# Introduction to Exponential-family Random Graph (ERG or p*) modeling with ergm

Version 3.2-11882-11883.1-2013.02.26-23.02.18

Carter T. Butts (University of California, Irvine)
Martina Morris (University of Washington)
Pavel N. Krivitsky (Penn State University)
Zack Almquist (University of California, Irvine)
Joint with the rest of the Statnet Development Team:

Mark S. Handcock (UCLA)
David R. Hunter (Penn State University)
Steven M. Goodreau (University of Washington)
Skye Bender de-Moll (Oakland)

March 15, 2013

## Contents

# 1 Getting Started

This vignette is based on the `ergm` tutorial presented at INSNA Sunbelt - St. Pete Beach, Florida, Feb 2011.

Open an R session, and set your working directory to the location where you would like to save this work. You can do this with the pull-down menus (File>Change Dir) or with the command:

```
> setwd('full.path.for.the.folder')
```

To install all of the packages in the statnet suite:

```
> install.packages('statnet')
> library(statnet)
```

Or, to only install the specific statnet packages needed for this tutorial:

```
> install.packages('network')
> install.packages('ergm')
> install.packages('sna')
> library(network)
> library(ergm)
> library(sna)
```

After the first time, to update the packages one can either repeat the commands above, or use:

```
> update.packages('name.of.package')
```

For this tutorial, we will need one additional package (coda), which is recommended (but not required) by ergm:

```
> install.packages('coda')
> library(coda)
```

# 2 Statistical network modeling; the *ergm* command and *ergm* object

Make sure the statnet package is attached:

```
> library(statnet)
```

or

```
> library(ergm)
> library(sna)
```

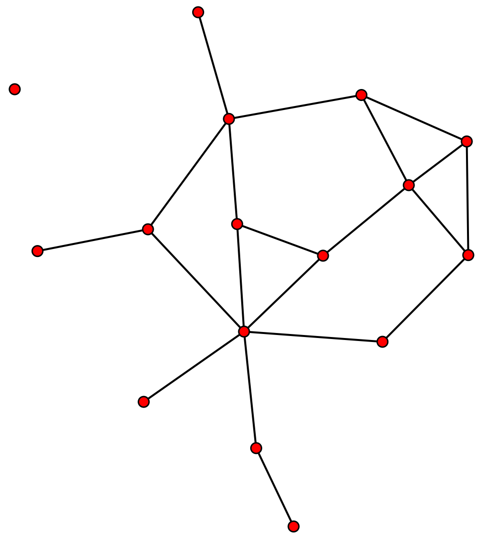
```
     Tools for Social Network Analysis
Version      2.2-0 created on      2010-11-21.
copyright (c) 2005, Carter T. Butts, University of California-Irvine
Type help(package="sna") to get started.
```

The ergm package contains several network data sets that you can use for practice examples.

```
> data(package='ergm') # tells us the datasets in our packages
> data(florentine) # loads flomarriage and flobusiness data
> flomarriage # Let's look at the flomarriage data
```

```
 Network attributes:
  vertices = 16
  directed = FALSE
  hyper = FALSE
  loops = FALSE
  multiple = FALSE
  bipartite = FALSE
  total edges= 20
    missing edges= 0
    non-missing edges= 20

 Vertex attribute names:
    priorates totalties vertex.names wealth
```

```
> plot(flomarriage) # Let's view the flomarriage network
```



Remember the general ergm representation of the probability of the observed network, and the conditional log-odds of a tie:

$$\Pr(Y = y) = \exp[\theta' g(y)]/k(\theta)$$

$Y$ is a network; $g(y)$ is a vector of network stats; $\theta$ is the vector of coefficients; $k(\theta)$ is a normalizing constant.

$$\text{logit}\left(\Pr(Y_{ij} = 1 | Y^c)\right) = \theta' \Delta \left(g(y)\right)_{ij}$$

$Y_{ij}$ is an actor pair in $Y$; $Y^c$ is the rest of the network; $\Delta \left(g(y)\right)_{ij}$ is the change in $g(y)$ when the value of $Y_{ij}$ is toggled on.

We begin with the simplest possible model, the Bernoulli or Erd?s-R?nyi model, which contains only an edge term.

```
> flomodel.01 <- ergm(flomarriage~edges) # fit model
> flomodel.01
```

```
MLE Coefficients:
 edges
-1.609
```

```
> summary(flomodel.01) # look in more depth
```

```
==========================
Summary of model fit
==========================

Formula:   flomarriage ~ edges

Iterations:  20

Monte Carlo MLE Results:
      Estimate Std. Error MCMC % p-value
edges  -1.6094     0.2449     NA  <1e-04 ***
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1

     Null Deviance: 166.4  on 120  degrees of freedom
 Residual Deviance: 108.1  on 119  degrees of freedom

AIC: 110.1    BIC: 112.9    (Smaller is better.)
```

How to interpret this model? The log-odds of any tie occurring is:

$$\begin{aligned} & -1.609 \times \text{change in the number of ties} \\ = & -1.609 \times 1 \end{aligned}$$

for all ties, since the addition of any tie to the network changes the number of ties by 1!

Corresponding probability is:

$$\begin{aligned} & \exp(-1.609)/(1 + \exp(-1.609)) \\ = & 0.1667 \end{aligned}$$

which is what you would expect, since there are 20/120 ties.

Let's add a term often thought to be a measure of "clustering": the number of completed triangles. Note we're in stochastic simulation now – your output will differ

```
> flomodel.02 <- ergm(flomarriage~edges+triangle)
```

```
Iteration 1 of at most 20:
Convergence test P-value: 9.3e-31
The log-likelihood improved by 0.002149
Iteration 2 of at most 20:
Convergence test P-value: 1e-05
The log-likelihood improved by 0.0003448
Iteration 3 of at most 20:
Convergence test P-value: 4.3e-01
The log-likelihood improved by < 0.0001
Iteration 4 of at most 20:
Convergence test P-value: 5.1e-01
Convergence detected. Stopping.
The log-likelihood improved by < 0.0001

This model was fit using MCMC.  To examine model diagnostics and check for degeneracy, use the mcmc.d
```

```
> summary(flomodel.02)
```

```
==========================
Summary of model fit
==========================

Formula:   flomarriage ~ edges + triangle

Iterations:  20

Monte Carlo MLE Results:
         Estimate Std. Error MCMC % p-value
edges     -1.6756     0.3509      0  <1e-04 ***
triangle   0.1633     0.5811      0   0.779
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1

     Null Deviance: 166.4  on 120  degrees of freedom
 Residual Deviance: 108.1  on 118  degrees of freedom

AIC: 112.1    BIC: 117.6    (Smaller is better.)
```

Again, how to interpret coefficients?

