Advanced Network Analysis

ERGMs for Valued Networks

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Readings

- Pavel N Krivitsky. Exponential-family random graph models for valued networks. *Electronic Journal of Statistics*, 6: 1110--1128, 2012.
- Bruce A. Desmarais and Skyler J. Cranmer. Statistical inference for valued-edge networks: The generalized exponential random graph model. *PloS One*, 7(1), 2012.

Overview

- Many networks of interest have valued rather than binary edges, e.g. trade network, friendships, romantic relationships.
- Can generalize ERGMs to modeling networks with count or rank-ordered valued edges.
- Similar properties and estimation approach.

The Sample Space

- For binary ERGMs, the sample space (or support) $\mathcal{Y}$ — the set of possible networks that can occur — is usually some subset of 2^N, the set of all possible ways in which relationships among the actors may occur.
- For the sample space of valued ERGMs, we need to define $\mathcal{S}$, the set of possible values each relationship may take. For example, for count data, that's $\mathcal{S} = \{0, 1, \ldots, s\}$ if the maximum count is s and $\{0, 1, \ldots\}$ if there is no a priori upper bound. Having specified that, $\mathcal{Y}$ is defined as some subset of $\mathcal{S}^N$: the set of possible ways to assign to each relationship a value.

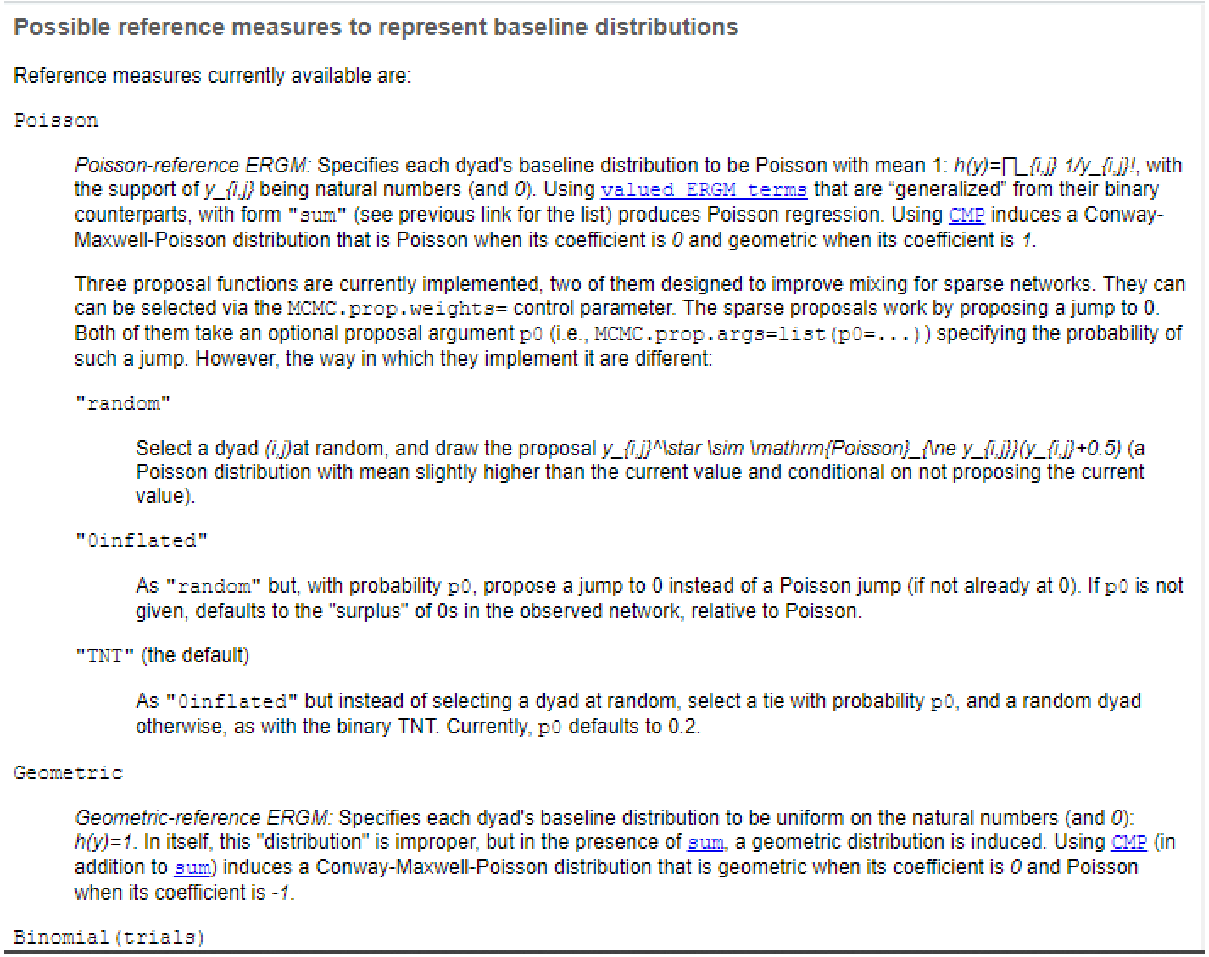
Estimation

Valued ERGMs

- The package `ergm.count` extends the `ergm` package to allow for modeling networks with valued edges. This is done by specifying the `response` argument with the name of the edge attribute to use as the response variable.
- New concept: a reference distribution
    - Need to think about how the values for connections we measure are distributed. The reference distribution specifies the model for the data before we add any ERGM terms.

```
help("ergm-references")
```

The Reference Distribution



Possible reference measures to represent baseline distributions

Reference measures currently available are:

`Poisson`

Poisson-reference ERGM: Specifies each dyad's baseline distribution to be Poisson with mean 1: *h(y)=∏_{i,j} 1/y_{i,j}!*, with the support of *y_{i,j}* being natural numbers (and *0*). Using valued ERGM terms that are "generalized" from their binary counterparts, with form `"sum"` (see previous link for the list) produces Poisson regression. Using CMP induces a Conway-Maxwell-Poisson distribution that is Poisson when its coefficient is *0* and geometric when its coefficient is *1*.

