

DETAILED REPORT OF BINARY ANALYSES

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1. Dataset

Binary networks formed by four kinds of species interaction, comprising almost all the networks analyzed by:

1. J. Bascompte, P. Jordano, C. J. Melian, J. M. Olesen, The nested assembly of plant-animal mutualistic networks. *Proc. Natl. Acad. Sci.* 100, 9383–9387 (2003).
2. P. Jordano, J. Bascompte, J. M. Olesen, Invariant properties in coevolutionary networks of plant-animal interactions. *Ecol. Lett.* 6, 69–81 (2003).

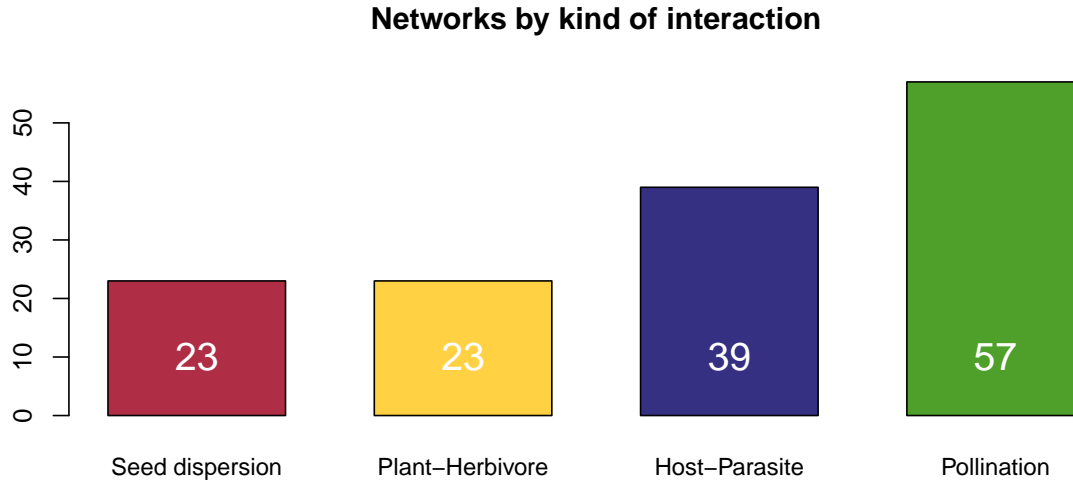
3. J. M. Olesen, J. Bascompte, Y. L. Dupont, P. Jordano, The modularity of pollination networks. *Proc. Natl. Acad. Sci.* 104, 19891–19896 (2007).
4. M. A. Fortuna, et al., Nestedness versus modularity in ecological networks: two sides of the same coin? *J. Anim. Ecol.* 79, 811–817 (2010).
5. E. Thebault, C. Fontaine, Stability of ecological communities and the architecture of mutualistic and trophic networks. *Science* (80-.). 329, 853–856 (2010).

[1] "Networks in the dataset: 142"

ID	Interaction	Reference	rows	cols
TP-001	disp	Beehler 1983	31	9
TP-002	disp	Sorensen 1981	7	6
TP-003	disp	Frost 1980	16	10
TP-004	disp	Gutián 1983	12	7
TP-005	disp	Galetti 1996	7	18
TP-006	disp	Galetti 1996	35	29
TP-007	disp	Kantak 1981	5	27
TP-008	disp	Snow 1988	11	14
TP-009	disp	Tutin 1997	19	8
TP-010	disp	Noma 1997	15	8
TP-011	disp	Wheelwright 1984	169	40
TP-012	disp	Crome 1975	71	7
TP-013	disp	Snow 1971	50	14
TP-014	disp	Jordano unpub	25	33
TP-015	disp	Jordano 1985	16	17
TP-016	disp	Herrera 1984	14	10
TP-017	pollin	Arroyo 1982	98	87
TP-018	pollin	Arroyo 1982	62	43
TP-019	pollin	Arroyo 1982	28	41
TP-020	pollin	Elberling 1999	118	23
TP-021	pollin	Olesen 2008	76	31
TP-022	pollin	Olesen 2002	13	14
TP-023	pollin	Herrera 1988	179	26
TP-024	pollin	Hocking 1968	86	29
TP-025	pollin	Inoue 1990	840	112
TP-026	pollin	Inouye 1988	91	41
TP-027	pollin	Kakutani 1990	314	113
TP-028	pollin	Kato 1996	187	64
TP-029	pollin	Kato 1990	679	91
TP-030	pollin	Kato 1993	356	90
TP-031	pollin	Kevan 1970	115	32
TP-032	pollin	McMullen 1993	54	105
TP-033	pollin	Mosquin 1967	18	11
TP-034	pollin	Montero 2005	82	28
TP-035	pollin	Olesen & Forfarg unpubl	55	29
TP-036	pollin	Montero 2005	42	8
TP-037	pollin	Montero 2005	40	10
TP-038	pollin	Olesen 2002	12	10
TP-039	pollin	Percival 1974	36	61
TP-040	pollin	Petanidou 1991	666	131
TP-041	pollin	Primack 1983	60	18
TP-042	pollin	Primack 1983	138	41
TP-043	pollin	Primack 1983	118	49
TP-044	pollin	Ramirez 1989	49	48

ID	Interaction	Reference	rows	cols
TP-045	pollin	Schemske 1978	33	7
TP-046	disp	Baird 1980	21	7
TP-047	disp	Lambert 1989	25	61
TP-048	disp	Jordano unpub	18	28
TP-053	disp	Jordano 1993	11	6
TP-056	disp	Silva 2002	207	110
TP-071	pollin	Kato 2000	678	91
TP-072	pollin	Gonzalez Alvaro 2004	46	477
TP-073	pollin	Yamazaki 2003	99	294
TP-074	pollin	Clements 1923	275	96
TP-075	pollin	Dupont 2009	30	236
TP-076	pollin	Bek 2006	37	225
TP-077	pollin	Dupont 2009	19	186
TP-079	pollin	Vázquez 2002	90	14
TP-080	pollin	Medan 2002	72	23
TP-081	pollin	Ingversen 2006	36	61
TP-082	pollin	Stald 2003	51	17
TP-083	pollin	Medan 2002	45	21
TP-084	pollin	Helenurm 1987	102	12
TP-085	pollin	Memmott 1999	79	25
TP-086	pollin	Ingversen 2006	44	31
TP-087	pollin	Bundgaard 2003	44	16
TP-088	pollin	Witt 1998	39	15
TP-089	pollin	Dupont 2003	38	11
TP-090	pollin	Stald 2003	35	14
TP-091	pollin	Lundgren 2005	26	17
TP-092	pollin	Philipp 2006	12	6
TP-093	disp	Jordano unpub	12	4
TP-094	disp	Jordano unpub	21	6
TP-095	pollin	Montero 2005	105	39
TP-096	paras	Alania 1964	20	15
TP-097	paras	Arthur 1976	29	7
TP-098	paras	Mikulin 1959	26	19
TP-099	paras	Vershinina 1967	17	28
TP-100	paras	deMoraes 2003	10	16
TP-101	paras	Linsdale 1956	22	19
TP-102	paras	Davis 2002	17	9
TP-103	paras	Elshanskaya 1972	18	8
TP-104	paras	Leong 1981	40	10
TP-105	paras	Burdelova 1996	22	15
TP-106	paras	Mikulin 1959	37	22
TP-107	paras	Morozkina 1971	25	8
TP-108	paras	Allred 1968	29	14
TP-109	paras	Syrvacheva 1964	21	13
TP-110	paras	Koshkin 1966	22	9
TP-111	paras	Leonov 1958	12	8
TP-112	paras	Reshetnikova 1959	19	17
TP-113	paras	Arai 1983	51	14
TP-114	paras	Vasiliev 1966	21	9
TP-115	paras	Labunets 1967	44	21
TP-116	paras	Popova 1968	31	18
TP-117	paras	Krasnov 1997	11	13

ID	Interaction	Reference	rows	cols
TP-118	paras	Morlan 1955	34	29
TP-119	paras	Yudin 1976	16	15
TP-120	paras	Shwartz 1958	35	16
TP-121	paras	Violovich 1969	34	27
TP-122	paras	Sineltshikov 1956	53	17
TP-123	paras	Vasiliev 1966	14	16
TP-124	paras	Bangham 1955	97	33
TP-125	paras	Pauller 1966	13	9
TP-126	paras	Stanko 2002	22	17
TP-127	paras	Chinniah 1978	25	6
TP-128	paras	Kunitsky 1962	23	13
TP-129	paras	Mikulin 1958	35	23
TP-130	paras	Zagniborodova 1960	42	18
TP-131	paras	Letov 1966	28	13
TP-132	paras	Kozlovskaya 1958	21	9
TP-133	paras	Nazarova 1981	35	29
TP-134	paras	Emelyanova 1967	29	15
TP-135	pollin	Motten 1986	44	13
TP-136	pollin	Ramirez 1992	53	28
TP-137	pollin	Robertson 1928	1427	454
TP-138	pollin	Small 1976	34	13
TP-139	pollin	Ollerton 2003	56	9
TP-140	pollin	Smith-Ramirez 2005	128	26
TP-141	herbiv	Basset 1996	32	10
TP-142	herbiv	Dawah 1995	17	10
TP-143	herbiv	Dyer 2002	443	293
TP-144	herbiv	Henneman 2001	23	22
TP-145	herbiv	Henneman 2001	25	26
TP-146	herbiv	Janzen 1980	110	98
TP-147	herbiv	Janzen 2005	301	776
TP-148	herbiv	Joern 1979	22	53
TP-149	herbiv	Joern 1979	21	53
TP-150	herbiv	Lewis 2002	93	71
TP-151	herbiv	Loye 1992	35	42
TP-152	herbiv	Memmott 1994	87	50
TP-153	herbiv	Muller 1999	25	26
TP-154	herbiv	Nakagawa 2003	29	20
TP-155	herbiv	Nakagawa 2003	36	13
TP-156	herbiv	Novotny 2005	29	29
TP-157	herbiv	Prado 2004	34	81
TP-158	herbiv	Tavakilian 1997	352	300
TP-159	herbiv	Tscharntke 2001	16	10
TP-160	herbiv	Ueckert 1971	14	43
TP-161	herbiv	Bluthgen 2006	14	38
TP-162	herbiv	Coley 2006	95	40
TP-163	herbiv	Cuevas-Reyes 2007	29	29



Warnings (matrix loadings)

```
## [1] "TP-027 was not binary"
## [1] "TP-099 had 1 empty columns"
## [1] "TP-108 had 1 empty columns"
## [1] "TP-111 had 1 empty columns"
## [1] "TP-113 had 1 empty columns"
## [1] "TP-121 had 1 empty columns"
## [1] "TP-126 had 2 empty columns"
## [1] "TP-128 had 1 empty columns"
## [1] "TP-133 had 1 empty columns"
## [1] "TP-001 was not binary"
## [1] "TP-072 was not binary"
```

2. Overall nestedness vs. Modularity

Binary nestedness: we applied the NODF index (Almeida-Neto et al. 2008).

Binary modularity: we calculated Barber's modularity index (Barber 2007) using the LPA and the DIRT LPA algorithms (Beckett 2016).