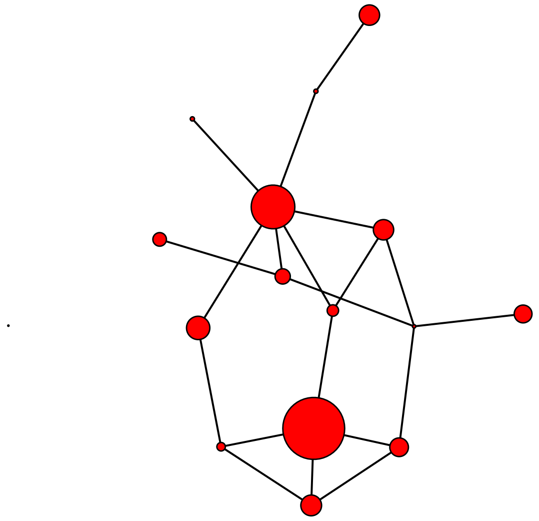
Conditional log-odds of two actors forming a tie is:

$$-1.673 \times \text{change in the number of ties} + 0.139 \times \text{change in number of triangles}$$

- if the tie will not add any triangles to the network, its log-odds is: $-1.673$.
- if it will add one triangle to the network, its log-odds is: $-1.673 + 0.139 = -1.534$
- if it will add two triangles to the network, its log-odds is: $-1.673 + 0.139 \times 2 = -1.395$
- the corresponding probabilities are 0.158, 0.177, and 0.199.

Let's take a closer look at the ergm object itself:

```
> class(flomodel.02) # this has the class ergm

[1] "ergm"

> names(flomodel.02) # let's look straight at the ERGM obj.

 [1] "coef"          "sample"        "sample.obs"    "iterations"
 [5] "MCMCtheta"     "loglikelihood" "gradient"      "hessian"
 [9] "covar"         "failure"       "mc.se"         "network"
[13] "newnetwork"    "coef.init"     "initialfit"    "coef.hist"
[17] "stats.hist"    "etamap"        "formula"       "target.stats"
[21] "constrained"   "constraints"   "control"       "reference"
[25] "estimate"      "offset"        "drop"          "estimable"
[29] "null.lik"      "mle.lik"


> flomodel.02$coef

     edges   triangle
-1.6755690  0.1633037

> flomodel.02$formula

flomarriage ~ edges + triangle

> flomodel.02$mle.lik

'log Lik.' -54.03589 (df=2)

> wealth <- flomarriage %v% 'wealth' # the %v% extracts vertex
> wealth # attributes from a network

 [1]  10  36  55  44  20  32   8  42 103  48  49   3  27  10 146  48

> plot(flomarriage, vertex.cex=wealth/25) # network plot with vertex size
>                                         # proportional to wealth
```



We can test whether edge probabilities are a function of wealth:

```
> flomodel.03 <- ergm(flomarriage~edges+nodecov('wealth'))
> summary(flomodel.03)

==========================
Summary of model fit
==========================

Formula:   flomarriage ~ edges + nodecov("wealth")

Iterations:  20

Monte Carlo MLE Results:
                Estimate Std. Error MCMC % p-value
edges          -2.594929   0.536056     NA  <1e-04 ***
nodecov.wealth  0.010546   0.004674     NA  0.0259 *
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1

     Null Deviance: 166.4  on 120  degrees of freedom
 Residual Deviance: 103.1  on 118  degrees of freedom

AIC: 107.1    BIC: 112.7    (Smaller is better.)
```

Yes, there is a significant positive wealth effect on the probability of a tie.

Let’s try a model or two on:

Is there a statistically significant tendency for ties to be reciprocated (’mutuality’)?

```
> data(samplk)
> ls() # directed data: Sampson's Monks
> samplk3
> plot(samplk3)
> sampmodel.01 <- ergm(samplk3~edges+mutual)
> summary(sampmodel.01)
```

Let’s try a larger network

```
> data(faux.mesa.high)
> mesa <- faux.mesa.high


> plot(mesa)
> mesa
> plot(mesa, vertex.col='Grade')
> legend('bottomleft',fill=7:12,legend=paste('Grade',7:12),cex=0.75)
> fauxmodel.01 <- ergm(mesa ~edges + nodematch('Grade',diff=T) + nodematch('Race',diff=T))
> summary(fauxmodel.01)
```

Note that two of the coefficients are estimated as -Inf (the nodematch coefficients for race Black and Other). Why is this?

```
> table(mesa %v% 'Race') # Frequencies of race
> mixingmatrix(mesa, "Race")
```

So the problem is that there are very few students in the Black and Other race categories, and these students form no homophilous (within-group) ties. The empty cells are what produce the -Inf estimates.

Time to consider some missing data:

```
> missnet <- network.initialize(10,directed=F)
> missnet[1,2] <- missnet[2,7] <- missnet[3,6] <- 1
> missnet[4,6] <- missnet[4,9] <- NA
> missnet
> plot(missnet)
> ergm(missnet~edges)
```

The coefficient equals -2.590. This is the log-odds of the probability .0698. Our network has 3 ties, out of the 43 nodal pairs (10 choose 2 minus 2) whose dyad status we have observed. $3/43 = 0.0698$.

```
> ergm(missnet~edges+degree(2))
> missnet[4,6] <- missnet[4,9] <- 0
> ergm(missnet~edges+degree(2))
```

The two estimates for the degree2 coefficient differ considerably. In the first case, there is one node we know for sure has degree 2, two that may or may not, and seven that we know for sure do not. In the latter, there is one node that has degree 2, and nine that do not.