Three proposal functions are currently implemented, two of them designed to improve mixing for sparse networks. They can can be selected via the `MCMC.prop.weights=` control parameter. The sparse proposals work by proposing a jump to 0. Both of them take an optional proposal argument `p0` (i.e., `MCMC.prop.args=list(p0=...)`) specifying the probability of such a jump. However, the way in which they implement it are different:

`"random"`

Select a dyad *(i,j)*at random, and draw the proposal *y_{i,j}^\star \sim \mathrm{Poisson}_{\ne y_{i,j}}(y_{i,j}+0.5)* (a Poisson distribution with mean slightly higher than the current value and conditional on not proposing the current value).

`"0inflated"`

As `"random"` but, with probability `p0`, propose a jump to 0 instead of a Poisson jump (if not already at 0). If `p0` is not given, defaults to the "surplus" of 0s in the observed network, relative to Poisson.

`"TNT"` (the default)

As `"0inflated"` but instead of selecting a dyad at random, select a tie with probability `p0`, and a random dyad otherwise, as with the binary TNT. Currently, `p0` defaults to 0.2.

`Geometric`

Geometric-reference ERGM: Specifies each dyad's baseline distribution to be uniform on the natural numbers (and *0*): *h(y)=1*. In itself, this "distribution" is improper, but in the presence of `sum`, a geometric distribution is induced. Using CMP (in addition to `sum`) induces a Conway-Maxwell-Poisson distribution that is geometric when its coefficient is *0* and Poisson when its coefficient is *-1*.

`Binomial(trials)`

Install Packages:

```r
library(devtools)
install_github("ochyzh/networkdata")
#install.packages("ergm.count")
library(statnet)
library(ergm.count)
library(networkdata)
```

Load the Data

We are going to use Gade et al's data. Our dependent variable--- the valued network--- records the number of collaborations between rebel groups.

```r
data(gadeData)
# data characs
actors = sort(unique(c(gadeData$Var1, gadeData$Var2)))
gadeData<-sort(gadeData)
gadeData$coopActions<-round(gadeData$coopActions^2)
#These are the dyadic variables. They
#must be in matrix form.
dyadVars = names(gadeData)[c(3,5:8)]
n = length(actors) ; p = length(dyadVars)
```

```r
# create empty arr object for all dyad vars
dyadArray = array(0,
    dim=c(n,n,p),
    dimnames=list(actors,actors,dyadVars)
    )
# loop through and fill in
for(param in dyadVars){
    for(i in 1:nrow(gadeData)){
        a1 = gadeData$Var1[i]
        a2 = gadeData$Var2[i]
        val =gadeData[i,param]
        dyadArray[a1,a2,param] = val
    }
}
```

```r
# These are node-level variables.
nodeVars = names(gadeData)[9:11]
nodeData = unique(gadeData[,c('Var1',nodeVars)])
rownames(nodeData) = nodeData$Var1
nodeData = nodeData[actors,c(-1)]
# The DV must be a network object
net = as.network(
    dyadArray[,,'coopActions'],
    directed=FALSE, loops=FALSE,
    matrix.type='adjacency',
    ignore.eval = FALSE,
  names.eval = "coopActions"
    )
```

Look at the first 10 rows and cols:

```
as.matrix(net[1:10,1:10])
```

```
##        101st 13th 1st AALS AARB AASB AASG ADF AF AFB
## 101st      0    1   0    0    0    0    0   0  0   0
## 13th       1    0   0    0    0    0    0   0  0   0
## 1st        0    0   0    0    0    0    0   0  0   1
## AALS       0    0   0    0    0    0    0   0  0   0
## AARB       0    0   0    0    0    0    0   0  1   0
## AASB       0    0   0    0    0    0    0   1  0   0
## AASG       0    0   0    0    0    0    0   0  0   1
## ADF        0    0   0    0    0    1    0   0  0   0
## AF         0    0   0    0    1    0    0   0  0   0
## AFB        0    0   1    0    0    0    1   0  0   0
```

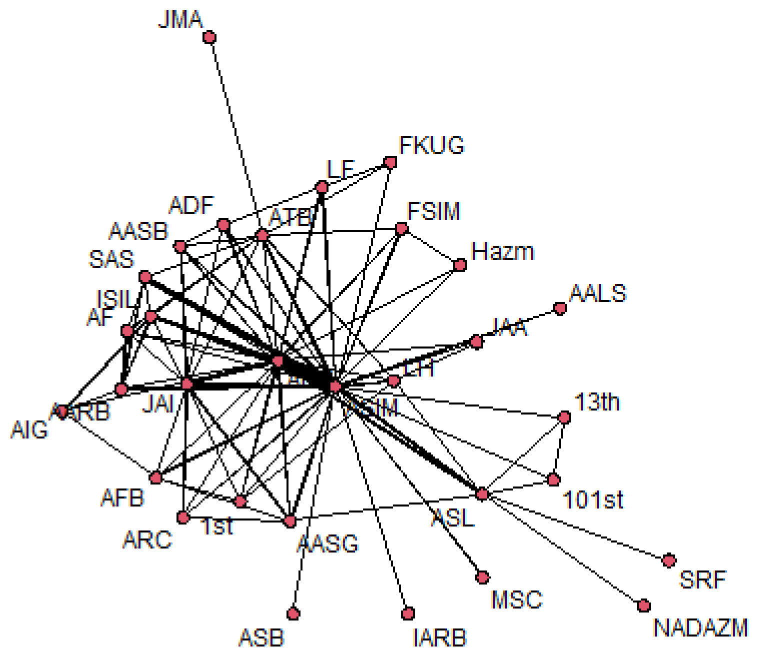
```r
# Set node attributes
for(param in nodeVars){
    network::set.vertex.attribute(net, param, nodeData[,param])
}

# Set network attributes:
set.network.attribute(net,'loc.dyad',dyadArray[,,'loc.dyad'])
set.network.attribute(net,'spons.dyad',dyadArray[,,'spons.dyad'])
# We can view the attribute as a sociomatrix.
as.matrix(net, attrname = "coopActions")[1:10, 1:10]
```

```
##        101st 13th 1st AALS AARB AASB AASG ADF AF AFB
## 101st      0    1   0    0    0    0    0   0  0   0
## 13th       1    0   0    0    0    0    0   0  0   0
## 1st        0    0   0    0    0    0    0   0  0   1
## AALS       0    0   0    0    0    0    0   0  0   0
## AARB       0    0   0    0    0    0    0   0  2   0
## AASB       0    0   0    0    0    0    0   1  0   0
## AASG       0    0   0    0    0    0    0   0  0   1
## ADF        0    0   0    0    0    1    0   0  0   0
## AF         0    0   0    0    2    0    0   0  0   0
## AFB        0    0   1    0    0    0    1   0  0   0
```