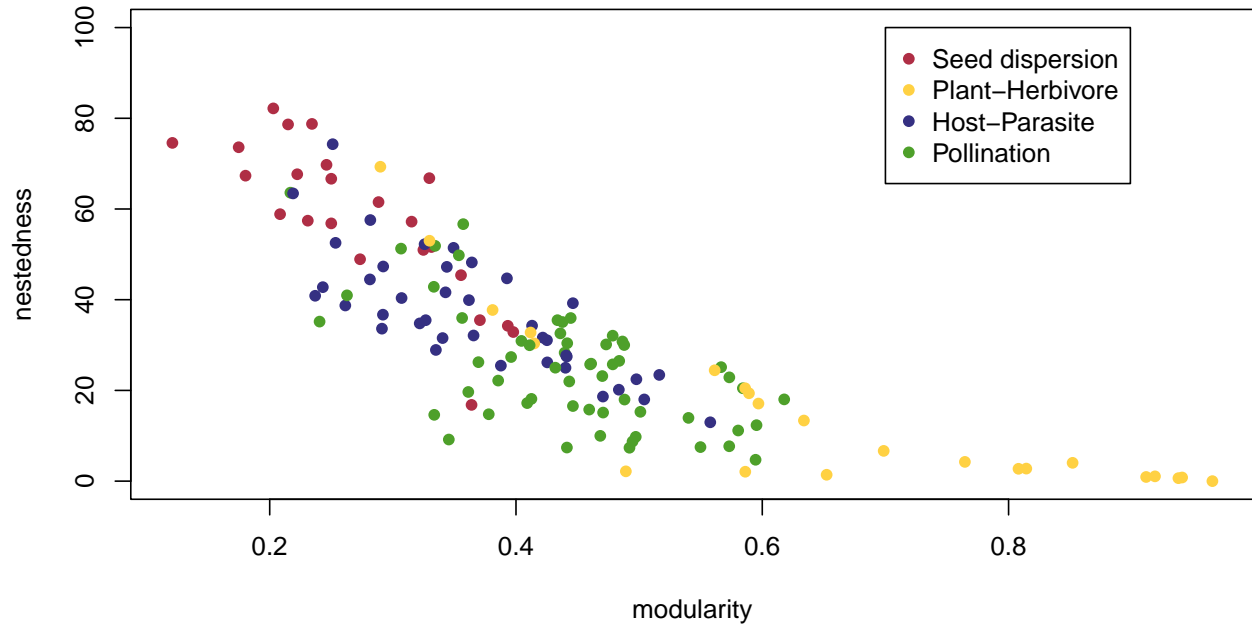
For too large networks (> 600 species), it was computational impracticable to apply the DIRT LPA algorithm, so we applied the faster, although a bit less effective, LPA.

List of large binary networks (>600 species)

ID	Interaction	Reference	rows	cols
TP-025	pollin	Inoue 1990	840	112
TP-029	pollin	Kato 1990	679	91
TP-040	pollin	Petanidou 1991	666	131
TP-071	pollin	Kato 2000	678	91
TP-137	pollin	Robertson 1928	1427	454
TP-143	herbiv	Dyer 2002	443	293

ID	Interaction	Reference	rows	cols
TP-147	herbiv	Janzen 2005	301	776
TP-158	herbiv	Tavakilian 1997	352	300

Plot and correlation test

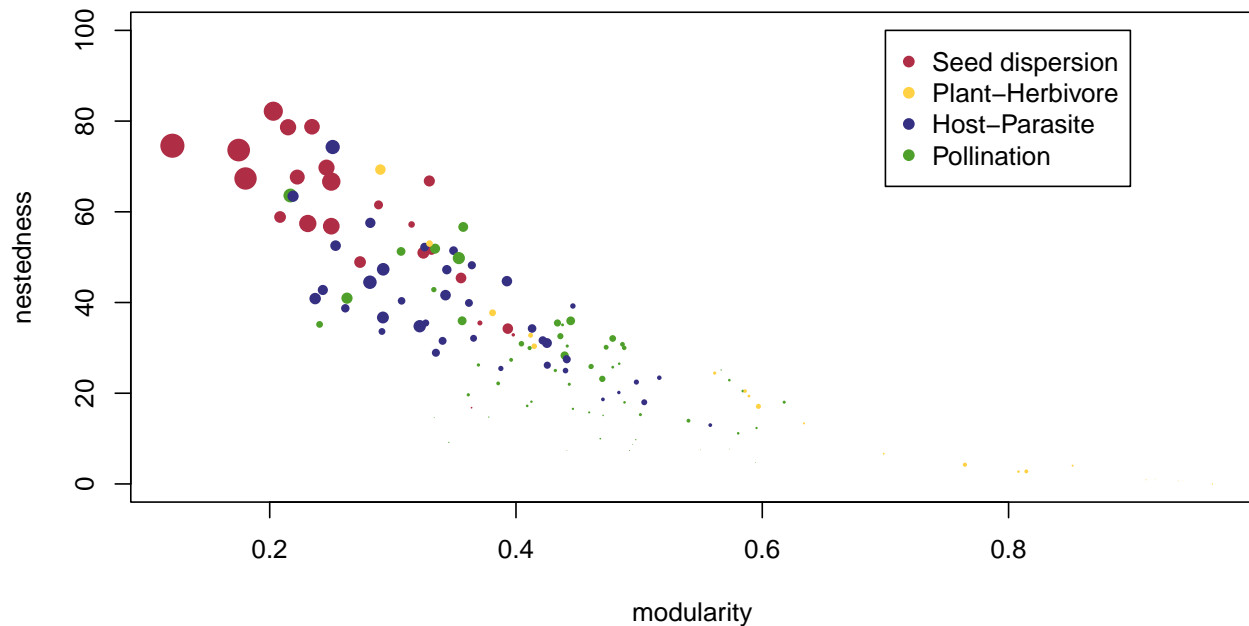


Testing the correlation between modularity and nestedness:

```
## Warning in cor.test.default(TABLE_RESULTS$modularity, TABLE_RESULTS$NODF, :
## Impossível calcular o valor exato de p com empates
##
## Spearman's rank correlation rho
##
## data: TABLE_RESULTS$modularity and TABLE_RESULTS$NODF
## S = 9e+05, p-value <2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
## -0.867
```

3. Correlations and comparisons

3.1. Connectance:



Correlation between modularity and connectance:

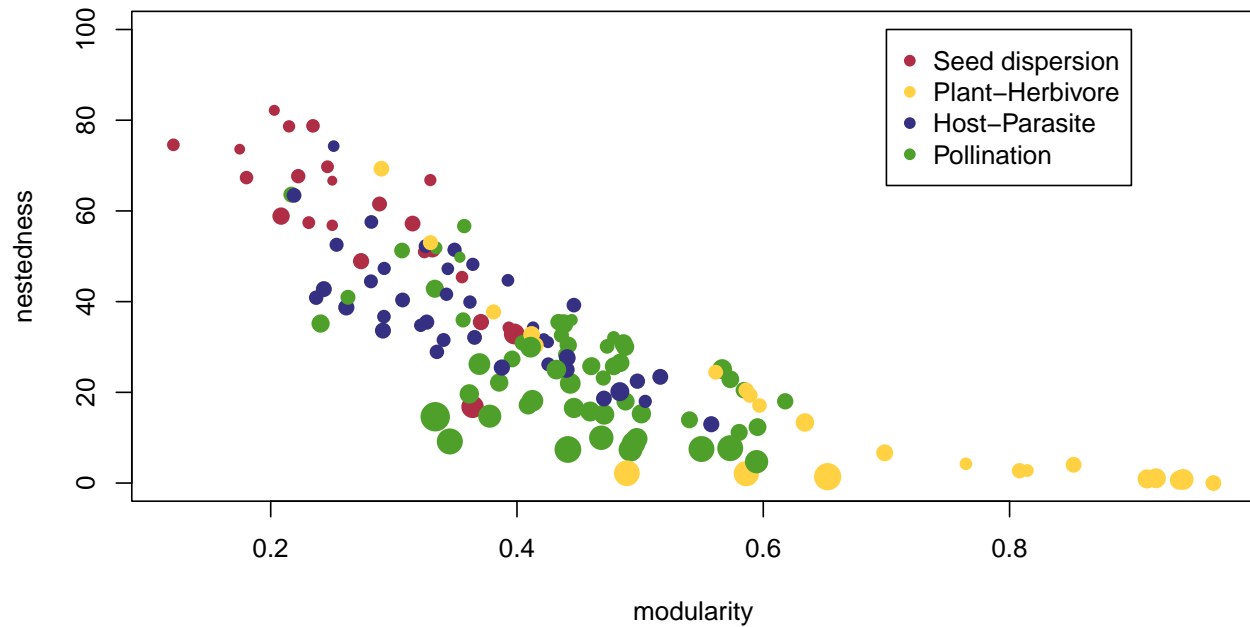
```
## Warning in cor.test.default(TABLE_RESULTS$modularity,
## TABLE_RESULTS$connectance, : Impossível calcular o valor exato de p com empates
##
## Spearman's rank correlation rho
##
## data: TABLE_RESULTS$modularity and TABLE_RESULTS$connectance
## S = 9e+05, p-value <2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
## -0.81
```

Correlation between nestedness and connectance:

```
## Warning in cor.test.default(TABLE_RESULTS$NODF, TABLE_RESULTS$connectance, :
## Impossível calcular o valor exato de p com empates
##
## Spearman's rank correlation rho
##
## data: TABLE_RESULTS$NODF and TABLE_RESULTS$connectance
## S = 42655, p-value <2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
## 0.911
```

3.2. Network size:

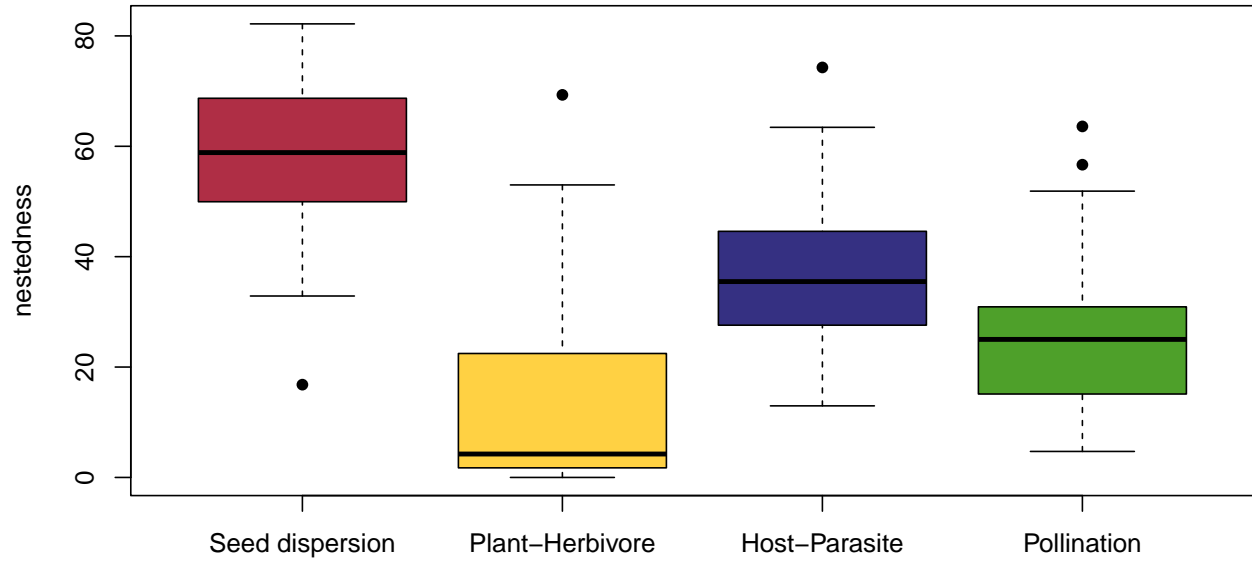
Size was log transformed (size = log(number of species))