# 3 Model terms available for *ergm* estimation and simulation

Model terms are the expressions (e.g. "triangle") used to represent predictors on the right-hand size of equations used in:

- calls to `ergm` (to estimate an ergm model)
- calls to `simulate` (to simulate networks from an ergm model fit)
- calls to `summary` (to obtain measurements of network statistics on a dataset)

## 3.1 Terms provided with ergm

For a list of available terms that can be used to specify an ERGM, see Appendix B, or type:

help('ergm-terms')

For a more complete discussion of these terms see the 'Specifications' paper in J Stat Software v. 24. (link is available online at `www.statnet.org`)

## 3.2 Coding new terms

We have recently released a new package (`ergm.userterms`) and tutorial aimed at making it much easier than before to write one's own terms. The package is available on CRAN, and installing it will also download the tutorial (ergmuserterms.pdf). We teach a workshop at the Sunbelt meetings, and are also hoping for the tutorial to appear soon in the *Journal of Statistical Software*. Note that writing up new `ergm` terms requires some knowledge of C and the ability to build R from source (although the latter is covered in the tutorial).

# 4 Network simulation: the *simulate* command and *network.list* objects

Once we have estimated the coefficients of an ERGM, the model is completely specified. It defines a probability distribution across all networks of this size. If the model is a good fit to the observed data, then networks drawn from this distribution will be more likely to "resemble" the observed data. To see examples of networks drawn from this distribution we use the `simulate` command:

```
> flomodel.03.sim <- simulate(flomodel.03,nsim=10)
> class(flomodel.03.sim)
```

```
[1] "network.list"
```

```
> summary(flomodel.03.sim)
```

```
Number of Networks: 10
Model: flomarriage ~ edges + nodecov("wealth")
Reference: ~Bernoulli
Constraints: ~.
Parameters:
         edges nodecov.wealth
   -2.59492903     0.01054591

Stored network statistics:
      edges nodecov.wealth
 [1,]    18           2261
 [2,]    20           2396
 [3,]    24           2831
 [4,]    19           2218
 [5,]    16           1733
 [6,]    19           2204
 [7,]    25           2915
 [8,]    23           2480
 [9,]    22           2591
[10,]    23           2591
```

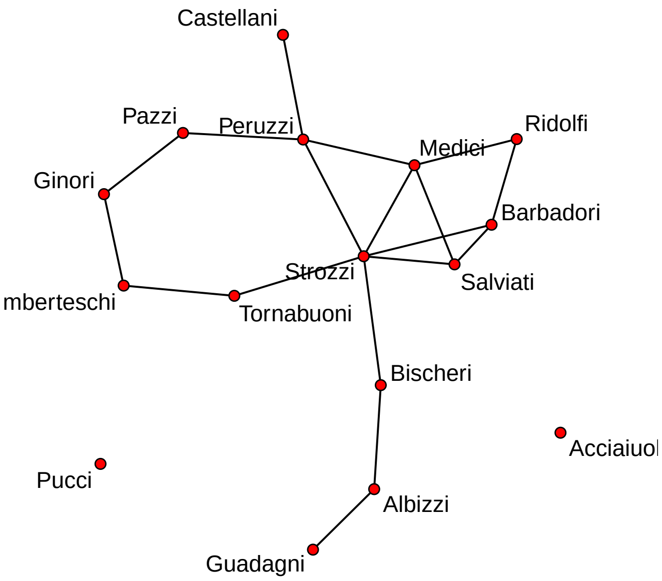
```
> length(flomodel.03.sim)
```

```
[1] 10
```

```
> flomodel.03.sim[[1]]
```

```
 Network attributes:
  vertices = 16
  directed = FALSE
  hyper = FALSE
  loops = FALSE
  multiple = FALSE
  bipartite = FALSE
  total edges= 18
    missing edges= 0
    non-missing edges= 18

 Vertex attribute names:
    priorates totalties vertex.names wealth
```

```
> plot(flomodel.03.sim[[1]], label= flomodel.03.sim[[1]] %v% "vertex.names")
```



Voil?. Of course, yours will look somewhat different.

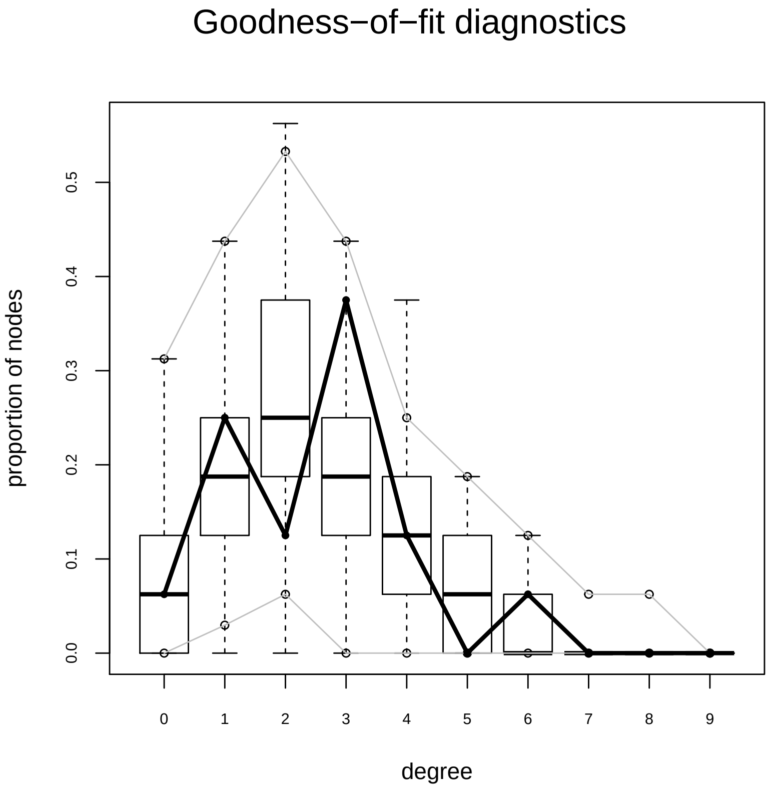
# 5 Examining the quality of model fit – *GOF*

