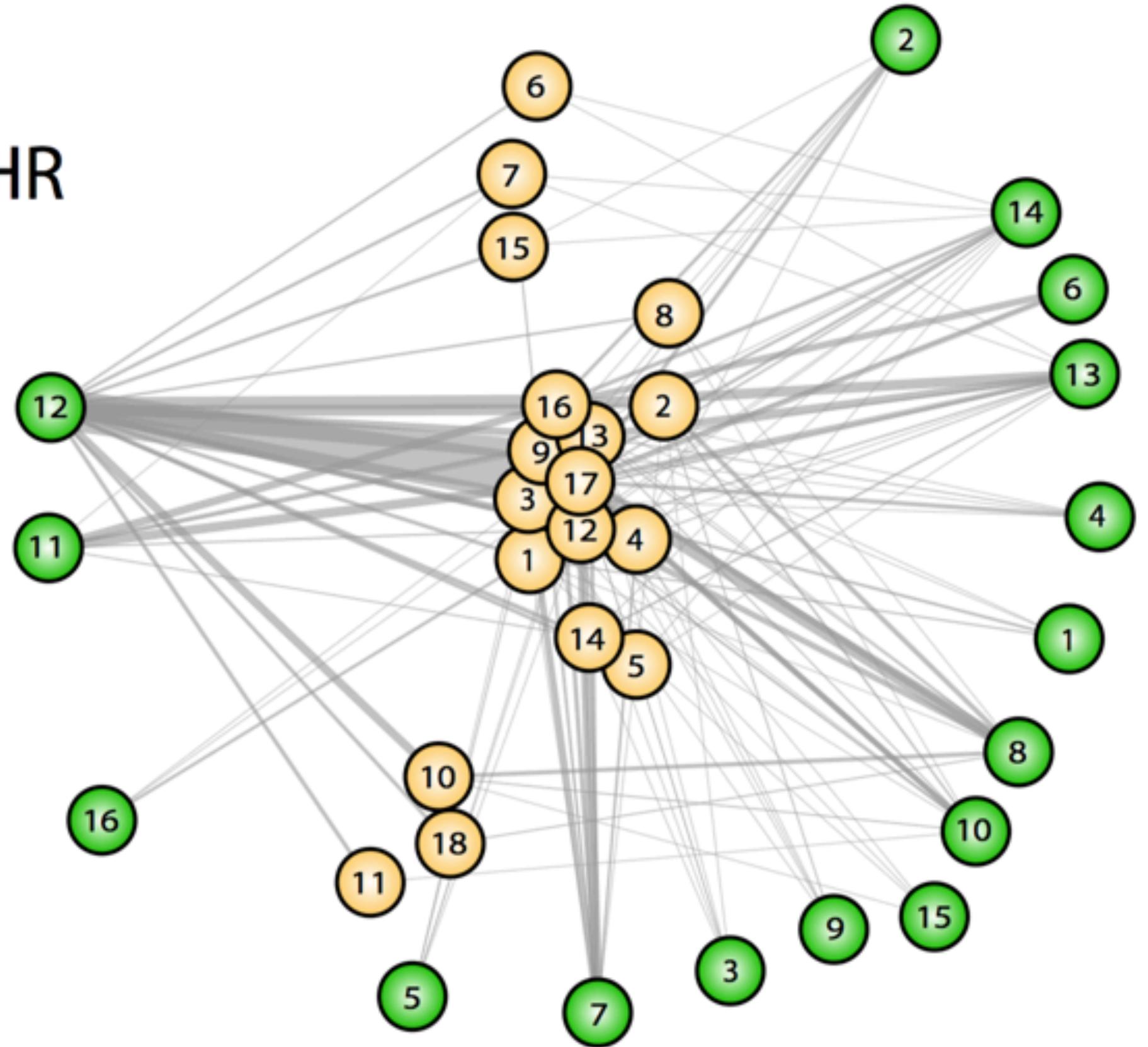


HR

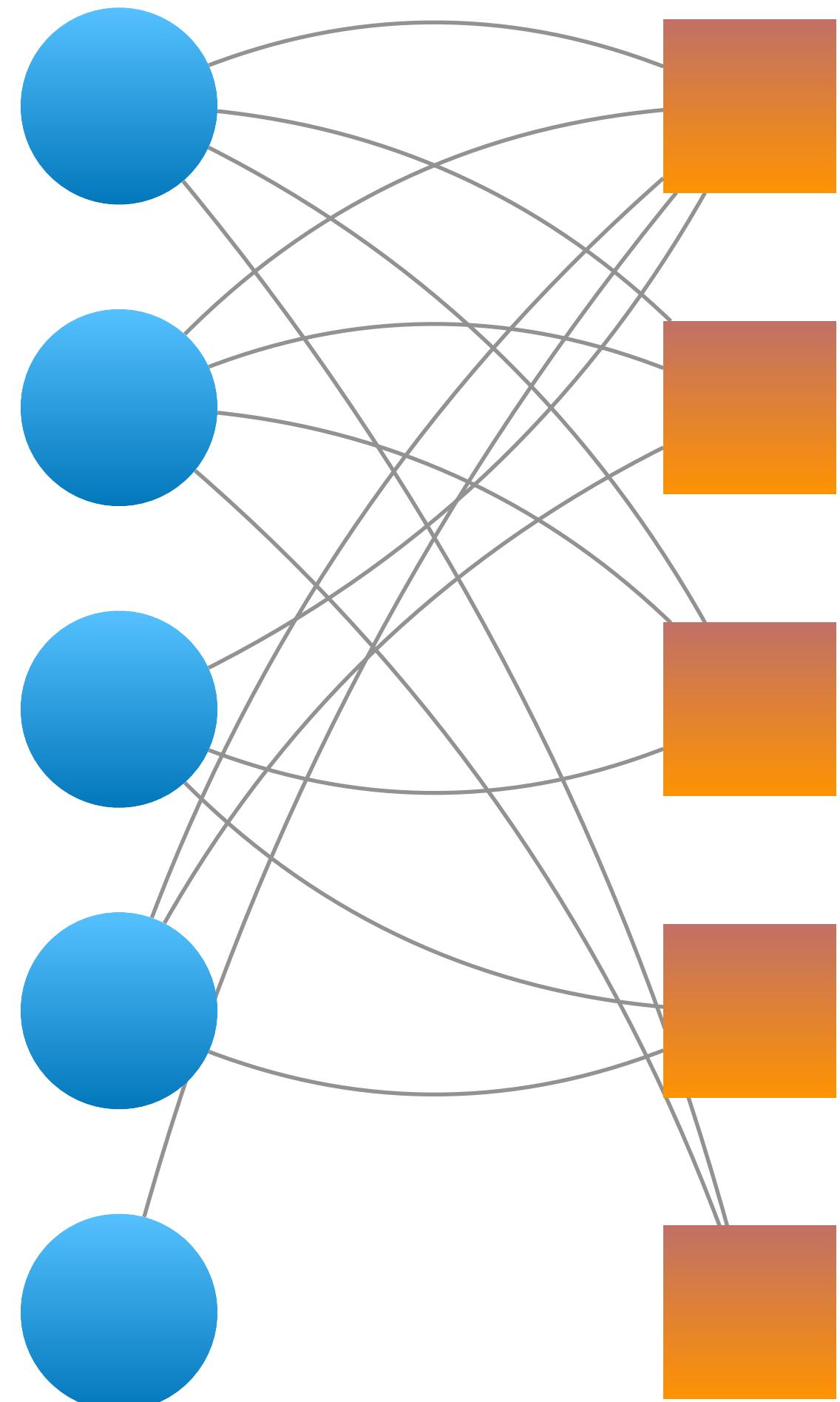


ERGMs

Pedro Jordano

$$\Pr(y_{ij} = 1 | Y_{ij}^C) = \frac{1}{c} \exp \sum_{k=1}^K \theta_k z_k(y)$$

Sevilla, 15 Sept 2021



ERGMs

An ERGM is a true generative statistical model of network structure and characteristics. Also known as p^* models.

Exponential random graph models (ERGMs) are statistical models for network structure, permitting inferences about how network links are patterned. ERGMs are link-based models for understanding how and why network links arise.

This means that inferential hypotheses can be proposed and tested. It is generative in the sense that characteristics of the individual elements in the network (i.e., nodes) and local structural properties can be used to predict properties of the entire network (e.g., diameter, degree distribution, etc.).

1. ERGMs can handle the complex dependencies of network data without the types of degeneracy problems that were frequently encountered in earlier network models.
2. ERGMs are flexible and can handle many different types of predictors and covariates.
3. The generative approach where overall network characteristics are predicted from individual node and local structural properties enhances the validity of the models.

ERGM specification

		Through a dependence assumption, a researcher makes claims about the type, extent, and accumulation of patterning that builds the network.
$G = (V, E)$.	A graph.	
$Y_{ij} = Y_{ji}$	Links.	Dependence is crucial. Independence of observations – the fundament of general linear model statistical techniques – cannot simply be presupposed. The presence of some links will encourage other links to come into existence, to be maintained, or to be destroyed.
$\mathbf{Y} = [Y_{ij}]$	An observed graph.	The dependence assumption is thereby a theory about the basis of link-formation processes. The network's self-organizing principles represent the way that links lead to other links (or their absence).
$\mathbf{y} = [y_{ij}]$	A realization.	The observable configurations of links then constitute the network's structural signature.

ERGM specification

Probability of graph G given parameters θ ; y_{ij} is a particular realization of Y

Probability of link=1 given the status of the rest of links in the network

$$Pr(y_{ij} = 1 | Y_{ij}^C) = \frac{1}{c} \exp \sum_{k=1}^K \theta_k z_k(y)$$

Parameter 1

Statistic 1

$$\theta_1 z_1(G) + \theta_2 z_2(G) + \cdots + \theta_p z_p(G)$$

Exponential random graph models (ERGMs)¹ are designed in direct analogy to the classical generalized linear models (GLMs).

ERGMs are fit using Monte Carlo Markov Chain maximum-likelihood estimation (MCMC).

ERGM specification

The model is predicting the probability of a link between nodes i and j , conditional on the rest of the network (all other links).

The thetas (θ_k) are the coefficients of the network statistics of interest, one for each of the K included statistics, $z_k(y)$.

$1/c$ is simply a normalizing constant that ensures that the probabilities stay within 0 and 1.

