

Advanced Network Analysis

ERGM Application

Olga Chyzh [www.olgachyzh.com]

Readings

- Steven M. Goodreau, James A. Kitts, and Martina Morris. Birds of a feather, or friend of a friend? using exponential random graph models to investigate adolescent social networks. *Demography*, 46(1):103--125, 2009.

Goodreau et al, 2009

Goal: to identify the determinants of friendship formation that lead to pervasive regularities in friendship structure among adolescent students

Three mechanisms:

- *Sociality*---heterogeneity among individuals in their propensity to establish friendship ties. Individuals with greater sociality have higher degree, although degree may be also influenced by other factors.
- *Selective mixing* is a dyad-level process by which pairs form (or break) relationships based on their combination of individual attributes. *Assortative mixing* is the greater propensity to partner with others having attributes similar to one's own. The resulting pattern---homophily--- is the predominance of within-group ties.
- *Triad Closure* leads to the outcome of transitivity. Possible mechanisms include increased chance for interaction and tendency for structural balance (i.e. a friend of my friend is my friend).

Goodreau et al, 2009

Additional mechanisms:

- Homophily may also be amplified by triad closure if there is already a tendency toward assortative mixing.
- Transitivity may also result from assortative mixing since increasing the likelihood of within category ties enhances the opportunity for completed triangles within categories, especially when groups are small.
- Population composition---the opportunity for partner selection is constrained by the available pool of partners.

Figure 2. Process and Outcome in Social Network Models

**Relationships between process and outcome
implied by individual analyses**

Process		Outcome
Sociality	→	Degree distribution
Selective mixing	→	Mixing pattern
Triad closure	→	Transitivity

**Relationships between process and outcome
considered here**

Process		Outcome
Sociality		Degree distribution
Selective mixing		Mixing pattern
Triad closure		Transitivity

Notes: Specific forms of selective mixing include assortative mixing and disassortative mixing. Corresponding specific forms of mixing pattern include homophily and heterophily.

Data

- Friendship data from the first wave of Add Health, a sample of more than 90,000 U.S. students in grades 7 through 12, obtained in 1994–1995 through a stratified sample of schools.
- The questionnaire provided a school roster and asked students to identify their five best male and five best female friends, in order of closeness.
- Students were allowed to nominate friends outside school or missing from the roster, or to stop before nominating five friends of either sex.
- Most students listed fewer friends than the maximum, but for the remainder, there may be some truncation. *When would this be a problem?*

Open Data

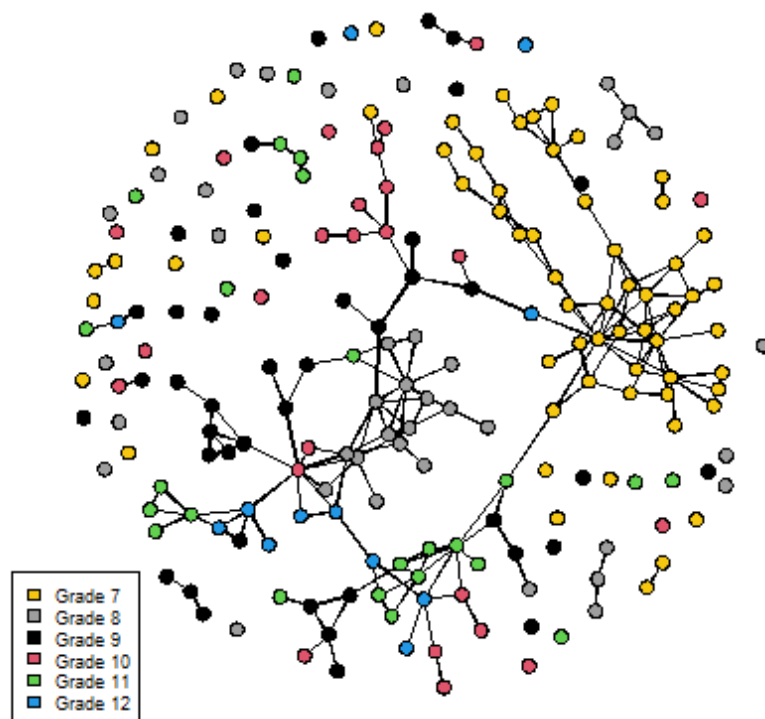
```
rm(list=ls())  
library(statnet)  
data(faux.mesa.high)  
mesa <- faux.mesa.high  
mesa
```

```
## Network attributes:  
##   vertices = 205  
##   directed = FALSE  
##   hyper = FALSE  
##   loops = FALSE  
##   multiple = FALSE  
##   bipartite = FALSE  
##   total edges= 203  
##     missing edges= 0  
##     non-missing edges= 203  
##  
## Vertex attribute names:  
##   Grade Race Sex  
##  
## No edge attributes
```