ERGMs are generative models – that is, they represent the process that governs tie formation at a local level. These local processes in turn aggregate up to produce characteristic global network properties, even though these global properties are not explicit terms in the model. One test of whether a model ”fits the data” is therefore how well it reproduces these global properties. We do this by choosing a network statistic that is not in the model, and comparing the value of this statistic observed in the original network to the distribution of values we get in simulated networks from our model.

```
> flomodel.03.gof <- gof(flomodel.03~degree)
> flomodel.03.gof

Goodness-of-fit for degree

   obs min mean max MC p-value
0    1   0 1.38   5       1.00
1    4   0 3.40   8       0.96
2    2   0 4.49   9       0.26
3    6   0 3.30   8       0.24
4    2   0 1.78   7       1.00
5    0   0 0.89   3       0.84
6    1   0 0.45   5       0.72
7    0   0 0.17   2       1.00
```

```
8    0    0 0.11   1       1.00
9    0    0 0.02   1       1.00
10   0    0 0.01   1       1.00
```

```
> plot(flomodel.03.gof)
> mesamodel.02 <- ergm(mesa~edges)
> mesamodel.02.gof <- gof(mesamodel.02~distance,nsim=10)
> plot(mesamodel.02.gof)
>
```



For a good example of model exploration and fitting for the Add Health Friendship networks, see Goodreau, Kitts & Morris, *Demography* 2009.

## 6 Diagnostics: troubleshooting and checking for model degeneracy

The computational algorithms in `ergm` use MCMC to estimate the likelihood function. Part of this process involves simulating a set of networks to approximate unknown components of the likelihood.

When a model is not a good representation of the observed network the estimation process may be affected. In the worst case scenario, the simulated networks will be so different from the observed network that the algorithm fails altogether. This can occur for two general reasons. First, the simulation algorithm may fail to converge, and the sampled networks are thus not from the specified distribution. Second, the model parameters used to simulate the networks are too different from the MLE, so even though the simulation algorithm is producing a representative sample of networks, this is not the sample that would be produced under the MLE.

For more detailed discussions of model degeneracy in the ERGM context, see the papers in *J Stat Software* v. 24. (link is available online at `www.statnet.org`)

We can use diagnostics to see what is happening with the simulation algorithm, and these can lead us to ways to improve it.

We will first consider a simulation where the algorithm works. To understand the algorithm, consider

```
> fit <- ergm(flobusiness~edges+degree(1),
+   control=control.ergm(MCMC.interval=1, MCMC.burnin=1000, seed=1))
```

This runs a version with every network returned. Let us look at the diagnostics produced:

```
> mcmc.diagnostics(fit, center=F)
```

Let's look more carefully at a default model fit:

```
> fit <- ergm(flobusiness~edges+degree(1))
> mcmc.diagnostics(fit, center=F)
```

Now let us look at a more interesting case, using a larger network:

```
> data('faux.magnolia.high')
> magnolia <- faux.magnolia.high
> plot(magnolia, vertex.cex=.5)
```

```
> fit <- ergm(magnolia~edges+triangle, control=control.ergm(seed=1))
> mcmc.diagnostics(fit, center=F)
```

```
Iteration 1 of at most 20:
Convergence test P-value: 9.7e-45
The log-likelihood improved by 1.645
Iteration 2 of at most 20:
Convergence test P-value: 7e-02
The log-likelihood improved by 0.599
Iteration 3 of at most 20:
Convergence test P-value: 1.7e-01
The log-likelihood improved by 0.2797
Iteration 4 of at most 20:

Error in ergm.MCMLE(init, nw, model, initialfit, control = control, MHproposal = MHproposal,  :
  Number of edges in a simulated network exceeds that in the observed by a factor of more than 20. Th
```

Very interesting. This model produced degenerate networks. You could have gotten some more feedback about this during the fitting, by using:

```
> fit <- ergm(magnolia~edges+triangle, control=control.ergm(seed=1), verbose=T)
```

You might try to increase the MCMC sample size:

```
> fit <- ergm(magnolia~edges+triangle,seed=1,
+  control = control.ergm(seed=1, MCMC.samplesize=20000),
+  verbose=T)
> mcmc.diagnostics(fit, center=F)
```

Now, try it again with a sample size of 50,000.

How about trying the more robust version of modeling triangles: GWESP? (For a technical introduction to GWESP see Hunter and Handcock; for a more intuitive description and empirical application see Goodreau Kitts and Morris 2009)

```
> fit <- ergm(magnolia~edges+gwesp(0.5,fixed=T),
+  control =  control.ergm(seed=1))
> mcmc.diagnostics(fit)
```

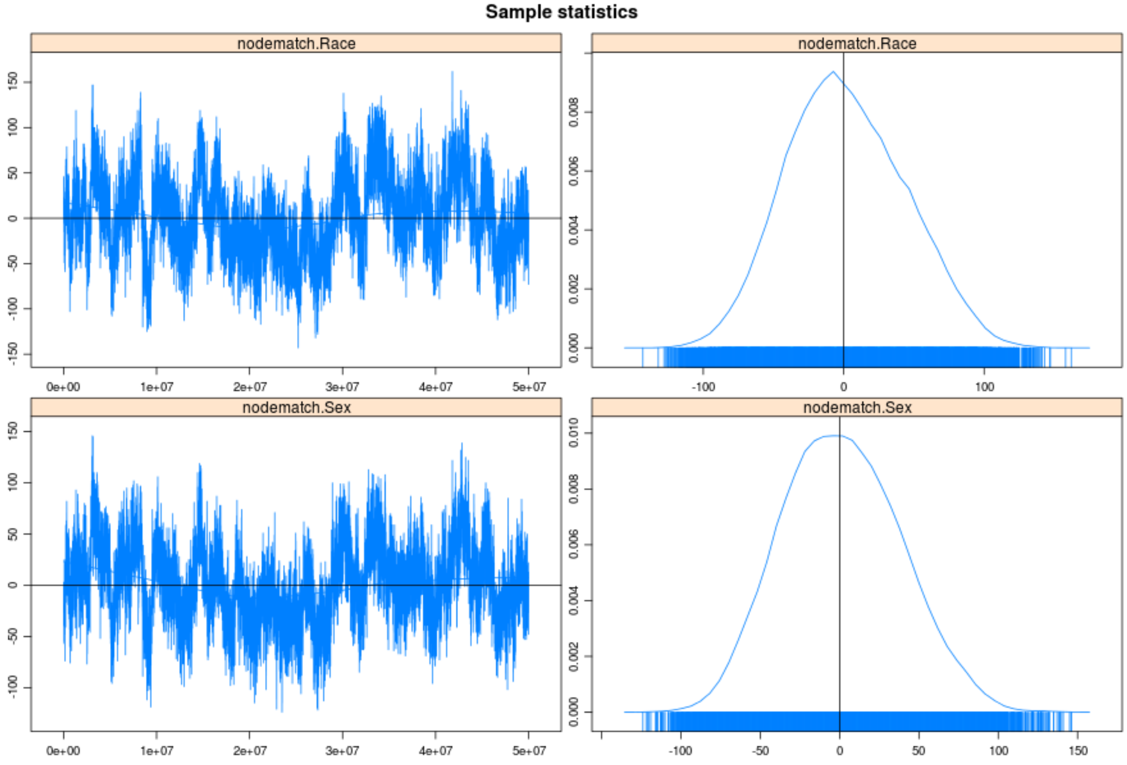
Still degenerate, but maybe getting closer?

```
> fit <- ergm(magnolia~edges+gwesp(0.5,fixed=T)+nodematch('Grade')+nodematch('Race')+
+   nodematch('Sex'),
+  control = control.ergm(seed=1),
+  verbose=T)
> pdf('diagnostics1.pdf')        #Use the recording function if possible, otherwise send to pdf
> mcmc.diagnostics(fit)
> dev.off()                        #If you saved to pdf, look at the file
> fit <- ergm(magnolia~edges+gwesp(0.25,fixed=T)+nodematch('Grade')+nodematch('Race')+
+         nodematch('Sex'),
+  control = control.ergm(seed=1))
> mcmc.diagnostics(fit)
> args(ergm)
```