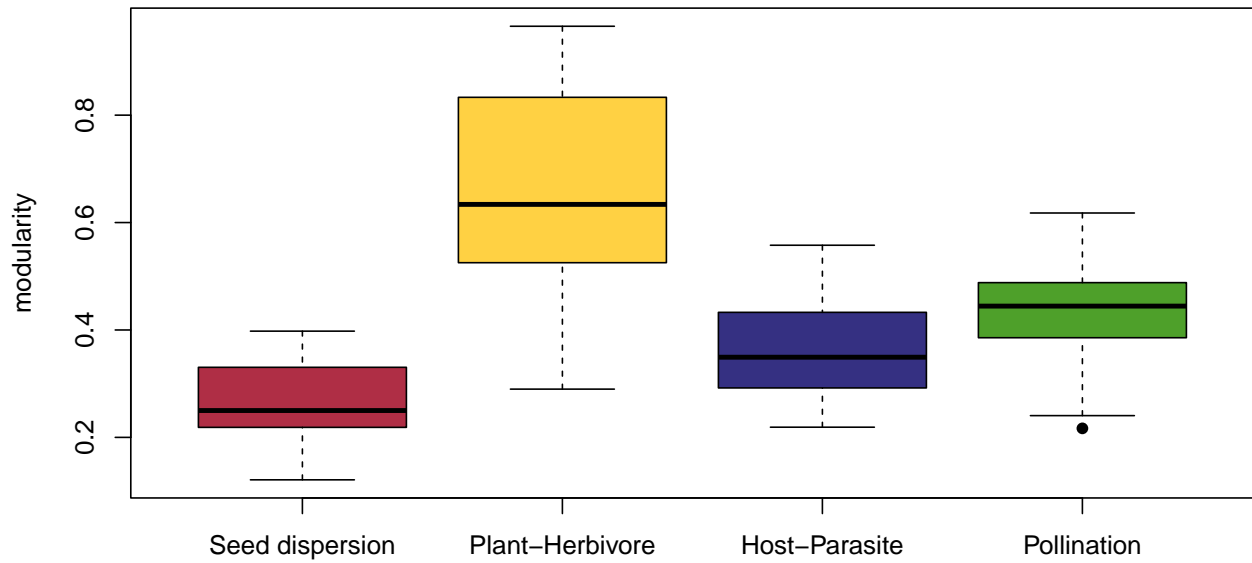
Correlation between size and connectance:

```
## Warning in cor.test.default((X$rows + X$cols), TABLE_RESULTS$connectance, :
## Impossível calcular o valor exato de p com empates
##
## Spearman's rank correlation rho
##
## data: (X$rows + X$cols) and TABLE_RESULTS$connectance
## S = 9e+05, p-value <2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
## rho
## -0.831
```


3.3. Nestedness vs. kind of interaction



3.4. Modularity vs. kind of interaction

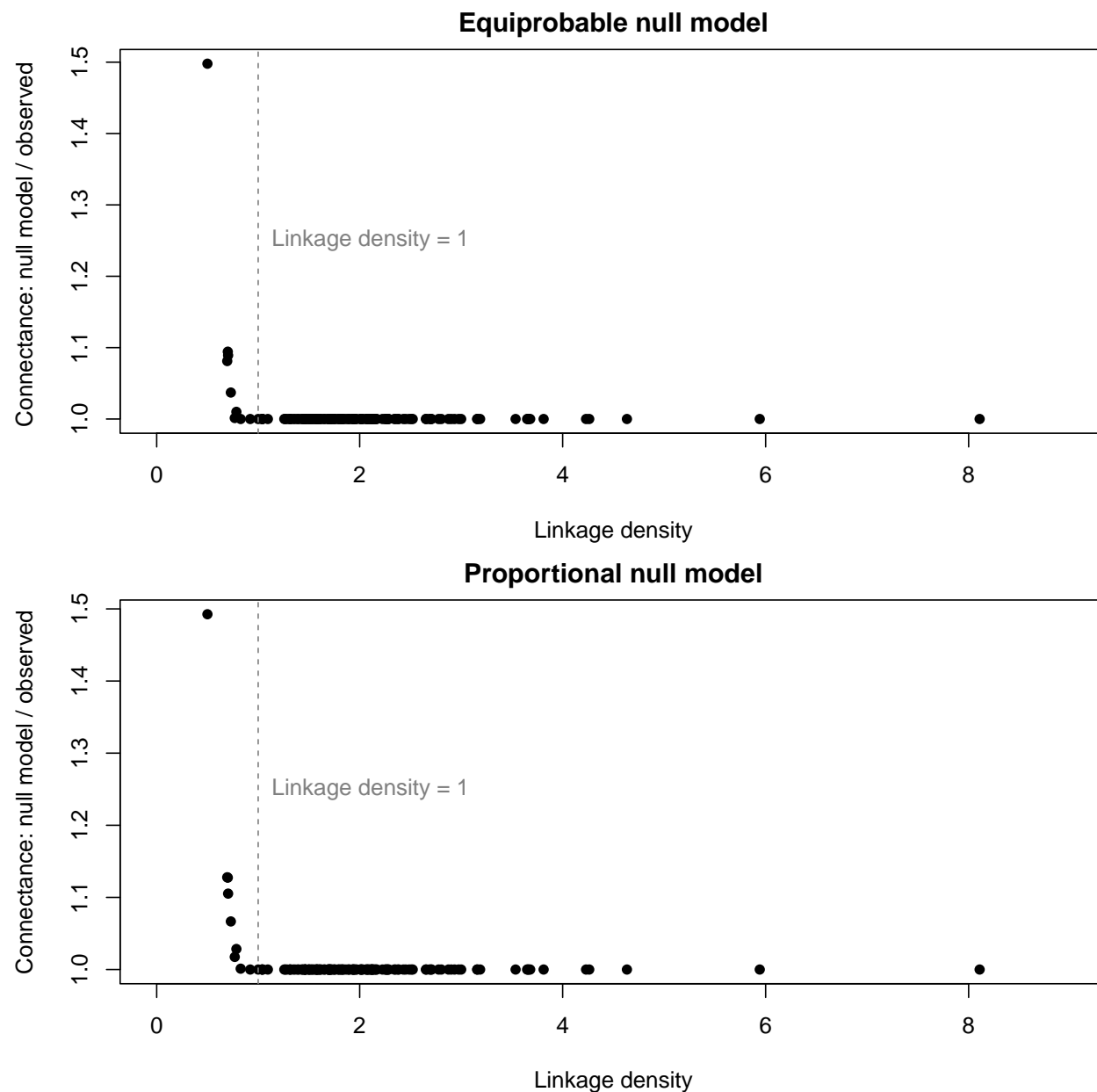


4. Distortions on null model connectance

We used a null model that forces the randomized matrix to keep the dimensions. It is based on the method developed by Vázquez (2007). However, because of conserving the dimensions, null models are not able to conserve connectance when the number of interactions divided by network size (linkage density) is lower than 1.

Here, to illustrate this problem, we built null models for all networks, regardless of linkage density. Then, we divided the average connectance in the null matrices by the connectance in the observed matrix.

Notice that, in networks with linkage density lower than 1, connectance in the null matrices is often higher than in the observed matrix. This problems never occur for matrices with linkage density equal or higher than 1.



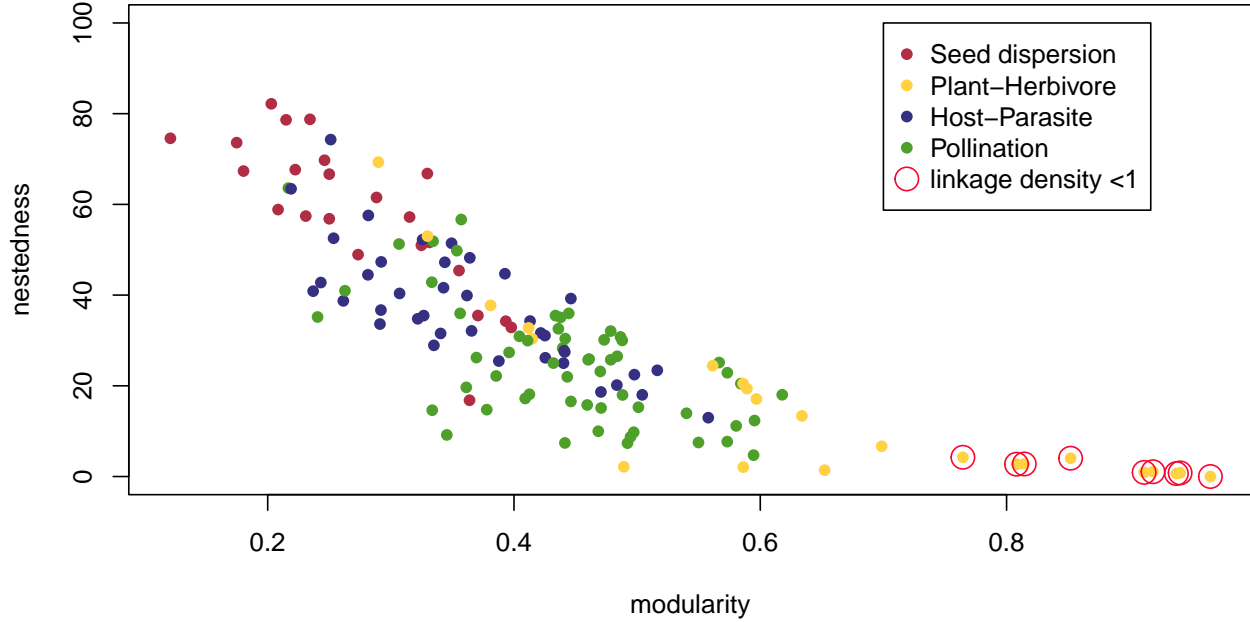
4.1. Networks with linkage density < 1

This is the list of networks in our dataset with linkage density lower than 1.