Plot Data

```
par(mfrow=c(1,1)) # Back to 1-panel plots
plot(mesa, vertex.col='Grade')
legend('bottomleft', fill=7:12,
      legend=paste('Grade', 7:12), cex=0.75)
```


Plot Data



Model Specification

Sociality

Goodreau et al (2009, 111) "infer sociality based on counts of ties observed: s represents the total number of ties, and k_i is the total number of ties for all persons with attribute value i . The s term acts as an intercept [edges], and the coefficient for s represents the conditional log-odds of a tie for the reference category (in these models, reference categories are grade 7, white, and male). The k_i terms assume homogeneity within attribute class, allowing each race, sex, and grade to have different mean sociality."

Sociality

Can also use the search function to find the relevant terms.

```
search.ergmTerms(keyword='sociality')
```

```
## Found 0 matching ergm terms:
```

Sociality

- None of these match the authors' description, which sounds like they are using the term `nodefactor`.
- Term `nodefactor` adds multiple network statistics to the model, one for each of the unique values of the attribute. Each of these statistics gives the number of times a node with that attribute or those attributes appears in an edge in the network.
- Note: `nodefactor` assumes non-numeric (e.g., character, factor) class, so recode "Grade" as a character.

Sociality

Based on this description, the model so far is specified as:

```
table(mesa %v% 'Race') # Frequencies of race
table(mesa %v% 'Sex') # Frequencies of sex
table(mesa %v% 'Grade') # Frequencies of Grade
mesa %v% "Grade" <- as.character(mesa %v% "Grade")

m1<- ergm(mesa~edges+nodefactor("Race",levels=c("Black","Hisp","Other",
nodefactor("Sex", levels="F")+
nodefactor("Grade", levels=c("8","9","10","11","12"))))
```

Sociality

- Note that we specified levels for each nodefactor as to make sure that the reference categories match those of Goodreau et al.
- The description of nodefactor in ?ergm.terms says that including each level is not a good idea (need a reference category, just like with categorical variables in OLS).
- If we get a positive coefficient on any categories within *Race*, *Sex*, and/or *Grade*, we will infer that students with that characteristic are, on average, more social.

Selective Mixing

Two selective mixing dynamics:

1. A homogeneous propensity for assortative mixing across attribute categories (“uniform homophily”).
2. A propensity that is specific to individual categories (“differential homophily”).

"Statistics are as follows: first, h is the total number of ties between persons in the same attribute category, regardless of category. This uniform homophily is used for sex since there are only three tie types (MM, MF, FF); with main effects included, only one degree of freedom remains. Second, h_i is the total number of ties between persons both in attribute category i . There is one such statistic for each category of the attribute. This differential homophily is used for race and grade."

Selective Mixing

Can also use the search function to find the relevant terms.

```
search.ergmTerms(keyword='homophily')
```

```
## Found 0 matching ergm terms:
```

- Term nodematch sounds like a good candidate.

Selective Mixing

Based on this description, we can further specify the model as:

```
m1<- ergm(mesa~edges+nodefactor("Race",levels=c("Black","Hisp","NatAr  
nodefactor("Sex", levels="F")+  
nodefactor("Grade", levels=c("8","9","10","11","12"))+  
nodematch("Sex")+nodematch("Race",diff=TRUE)+nodematch("(  
)
```

Note: option `diff` specifies whether there can be differences in probability of friendships between groups.

- Use `absdiff` instead of `nodematch` for continuous variables (e.g. wealth).

Selective Mixing: Interpretation

- To calculate the probability of a tie between two women, set `nodefactor("Sex", levels="F")=1` and `nodematch("Sex")=1`, and all other variables to the values of interest.
- To calculate the probability of a tie between two men, set `nodefactor("Sex", levels="F")=0` and `nodematch("Sex")=1`, and all other variables to the values of interest.
- To calculate the probability of a tie between a woman and a man, set `nodefactor("Sex", levels="F")=1` and `nodematch("Sex")=0`, and all other variables to the values of interest.