One more try...

```
> fit <- ergm(magnolia~edges+gwesp(0.25,fixed=T)+nodematch('Grade')+nodematch('Race')+
+   nodematch('Sex'),
+  control = control.ergm(seed=1,MCMC.samplesize=50000,MCMC.interval=1000),
+  verbose=T)


> png( 'fig1.png', width=900, height=900, units='px')
> mcmc.diagnostics(fit)

Sample statistics summary:

Iterations = 10000:50009000
Thinning interval = 1000
Number of chains = 1
Sample size per chain = 50000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

                   Mean    SD Naive SE Time-series SE
edges             1.769 46.97   0.2101          4.268
```

```
gwesp.fixed.0.25 -2.144 42.42   0.1897          5.978
nodematch.Grade   1.890 44.57   0.1993          4.503
nodematch.Race    1.658 42.11   0.1883          3.885
nodematch.Sex     1.168 37.30   0.1668          3.195

2. Quantiles for each variable:

                   2.5%    25%    50%   75% 97.5%
edges            -85.00 -32.00  0.000 35.00 94.00
gwesp.fixed.0.25 -75.66 -34.53 -4.207 28.82 82.51
nodematch.Grade  -80.00 -31.00  0.000 33.00 89.00
nodematch.Race   -76.00 -29.00 -1.000 31.00 86.00
nodematch.Sex    -67.00 -26.00  0.000 27.00 76.00


Are sample statistics significantly different from observed?
               edges gwesp.fixed.0.25 nodematch.Grade nodematch.Race
diff.      1.7687600       -2.1437427       1.8900800      1.6576600
test stat. 0.4144720       -0.3586236       0.4197362      0.4266697
P-val.     0.6785284        0.7198767       0.6746782      0.6696199
           nodematch.Sex Overall (Chi^2)
diff.          1.1678800              NA
test stat.     0.3655582        2.555655
P-val.         0.7146948        0.768091

Sample statistics cross-correlations:
                     edges gwesp.fixed.0.25 nodematch.Grade nodematch.Race
edges            1.0000000        0.8489831       0.9608950      0.9459269
gwesp.fixed.0.25 0.8489831        1.0000000       0.8697887      0.8426413
nodematch.Grade  0.9608950        0.8697887       1.0000000      0.9153498
nodematch.Race   0.9459269        0.8426413       0.9153498      1.0000000
nodematch.Sex    0.9050979        0.7830149       0.8725909      0.8615647
                 nodematch.Sex
edges                0.9050979
gwesp.fixed.0.25     0.7830149
nodematch.Grade      0.8725909
nodematch.Race       0.8615647
nodematch.Sex        1.0000000

Sample statistics auto-correlation:
Chain 1
             edges gwesp.fixed.0.25 nodematch.Grade nodematch.Race
Lag 0    1.0000000        1.0000000       1.0000000      1.0000000
Lag 1000 0.9398119        0.9976842       0.9620886      0.9499676
Lag 2000 0.8967237        0.9953958       0.9319044      0.9137642
Lag 3000 0.8644365        0.9931684       0.9073775      0.8858762
Lag 4000 0.8397903        0.9909569       0.8870391      0.8639448
Lag 5000 0.8206954        0.9887777       0.8699429      0.8461555
         nodematch.Sex
Lag 0        1.0000000
Lag 1000     0.9439161
Lag 2000     0.9026602
Lag 3000      0.8715295
Lag 4000      0.8469837
Lag 5000      0.8271042

Sample statistics burn-in diagnostic (Geweke):
Chain 1

Fraction in 1st window = 0.1
Fraction in 2nd window = 0.5

           edges gwesp.fixed.0.25  nodematch.Grade   nodematch.Race
          0.9231           0.8506           0.9895           1.0093
   nodematch.Sex
          2.3882

P-values (lower = worse):
           edges gwesp.fixed.0.25  nodematch.Grade   nodematch.Race
      0.35596355       0.39499110       0.32243893       0.31283789
   nodematch.Sex
      0.01692995

> invisible(dev.off())
```



Success! Of course, in real life one might have a lot more trial and error.

# 7 Working with egocentrically sampled network data

In many empirical contexts, it is not feasible to collect a network census or even an adaptive (link-traced) sample. Even when one of these may be possible in practice, egocentrically sampled data are typically cheaper and easier to collect.

Long regarded as the poor country cousin in the network data family, egocentric data contain a remarkable amount of information. With the right statistical methods, such data can be used to explore the properties of the complete networks in which they are embedded. The basic idea here is to combine what is observed, with assumptions, to define a class of models that describe the distribution of networks that are centered on the observed properties. The variation in these networks quantifies some of the uncertainty introduced by the assumptions.