ID	Interaction	Reference	rows	cols
TP-142	herbiv	Dawah 1995	17	10
TP-146	herbiv	Janzen 1980	110	98
TP-150	herbiv	Lewis 2002	93	71
TP-152	herbiv	Memmott 1994	87	50
TP-153	herbiv	Muller 1999	25	26

ID	Interaction	Reference	rows	cols
TP-156	herbiv	Novotny 2005	29	29
TP-159	herbiv	Tscharntke 2001	16	10
TP-162	herbiv	Coley 2006	95	40
TP-163	herbiv	Cuevas-Reyes 2007	29	29

Notice that these networks correspond to the 9 networks with higher modularity:

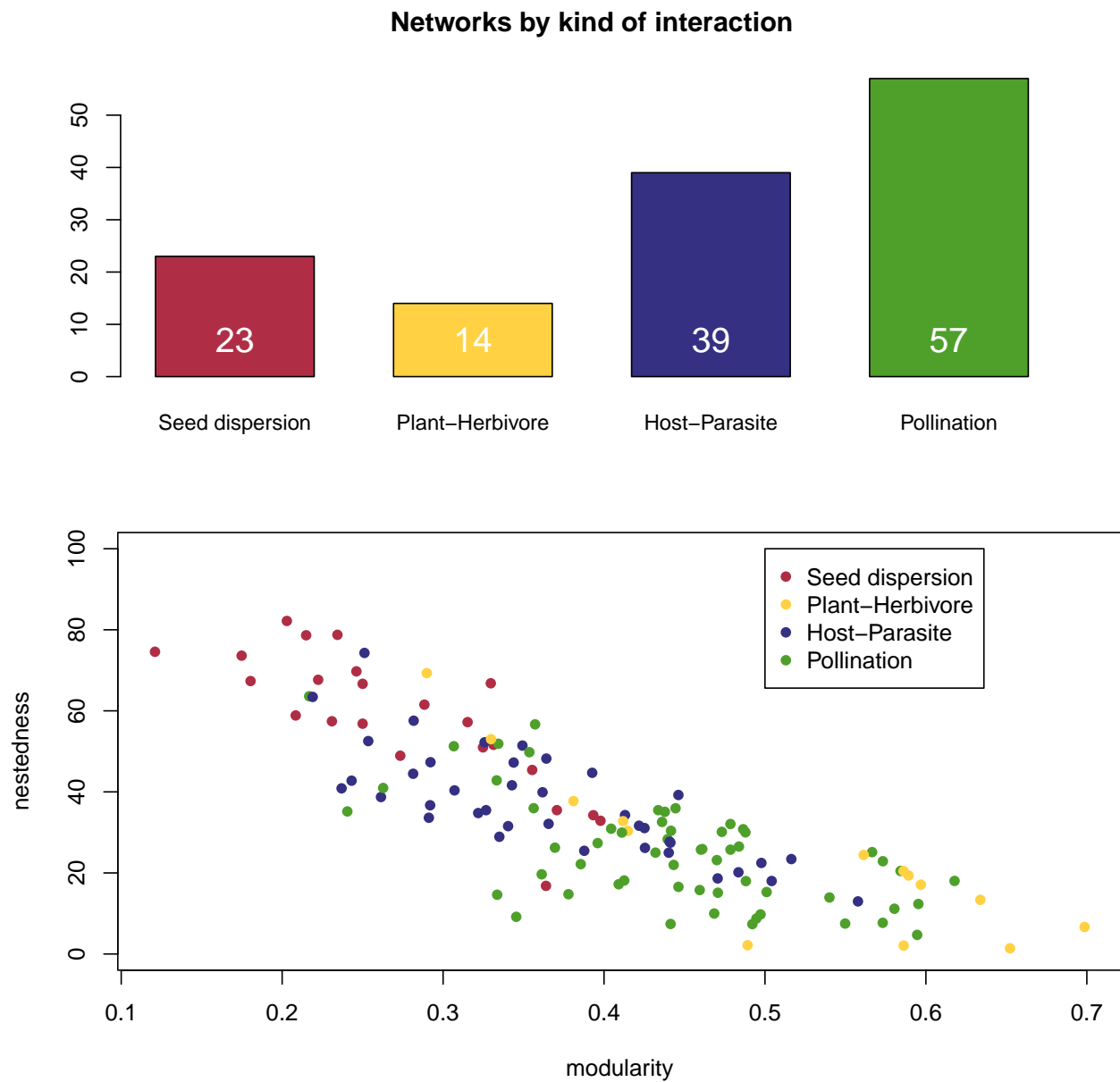


5. Modularity and nestedness significance

For these analysis we only included networks with linkage density equal or higher to 1.

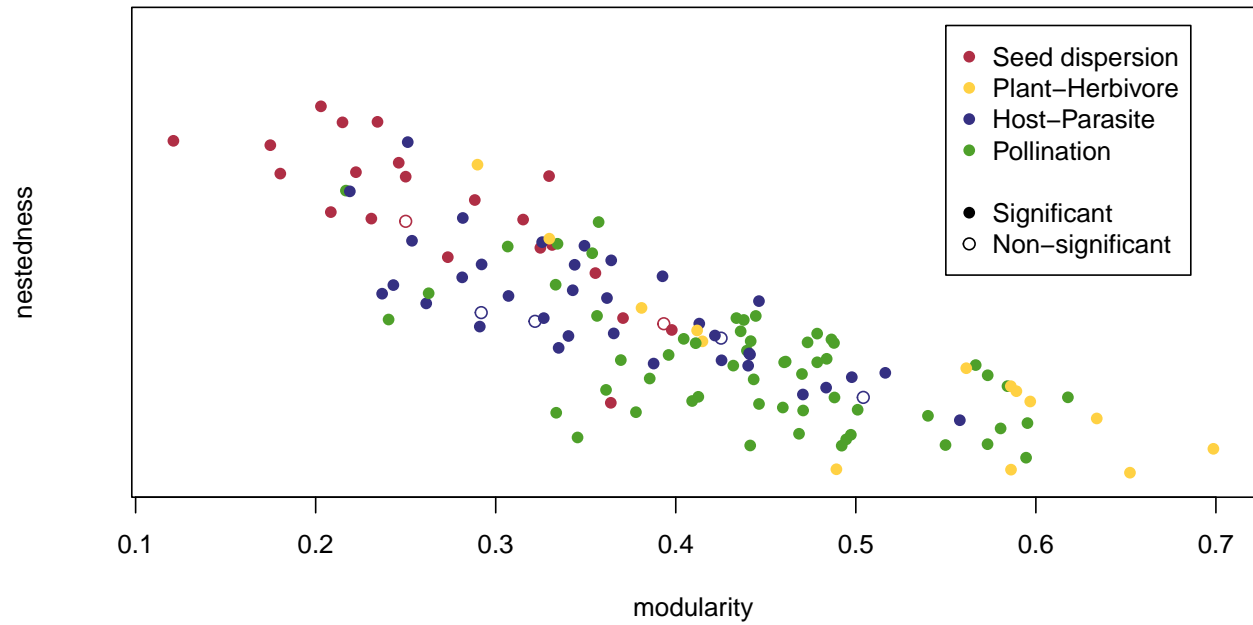
Null models in our study are composed of 105 randomized matrices each. This is not a very high number of matrices, but for computational limitations it was impracticable to produce larger null models. We analyzed a large number of real networks (binary: 142, weighted: 68), some of which including a very large number of species (max= 1881 species).

```
## [1] "Number of remaining networks: 133"
```

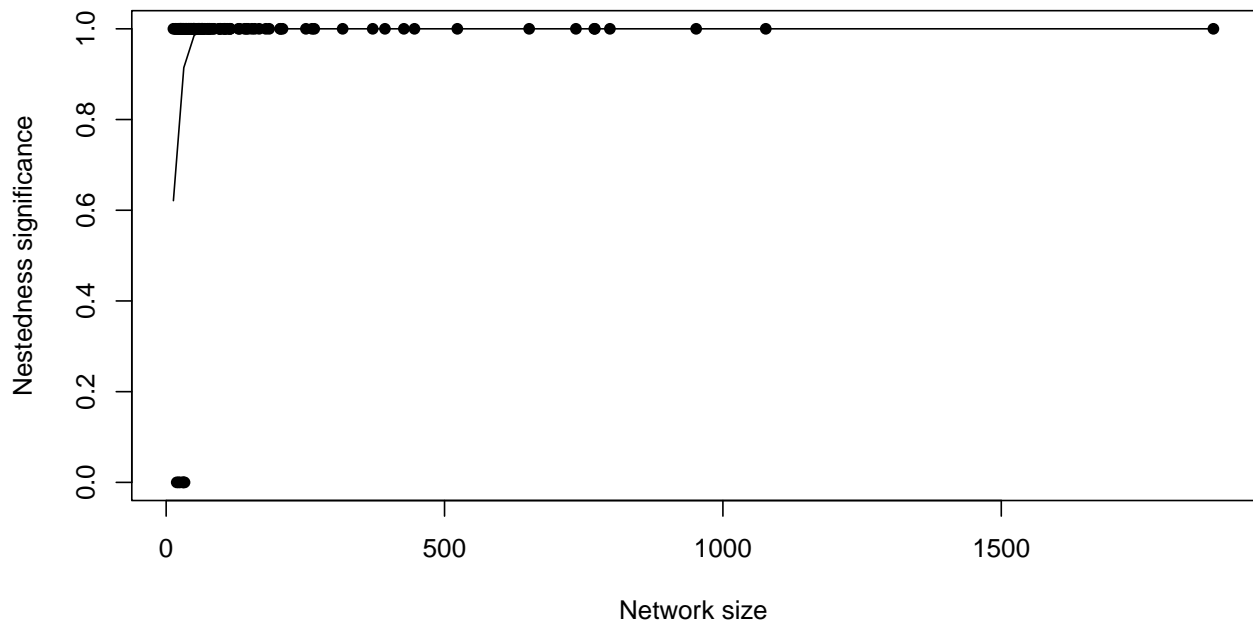


5.1. Significantly nested

Nestedness significance was assessed through comparisons with the equiprobable null model.



