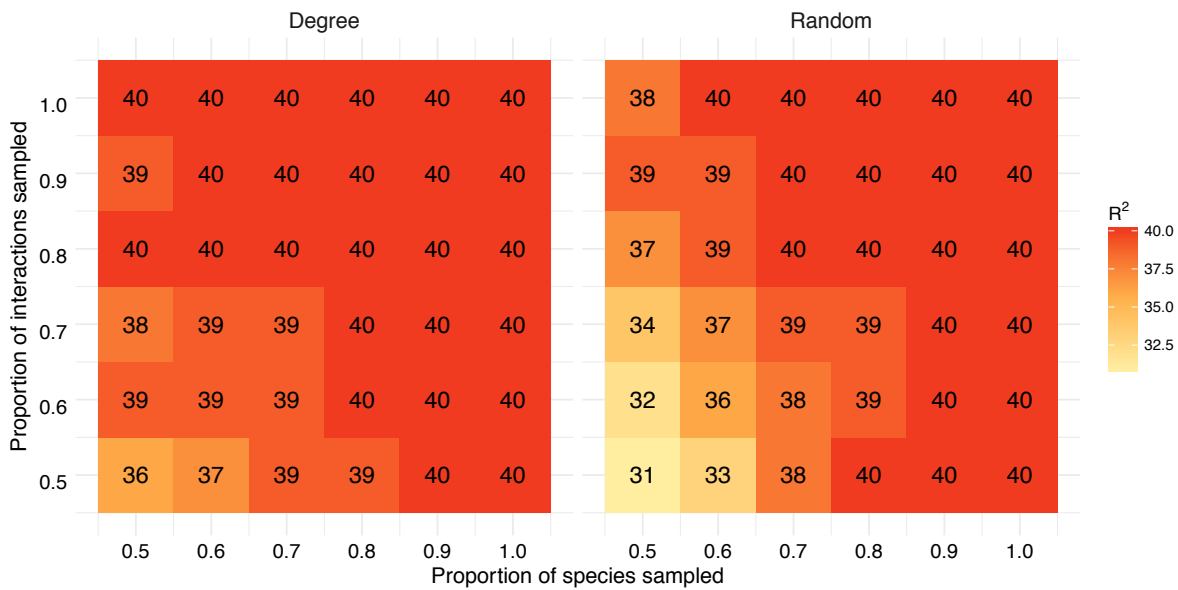


Figure A7. The number of networks used for each level of species and interaction removal in the sampling analysis of structural signatures. Some combinations of species and interaction removal resulted in sampled versions of some smaller networks which were too small or disconnected to contain larger motifs. For these sampled networks we could not calculate a structural signature which was comparable to that of the 'true' network and therefore these networks were excluded. Each cell shows the number of networks for which we were able to calculate the mean R^2 in the corresponding cells of Figure 5a (when plant species with higher degree had a higher probability of being sampled) and Supplementary material Fig. A4a (when plant species were sampled randomly).

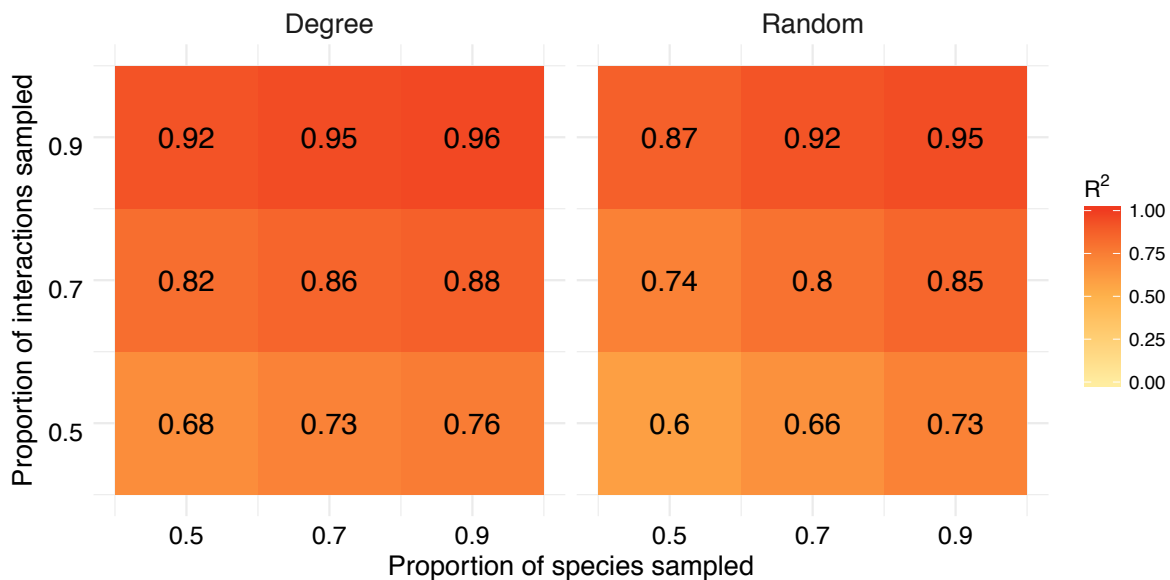


Figure A8. The proportion of species used for each level of species and interaction removal in the sampling analysis of species roles. Some species in sampled versions of smaller networks did not appear in larger motifs, particularly at high levels of species and interaction removal. For these species we could not calculate a species role signature which was comparable to that of the ‘true’ role and therefore these species were excluded. Each cell shows the proportion of species for which we were able to calculate the mean R^2 in the corresponding panels of Figure 5b (when plant species with higher degree had a higher probability of being sampled) and Supplementary material Fig. A4b (when plant species were sampled randomly).

References

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