The statistics (Z) are analogous to independent variables- they can be node covariates, dyad predictors, and or local network structural characteristics (~motifs).

$$Pr(y_{ij} = 1 | Y_{ij}^C) = \frac{1}{c} \exp \sum_{k=1}^K \theta_k z_k(y)$$

$$\theta_1 z_1(G) + \theta_2 z_2(G) + \cdots + \theta_p z_p(G)$$

ERGM specification

ERGM terms	
Predictor type	Term
Node	nodefactor
	nodecov
Dyad	nodemix
	nodematch
Relation Structure	absdiff
	edgecov
	gwdegree
	gwdsp
	gwesp

$$Pr(y_{ij} = 1 | Y_{ij}^C) = \frac{1}{c} \exp \sum_{k=1}^K \theta_k z_k(y)$$

- ~ Node characteristics
- ~ Dyad predictors (links). When you hypothesize that the characteristics of both nodes in a dyad may influence the probability of observing a link between those two nodes.
- ~ Information about local structural properties of the observed network can be used as model covariates. Allows the network model to be conditioned on e.g., the observed degree distribution, or on the level of transitivity (closed triangles), etc., that is observed or any other motif(s).

ERGM specification

Null model.

It is the one with no substantive structural predictors. A baseline model.

The simplest ERGM model has just a term, `edges`. It yields a network that has exactly the same number of links as the observed network.

```
Model01 <- ergm(TCdiss ~ edges,  
                  control= control.ergm(seed=40))
```

`edges` is a type of intercept for the model, and ensures that the simulated networks have the same number of edges as the observed network.

The probability of any link (aka the density of the network) is the inverse-logit of the coefficient on `edges`.

The logistic transformation of the `edges` parameter, gives the overall density of network.

```
plogis(coef(Model01))  
## edges # log-odds of p/n equals log(p / (n-p))  
## 0.343 log(89 / (252 - 89))
```

```
library(ergm)  
DSmod0 <- ergm(TCdiss ~ edges,  
                 control=control.ergm(seed=40))  
class(DSmod0)  
## [1] "ergm"  
summary(DSmod0)  
##  
## =====  
## Summary of model fit  
## =====  
## Formula: TCdiss ~ edges  
##  
## Iterations: 4 out of 20  
##  
## Monte Carlo MLE Results:  
## Estimate Std. Error MCMC % p-value  
## edges -0.648 0.122 0 <1e-04  
##  
## Null Deviance: 416 on 300 degrees of freedom  
## Residual Deviance: 386 on 299 degrees of freedom  
##  
## AIC: 388 BIC: 392 (Smaller is better.)
```

ERGM specification

Models

Including predictors

- Main effects terms based on node traits.
- Dyad predictors based on properties of links.
- Structural predictors based on counts of “motifs” that have biological interpretation.

```
305 ## Bipartite network: models with explanatory variables (valued ERGMs)
306
307 I set models including different descriptor variables:
308
309 `# Variables:
310 `# class, order, family, genus, species: higher taxonomic level and species`
311 `# spcode, code for species name` `# w, body mass (g)`
312 `# g, gape width for animals, fruit diameter for plants, mm`
313 `# f, proportion of fruits in diet` `# a, local abundance (no. birds/ha)`
314 `# geog,geographic area (no. localities with presence in 19 sites in S Spain)`
315 `# ph, phenology, no. months present in the area or with ripe fruits available`
316 `# pp, ps, pa, pu, proportions of forbidden interactions due to plehnological`
317 `# mismatch, size mismatch, accesibility constraints, and unknown causes`
318 `# hab, main habitat type` `# diet, diet category` `# forag, foraging mode`
319 `# noct, is nocturnal?` `# nativ,is native? (0 codes non native species)`
320 `# frlen, fruit length, mm` `# fleshy, is the fruit fleshy?` `# seedm, seed dry mass (mg)`
321 `# height, plant height (m)` `# grwform, growth form`
```

ERGM specification

Models

Including predictors

We can model quantitative networks by specifying "form="sum" argument for one of the terms inherited from binary ERGMs, though this not required, as it's the default.

Also, note that for valued ERGMs, the "intercept" term is sum, not edges. The sum-term represents an intercept term for edge counts. It controls for the expected number of interactions (i.e., edge counts) in the multi-edge network.

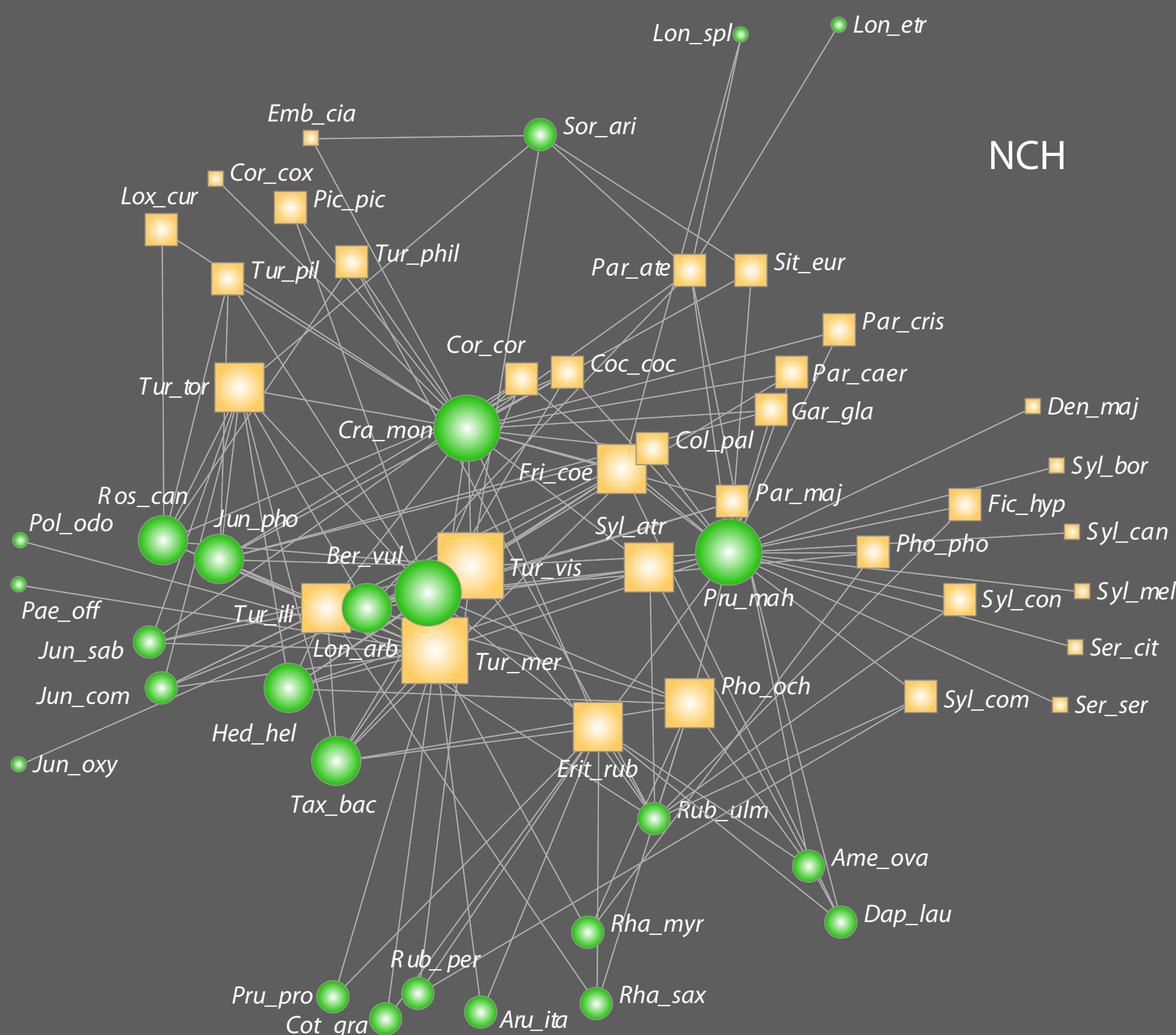
The `b1cov` terms represent the effects of each attribute of the plant nodes (first set of nodes in the bipartite network). The `b2cov` terms represent the effects of attributes of the animals (second set of nodes).

```
361 ergm01 <- ergm(int.s.NCH ~ edges
362                                     #+ b1cov("w")
363                                     + b1cov("g")
364                                     #+ b1cov("f")
365                                     + b1cov("a")
366                                     + b1cov("geog")
367                                     + b1cov("ph")
368                                     #+ b1cov("pp")
369                                     #+ b1cov("ps")
370                                     #+ b1cov("pu")
371                                     #+ b1cov("hab")
372                                     #+ b1cov("diet")
373                                     #+ b2cov("w")
374                                     + b2cov("g")
375                                     #+ b2cov("f")
376                                     + b2cov("a")
377                                     + b2cov("geog")
378                                     + b2cov("ph")
379                                     #+ b2cov("pp")
380                                     #+ b2cov("ps")
381                                     #+ b2cov("pu")
382                                     #+ b2cov("hab")
383                                     #+ b2cov("diet")
384                                     , response = "weight", reference= ~Poisson
385 )
386 summary(ergm01)
387 mcmc.diagnostics(ergm01)
```

ERGM specification

Models

Including predictors.



```
361 ergm01 <- ergm(int.s.NCH ~ edges
362               #+ b1cov("w")
363               + b1cov("g")
364               #+ b1cov("f")
365               + b1cov("a")
366               + b1cov("geog")
367               + b1cov("ph")
368               #+ b1cov("pp")
369               #+ b1cov("ps")
370               #+ b1cov("pu")
371               #+ b1cov("hab")
372               #+ b1cov("diet")
373               #+ b2cov("w")
374               + b2cov("g")
375               #+ b2cov("f")
376               + b2cov("a")
377               + b2cov("geog")
378               + b2cov("ph")
379               #+ b2cov("pp")
380               #+ b2cov("ps")
381               #+ b2cov("pu")
382               #+ b2cov("hab")
383               #+ b2cov("diet")
384 , response = "weight", reference= ~Poisson
385 )
386 summary(ergm01)
387 mcmc.diagnostics(ergm01)
```

ERGM specification

Models

Interpretation of outputs.

```
NCH1 <- ergm(NCH ~ ergm(int.s.NCH ~ edges
                  + b1cov(c("g"))
                  + b2cov(c("g"))),
                  control= control.ergm(seed=40))
summary(NCH1)

##
## =====
## Summary of model fit
## =====
##
## Formula:
##
## NCH ~ ergm(int.s.NCH ~ edges
##                  + b1cov(c("g"))
##                  + b2cov(c("g")))
##
## Iterations: 16 out of 20
##
```

```
## Monte Carlo MLE Results:
##
##          Estimate   Std. Error
## edges     -1.6783    0.3293
## b1cov.g  -3.447E-04 93.5551. # fruit diameter
## b2cov.g   0.3677    0.0228 # gape width
##
##          MCMC % p-value
## edges        0 <1e-04
## b1cov.g      0  0.9847
## b2cov.g      0  0.0091
##
##          Null Deviance: 416 on 300 degrees of freedom
## Residual Deviance: 323 on 297 degrees of freedom
##
## AIC: 329    BIC: 341 (Smaller is better.)
```

The `b1cov` terms represent the effects of each attribute of the plant nodes (first set of nodes in the bipartite network).