Let's start with a simple fictional example: You have a sample of persons who were asked about the friends they had seen face-to-face more than once in the last week. The respondent was asked their own sex, and the sex of each friend (for up to three friends). Summary statistics from these data thus include the sex distribution, the degree distribution (it could be broken down by sex, but we will just examine the marginal distribution here), and the joint distribution of the respondent and friend's sex (the sex mixing matrix). Let's assume there are equal numbers of men and women in the sampled respondents. The other distributions are shown below:

**Degree distribution**

| **Degree** | **Frequency** | **Fraction** | **Ties** |
|---|---|---|---|
| 0 | 180 | 0.36 | 0 |
| 1 | 245 | 0.49 | 245 |
| 2 | 60 | 0.12 | 120 |
| 3 | 15 | 0.03 | 45 |
| Total | 500 | 1.00 | 410 |

**Sex mixing matrix**

| (410 total) | | **Friend** | |
|---|---|---|---|
| | | M | F |
| **Respondent** | M | 164 | 44 |
| | F | 26 | 176 |

So, total N respondents = 500, total N friends reported = 410.

We can use an ERGM to fit the parameters associated with these observed statistics, then use the fitted model to simulate complete networks that are drawn from the distribution of networks that is centered around these statistics. As a theoretical exercise, this provides a method for investigating the complete network implications of these observed summary statistics. As an empirical exercise, the primary assumption needed for inference is that the data we have is sampled from a population in equilibrium (and, as in all statistical inference, that our model is correct). The theory for this is developed in Krivitsky, 2009.

We need to make assumptions about size, directedness and bipartite-ness when we model and simulate the complete network.

- **Size**: any size can be simulated, but if the model is fit using the observed frequencies, it should be used to simulate a population of that size, unless a size adjustment is made in the simulation (see Krivitsky, Handcock and Morris 2011). We are going to work with a population size 500 here, equal to the number of respondents.
- **Directedness**: Ego data are in one sense inherently directed (respondents nominate alters, alters are not observed), but the relationship may be either. In this case ("seen more than once") it is undirected, so we will fit and simulate an undirected network.
- **Bipartite**: Ego data can be bipartite (if no alters are also respondents, or data are collected on 2-mode networks) or not (if respondents are also alters). But again, the relationship may be either. "Seen" is undirected, and we will fit and simulated and undirected network.

In sum, we will simulate a one-mode, undirected network of size 500, assuming the ego statistics we observed contain the information we need to calculate the statistics that would have been observed in a self-contained population of that size, noting that other assumptions are possible.

To ensure consistency between the degree distribution (which is a tabulation of nodes) and the mixing matrix (which is a cross-tabulation of ties) in our simulated "complete network," it is important to recognize that in a complete network, the degree distribution should imply twice the number of ties observed in the mixing matrix, because every tie is being reported by both nodes in the degree distribution. If we are fixing the population size at 500 in this simulation, then our observed mixing matrix data needs to be divided by 2.

Start by initializing an empty network of the desired size and assign the "sex" attribute to the nodes:

```
> ego.net <- network.initialize(500, directed=F)
> ego.net %v% 'sex' <- c(rep(0,250),rep(1,250))
```

Set up the observed statistics (adjusted for this "complete" network) as we will use them to assess the accuracy of the simulation later:

```
> ego.deg <- c(180, 245, 60, 15)                                  # node distn
> ego.mixmat <- matrix(c(164,44,26,176)/2, nrow=2, byrow=T)        # adjusted tie distn
```

Then, pick the observed statistics you want to target – we will start with a simple model here: the total number of ties (edges), and the number of sex-matched ties (homophily). These are both functions of the observed statistics:

```
> ego.edges <- sum(ego.mixmat)
> ego.sexmatch <- ego.mixmat[1,1]+ego.mixmat[2,2]
```

And combine these into a vector

```
> ego.target.stats <- c(ego.edges, ego.sexmatch)
> ego.target.stats

[1] 205 170
```

Now, fit an ERGM to this "network", with terms for the statistics you want to match, and the "`target.stats`" argument for **ergm** that specifies the target values for those statistics:

```
> ego.fit <- ergm(ego.net ~ edges + nodematch('sex'),
+  target.stats = ego.target.stats)
```

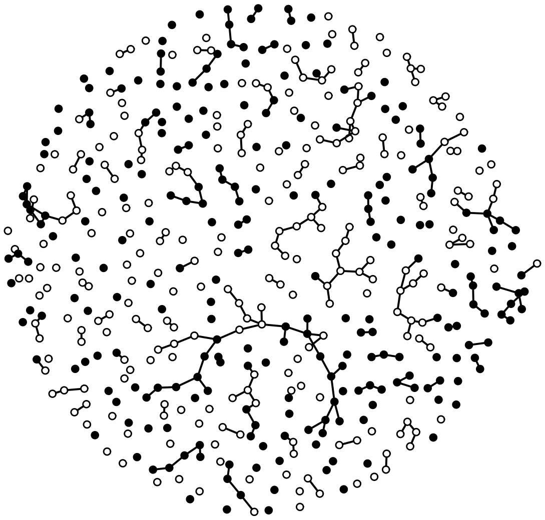
Take a look at the fitted model:

```
> summary(ego.fit)

==========================
Summary of model fit
==========================

Formula:   nw ~ edges + nodematch("sex")
<environment: 0xba1d6c8>

Iterations:  20

Monte Carlo MLE Results:
```

```
              Estimate Std. Error MCMC % p-value
edges          -7.4870     0.1690     NA  <1e-04 ***
nodematch.sex   1.5866     0.1857     NA  <1e-04 ***
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1

     Null Deviance: 172940  on 124750  degrees of freedom
 Residual Deviance:   2941  on 124748  degrees of freedom

AIC: 2945    BIC: 2964    (Smaller is better.)
```

Now that you have a fitted model, you can simulate a complete network from it, and look at the results:

```
> ego.sim1 <- simulate(ego.fit)
> plot(ego.sim1, vertex.cex=.65, vertex.col="sex")
```



Does it reproduce the observed degree and mixing frequencies? We only targeted the total number of edges, not the full degree distribution.

```
> rbind(summary(ego.sim1 ~ degree(c(0:3))), ego.deg)

        degree0 degree1 degree2 degree3
            212     185      79      21
ego.deg     180     245      60      15
```

```
> mixingmatrix(ego.sim1, "sex")
```

```
Note:  Marginal totals can be misleading
 for undirected mixing matrices.
   0  1
0 93 31
1 31 85
```

```
> ego.mixmat
```

```
     [,1] [,2]
[1,]   82   22
[2,]   13   88
```

We only targeted the number of same-sex ties, not the full mixing matrix.