Triad Closure

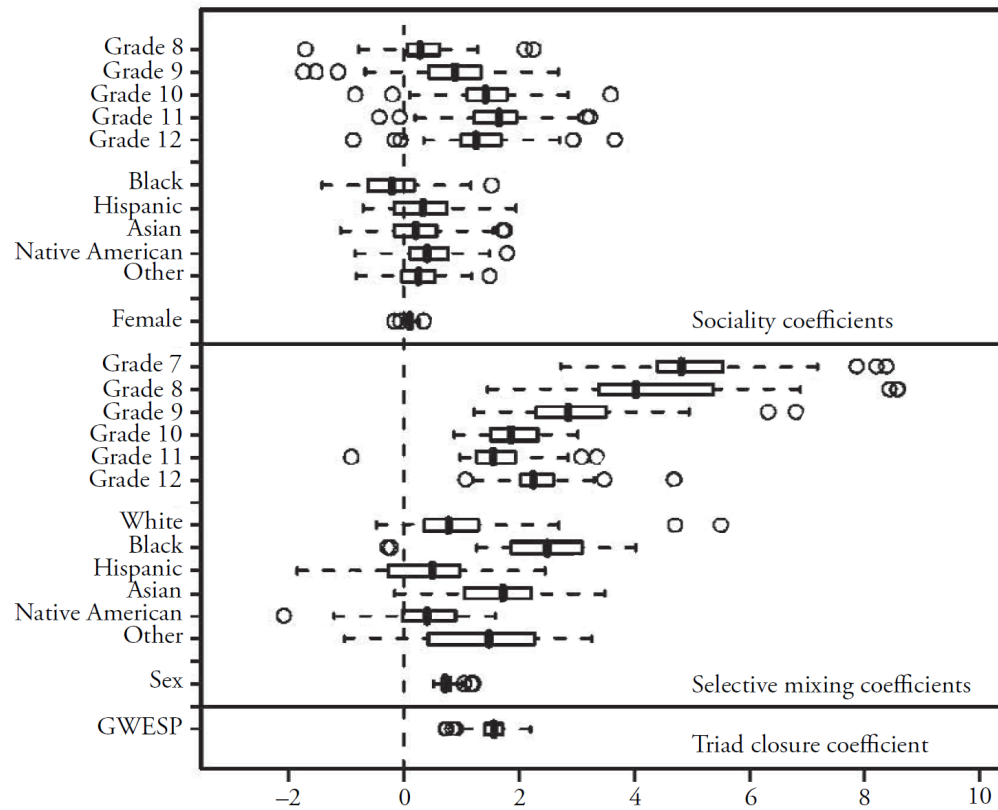
"For the reasons described above, we investigate triad closure using the GWESP statistic. We adopt a value of 0.25 for decay, although results are robust to this choice."

Based on this description, we can further specify the model as:

```
mesa %v% "Grade" <- as.character(mesa %v% "Grade")
m1 <- ergm(mesa ~ edges + nodefactor("Race", levels = c("Black", "Hispanic", "Native American")) +
  nodefactor("Sex", levels = c("Female", "Male")) +
  nodefactor("Grade", levels = c("8", "9", "10", "11", "12")) +
  nodematch("Sex") + nodematch("Race", diff = TRUE) + nodematch("Grade") +
  gwesp(decay = 0.25)
par(mfrow = c(3, 2))
mcmc.diagnostics(m1)
```