The `b2cov` terms represent the effects of attributes of the animals (second set of nodes).

ERGM specification

Models

Interpretation of outputs

```
> summary(ergm01)
Call:
ergm(formula = int.s.NCH ~ edges + b1cov("g") + b1cov("a") +
      b1cov("geog") + b1cov("ph") +
      b2cov("g") + b2cov("a") +
      b2cov("geog") + b2cov("ph"),
      response = "weight", reference = ~Poisson)
```

Monte Carlo Maximum Likelihood Results:

	Estimate	Std. Error	MCMC %	z value	Pr(> z)
nonzero	-1.457e+01	2.953e-01	0	-49.331	<1e-04 ***
b1cov.sum.g	6.770e-02	5.138e-03	0	13.176	<1e-04 ***
b1cov.sum.a	-4.400e-02	2.828e-03	0	-15.562	<1e-04 ***
b1cov.sum.geog	2.113e-01	3.972e-03	0	53.209	<1e-04 ***
b1cov.sum.ph	-9.440e-02	4.550e-03	0	-20.744	<1e-04 ***
b2cov.sum.g	-3.447e-04	2.085e-03	0	-0.165	0.869
b2cov.sum.a	1.125e-01	3.223e-03	0	34.899	<1e-04 ***
b2cov.sum.geog	2.829e-02	3.273e-03	0	8.645	<1e-04 ***
b2cov.sum.ph	-1.343e-03	2.267e-03	0	-0.593	0.553

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

The `b1cov` terms represent the effects of each attribute of the plant nodes (first set of nodes in the bipartite network). The `b2cov` terms represent the effects of attributes of the animals (second set of nodes).

NOTE on P-values:

the theoretical justification for the asymptotic chi-square and F-distributions used by ergm to compute these values has not been established formally to date. Therefore, **INTERPRET THESE VALUES INFORMALLY**, just as additional summary statistics.

ERGM specification

Models

Interpretation of outputs

Coefficient interpretation

As in a logistic regression.

In order to interpret the coefficients, it is useful to think in terms of the probability of a given node pair having a link, conditional on the link status between all other pairs.

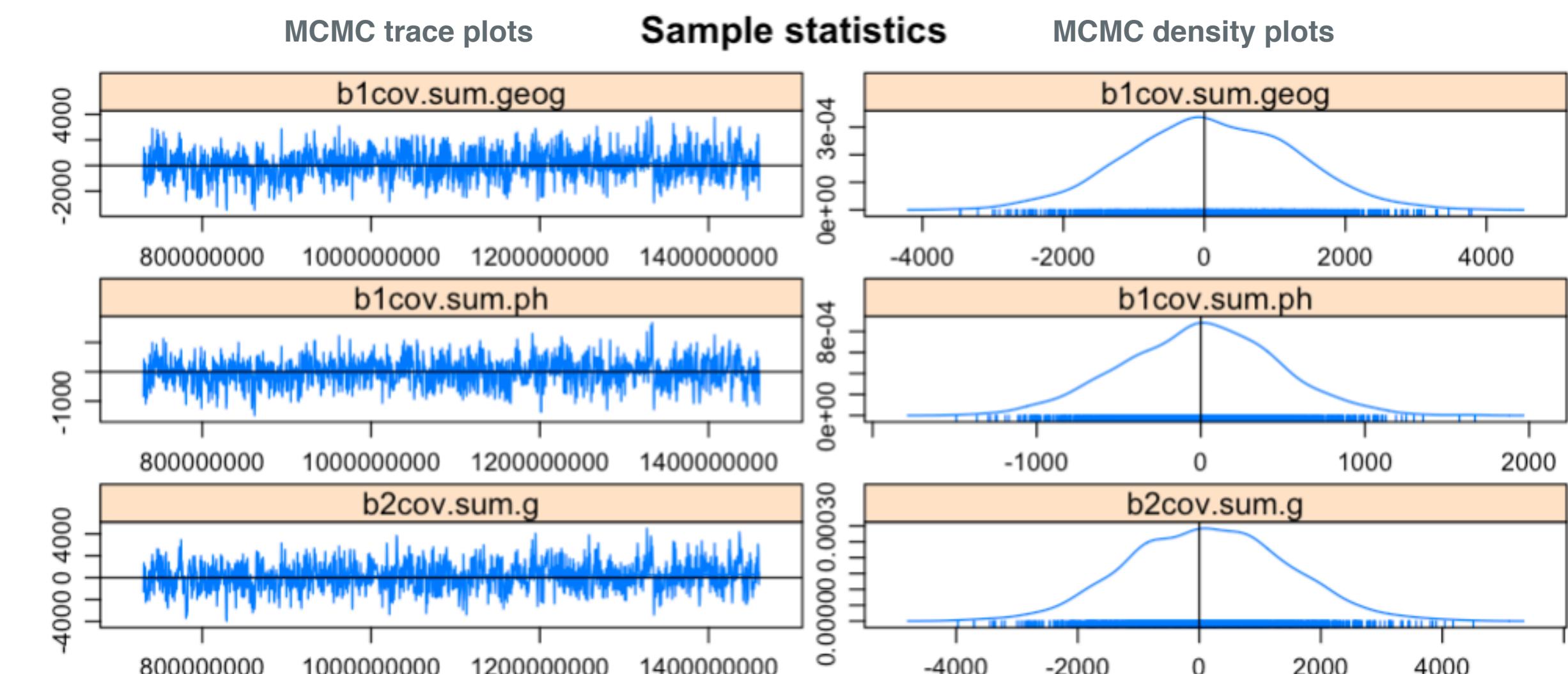
```
# Prob interaction fruit diameter and gape size  
> plogis(-1.6783 + (0.0677*8.3) + (-0.0003447*5.2))  
[1] 0.2463486
```

MCMC diagnostics available.

```
summary(ergm03)  
mcmc.diagnostics(ergm03)
```

GOF not available for bipartite networks (either binary or weighted).

```
## Monte Carlo MLE Results:  
##  
## Estimate Std. Error  
## edges -1.6783 0.3293  
## b1cov.g 7.9366 93.5551  
## b2cov.g 0.0599 0.0228  
##  
## MCMC % p-value  
## edges 0 <1e-04  
## b1cov.g 0 0.0091  
## b2cov.g 0 0.9847  
##  
## Null Deviance: 416 on 300 degrees of freedom  
## Residual Deviance: 323 on 297 degrees of freedom  
##  
## AIC: 329 BIC: 341 (Smaller is better.)
```



ERGM specification

Models

Interpretation of outputs.

More on coefficient interpretation

The model coefficients for exogenous variables represent the effects of plant or animal attributes on the likelihood of any plant–animal pair to increase the number of interactions. They indicate the expected change in the logged number of interactions between any plant–animal pair increasing (or decreasing) as a function of a given one-unit change in a specific plant or pollinator attribute.

The estimated coefficient of each attribute statistic in ERGM may be interpreted as a conditional log-odds ratio for fruit diameter or gape width.

For example, fruit diameter, just slightly increases the odds of interaction by a factor of $\exp(-3.447E-04) \approx 0.9996554$, or <50 %.

Similarly, gape size more than doubles the odds of interaction, since $\exp(0.3677) \approx 1.444409$.

Note for which variables the coefficient differs from zero by at least one standard error, suggesting some nontrivial effect of these variables on the formation of network ties.

```
## Monte Carlo MLE Results:  
##  
## Estimate Std. Error  
## edges -1.6783 0.3293  
## b1cov.g -3.447E-04 93.5551. # fruit diameter  
## b2cov.g 0.3677 0.0228 # gape width  
##  
## MCMC % p-value  
## edges 0 <1e-04  
## b1cov.g 0 0.9847  
## b2cov.g 0 0.0091  
##  
## Null Deviance: 416 on 300 degrees of freedom  
## Residual Deviance: 323 on 297 degrees of freedom  
##  
## AIC: 329 BIC: 341 (Smaller is better.)
```

```
# Prob interaction fruit diameter and gape size  
> plogis(-1.6783 + (-0.0003447*8.3) + (0.3677*5.2))  
[1] 0.5574647
```

ERGM specification

$$\theta_1 z_1(G) + \theta_2 z_2(G) + \cdots + \theta_p z_p(G)$$

Parameter 1 Statistic 1

The diagram shows two blue arrows pointing downwards from the labels 'Parameter 1' and 'Statistic 1' towards the corresponding terms in the equation below. The first arrow points to θ_1 , and the second arrow points to $z_1(G)$.

Models

Including Dyadic Predictors and Relational Terms (Network predictors)

Dyadic Predictors

Hypotheses for network structures derive from questions about homophily and heterophily.

That is, are ties more or less likely between network members who are similar to each other on some characteristic (homophily) or dissimilar (heterophily). This is a type of dyadic interaction predictor, and ergm includes a number of these terms.

ERGM specification

Relational Terms (Network Predictors)

Hypotheses for network structures also derive from local structure, i.e., frequencies of interaction modes. ERGMs can include some information about local structural tendencies, such as the tendency for directed ties to be reciprocated, or transitivity of links (e.g., in unipartite networks).

These types of predictors lead to what are called dyadic-dependency models, and these present many more computational and statistical challenges. THERE IS NO THEORY FOR DYADIC DEPENDENCE MODELS OR LOCAL STRUCTURAL COVARIATES IN ECOLOGY.

RECALL: Predictor variables can be node-based, dyadic and local structural covariates.

Node-based covariates model how node attributes affect the number of links they establish (e.g. plant size).

Dyadic covariates explain differences in link values between two nodes as outcomes of other kinds of relationships between those nodes (i.e. link attributes, e.g., spatial distance between plants).