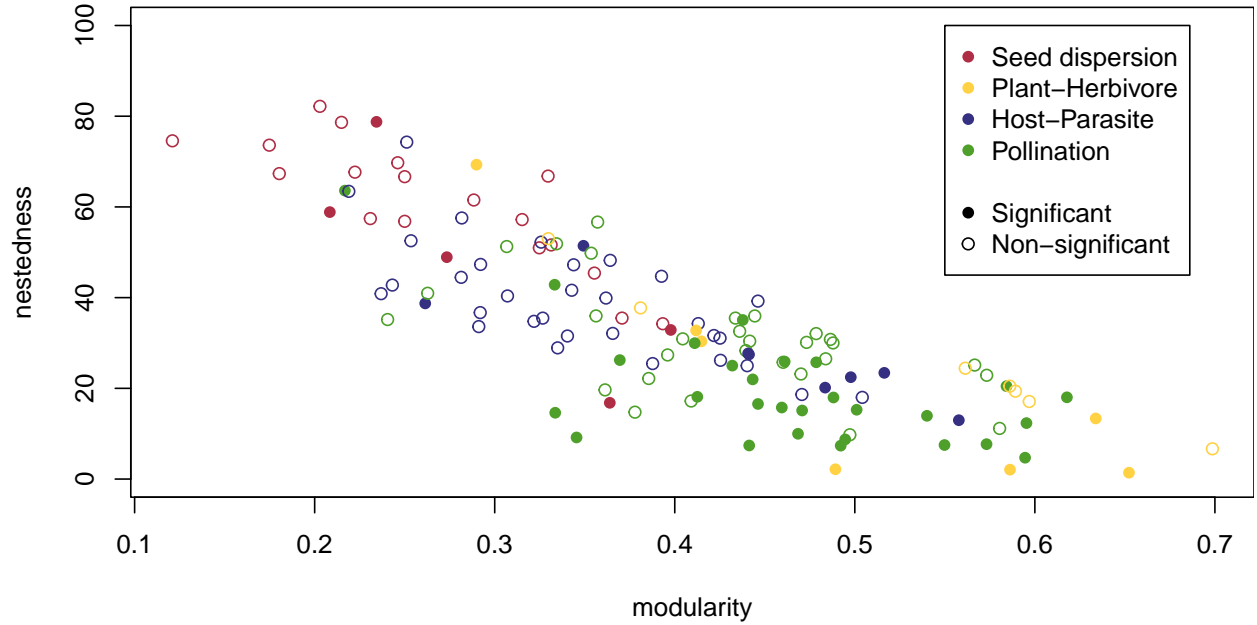
```
## [1] "Number of significantly nested networks: 127"
```



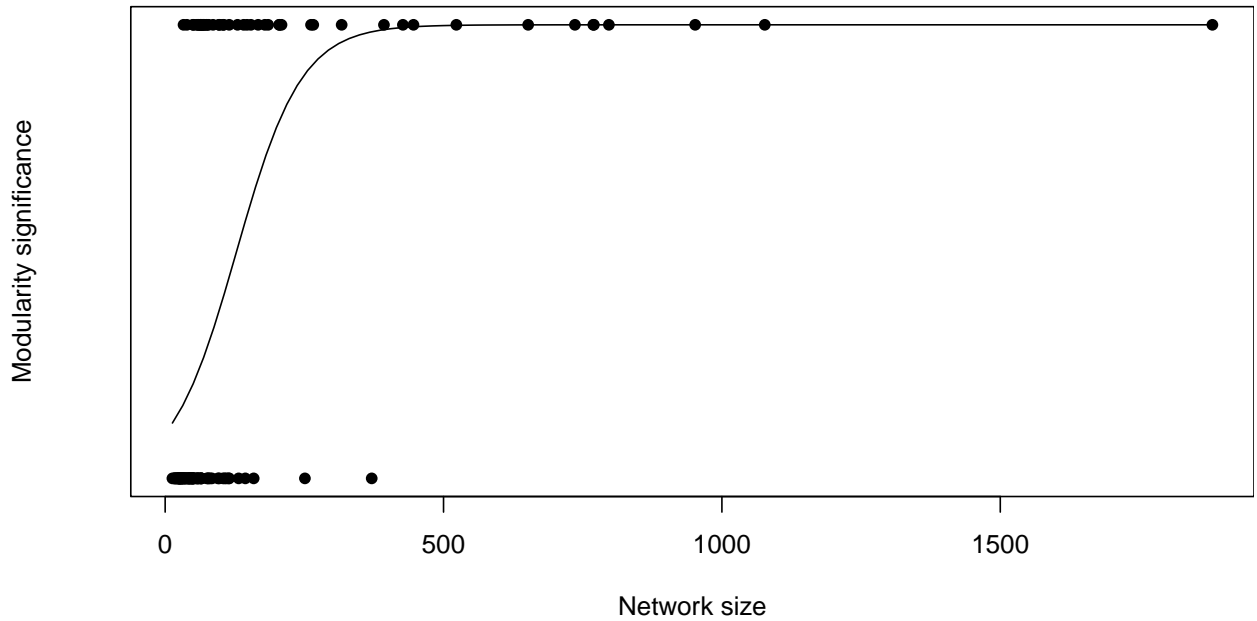
All the networks with more than 34 species were significantly nested.

5.2. Significantly modular

Modularity significance was assessed through comparisons with the proportional null model.



```
## [1] "Number of significantly modular networks: 48"
```



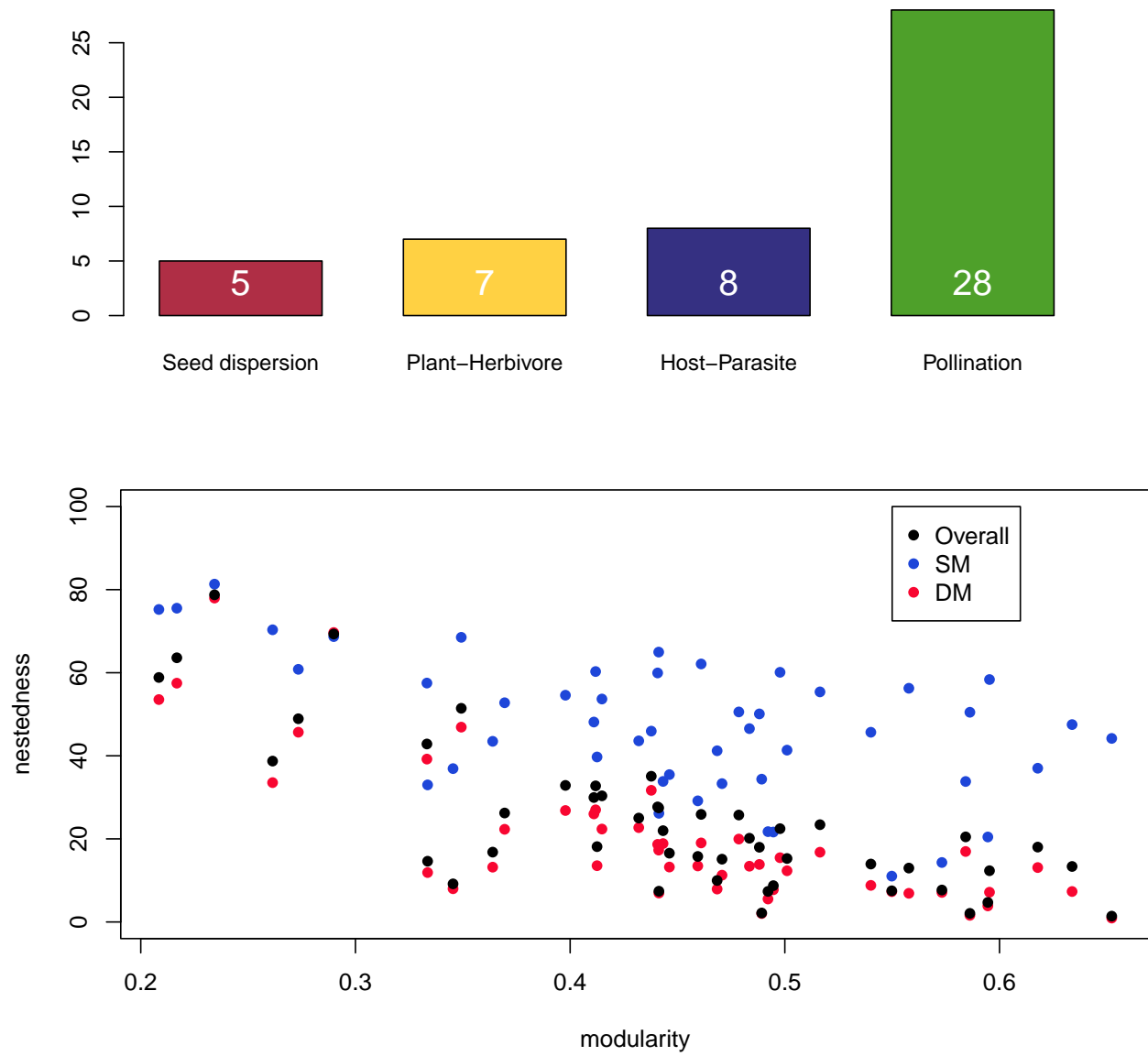
Almost all the networks (except from two) with more than 160 species were significantly modular.

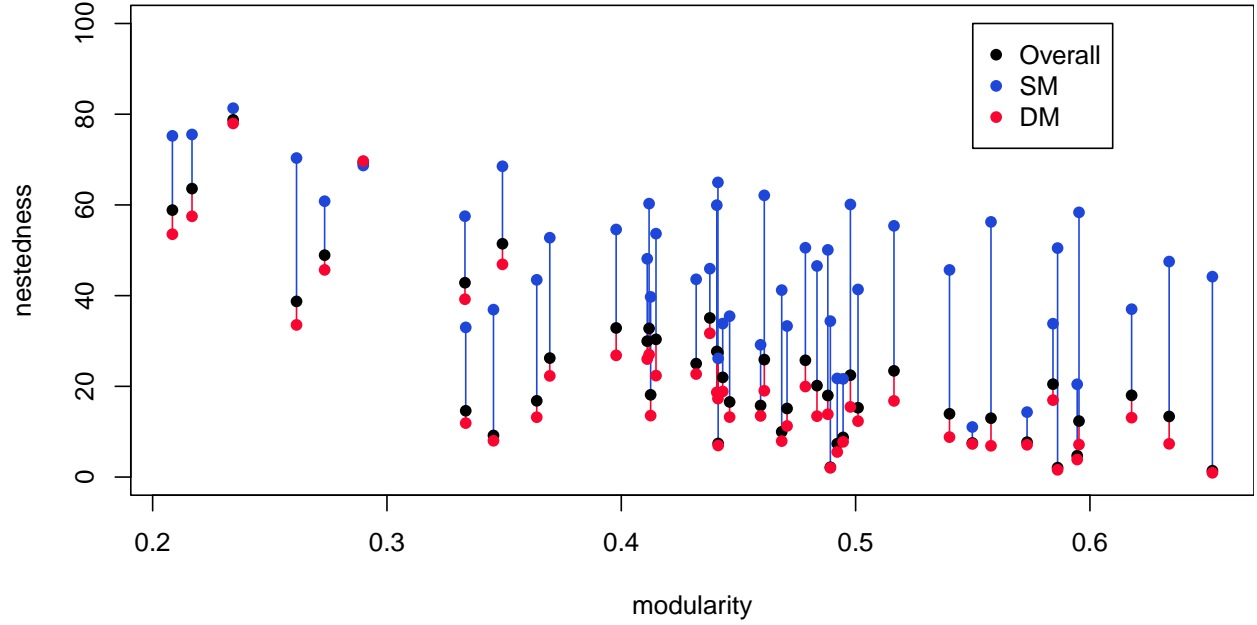
6. Nestedness SM and DM

For significant modular networks we calculated nestedness between species belonging to the same module (N_{SM}) and nestedness between species in different modules (N_{DM}) (Flores et al. 2013, Pinheiro et al. 2019, Felix et al. 2022).