Results

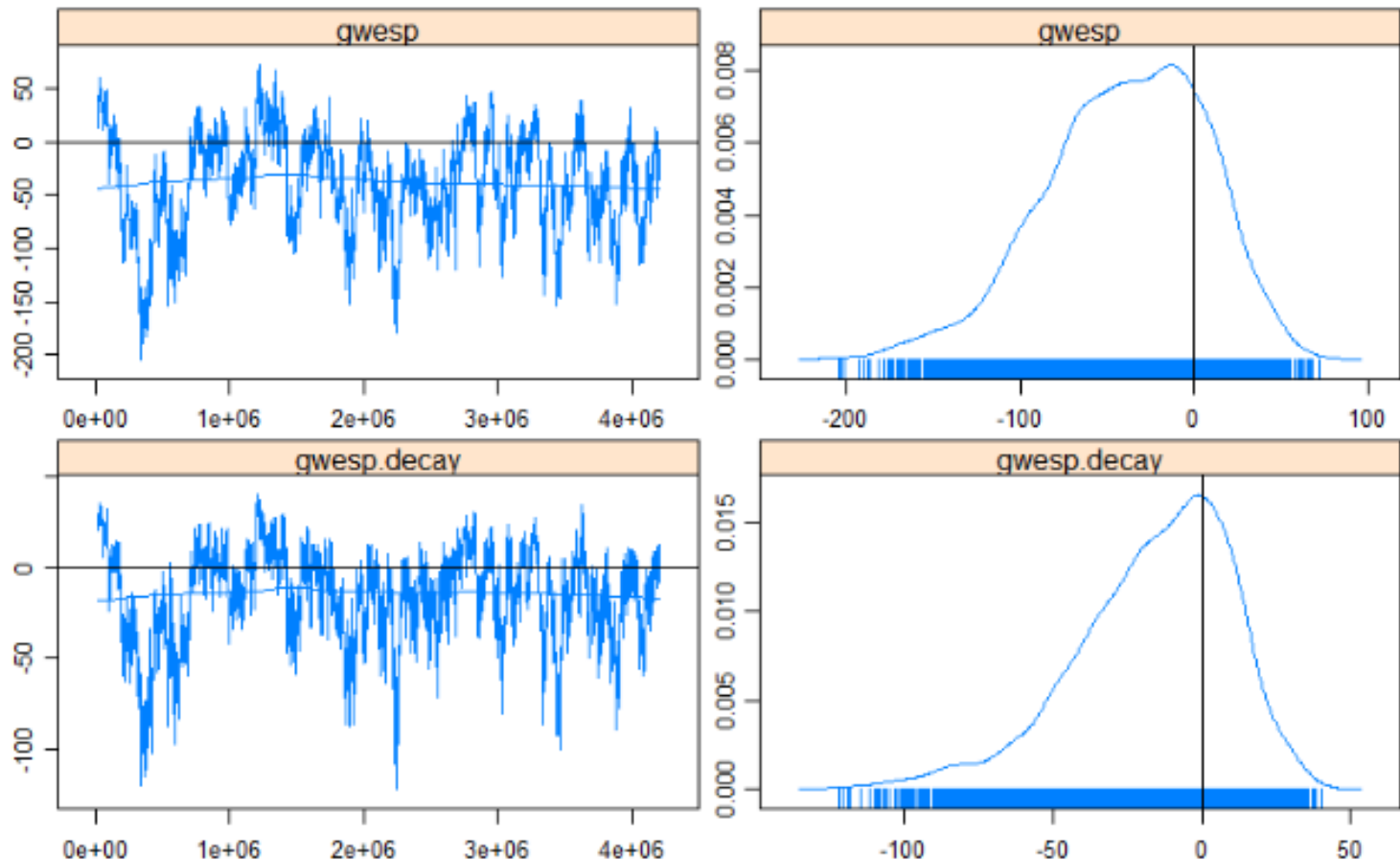
Figure 3. Coefficients From the Full Model, Plotted Across All 59 Schools



Notes: Boxplots follow the Tukey method. Boxes represent quartiles; whiskers extend to the most extreme data point within 1.5 times the interquartile range from the edge of the box; and points represent outliers.