Structural covariates, also called ‘network statistics’, describe aspects of network topology that are expected to affect link formation, being the total number of link weights the most basic structural term in weighted ERGMs.

ERGM specification

Relational Terms (Network Predictors)

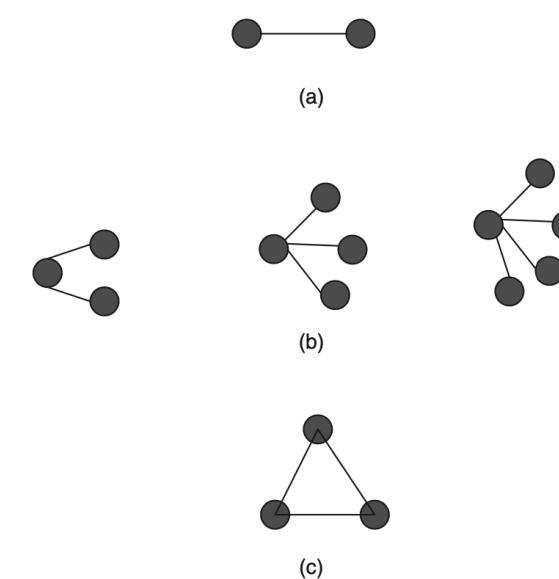
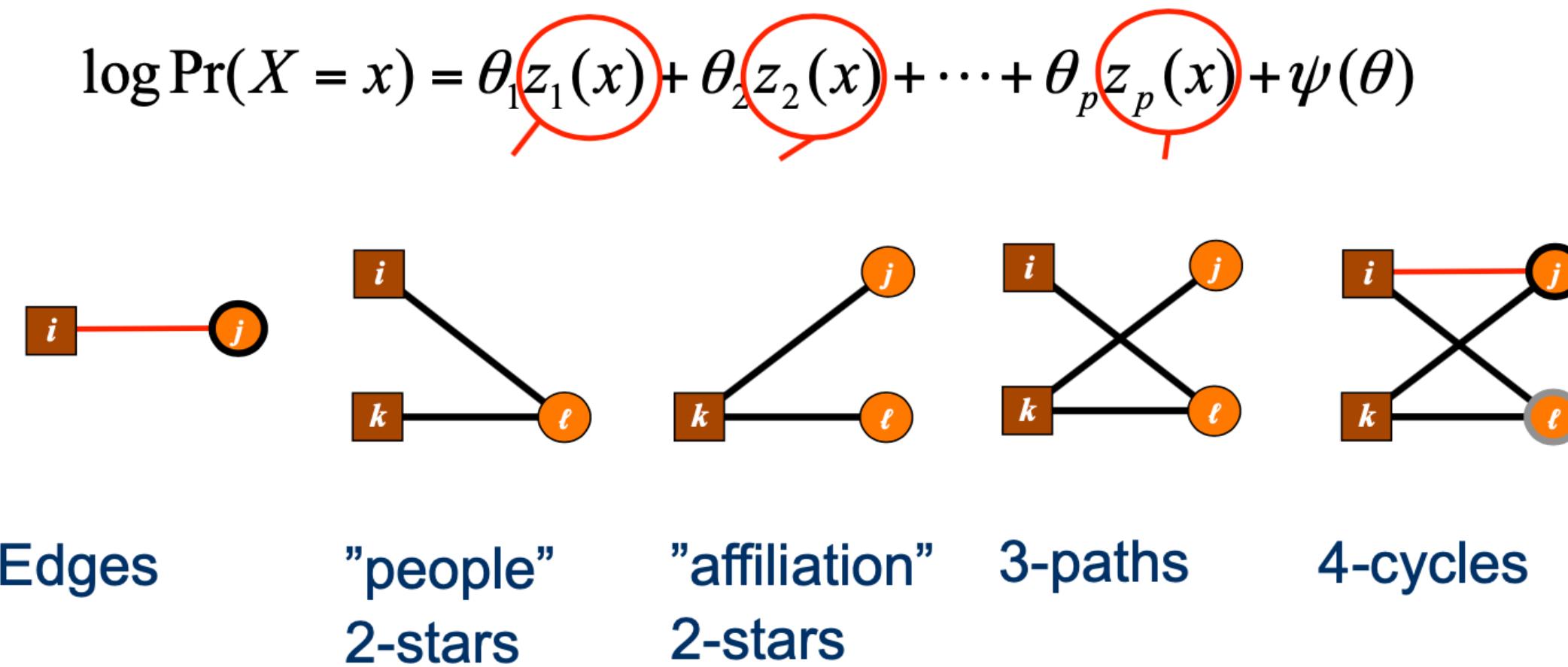


Figure 32.1 Configurations for Markov random graph model for undirected graphs (a) edge; (b) 2-star, 3-star, 4-star (higher-order star configurations may also be included); (c) triangles

The model is the same as for one-mode networks (Wang et al., 2007)



The network statistics are counts of the number of network configurations in the given network G , or some function of those counts. These configurations are small, local subgraphs in the network. In short, the probability of the network depends on how many of those configurations are present, and the parameters inform us of the importance of each configuration.

$$L(x) = \# \text{ (edge)} \quad S_2(x) = \# \text{ (2-star)} \quad S_3(x) = \# \text{ (3-star)} \quad T(x) = \# \text{ (triangle)}$$

```
Estim2 <- ergm(BusyNetNet ~ kstar(1:3) + triangles)
summary(Estim2)
```

Summary of model fit

Formula: BusyNetNet ~ kstar(1:3) + triangles

Newton-Raphson iterations: 42
MCMC sample of size 10000

Monte Carlo MLE Results:

	Estimate	Std. Error	MCMC s.e.	p-value
kstar1	-1.6130	0.6699	0.462	0.0176 *
kstar2	0.7492	0.6407	0.455	0.2446
kstar3	-0.5408	0.3574	0.225	0.1330
triangle	1.4837	0.4592	0.138	0.0016 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

$\hat{\tau}_{MLE}$

ERGM specification

Relational Terms (Network Predictors) Bipartite networks

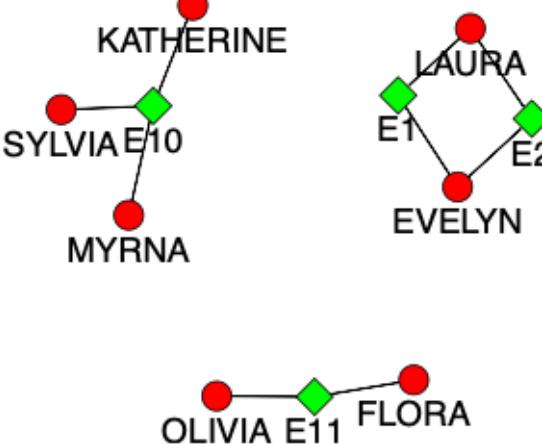
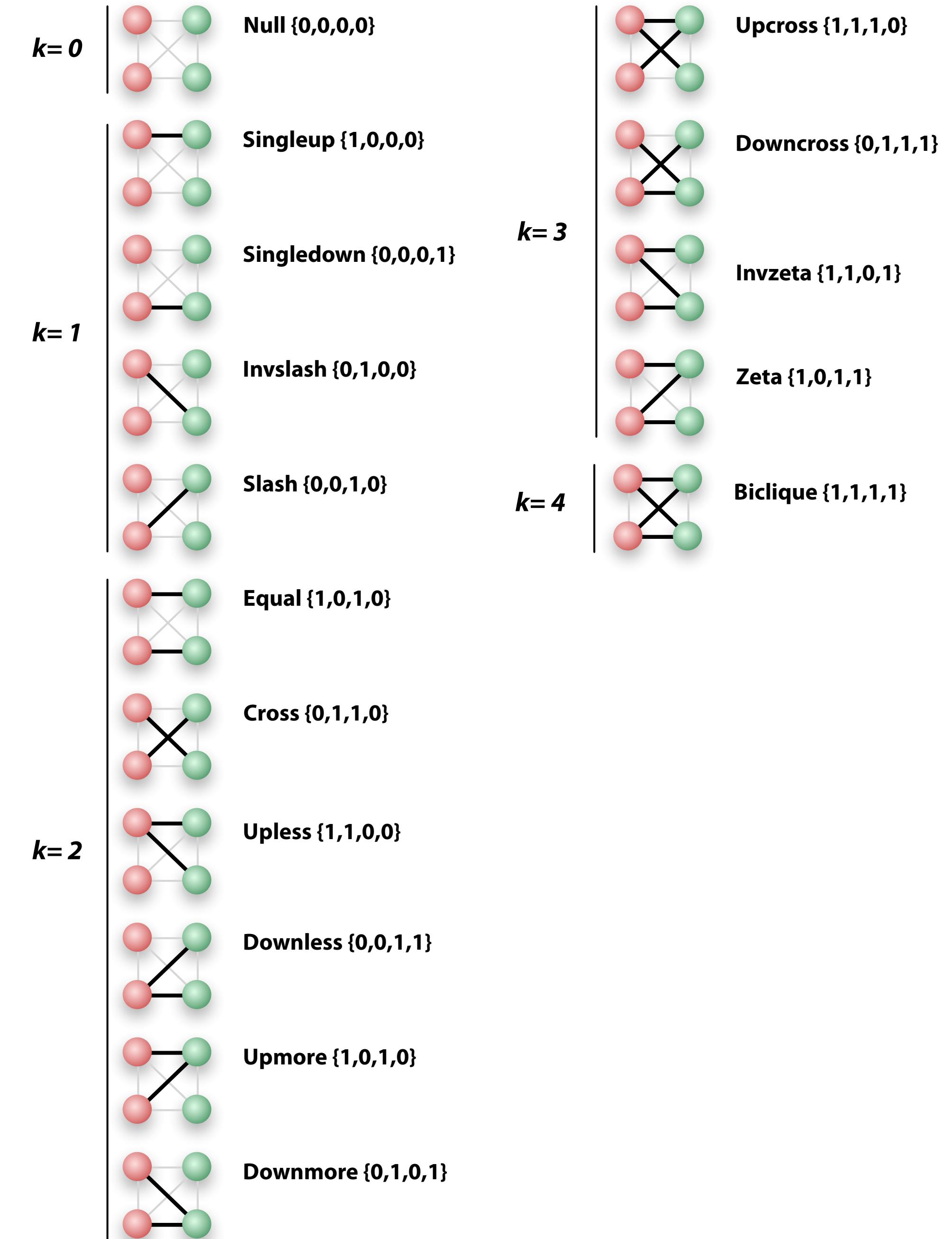