Make a Network Graph with Valued Edges:

```
plot(net, edge.col = "black", usecurve = TRUE,
     edge.curve = 0, edge.lwd=.25*dyadArray[,,"coopActions"],
     displaylabels = TRUE)
```

Make a Network Graph with Valued Edges:



Estimate a Valued ERGM

```r
m0 <- ergm(net ~ sum +
    nodecov('averageId.node') +
    nodecov('size.node') +
    nodecov('spons_actor.node') +
    absdiff('averageId.node') +
    absdiff('size.node') +
    edgecov('loc.dyad') +
    edgecov('spons.dyad'),
    response = "coopActions", reference = ~Poisson)
mcmc.diagnostics(m0)
```

Diagnostics

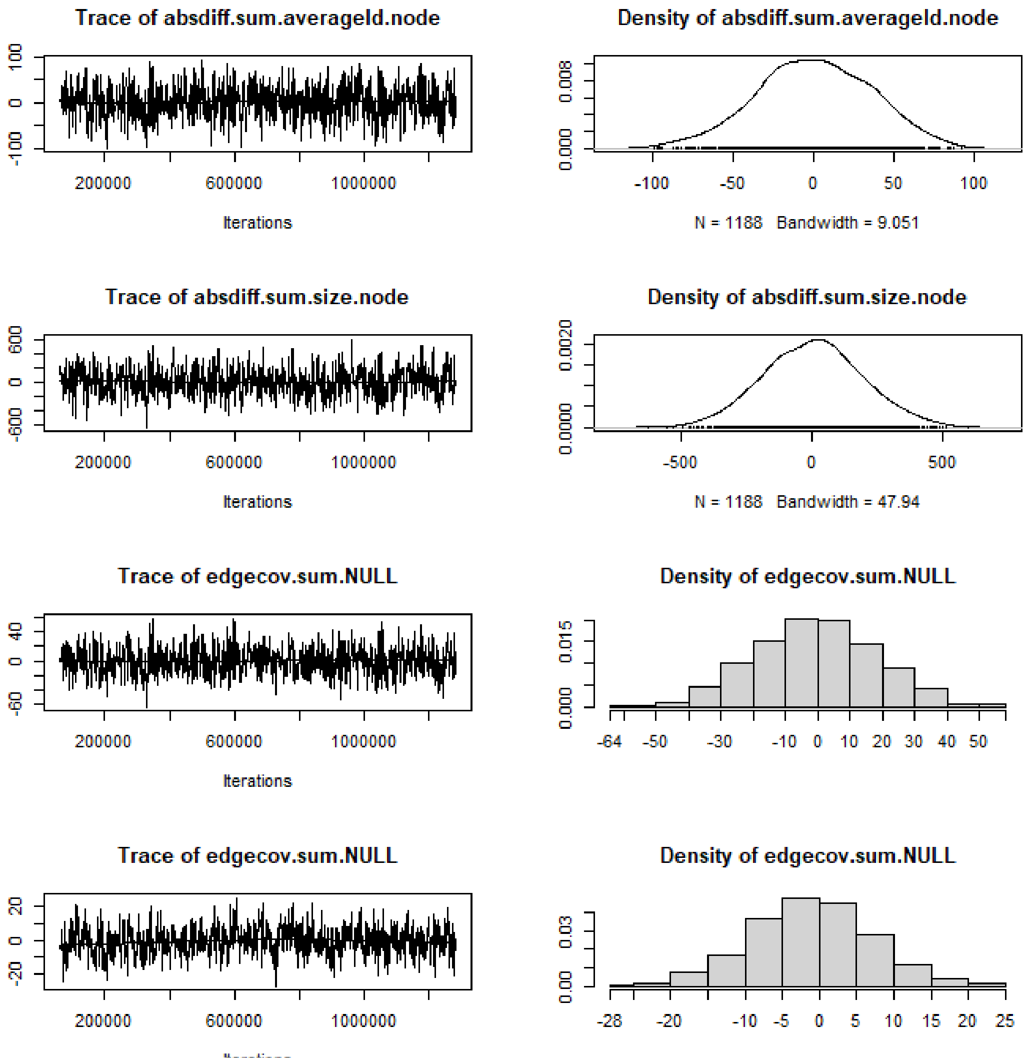


Table of Results

```
summary(m0)
```

```
## Call:
## ergm(formula = net ~ sum + nodecov("averageId.node") + nodecov("size.node"
##     nodecov("spons_actor.node") + absdiff("averageId.node") +
##     absdiff("size.node") + edgecov("loc.dyad") + edgecov("spons.dyad"),
##     response = "coopActions", reference = ~Poisson)
##
## Monte Carlo Maximum Likelihood Results:
##
##                               Estimate Std. Error MCMC % z value Pr(>|z|)
## sum                          -8.012597   1.117417      0  -7.171  < 1e-04
## nodecov.sum.averageId.node    0.564307   0.049284      0  11.450  < 1e-04
## nodecov.sum.size.node         0.074916   0.005851      0  12.803  < 1e-04
## nodecov.sum.spons_actor.node  0.748998   0.140239      0   5.341  < 1e-04
## absdiff.sum.averageId.node   -0.179775   0.050796      0  -3.539 0.000401
## absdiff.sum.size.node        -0.089858   0.010511      0  -8.549  < 1e-04
## edgecov.sum.NULL              3.834232   1.094595      0   3.503 0.000460
## edgecov.sum.NULL              0.597594   0.149731      0   3.991  < 1e-04
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##      Null Deviance:    0.0  on 465  degrees of freedom
```