Our Replication: M1 Diagnostics

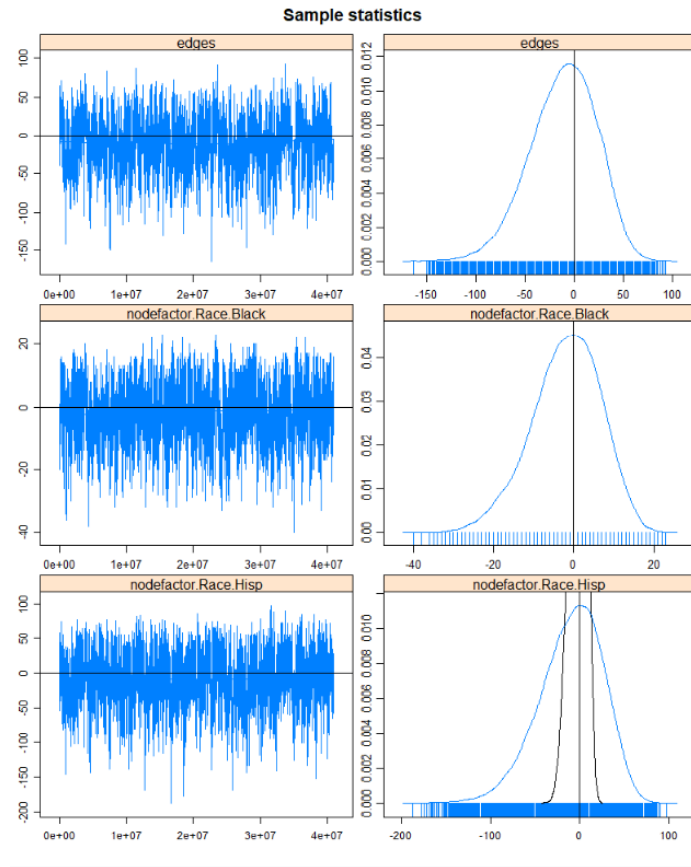
Sample statistics



Increase the Number of Simulations.

```
m2<- ergm(mesa~edges+nodefactor("Race",levels=c("Black","Hispanic","Native American"),
nodefactor("Sex", levels="F")+
nodefactor("Grade", levels=c("8","9","10","11","12"))+
nodematch("Sex")+nodematch("Race",diff=TRUE)+
nodematch("Grade",diff=TRUE)+gwesp(decay=0.25),
control=control.ergm(seed=6886, MCMC.samplesize=10000)
)
par(mfrow = c(3, 2))
mcmc.diagnostics(m2)
```

Results



Results

Results:

##

##	Estimate	Std. Error	MCMC %	z value	Pr(> z)	
## edges	-10.22281	1.17910	0	-8.670	< 1e-04	***
## nodefactor.Race.Black	0.61845	0.24268	0	2.548	0.010822	*
## nodefactor.Race.Hisp	-0.49867	0.23138	0	-2.155	0.031144	*
## nodefactor.Race.NatAm	-0.47808	0.20968	0	-2.280	0.022603	*
## nodefactor.Race.Other	-1.54877	0.96497	0	-1.605	0.108496	
## nodefactor.Sex.F	0.13086	0.06715	0	1.949	0.051314	.
## nodefactor.Grade.8	1.45656	0.66174	0	2.201	0.027729	*
## nodefactor.Grade.9	2.22394	0.62197	0	3.576	0.000349	***
## nodefactor.Grade.10	2.55889	0.62167	0	4.116	< 1e-04	***
## nodefactor.Grade.11	2.30632	0.62423	0	3.695	0.000220	***
## nodefactor.Grade.12	2.93496	0.62202	0	4.718	< 1e-04	***
## nodematch.Sex	0.52444	0.13175	0	3.980	< 1e-04	***
## nodematch.Race.Black	-Inf	0.00000	0	-Inf	< 1e-04	***
## nodematch.Race.Hisp	0.57111	0.31521	0	1.812	0.070013	.
## nodematch.Race.NatAm	1.08712	0.30657	0	3.546	0.000391	***
## nodematch.Race.Other	-Inf	0.00000	0	-Inf	< 1e-04	***
## nodematch.Race.White	0.30392	0.62741	0	0.484	0.628101	
## nodematch.Grade.10	1.07180	0.53553	0	2.001	0.045352	*
## nodematch.Grade.11	1.83540	0.51002	0	3.599	0.000320	***
## nodematch.Grade.12	0.98219	0.57182	0	1.718	0.085858	
## nodematch.Grade.7	6.01282	1.14075	0	5.230	< 1e-04	***

Results

- Another problem is that several of our parameters are estimated as $-\infty$.
- Check Our Summary Statistics

```
summary(mesa~edges+nodefactor("Race")+
        nodefactor("Sex", levels="F")+
        nodefactor("Grade", levels=c("8","9","10","11","12"))+
        nodematch("Sex")+
        nodematch("Race",diff=TRUE)+
        nodematch("Grade",diff=TRUE)+
        gwesp(decay=0.25)
)
#Also can:
mixingmatrix(mesa, "Race")
```