Figure 6: A 3-b2star (left), a 4-cycle (right), and a 2-b2star (bottom)

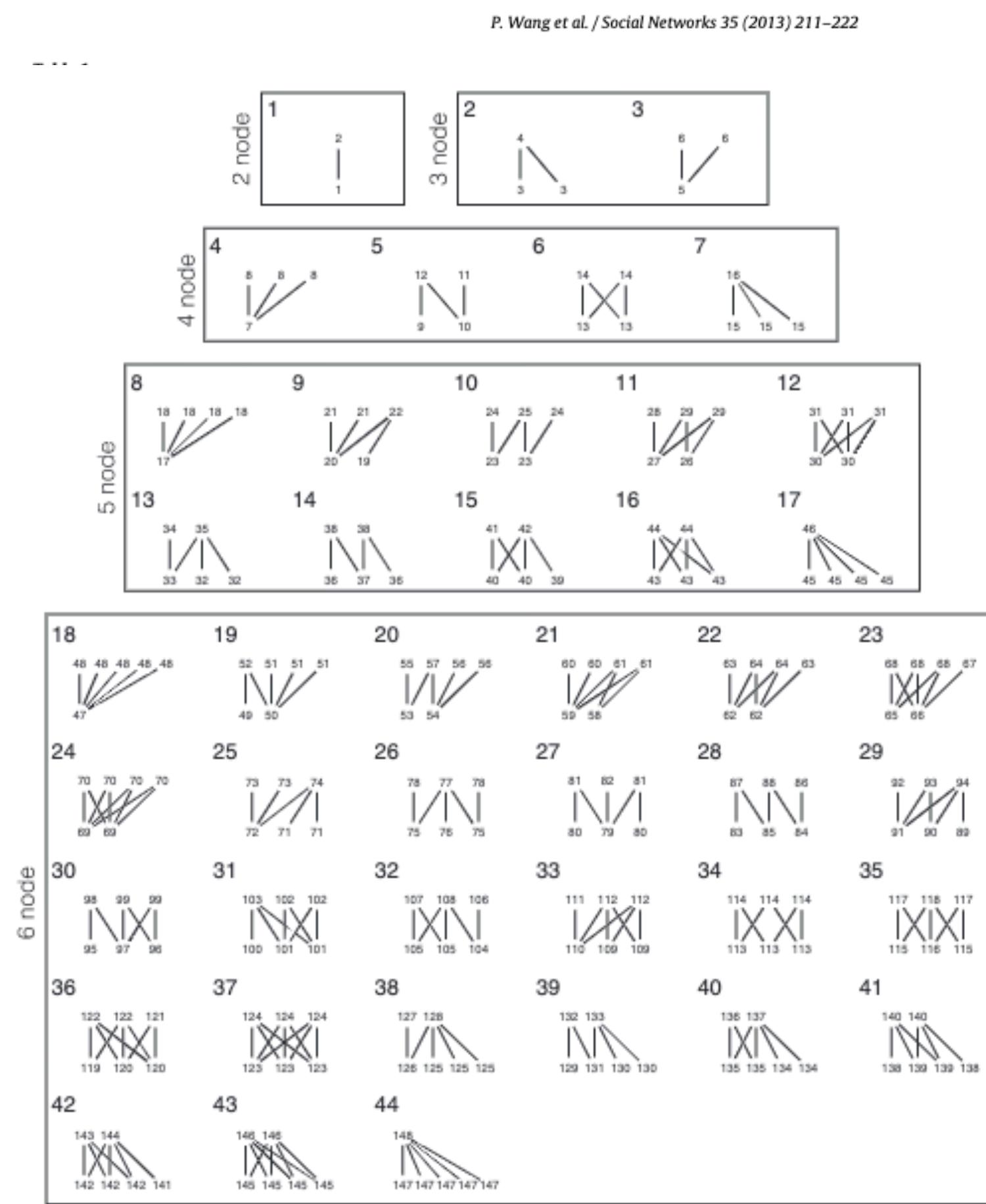
```
summary(davis ~ b2star(3) + cycle(4) + b2star(2) + b1star(2))
```

```
## b2star3  cycle4 b2star2 b1star2
##     878     341    322    214
```



ERGM specification

Relational Terms (Network Predictors) Bipartite networks



ERGM specification

Relational Terms (Network Predictors)

Bipartite networks

```
search.ergmTerms(categories=c('bipartite', 'dyad-independent'))

> search.ergmTerms(keyword='bipartite')
Found 43 matching ergm terms:
S(formula, attrs)
  Evaluation on an induced subgraph

b1concurrent(by=NULL, levels=NULL)
  Concurrent node count for the first mode in a bipartite (aka two-mode) network

b1cov(attr)
  Main effect of a covariate for the first mode in a bipartite (aka two-mode) network

b1cov(attr, form="sum")
  Main effect of a covariate for the first mode in a bipartite (aka two-mode) network

b1degrange(from, to=+Inf, by=NULL, homophily=FALSE, levels=NULL)
  Degree range for the first mode in a bipartite (a.k.a. two-mode) network

b1degree(d, by=NULL, levels=NULL)
  Degree for the first mode in a bipartite (aka two-mode) network

b1dsp(d)
  Dyadwise shared partners for dyads in the first bipartition

b1factor(attr, base=1, levels=-1)
  Factor attribute effect for the first mode in a bipartite (aka two-mode) network

b1factor(attr, base=1, levels=-1, form="sum")
  Factor attribute effect for the first mode in a bipartite (aka two-mode) network

b1mindegree(d)
  Minimum degree for the first mode in a bipartite (aka two-mode) network
.../...
```

Basic / Frequently-used term category matrix

For convenience, this table lists a subset of the most commonly-used ergm terms and categories.

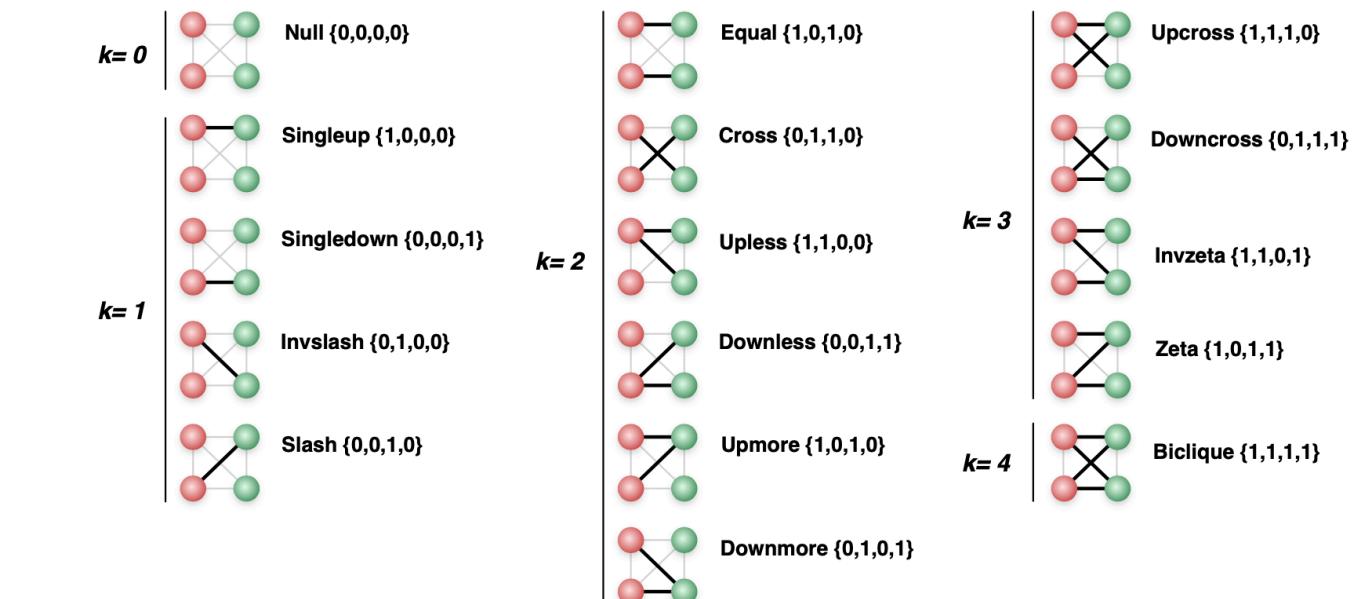
Term name	binary	valued	directed	undirected	bipartite	dyad-independent	operator	layer-aware
absdiff	✓			✓	✓		✓	
b1cov	✓			✓	✓	✓	✓	
b1cov			✓	✓	✓	✓	✓	
b1degree	✓			✓	✓	✓		
b1factor	✓			✓	✓	✓	✓	
b1factor			✓	✓	✓	✓	✓	
b1nodematch	✓			✓	✓	✓	✓	
b2concurrent	✓			✓	✓	✓		
b2cov	✓			✓	✓	✓	✓	
b2cov			✓	✓	✓	✓	✓	
b2degree	✓			✓	✓	✓		
b2factor	✓			✓	✓	✓	✓	
b2factor			✓	✓	✓	✓	✓	
b2nodematch	✓			✓	✓	✓	✓	
degree	✓			✓	✓			
diff	✓			✓	✓		✓	
edgecov	✓			✓	✓			
edges	✓		✓	✓	✓			
gwdegree	✓				✓			
gwesp	✓			✓	✓			
idegree	✓			✓				
isolates	✓			✓	✓			
mm	✓			✓	✓			✓
mm			✓	✓	✓			✓
mutual	✓			✓				
nodecov	✓			✓	✓			
nodefactor	✓			✓	✓			
nodeicov	✓			✓				
nodeifactor	✓			✓				
nodematch	✓			✓	✓			
nodemix	✓			✓	✓			
odegree	✓			✓				
triangle	✓			✓	✓			

ERGM specification

Relational Terms (Network Predictors)