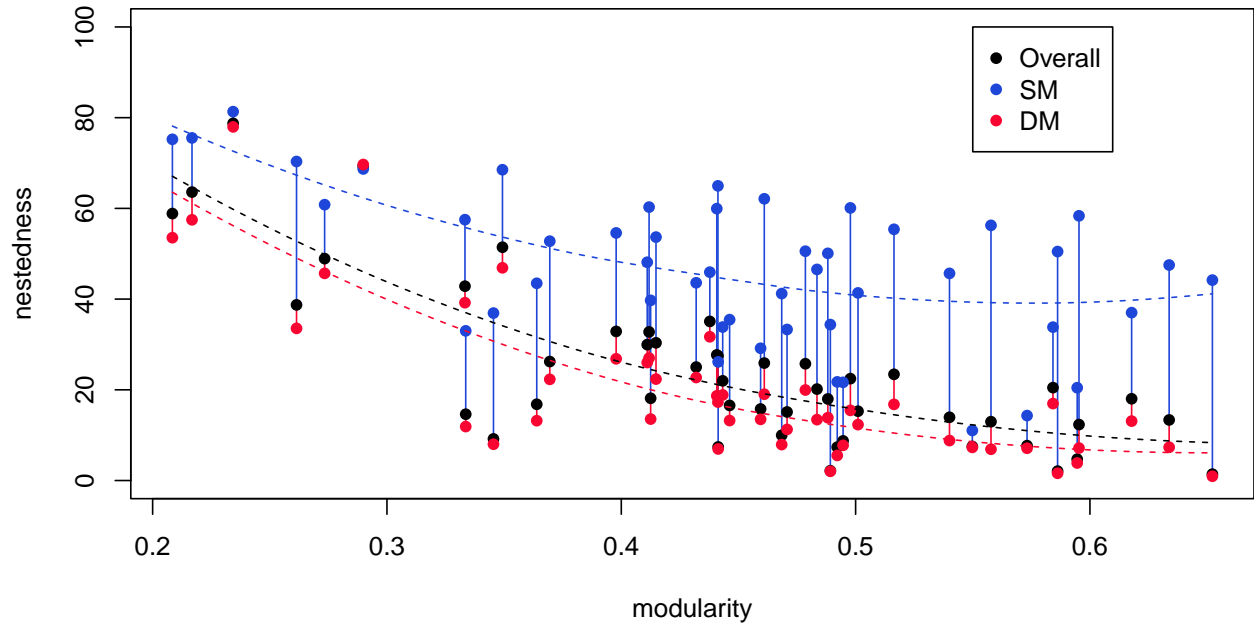
```
## [1] "Modular networks: 48"
```

Modular networks by kind of interaction





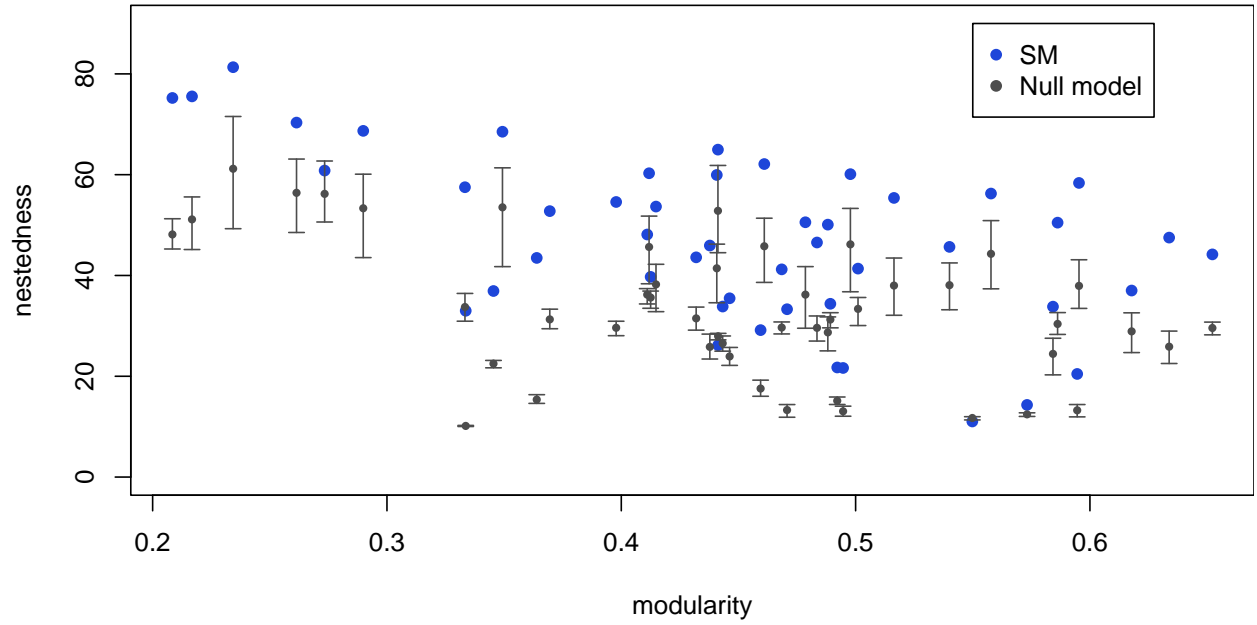
I applied local regressions (R function loess), very smoothly, to see the general trend of $NODF_O$, $NODF_{SM}$ and $NODF_{DM}$, with increasing modularity.



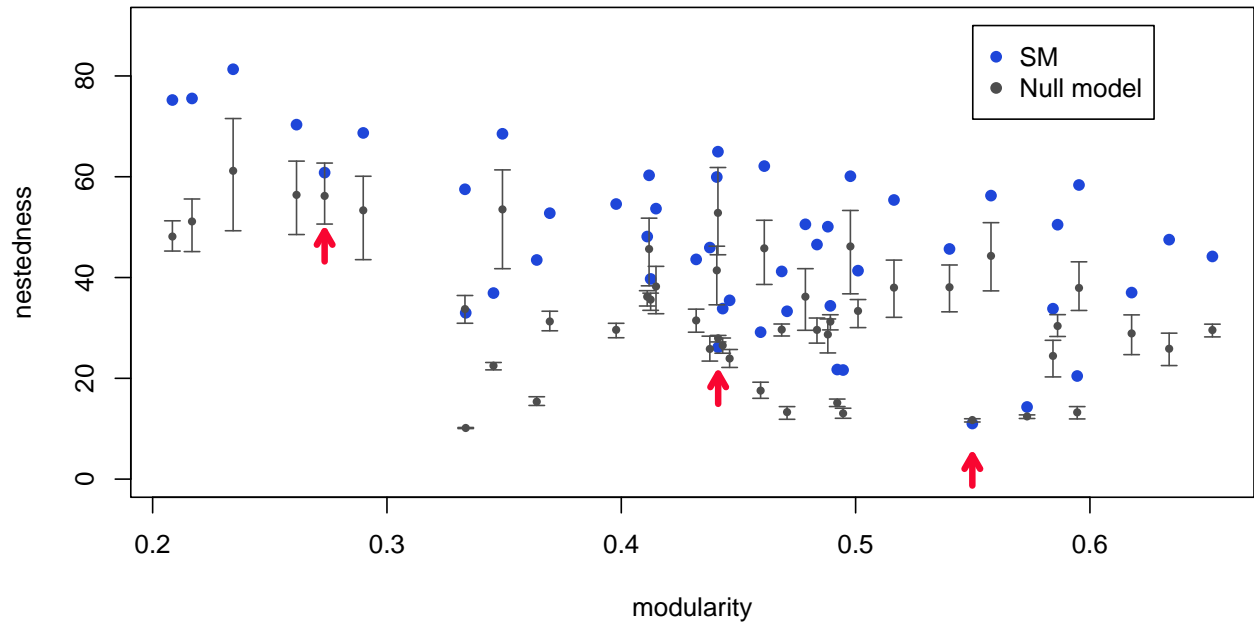
7. Significance of nestedness SM

We used restricted null models (models that conserve the modular structure on the networks) to test N_{SM} significance.

Brackets represent 95% of values in the null model.



Only a few modular networks do not present significant nestedness SM (red arrows).



8. Network topologies

Significance tests:

Equiprobable null model for N_O significance.

Proportional null model for modularity significance.

Equiprobable restricted null model for N_{SM} significance.

Topologies:

Nested network: non-significant modularity and significant N_O

Pure modular network: significant modularity and non-significant N_{SM}

Compound topology: significant modularity and significant N_{SM}

Unstructured: non significant N_O and non significant modularity

topology	Number of networks
compound	45
nested	79
pure modular	3
unstructured	6

8.1. Topology vs. kind of interaction

	seed dispersal	plant-herbivore	host-parasite	pollination
nested	16	7	27	29
unstructured	2	0	4	0
compound	4	7	8	26
pure modular	1	0	0	2
linkage density <1	0	9	0	0

9. Network robustness

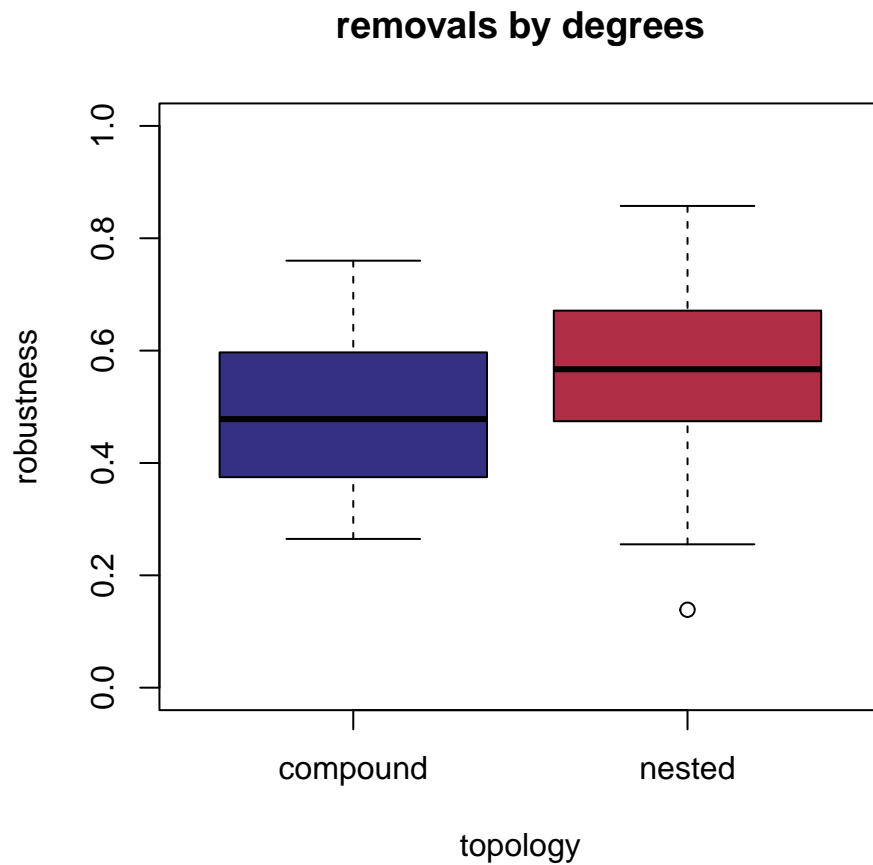
Here, we simulate the exclusion of species on one side of the network (row or columns in the matrix) and analyze the secondary extinctions: species on the other side that lose all interactions. We only used the binary matrices for this analysis.

As the measure of robustness we applied the index proposed by Burgos et al. (2007), which is the area under the secondary extinction curve. We restricted this analysis to nested and compound networks, as they represent the large majority of binary networks (124 out of 142).