Check Our Summary Statistics

##	edges	nodefactor.Race.Hisp	nodefactor.Race.NatAm
##	203	178	156
##	nodefactor.Race.Other	nodefactor.Race.White	nodefactor.Sex.F
##	1	45	235
##	nodefactor.Grade.8	nodefactor.Grade.9	nodefactor.Grade.10
##	75	65	36
##	nodefactor.Grade.11	nodefactor.Grade.12	nodematch.Sex
##	49	28	132
##	nodematch.Race.Black	nodematch.Race.Hisp	nodematch.Race.NatAm
##	0	53	46
##	nodematch.Race.Other	nodematch.Race.White	nodematch.Grade.10
##	0	4	9
##	nodematch.Grade.11	nodematch.Grade.12	nodematch.Grade.7
##	17	6	75
##	nodematch.Grade.8	nodematch.Grade.9	esp#1
##	33	23	70
##	esp#2	esp#3	esp#4
##	36	13	0
##	esp#5	esp#6	esp#7
##	1	0	0
##	esp#8	esp#9	esp#10
##	0	0	0
##	esp#11	esp#12	esp#13
##	0	0	0

Remove the Categories with Empty Cells:

```
m3<- ergm(mesa~edges+nodefactor("Race",levels=c("Black","Hisp","NatAr
nodefactor("Sex", levels="F")+
nodefactor("Grade", levels=c("8","9","10","11","12"))+
nodematch("Sex")+
nodematch("Race",levels=c("White","Hisp","NatAm"),diff=TRUE)+
nodematch("Grade",diff=TRUE)+
gwesp(decay=0.25),
control=control.ergm(seed=6886, MCMC.samplesize=10000)
summary(m3)
```

Results

Monte Carlo MLE Results:

	Estimate	Std. Error	MCMC %	z value	Pr(> z)	
edges	-10.23242	1.17306	0	-8.723	< 1e-04	***
nodefactor.Race.Black	0.50708	0.22028	0	2.302	0.021338	*
nodefactor.Race.Hisp	-0.48685	0.22539	0	-2.160	0.030774	*
nodefactor.Race.NatAm	-0.46212	0.20547	0	-2.249	0.024505	*
nodefactor.Race.Other	-1.53903	0.95837	0	-1.606	0.108301	
nodefactor.Sex.F	0.13052	0.06733	0	1.938	0.052569	.
nodefactor.Grade.8	1.45427	0.65789	0	2.211	0.027070	*
nodefactor.Grade.9	2.22469	0.62209	0	3.576	0.000349	***
nodefactor.Grade.10	2.54794	0.62156	0	4.099	< 1e-04	***
nodefactor.Grade.11	2.30707	0.62273	0	3.705	0.000212	***
nodefactor.Grade.12	2.91888	0.61877	0	4.717	< 1e-04	***
nodematch.Sex	0.53114	0.13293	0	3.996	< 1e-04	***
nodematch.Race.white	0.34575	0.61488	0	0.562	0.573916	
nodematch.Race.Hisp	0.56367	0.30562	0	1.844	0.065137	.
nodematch.Race.NatAm	1.06819	0.30388	0	3.515	0.000439	***
nodematch.Grade.10	1.08583	0.53473	0	2.031	0.042295	*
nodematch.Grade.11	1.83819	0.51002	0	3.604	0.000313	***
nodematch.Grade.12	1.04165	0.56946	0	1.829	0.067373	.
nodematch.Grade.7	6.00230	1.14645	0	5.236	< 1e-04	***
nodematch.Grade.8	3.24257	0.64615	0	5.018	< 1e-04	***
nodematch.Grade.9	1.63799	0.47345	0	3.460	0.000541	***
gwesp	1.22453	0.12893	0	9.498	< 1e-04	***
gwesp.decay	0.50137	0.12661	0	3.960	< 1e-04	***

Summary of Results

- Sociality increases by grade.
- Grade-based selective mixing is consistently assortative (i.e., the selective mixing coefficient is positive), but is strongest among 7th graders and declines with seniority.
- The triad closure (GWESP) coefficient is positive.

Interpreting GWESP coefficient

- Two nodes i and j have an edgewise shared partner when they are (1) connected to each other and (2) both i and j are also connected to a third individual k .
- If i and j were also connected to node l , then i and j would have two edgewise shared partners.
- When nodes have edgewise shared partnerships, they form triangles.
- The GWESP term models the tendency for ties that close triangles to be more likely than ties that do not close triangles.
- The GWESP term gradually decreases as pairs of individuals have more existing shared partners.

Interpreting GWESP coefficient

$$\omega = e^{\alpha} \sum_{i=1}^{n-2} (1 - (1 - e^{-\alpha})^i) p_i,$$

where α is the decay parameter, p_i is the number of actor pairs who have exactly i shared edgewise partners, and n is the number of nodes in the network.