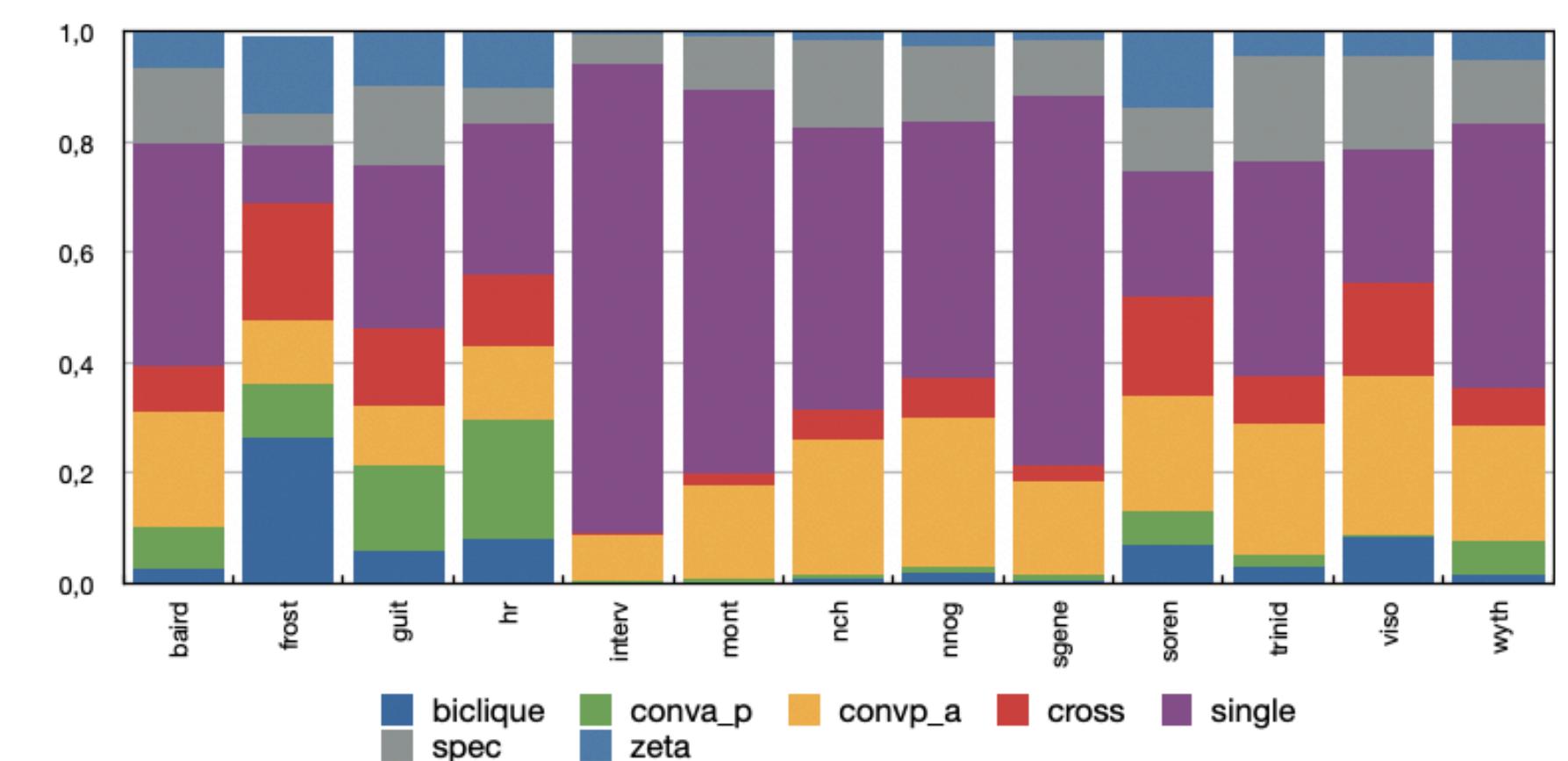
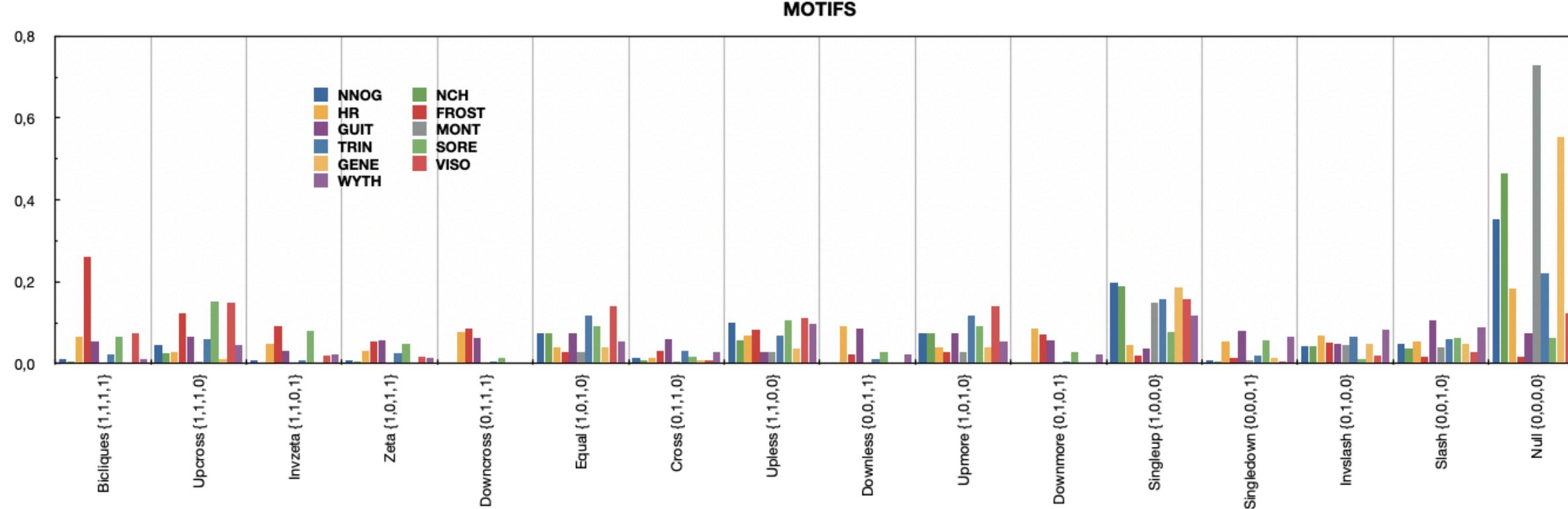
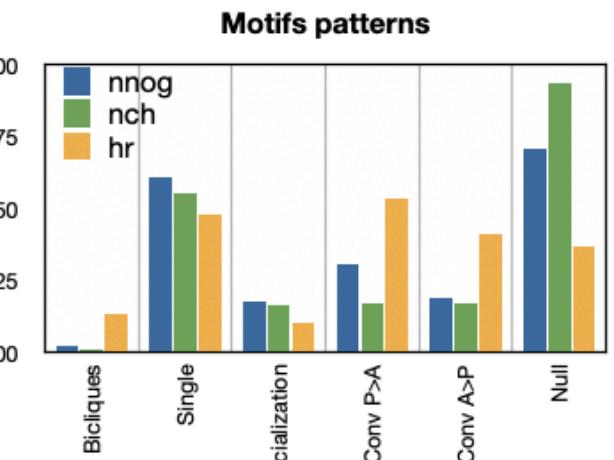
Bipartite networks

Motif		NNOG	NCH	HR	FROST	GUIT	MONT	TRIN	SORE	GENE	VISO	WYTH
Bicliques {1,1,1,1}	783	0,012676	928	0,005459	1247	0,066080	1432	0,261076	80	0,055287	9004	0,000854
Upcross {1,1,1,0}	2837	0,045928	4527	0,026633	541	0,028668	683	0,124521	94	0,064962	68112	0,006457
Invzeta {1,1,0,1}	601	0,009729	666	0,003918	941	0,049865	498	0,090793	45	0,031099	13595	0,001289
Zeta {1,0,1,1}	463	0,007495	785	0,004618	604	0,032007	293	0,053418	84	0,058051	12827	0,001216
Downcross {0,1,1,1}	151	0,002445	211	0,001241	1467	0,077738	465	0,084777	92	0,063580	2912	0,000276
Equal {1,0,1,0}	4592	0,074339	12627	0,074285	740	0,039214	154	0,028077	108	0,074637	308752	0,029270
Cross {0,1,1,0}	891	0,014424	1563	0,009195	256	0,013566	169	0,030811	89	0,061507	53198	0,005043
Upless {1,1,0,0}	6210	0,100533	9637	0,056695	1304	0,069101	459	0,083683	40	0,027643	316063	0,029963
Downless {0,0,1,1}	191	0,003092	270	0,001588	1727	0,091516	123	0,022425	123	0,085003	9819	0,009931
Upmore {1,0,1,0}	4592	0,074339	12627	0,074285	740	0,039214	154	0,028077	108	0,074637	308752	0,029270
Downmore {0,1,0,1}	185	0,002995	304	0,001788	1613	0,085475	398	0,072562	83	0,057360	16494	0,001564
Singleup {1,0,0,0}	12304	0,199187	32050	0,188552	879	0,046579	114	0,020784	55	0,038010	1565243	0,148386
Singledown {0,0,0,1}	498	0,008062	920	0,005412	1049	0,055588	82	0,014950	118	0,081548	87596	0,008304
Invslash {0,1,0,0}	2665	0,043143	7209	0,042411	1281	0,067882	276	0,050319	70	0,048376	467709	0,044339
Slash {0,0,1,0}	3008	0,048696	6454	0,037969	1026	0,054369	89	0,016226	152	0,105045	428346	0,040607
Null {0,0,0,0}	21800	0,352916	79202	0,465949	3456	0,183138	96	0,017502	106	0,073255	7674344	0,727531
Total	61771		169980		18871		5485		1447		10548484	
											123171	
											328	
											248066	
											4692	
											5133	



dataset	biclique	conv_a_p	conv_p_a	cross	single	spec	zeta
baird	0,02568	0,07620	0,20872	0,08531	0,40282	0,13556	0,06571
frost	0,26573	0,09668	0,11375	0,21303	0,10410	0,05994	0,14000
guit	0,05966	0,15362	0,11037	0,13870	0,29460	0,14691	0,09600
hr	0,08090	0,21667	0,13260	0,13026	0,27470	0,06461	0,10023
interv	0,00048	0,00444	0,08355	0,00467	0,84860	0,05435	0,00389
mont	0,00245	0,00717	0,17032	0,01936	0,69480	0,09867	0,00720
nch	0,01022	0,00632	0,24526	0,05219	0,51370	0,15632	0,01598
n nog	0,01959	0,00941	0,27025	0,07475	0,46221	0,13717	0,02662
sgene	0,00463	0,00974	0,17216	0,02634	0,67004	0,10405	0,01303
soren	0,07166	0,05863	0,21173	0,17915	0,22476	0,11726	0,13681
trinid	0,02919	0,02292	0,23888	0,08468	0,39095	0,18838	0,04500
viso	0,08546	0,00243	0,28793	0,16824	0,24472	0,16946	0,04176
wyth	0,01629	0,06252	0,20751	0,06856	0,48017	0,11374	0,05122

pattern	%	n nog	%	n ch	%	hr
Bicliques	783	0,0127	0,0127	928	0,0055	0,0055
Single	18475	0,3029	0,3029	46633	0,2759	0,2759
Specialization	5483	0,0888	0,0888	14190	0,0835	0,0835
Conv P>A	6401	0,1036	0,1520	9907	0,0583	0,0862
Conv A>P	4777	0,0773	0,0946	12931	0,0761	0,0846
Conv P>A_3	2988	0,0484		4738	0,0279	0,0208
Conv A>P_3	1064	0,0172		1451	0,0085	0,0081
Null	21800	0,3529	0,3529	79202	0,4659	0,4659