9.1 Removal of resource species

We removed the resource species (rows): plants in seed dispersal, pollination and plant-herbivore networks, and hosts in host-parasite networks.

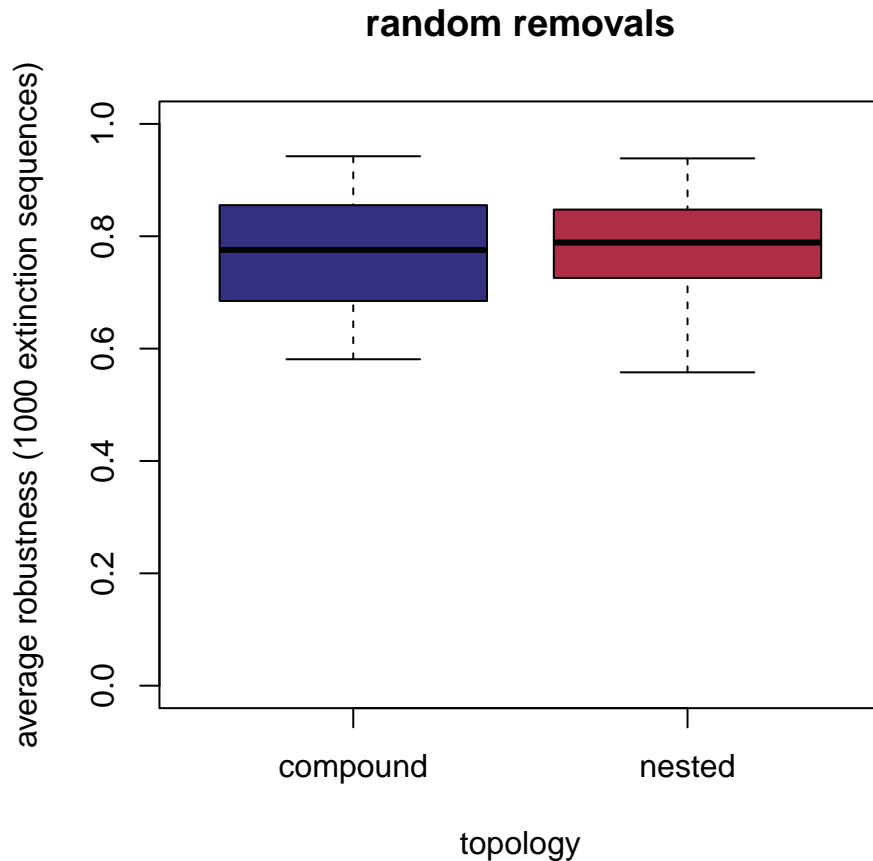
For all nested or compound networks, we measured robustness to resource species removals (1) based on species degrees (more connected to less connected) and (2) randomly. For each network, we made 1000 random extinction sequences and calculated the average robustness.



We performed a non-parametrical Mann-Whitney test to compare the robustness of nested and compound binary networks:

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: ROB_RESULTS$rob_low_deg[criterium3 & ROB_RESULTS$topology == "nested"] and ROB_RESULTS$rob_low_deg[criterium3 & ROB_RESULTS$topology == "compound"]
## W = 2418, p-value = 9e-04
## alternative hypothesis: true location shift is not equal to 0
```

Nested networks were significantly more robust to removals of resource species following decreasing degrees than networks with compound topologies.



We performed a non-parametrical Mann-Whitney test to compare the robustness of nested and compound binary networks:

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: ROB_RESULTS$rob_low_ran[criterium3 & ROB_RESULTS$topology == "nested"] and ROB_RESULTS$rob_low_ran[criterium3 & ROB_RESULTS$topology == "compound"]
## W = 2006, p-value = 0.2
## alternative hypothesis: true location shift is not equal to 0
```

We did not find statistically significant differences in the robustness of nested and compound networks to random sequences of resource species removals.

For networks with compound topologies (n=45) we compared the robustness following two different rules for the sequences of species removals. For each network, using each rule, we made 1000 different sequences of extinctions.

In the first rule, we maximally delay the exclusion of modules (removal of all species of the module). For this, in each round, the resource species to be removed is randomly selected from the module or modules with more remaining resources.

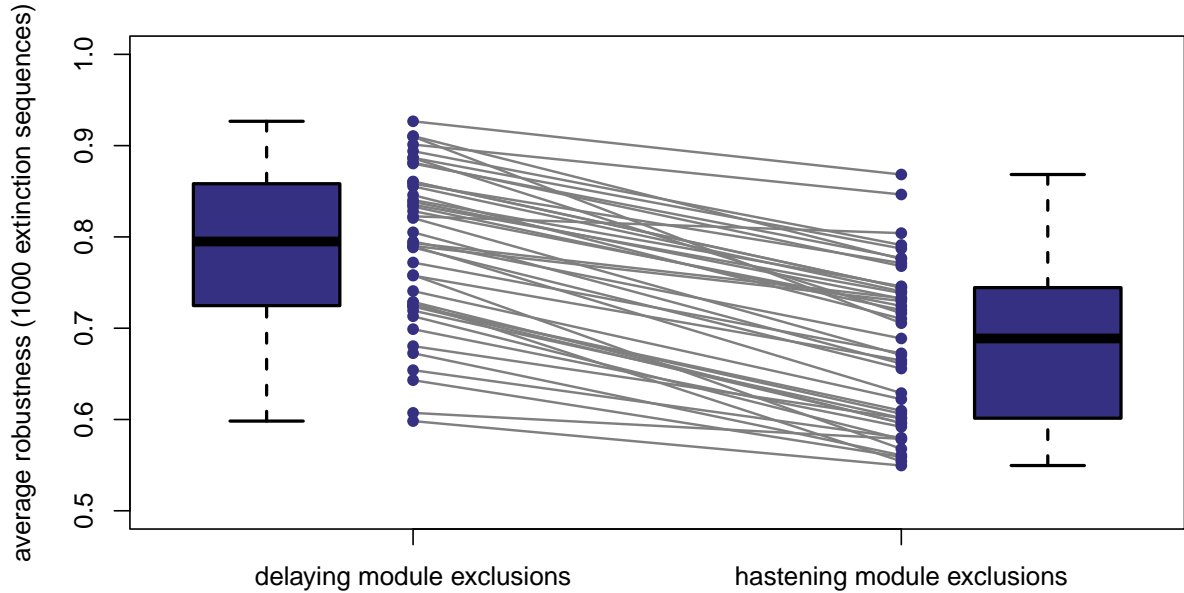
Imagine a network with 15 resource species, distributed among 3 modules: A, B and C. Initially, A has 8 resources, B has 4 and C has 3. This is a possible sequence of removals following rule 1.

remaining species in each module -> action

A=8 B=4 C=3 -> remove a random species from A
 A=7 B=4 C=3 -> remove a random species from A
 A=6 B=4 C=3 -> remove a random species from A
 A=5 B=4 C=3 -> remove a random species from A
 A=4 B=4 C=3 -> remove a random species from A or B
 A=4 B=3 C=3 -> remove a random species from A
 A=3 B=3 C=3 -> remove a random species from A, B or C
 A=2 B=3 C=3 -> remove a random species from B or C
 A=2 B=3 C=2 -> remove a random species from B
 A=2 B=2 C=2 -> remove a random species from A, B or C
 A=2 B=1 C=2 -> remove a random species from A or C
 A=2 B=1 C=1 -> remove a random species from A
 A=1 B=1 C=1 -> remove a random species from A, B or C
 A=1 B=0 C=1 -> remove a random species from A or C
 A=0 B=0 C=1 -> remove a random species from C
 A=0 B=0 C=0 - End of extinction sequence

The second rule for species removals aims at hastening the exclusion of modules. Therefore, for each sequence of removals, we randomly define the order of modules to be tackled. All modules have the same chance of being selected in any position. Then, we proceed by removing species from the first defined module, until it is fully excluded, then we move to the next and so on.

Imagine a network with 15 resource species, distributed among 3 modules: A, B and C. Initially, A has 8 resources, B has 4 and C has 3. First we define a random order of modules: B - A - C. In the first 4 rounds, random species of module B would be removed, then in the next 8 rounds, the species of A are removed, and finally, in the last 3 rounds, the species of C are removed.



We performed non-parametrical Mann-Whitney tests for each compound network to compare its robustness

to sequences of removals following the two rules:

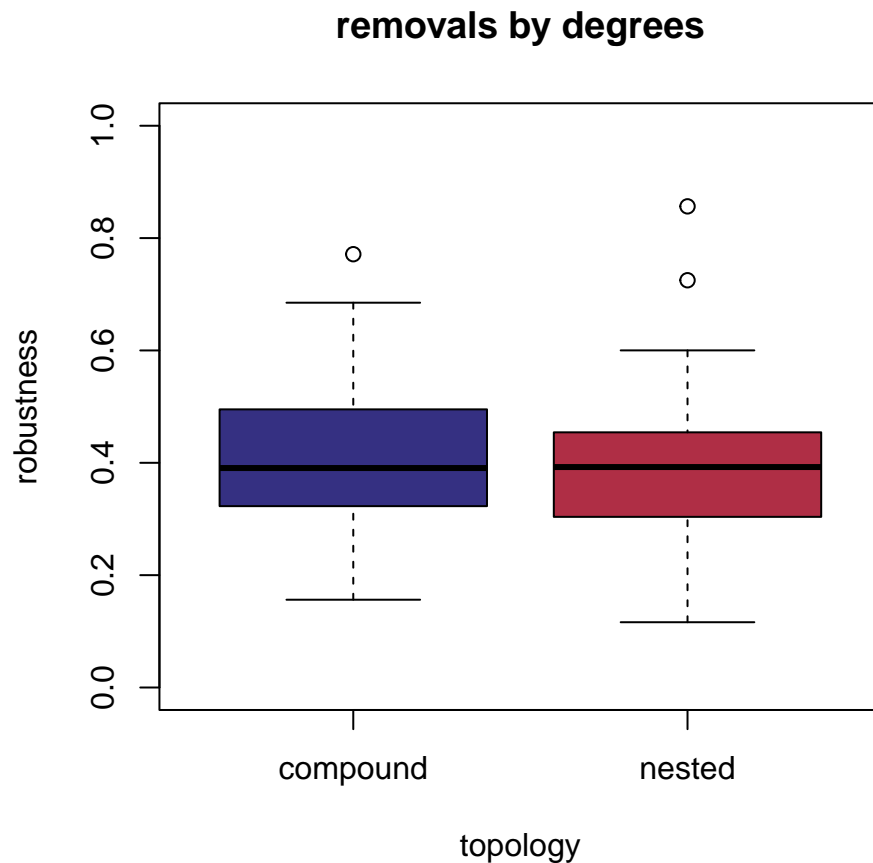
networks	statistic	pvalue
TP-011	188926	3.21e-128
TP-015	299648	2.69e-54
TP-017	171359	7.06e-143
TP-018	135961	7.49e-175
TP-019	137192	1.10e-173
TP-020	45698	3.87e-271
TP-023	170517	1.34e-143
TP-027	11434	0.00e+00
TP-030	71585	2.35e-241
TP-031	107008	1.99e-203
TP-040	166078	1.93e-147
TP-041	62911	3.85e-251
TP-042	66638	6.51e-247
TP-043	208392	6.49e-113
TP-044	96950	7.26e-214
TP-047	185436	4.55e-131
TP-056	105951	1.64e-204
TP-071	675	0.00e+00
TP-081	254008	6.61e-81
TP-082	166063	1.87e-147
TP-083	61636	1.35e-252
TP-085	214515	2.65e-108
TP-087	255918	1.10e-79
TP-104	142382	8.16e-169
TP-106	87285	3.83e-224
TP-118	6233	0.00e+00
TP-120	20352	5.47e-302
TP-122	127267	3.33e-183
TP-124	149919	7.44e-162
TP-126	215239	9.15e-108
TP-133	30804	4.59e-289
TP-137	434183	3.45e-07
TP-140	139086	6.73e-172
TP-143	0	0.00e+00
TP-147	3364	0.00e+00
TP-148	187812	3.99e-129
TP-149	161120	8.61e-152
TP-157	305363	2.45e-51
TP-158	9	0.00e+00
TP-160	353891	1.11e-29
TP-073	29056	3.31e-291
TP-075	203579	1.32e-116
TP-076	153945	3.36e-158
TP-077	246706	1.15e-85
TP-072	306349	7.76e-51

All networks were significantly more robust to sequences of removals that delay the exclusion of modules than to sequences of removals that hasten the exclusion of modules.