The simulation stats seem quite different than the observed stats, and there are two possible reasons: either we mis-specified the original model (bias), or this one random draw may be unrepresentative of the distribution described by the model (variance). The latter is easily examined by simulating 100 networks, to see where the observed data fall in the distribution of networks produced by the model:

```
> ego.sim100 <- simulate(ego.fit, nsim=100)
> ego.sim100
```

```
Number of Networks: 100
Model: nw ~ edges + nodematch("sex")
Reference: ~Bernoulli
Constraints: ~.
Parameters:
        edges nodematch.sex
    -7.487013      1.586633
```

More information can be obtained with

```
> summary(ego.sim100)
```

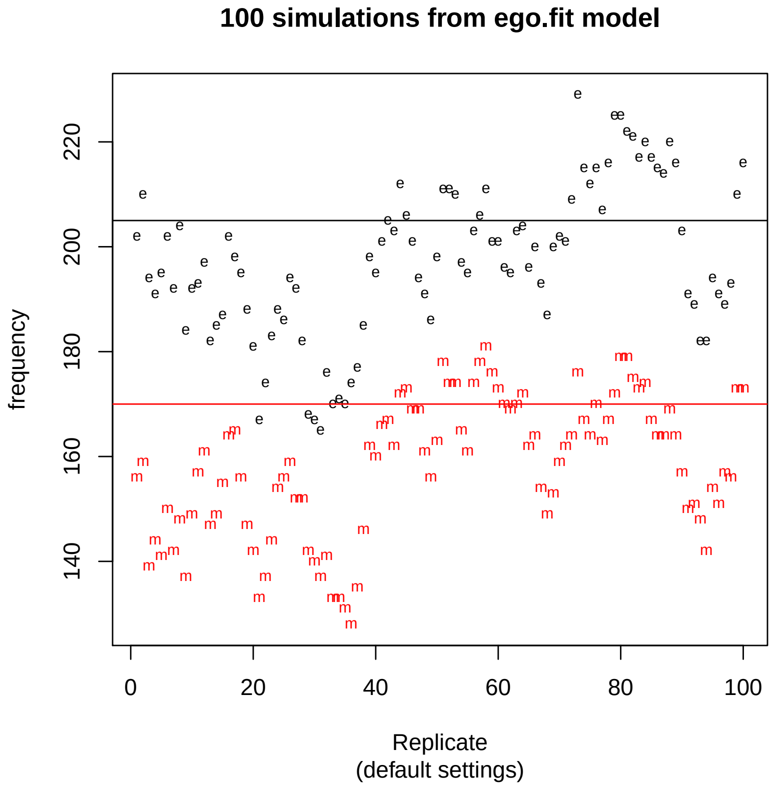
First, we'll look at how well the simulations reproduced the target statistics that were included in the model (note, not the observed full distributions):

```
> sim.stats <- attr(ego.sim100,"stats")
> rbind(colMeans(sim.stats), ego.target.stats)
```

```
                  edges nodematch.sex
                 197.31        158.22
ego.target.stats 205.00        170.00
```

These look pretty good – the means of the simulated target stats are within 1% of the observed. We can plot the 100 replicates to see check the variation for any problematic patterns:

```
> matplot(1:nrow(sim.stats), sim.stats,
+   pch=c("e","m","0","+"), cex=.65,
+   main="100 simulations from ego.fit model", sub="(default settings)",
+   xlab="Replicate", ylab="frequency")
> abline(h=ego.target.stats, col=c(1:4))
```

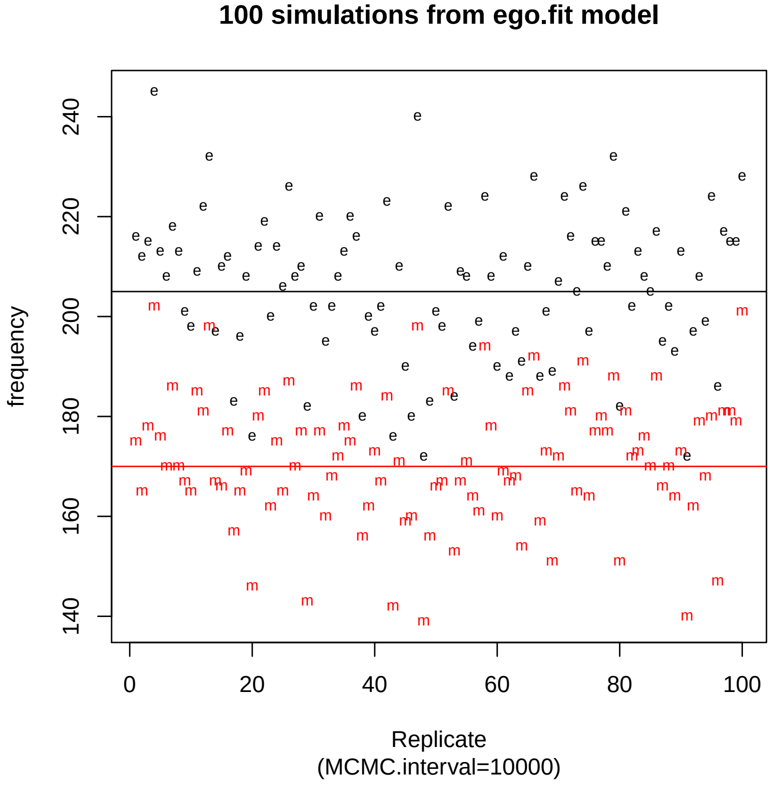


The lines mark the target statistic frequencies in the observed data. The points represent the frequencies in the simulated networks.

The simulated network statistics vary stochastically around the target values, not trending over time.