- The maximum number of edgewise-shared partners for any pair of nodes is $n - 2$.

Interpreting GWESP coefficient

Goal: calculate the change in GWESP statistic that will result from adding a particular tie.

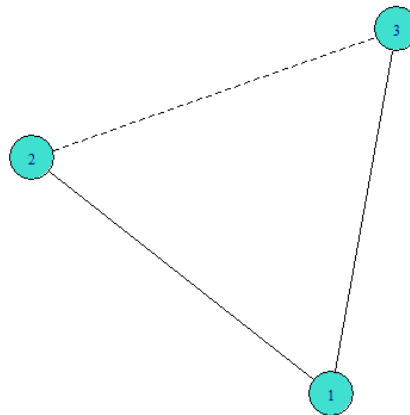
Depends on (1) the number of triangles that the tie closes and (2) the existing number of edgewise shared partnerships that the nodes involved in the triangles already belong to.

- Adding a tie that closes no triangles has no effect on GWESP.

Adding a Tie That Closes One Triangle

Adding a tie that closes one triangle and no nodes in the group have any existing ESPs will:

- add *three* ties with one edgewise shared partnership: 1 and 2 share partner 3, 1 and 3 share partner 2, and 2 and 3 share partner 1
- and *remove* two cases of a tie with zero shared partners: 1 – 2 and 1 – 3.



Adding a Tie That Closes One Triangle

- The corresponding change in the *gwesp* statistic for this toy network is:

$$\delta w = e^{\alpha} \{1 - (1 - e^{-\alpha})^1\} * 3 - e^{\alpha} \{1 - (1 - e^{-\alpha})^0\} * 2$$

- Assume the decay parameter, $\alpha = .25$, then

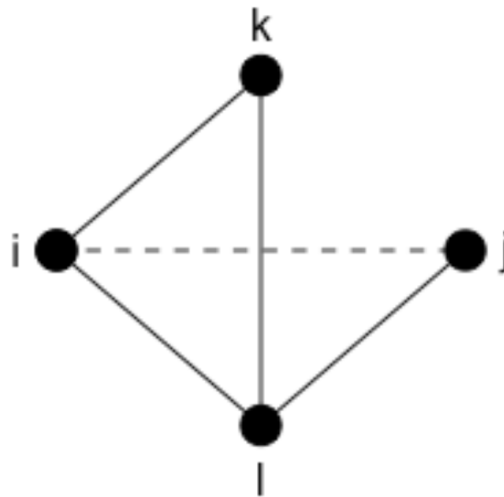
```
exp(.25)*(1-(1-exp(-.25))^1)*3-exp(.25)*(1-(1-exp(-.25))^0)*2
```

```
## [1] 3
```

- Consider a GWESP coefficient of 1.8.
- If a tie will close one triangle, and all actor pairs in that triangle currently have no shared partners, the log-odds of the tie are increased by 5.4 ($1.8*3$), and the odds of such a tie are increased by $\exp(5.4) = 221$.

Your Turn

- Suppose a tie closes one triangle, but nodes in the triangle to be closed already have some *esps*:



- Calculate the change in the *gwesp* statistic that results from this change.
- How many ties with one *esps* does this tie add? How many ties with two *esps* does this tie add?

Your Turn 2

- Remember this model we estimated on the Sampson monastery data. Calculate the probability of a non-reciprocated tie that closes one triangle among nodes with no *esps*.

```
m2<-ergm(samplike~edges+mutual+nodematch('group')+gwesp(.25,fixed=TRUE)
summary(m2)
```

```
## Call:
## ergm(formula = samplike ~ edges + mutual + nodematch("group") +
##       gwesp(0.25, fixed = TRUE))
##
## Monte Carlo Maximum Likelihood Results:
##
##               Estimate Std. Error MCMC % z value Pr(>|z|)
## edges           -1.8962     0.4092      0  -4.634 < 1e-04 ***
## mutual            1.3910     0.4863      0   2.860 0.00423 **
## nodematch.group    2.2846     0.3863      0   5.914 < 1e-04 ***
## gwesp.OTP.fixed.0.25 -0.2808     0.2359      0  -1.191 0.23382
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##      Null Deviance: 424.2  on 306  degrees of freedom
## Residual Deviance: 267.4  on 302  degrees of freedom
```