Interpretation

Let's calculate the expected number of links between two average rebel groups:

- Set all xs to their mean values
- Calculate the expected number as $e^{X^T\beta}$

```
#to get the mean values (in same order as in our model)
x_mean<-apply(data[,c(9,10,11,5,6,7,8)],2,mean)
exp(c(1,x_mean)%*%m0$coef) #expected number of collaborations
```

Your Turn

Calculate the expected number of links between two average rebel groups with no ideological differences:

Accounting for Network Dependencies

Network Dependencies with Valued Edges

- Goal: model endogenous network dependencies
- Complication: valued edges obviate intuitive network measures, such as triangles and k-stars.
- Need to re-conceptualize existing measures to adapt to the context of valued edges.

Individual Heterogeneity.

- A count equivalent to k-stars:

Actors may have different overall propensities to interact. This has been modeled using using degeneracy-prone terms like k-star counts. With valued ERGMs, a more robust measure is:

$$\boldsymbol{g}_{\boldsymbol{actor\ cov.}}(\boldsymbol{y}) = \sum_{i \in N} \frac{1}{n-2} \sum_{j,k \in \mathbb{Y}_{\mathrm{i}} \wedge j<k} \left(\sqrt{\boldsymbol{y}_{i,j} - \overline{\sqrt{\boldsymbol{y}}}}\right)\left(\sqrt{\boldsymbol{y}_{i,k} - \overline{\sqrt{\boldsymbol{y}}}}\right)$$

This is essentially a measure of covariance between the squared values of edges incident (originating) from the same actor. Implemented with the term `nodecovar(transform="sqrt")`.

Triadic Closure

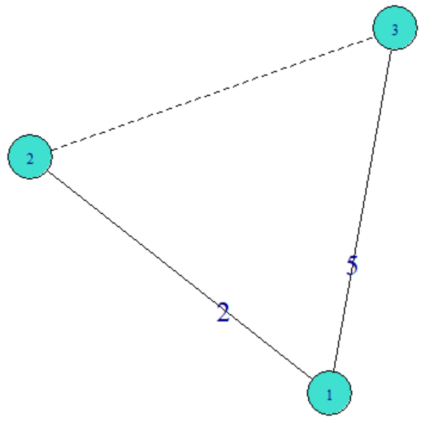
$$\boldsymbol{g}_{\boldsymbol{v}}(\boldsymbol{y}) = \sum_{(i,j)\in\mathbb{Y}} v_{\text{affect}}\left(\boldsymbol{y}_{i,j}, v_{\text{combine}}\left(v_{\text{2-path}}(\boldsymbol{y}_{i,k}, \boldsymbol{y}_{k,j})_{k\in N\setminus\{i,j\}}\right)\right),$$

Triadic Closure

`transitiveweights(twopath, combine, affect)`

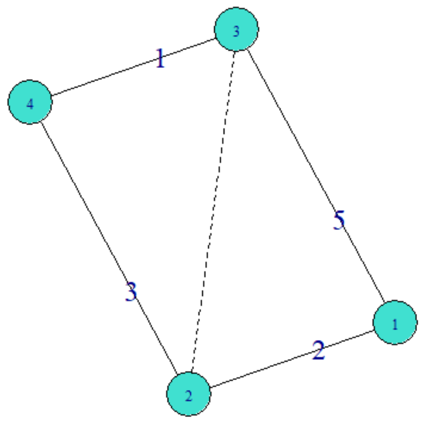
- `twopath`---given $\boldsymbol{y}_{i,j}$ and $\boldsymbol{y}_{k,j}$, how to compute the value for the two-path?
    - `"min"`---the minimum of their values
    - `"geomean`---geometric mean
- `combine`---given the strength of the two-paths $\boldsymbol{y}_{i->k->j}$ for all $k \neq i, j$, how to combine the values?
    - `"max"`--- the strength of the strongest path
    - `"sum"`---the sum of path strength
- `affect` ---given the combined strength of the two-paths between i and j, how should they affect $\boldsymbol{Y}_{i,j}$?
    - `"min"`
    - `"geomean"`

Transitiveweights, Two-Path



- $\text{Two-Path}_{min}(2,5) = 2$
- $\text{Two-Path}_{geomean}(2,5) = \sqrt{(2*5)} = \sqrt{10}$

Transitiveweights, Combine



- $\text{Combine}_{max} = max(\text{Two-path}_{23})$
- $\text{Combine}_{sum} = sum(\text{Two-path}_{23})$

Transitiveweights, Affect

For all pairs connected by two-paths:

- $\text{Affect}_{min} = min(\text{Combine}_{ij})$
- $\text{Affect}_{geomean} = geomean(\text{Combine}_{ij})$

Example

```
m1 <- ergm(net ~ sum +
    nodecov('averageId.node') +
    nodecov('size.node') +
    nodecov('spons_actor.node') +
    absdiff('averageId.node') +
    absdiff('size.node') +
    edgecov('loc.dyad') +
    edgecov('spons.dyad')+
    transitiveweights("min","max","min"),
    response = "coopActions", reference = ~Poisson)
par(mfrow = c(3,2))
mcmc.diagnostics(m1)
```