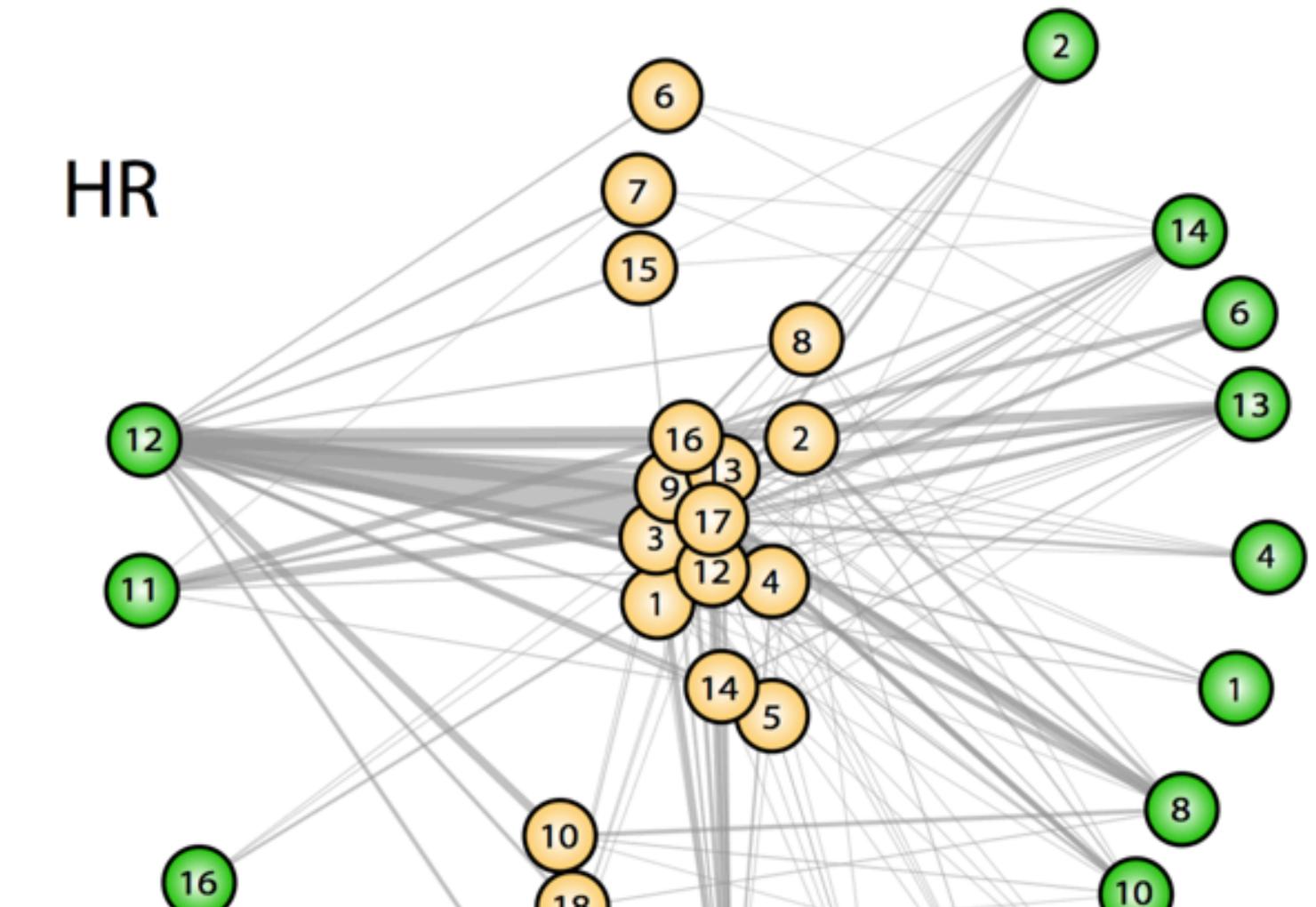
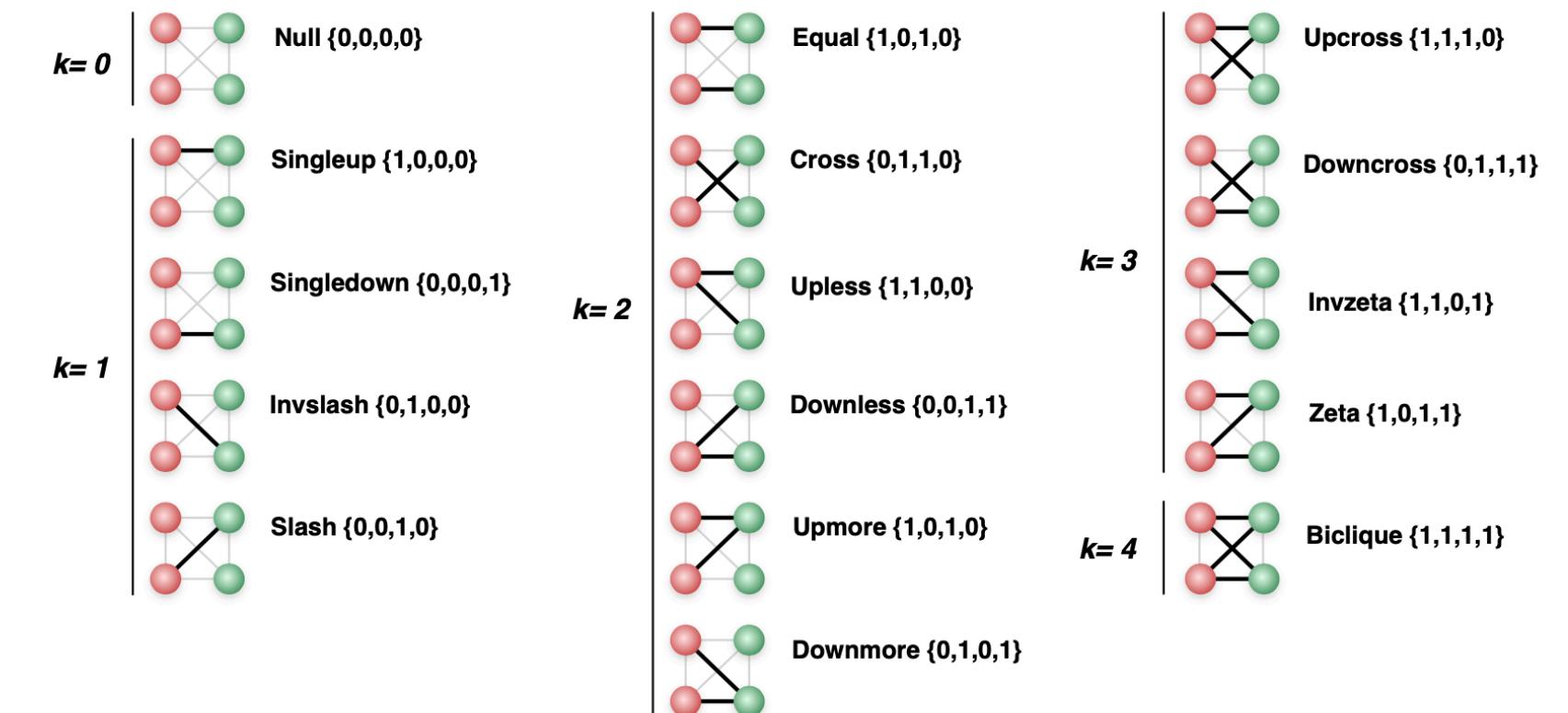
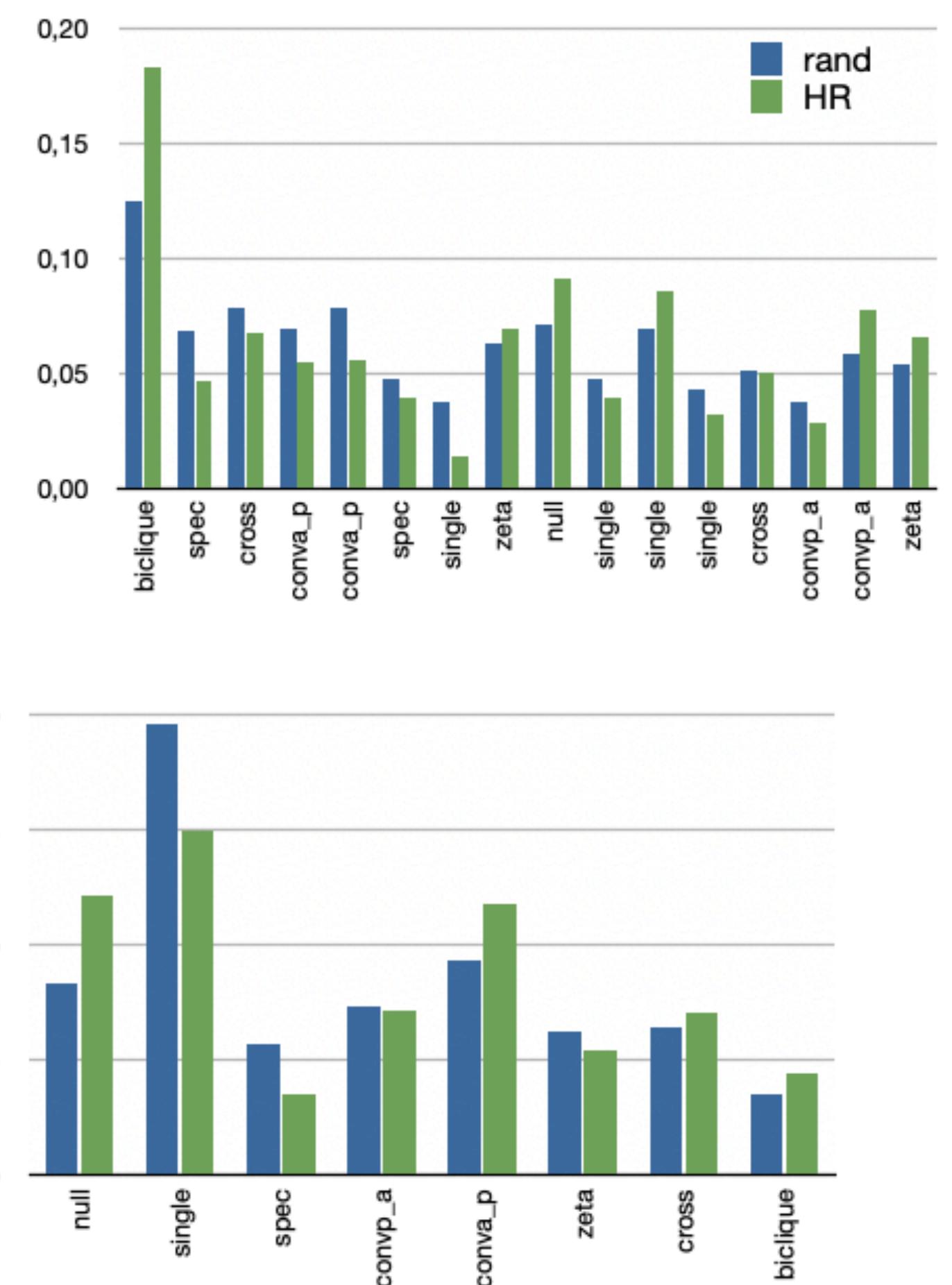