9.1 Removal of consumer species

We removed the consumer species (rows): animals in seed dispersal, pollination and plant-herbivore networks, and parasites in host-parasite networks.

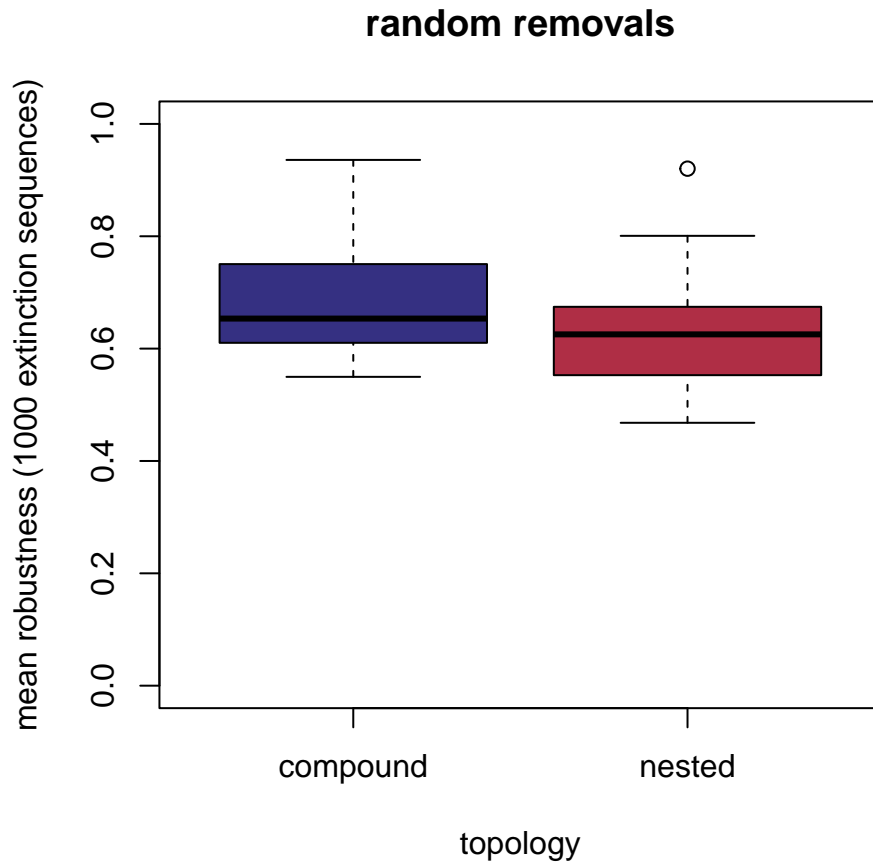
For all nested or compound networks, we measured robustness to consumer species removals (1) based on species degrees (more connected to less connected) and (2) randomly. For each network, we made 1000 random extinction sequences and calculated the average robustness.



We performed a non-parametrical Mann-Whitney test to compare the robustness of nested and compound binary networks:

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: ROB_RESULTS$rob_high_deg[criterium3 & ROB_RESULTS$topology == "nested"] and ROB_RESULTS$rob_h
## W = 1601, p-value = 0.4
## alternative hypothesis: true location shift is not equal to 0
```

We did not find statistically significant differences in the robustness of nested and compound networks to sequences of consumer species removals by decreasing degrees.



We performed a non-parametrical Mann-Whitney test to compare the robustness of nested and compound binary networks:

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: ROB_RESULTS$rob_high_ran[criterium3 & ROB_RESULTS$topology == "nested"] and ROB_RESULTS$rob_h
## W = 1190, p-value = 0.002
## alternative hypothesis: true location shift is not equal to 0
```

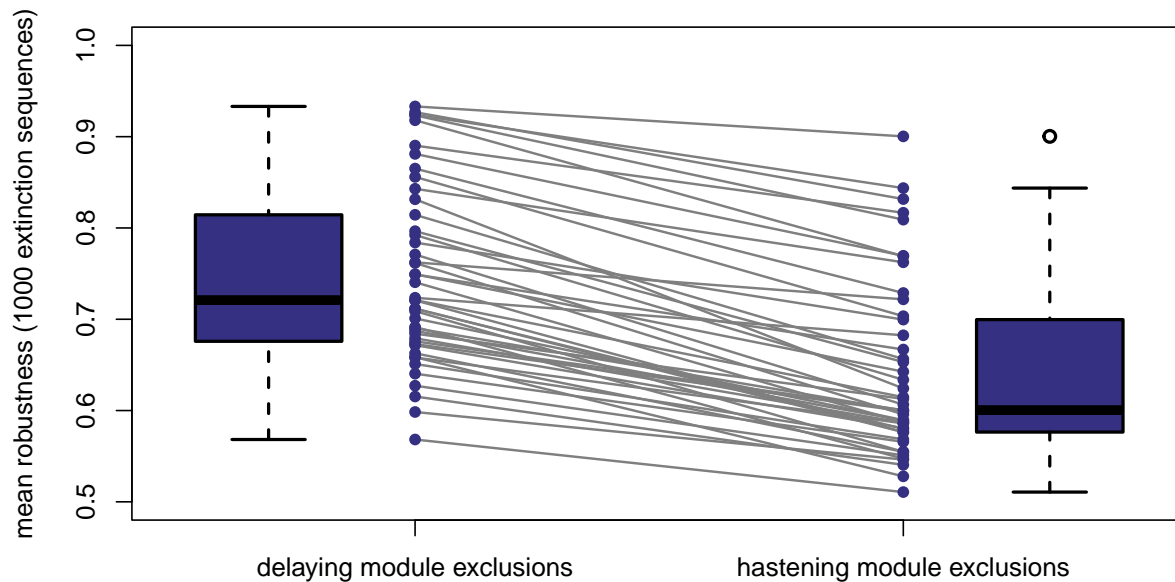
Networks with compound topologies were significantly more robust to random removals of consumer species than nested networks.

For networks with compound topologies (n=45) we compared the robustness following two different rules for the sequences of species removals. For each network, using each rule, we made 1000 different sequences of extinctions.

In the first rule, we maximally delay the exclusion of modules (removal of all species of the module). For this, in each round, the consumer species to be removed is randomly selected from the module or modules with more remaining resources.

The second rule for species removals aims at hastening the exclusion of modules. Therefore, for each sequence of removals, we randomly define the order of modules to be tackled. All modules have the same chance of

being selected in any position. Then, we proceed by removing species from the first defined module, until it is fully excluded, then we move to the next and so on.



We performed non-parametrical Mann-Whitney tests for each compound network to compare its robustness to sequences of removals following the two rules:

networks	statistic	pvalue
TP-011	131410	3.36e-179
TP-015	271383	3.53e-70
TP-017	176814	3.06e-138
TP-018	124170	3.16e-186
TP-019	140845	3.02e-170
TP-020	231557	5.53e-96
TP-023	289071	5.62e-60
TP-027	141808	2.40e-169
TP-030	176688	2.40e-138
TP-031	152307	1.11e-159
TP-040	27135	1.44e-293
TP-041	121205	3.83e-189
TP-042	249403	6.83e-84
TP-043	173194	2.61e-141
TP-044	16402	6.02e-307
TP-047	277304	1.21e-66
TP-056	268833	1.15e-71
TP-071	48358	5.35e-268
TP-081	56333	1.08e-258
TP-082	178684	1.14e-136
TP-083	202248	1.22e-117
TP-085	262847	2.50e-75

networks	statistic	pvalue
TP-087	355728	5.56e-29
TP-104	187061	9.73e-130
TP-106	92197	6.87e-219
TP-118	49434	9.85e-267
TP-120	217014	1.89e-106
TP-122	95373	1.59e-215
TP-124	74916	1.19e-237
TP-126	226009	6.53e-100
TP-133	118776	1.50e-191
TP-137	5767	0.00e+00
TP-140	130261	2.64e-180
TP-143	6468	0.00e+00
TP-147	0	0.00e+00
TP-148	177121	5.56e-138
TP-149	169544	1.94e-144
TP-157	3943	0.00e+00
TP-158	132	0.00e+00
TP-160	277363	1.21e-66
TP-073	3879	0.00e+00
TP-075	184494	7.66e-132
TP-076	144690	1.15e-166
TP-077	98663	4.54e-212
TP-072	19113	1.54e-303

All networks were significantly more robust to sequences of removals that delay the exclusion of modules than to sequences of removals that hasten the exclusion of modules.

10. References

- D. P. Vázquez, et al., Species abundance and asymmetric interaction strength in ecological networks. *Oikos* 116, 1120–1127 (2007).
- E. Burgos, et al. Why nestedness in mutualistic networks? *Journal of Theoretical Biology* 249, 307–313 (2007).
- M. Almeida-Neto, P. Guimarães, P. R. Guimarães, R. D. Loyola, W. Ulrich, A consistent metric for nestedness analysis in ecological systems: reconciling concept and measurement. *Oikos* 117, 1227–1239 (2008).
- C. O. Flores, S. Valverde, J. S. Weitz, Multi-scale structure and geographic drivers of cross-infection within marine bacteria and phages. *ISME J.* 7, 520–532 (2013).
- S. J. Beckett, Improved community detection in weighted bipartite networks. *R. Soc. Open Sci.* 3, 140536 (2016).
- R. B. P. Pinheiro, G. M. F. Felix, C. F. Dormann, M. A. R. Mello, A new model explaining the origin of different topologies in interaction networks. *Ecology* 100, 1–30 (2019).
- G. M. Felix, R. B. P. Pinheiro, R. Poulin, B. R. Krasnov, M. A. R. Mello, The compound topology of host–parasite networks is explained by the integrative hypothesis of specialization. *Oikos* 2022 (2022).