Diagnostics

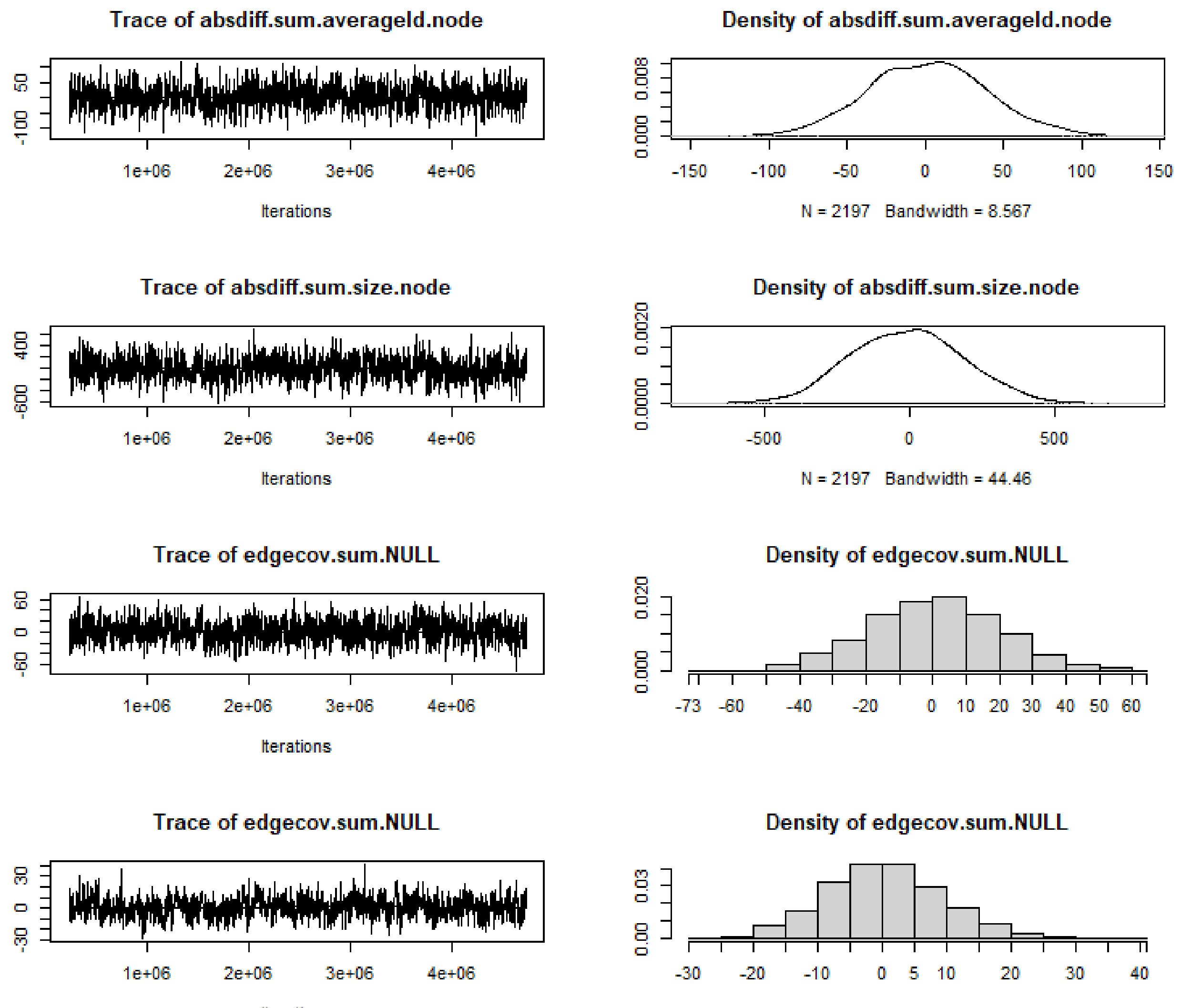


Table of Results

```
summary(m1)
```

```
## Call:
## ergm(formula = net ~ sum + nodecov("averageId.node") + nodecov("size.node"
##     nodecov("spons_actor.node") + absdiff("averageId.node") +
##     absdiff("size.node") + edgecov("loc.dyad") + edgecov("spons.dyad") +
##     transitiveweights("min", "max", "min"), response = "coopActions",
##     reference = ~Poisson)
##
## Monte Carlo Maximum Likelihood Results:
##
##                               Estimate Std. Error MCMC % z value Pr(>|z|)
## sum                          -7.454511   1.063267      0  -7.011  < 1e-04
## nodecov.sum.averageId.node    0.551644   0.049526      0  11.138  < 1e-04
## nodecov.sum.size.node         0.067389   0.005726      0  11.770  < 1e-04
## nodecov.sum.spons_actor.node  0.828172   0.132405      0   6.255  < 1e-04
## absdiff.sum.averageId.node   -0.159866   0.044402      0  -3.600 0.000318
## absdiff.sum.size.node        -0.078650   0.009654      0  -8.147  < 1e-04
## edgecov.sum.NULL              3.805675   1.017857      0   3.739 0.000185
## edgecov.sum.NULL              0.528179   