ERGM specification

Relational Terms (Network Predictors) Bipartite networks

motif	pattern	rand	HR	morder
Null {0,0,0}	null	0,124720913794871	0,183138	1
Singleup {1,0,0,0}	single	0,0686975617388865	0,046579	2
Invslash {0,1,0,0}	single	0,0780815487463378	0,067882	3
Slash {0,0,1,0}	single	0,0694135547678014	0,054369	4
Singledown {0,0,0,1}	single	0,0786318975703718	0,055588	5
Equal {1,0,1,0}	spec	0,0474853914760679	0,039214	6
Cross {0,1,1,0}	spec	0,0378229927105759	0,013566	7
Upless {1,1,0,0}	convp_a	0,0628282533978644	0,069101	8
Downless {0,0,1,1}	convp_p	0,0711012911615058	0,091516	9
Upmore {1,0,1,0}	convp_a	0,0474853914760679	0,039214	10
Downmore {0,1,0,1}	convp_p	0,0693331606748787	0,085475	11
Zeta {1,0,1,1}	zeta	0,0430669537113474	0,032007	12
Invzeta {1,1,0,1}	zeta	0,0514916071804335	0,049865	13
Upcross {1,1,1,0}	cross	0,0375381062604877	0,028668	14
Downcross {0,1,1,1}	cross	0,0585382303587519	0,077738	15
Bicliques {1,1,1,1}	biclique	0,0537631449737505	0,06608	16

pattern	rand	HR	chi-sq		
null	0,124720913794871	0,183138	566,7354		
single	0,294824562823398	0,224418	276,4321		
spec	0,0853083841866438	0,05278	216,4649		
convp_a	0,110313644873932	0,108315	0,0001		
convp_p	0,140434451836385	0,176991	208,8811		
zeta	0,0945585608917809	0,081872	24,5566		
cross	0,0960763366192396	0,106406	29,0427		
biclique	0,0537631449737505	0,06608	63,0294		
		1385,1423			



ERGMs

Use R!

Eric D. Kolaczyk
Gábor Csárdi

Statistical
Analysis of
Network Data
with R



Use R!

Douglas A. Luke

A User's
Guide to
Network
Analysis in R



STRUCTURAL ANALYSIS IN THE SOCIAL SCIENCES 35

Exponential Random
Graph Models for
Social Networks

THEORY, METHODS, AND APPLICATIONS

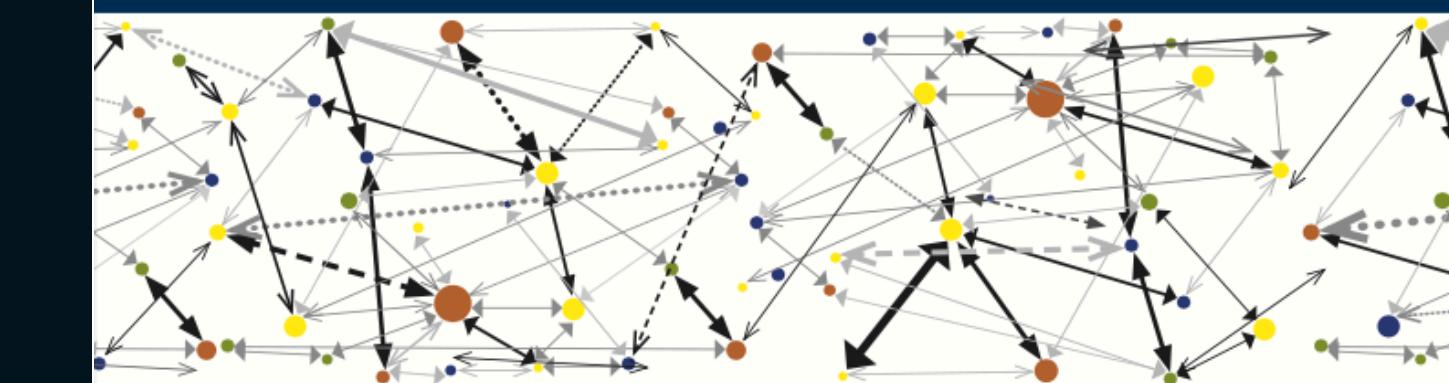
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The SAGE Handbook of
Social Network Analysis



Edited by
John Scott and
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ERGMs

- Handcock, M. S., D. R. Hunter, C. T. Butts, S. M. Goodreau and M. Morris (2008). statnet: Software Tools for the Representation, Visualization, Analysis and Simulation of Network Data. *Journal of Statistical Software* 42(01).
- Hunter DR, Handcock MS, Butts CT, Goodreau SM, Morris M (2008b). ergm: A Package to Fit, Simulate and Diagnose Exponential-Family Models for Networks. *Journal of Statistical Software*, 24(3). <http://www.jstatsoft.org/v24/i03/>.
- Krivitsky, P. N., M. S. Handcock and M. Morris (2011). Network Size and Composition Effects in Exponential-Family Random Graph Models. *Statistical Methodology* 8:319-339.
- Krivitsky PN (2012). Exponential-family random graph models for valued networks. *Electronic Journal of Statistics* 6:1100-1128.
- Wang, P. (2012). Exponential Random Graph Model Extensions: Models for Multiple Networks and Bipartite Networks. In D. Lusher, J. Koskinen, & G. Robins (Eds.), *Exponential Random Graph Models for Social Networks: Theory, Methods, and Applications* (Structural Analysis in the Social Sciences, pp. 115-129). Cambridge: Cambridge University Press. doi:10.1017/CBO9780511894701.012

ERGMs

8.3 R packages that build on statnet

There is a growing number of R packages written by other folks that build on or extend the functionality of the statnet suite. You can get a current list of those packages by looking at the reverse depends/suggests on CRAN. A partial list includes:

- [EpiModel package](#) – Mathematical Modeling of Infectious Disease, includes functions for deterministic compartmental modeling, stochastic individual contact modeling, and stochastic network modeling
- [RDS package](#) – Estimation with data collected using Respondent-Driven Sampling.
- ✓ • [Bergm package](#) – Bayesian ERGM estimation
- ✓ • [hergm package](#) – Hierarchical Exponential-Family Random Graph Models with Local Dependence (for latent groups).
- ✓ • [lvm4net package](#) – Latent variable models.
- [VBLPCM package](#) – Variational Bayes Latent Position Cluster Models.
- [xergm package](#) – Temporal exponential random graph models (TERGM) by bootstrapped pseudolikelihood, MCMC MLE and (temporal) network autocorrelation models.

ERGMs



Research

Context-dependency and anthropogenic effects on individual plant-frugivore networks

M. Florencia Miguel, Pedro Jordano, Solana Tabeni and Claudia M. Campos

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Oikos
127: 1045–1059, 2018
doi: 10.1111/oik.04978

Subject Editor: Sa Xiao
Editor-in-Chief: Dries Bonte
Accepted 23 December 2017

Anthropogenic activities, such as grazing by domestic animals, are considered drivers of environmental changes that may influence the structure of interaction networks. The study of individual-based networks allows testing how species-level interaction patterns emerge from the pooled interaction modes of individuals within populations. Exponential random graph models (ERGMs) examine the global structure of networks by allowing the inclusion of specific node (i.e. interacting partners) properties as explanatory covariates. Here we assessed the structure of individual plant-frugivore interaction networks and the ecological variables that influence the mode of interactions under

Received: 6 November 2020 | Accepted: 4 May 2021

DOI: 10.1111/1365-2745.13694

RESEARCH ARTICLE

Journal of Ecology

BRITISH
ECOLOGICAL
SOCIETY

Individual-based plant-pollinator networks are structured by phenotypic and microsite plant traits

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Funding information
Consejo Superior de Investigaciones Científicas, Grant/Award Number: JAEINT18_EX_0080; Ministerio de Ciencia e Innovación, Grant/Award Number: CGL2017-082847P, CGL2017-92436EXP and FPU19_02552

Handling Editor: Ryan Phillips

Abstract

1. The biotic and abiotic context of individual plants within animal-pollinated plant populations can influence pollinator foraging behaviour. Pollinator movements regulate pollen flow among plant individuals, and ultimately determine individual plant reproductive success. Yet the underlying drivers of this context dependency of interactions at the population level and their functional consequences for individuals remain poorly known.
2. Here we used a well-characterised population of *Halimium halimifolium* (Cistaceae), a Mediterranean shrub species, in combination with exponential random graph models (ERGMs) to evaluate how the intrapopulation variation in plant attributes configures individual-based plant-pollinator networks and determines their reproductive outcomes. Specifically, we assessed (a) how the intrinsic (i.e. phenotype and phenology) and extrinsic (i.e. microsite) plant attributes influenced the emerging configuration of the bipartite plant-pollinator network and the unipar-