0.126521      0   4.175  < 1e-04
## transitiveweights.min.max.min -0.628822   0.046141      0 -13.628  < 1e-04
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Simulating Networks

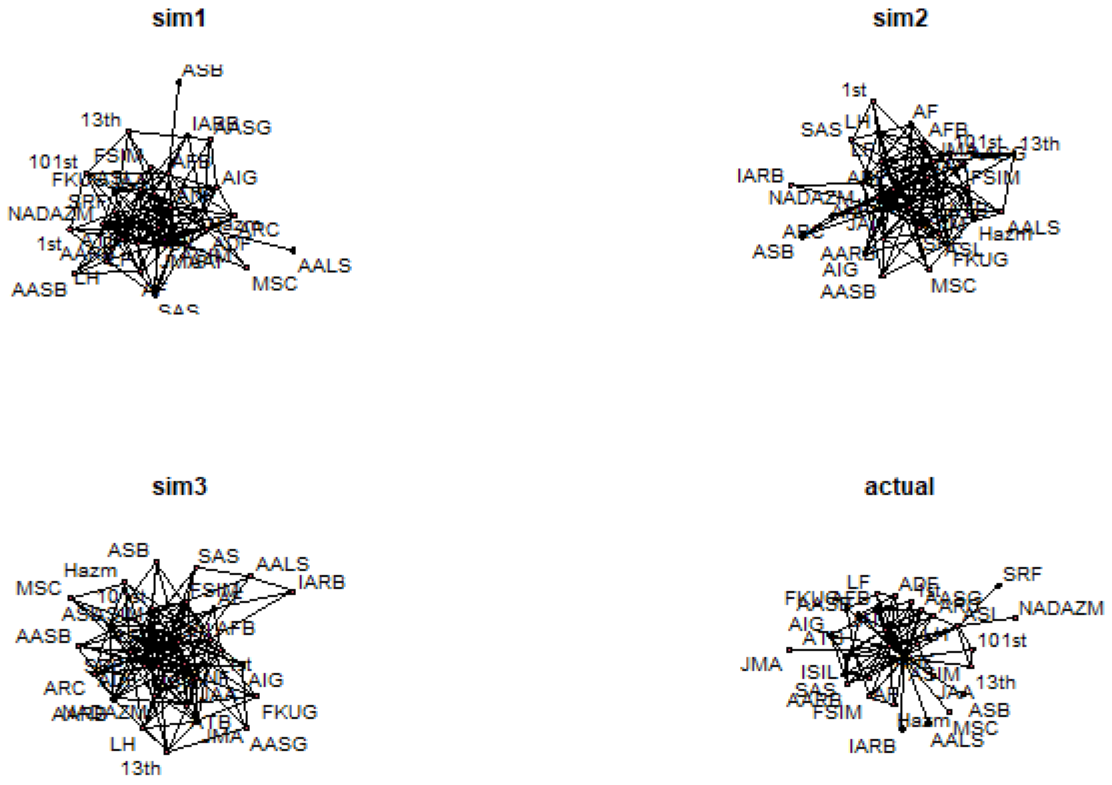
Simulating Networks

We can use the estimates from our model to simulate a network (just like with ERGMs). If the simulated networks look similar to the observed network, then our model has a good fit.

```r
# Simulate from model fit:
simNets <- simulate(m1, nsim = 3)

# Define a plotting function:
plotSimNet = function(net, label){
    set.seed(6886)
    plot(net, edge.col = "black", usecurve = TRUE,
     edge.curve = 0, edge.lwd=.1*dyadArray[,,"coopActions"],
     displaylabels = TRUE)
    title(label) }
```

```r
par(mfrow = c(2, 2))
# add actual network to list of sim nets
# for comparison
simNets[[4]] = net
labels = c(paste0("sim",1:3), 'actual')
lapply(1:length(simNets), function(i){
    plotSimNet(simNets[[i]], labels[i]) })
```

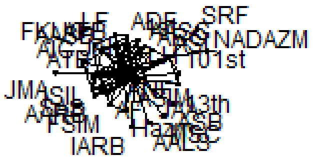
Observed vs. Simulated Networks



```
## [[1]]
## NULL
```

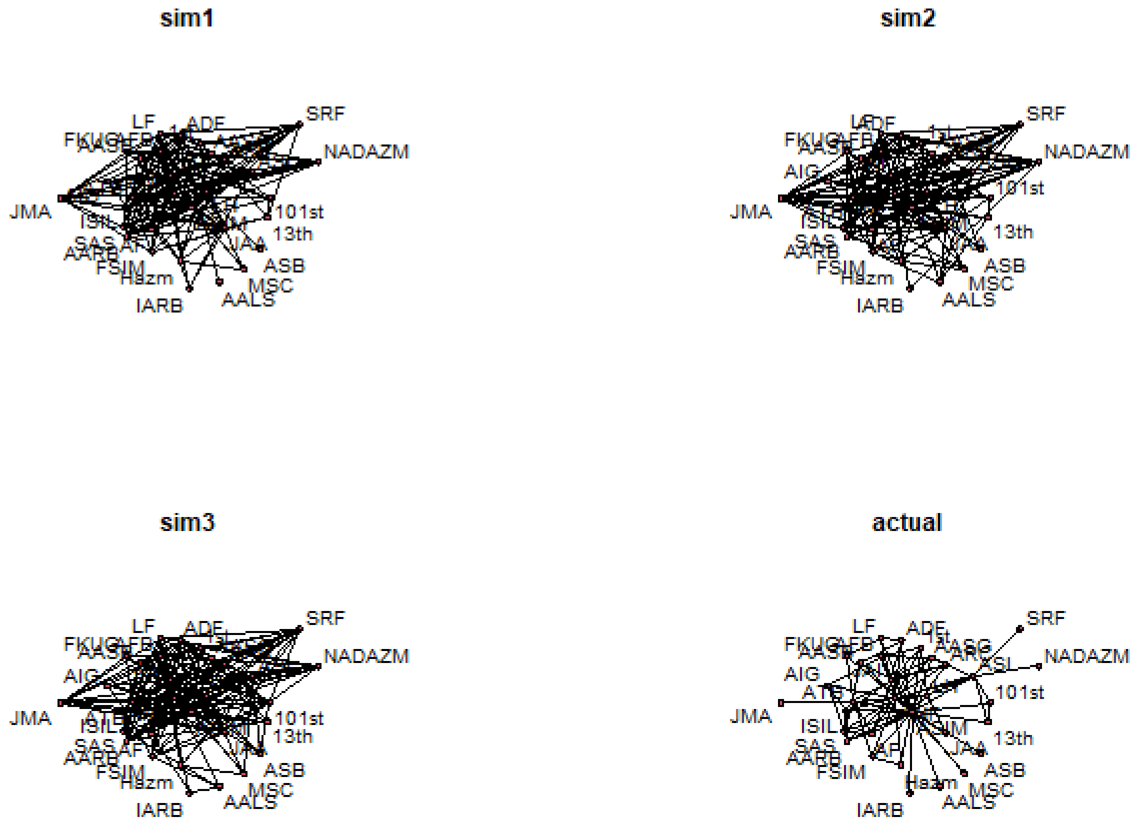
With Fixed Coordinates:

```r
#Plot the original network to get the layout:
set.seed(6886)
p<-plot(net, edge.col = "black", usecurve = TRUE,
     edge.curve = 0, edge.lwd=.25*dyadArray[,,"coopActions"],
     displaylabels = TRUE)
```



```
# Define a plotting function:
plotSimNet = function(net, label){
    set.seed(6886)
    plot(net, edge.col = "black", usecurve = TRUE,
     edge.curve = 0, edge.lwd=.1*dyadArray[,,"coopActions"],
     displaylabels = TRUE, coord=p)
    title(label) }
```

Observed vs. Simulated Networks (Fixed Coord.)



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

Assessing Model Fit

In the above exercise, we compared our network to only 3 simulated networks. Ideally, we would like to compare it to more than 3. Since it's difficult to look at thousands of simulated networks on a graph, a way to compare our network to thousands of such simulated networks is by summarizing the characteristics of these simulated networks, such as the sum of edges or various other measures.

Notice that in the code below that, in addition to network statistics included in model `m1`, we can also summarize statistics that were not explicitly included in `m1`, such as `nodecovar(transform="sqrt")`. This is because our simulated networks may still exhibit vertex heterogeneity as a function of the modeled network properties (e.g. triangles), i.e. more triangles may also lead to more k-stars.

Also notice that I specified `output="stats"`. Since I only care about network summaries, I am telling the function to NOT save the actual simulated networks, but only their summary statistics. This saves memory space.

```r
# Simulate from model fit:
simNets1000 <- simulate(m1, monitor = ~ nodecovar(transform="sqrt"),
    nsim = 1000, output = "stats")
```

Results of the Simulation

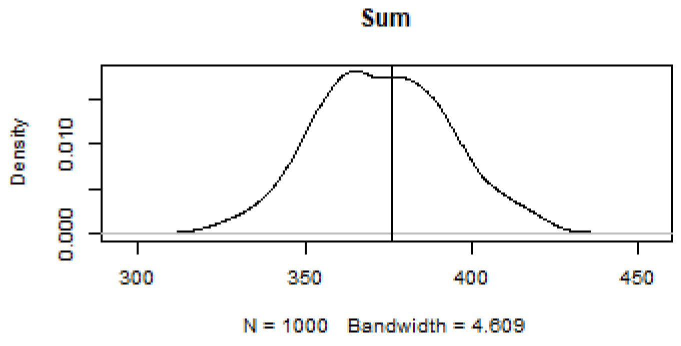
```
colnames(simNets1000)
```

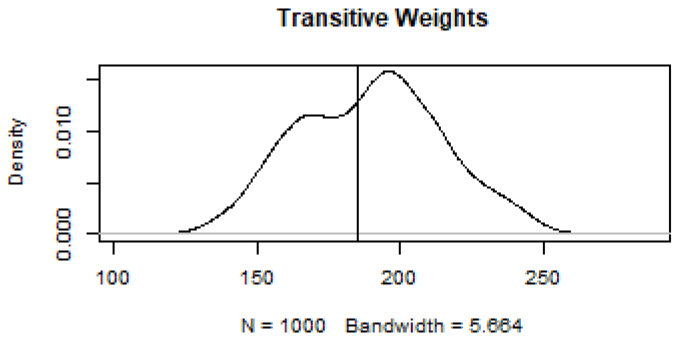
```
##  [1] "sum"                             "nodecov.sum.averageId.node"
##  [3] "nodecov.sum.size.node"           "nodecov.sum.spons_actor.node"
##  [5] "absdiff.sum.averageId.node"      "absdiff.sum.size.node"
##  [7] "edgecov.sum.loc.dyad"            "edgecov.sum.spons.dyad"
##  [9] "transitiveweights.min.max.min" "nodecovar"
```

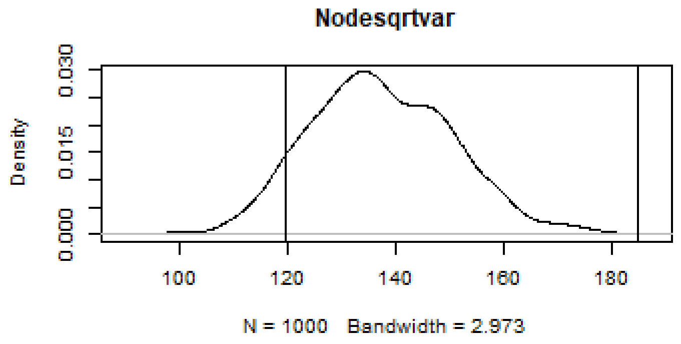
Plot the Summary of the Simulations

```
#How prevalent are k-stars in the observed network?
obsNet<-summary(net~sum+transitiveweights("min","max","min")+nodecova
                response = "coopActions")
par(mfrow = c(2, 2))
#1st col.=sum
plot(density(simNets1000[,1]), main="")
abline(v = obsNet[1])
title("Sum")

# 9th col. = transitiveweights
plot(density(simNets1000[,9]), main="")
abline(v = obsNet[2])
title("Transitive Weights")

# 10th col. = nodesqrtcovar
plot(density(simNets1000[,10]), main="")
abline(v = obsNet)
title("Nodesqrtvar")
```

Plot the Summary of the Simulations







Improve Model Specofication

```
m2 <- ergm(net ~ sum +
    nodecov('averageId.node') +
    nodecov('size.node') +
    nodecov('spons_actor.node') +
    absdiff('averageId.node') +
    absdiff('size.node') +
    edgecov('loc.dyad') +
    edgecov('spons.dyad')+
    transitiveweights("min","max","min")+
    nodecovar(transform="sqrt"),
    response = "coopActions", reference = ~Poisson)
```

Improve Model Specification

```
## Call:
## ergm(formula = net ~ sum + nodecov("averageId.node") + nodecov("size.node"
##     nodecov("spons_actor.node") + absdiff("averageId.node") +
##     absdiff("size.node") + edgecov("loc.dyad") + edgecov("spons.dyad") +
##     transitiveweights("min", "max", "min") + nodecovar(transform = "sqrt")
##     response = "coopActions", reference = ~Poisson)
##
## Monte Carlo Maximum Likelihood Results:
##
##                              Estimate Std. Error MCMC % z value Pr(>|z|)
## sum                         -6.594598   1.084880      0  -6.079  < 1e-04
## nodecov.sum.averageId.node   0.510330   0.047484      0  10.747  < 1e-04
## nodecov.sum.size.node        0.057320   0.005981      0   9.584  < 1e-04
## nodecov.sum.spons_actor.node  0.808021   0.126655      0   6.380  < 1e-04
## absdiff.sum.averageId.node  -0.085453   0.036289      0  -2.355 0.018535
## absdiff.sum.size.node       -0.052703   0.009241      0  -5.703  < 1e-04
## edgecov.sum.NULL             3.580399   1.020037      0   3.510 0.000448
## edgecov.sum.NULL             0.304451   0.124577      0   2.444 0.014530
## transitiveweights.min.max.min -0.432002   0.066354      0  -6.511  < 1e-04
## nodecovar                   -1.109736   0.242183      0  -4.582  < 1e-04
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##      Null Deviance:     0.0  on 465  degrees of freedom
```

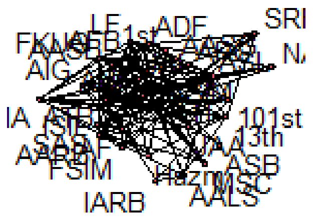
Your Turn

Follow the steps we did for `m1` to evaluate the fit of model `m2`. Start by simulating a small number of networks, plot them and compare them to the observed network. Then simulate 1000 networks and compare them to the observed network on the key network statistics. Does `m2` have a better fit?

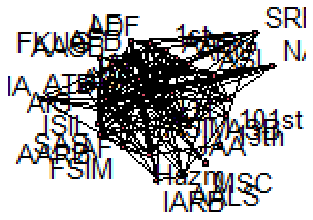
sim1

LE
ADF
SRI
N
AIG
IA
101st
13th
ASB
MSC
FSIM
AALS
IARB

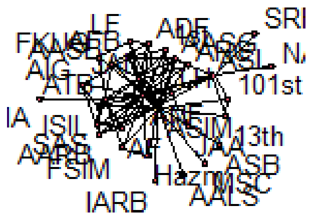
sim2

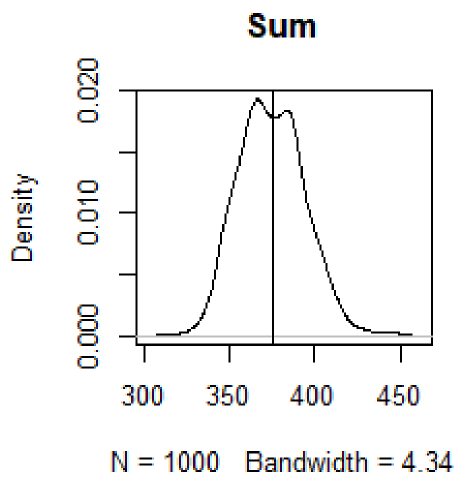


sim3



actual




Sum
Density
0.000
0.010
0.020
300
350
400
450
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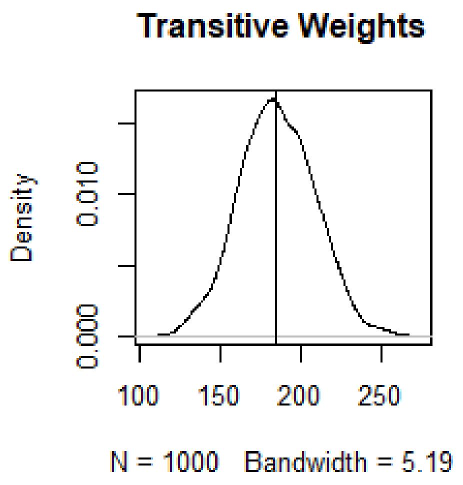
Transitive Weights
Density
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0.010
100
150
200
250
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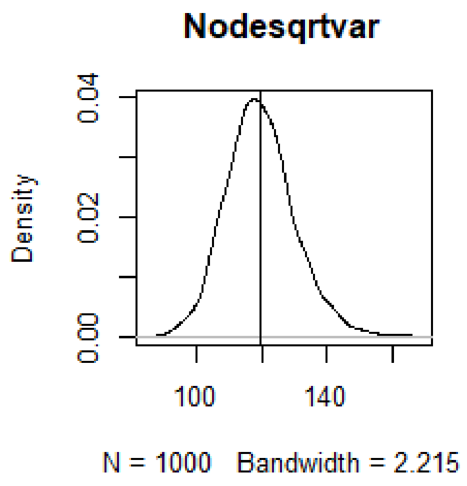
Nodesqrtvar
Density
0.00
0.02
0.04
100
140
N = 1000 Bandwidth = 2.215