But, there is clear autocorrelation across the replicates, which suggests we might want to increase the MCMC interval to draw more independent realizations.

```
> ego.sim100 <- simulate(ego.fit, nsim=100,
+   control=control.simulate.ergm(MCMC.interval=10000))
> sim.stats <- attr(ego.sim100,"stats")
> matplot(1:nrow(sim.stats), sim.stats,
+   pch=c("e","m"), cex=.65,
+   main="100 simulations from ego.fit model", sub="(MCMC.interval=10000)",
+   xlab="Replicate", ylab="frequency")
> abline(h=ego.target.stats, col=c(1:2))
```



With the larger interval, the autocorrelation is no longer detectable, and all of the statistics from the simulated networks vary in a symmetric band around their targets.

The variation (about +/- 10%) represents the range of target statistics that are consistent with the fitted coefficients.

If you wanted instead to constrain these statistics to equal a specified value, then you can use the “constraints=” argument during the `ergm` fit instead.

This is good for verifying that the simulation reproduces the target values we specified. So now let’s see whether the simulated complete networks also match statistics that were not set by the targets. We targeted edges and homophily. How well does this model reproduce the full degree distribution?

```
> sim.fulldeg <- summary(ego.sim100 ~ degree(c(0:10)))
> colnames(sim.fulldeg) <- paste("deg",0:10, sep='')
> sim.fulldeg[1:5,]
```

```
     deg0 deg1 deg2 deg3 deg4 deg5 deg6 deg7 deg8 deg9 deg10
[1,]  211  174   87   28    0    0    0    0    0    0     0
[2,]  209  185   84   19    2    0    1    0    0    0     0
[3,]  210  184   76   26    4    0    0    0    0    0     0
[4,]  186  185   88   35    6    0    0    0    0    0     0
[5,]  204  191   82   21    2    0    0    0    0    0     0
```

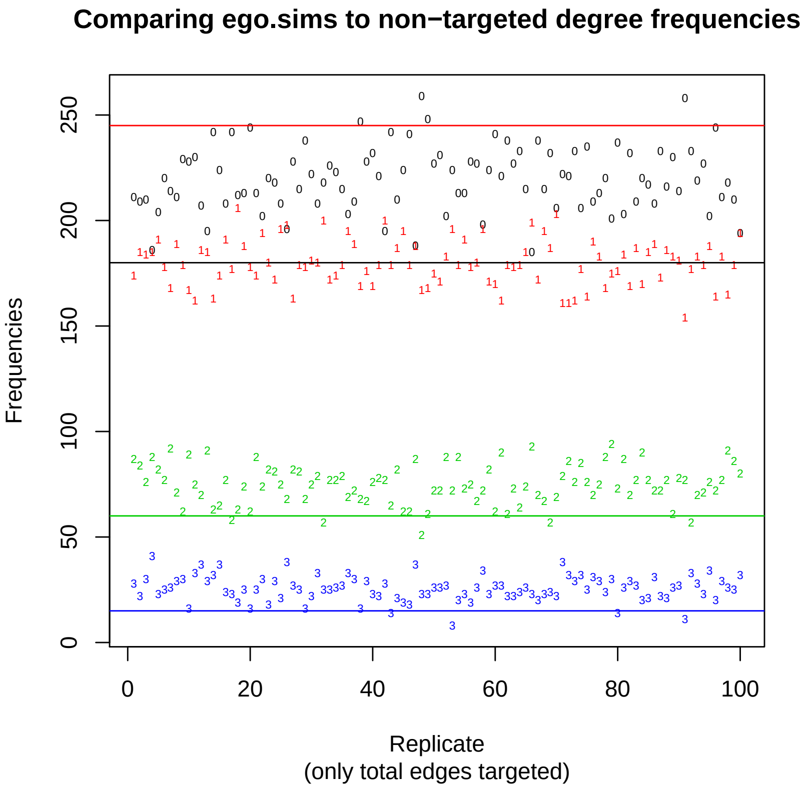
Recall that the degree range in our data was [0,3] by design, but we did not constrain the simulations to this range. If our model correctly captured the processes that led to the aggregate statistics we observe in our data, the simulated networks would show us what we missed. Here the simulated networks suggest that the fully observed network would have a wider range of degrees, which we might have observed, had we not truncated the data collection at 3 friends per respondent. About 1% of nodes have degree 4 or 5, and the max observed is 6.

But did our model did correctly capture the underlying processes? How well does the simulated degree distribution from this model match the frequencies we did observe? Aggregating the degrees of 3 or more in the simulations, we find:

```
> sim.deg <- cbind(sim.fulldeg[,1:3], apply(sim.fulldeg[,4:11],1,sum))
> colnames(sim.deg) <- c(colnames(sim.fulldeg)[1:3],"degree3+")
> rbind(colMeans(sim.deg),ego.deg)

          deg0   deg1  deg2 degree3+
        219.69 179.89 74.87    25.55
ego.deg 180.00 245.00 60.00    15.00
```

As with the single simulation above, the discrepancies between the simulation averages and the observed statistics are quite large. We can see this more clearly by plotting the degree frequencies for the 100 replicate networks we simulated:

```
> matplot(1:nrow(sim.deg), sim.deg, pch=as.character(0:3), cex=.5,
+    main="Comparing ego.sims to non-targeted degree frequencies",
+    sub = "(only total edges targeted)",
+    xlab = "Replicate", ylab = "Frequencies")
> abline(h=c(180, 245, 60, 15), col=c(1:4))
```



The simulations are producing systematically more isolates than expected (the "0" points vs. the black line), and systematically more degree 1 nodes. In fact, the two degree frequencies are essentially reversed in the simulation.

The fraction of nodes with 2 or 3+ partners is systematically off but by a much smaller amount.

So our observed network has fewer isolates than expected in a network of this density, more degree 1 nodes than expected, and fewer degree 2 and 3+ nodes.

This suggests the model is mis-specified. Since the degree 0 vs. degree 1 is the worst fitting aspect, we will try using the number of isolates as a target statistic in the model.

```
> ego.isolates <- ego.deg[1]
> ego.target.stats <- c(ego.edges, ego.sexmatch, ego.isolates)
> ego.fit <- ergm(ego.net ~ edges + nodematch('sex') + degree(0),
+  target.stats = ego.target.stats)
```

```
Iteration 1 of at most 20:
Convergence test P-value: 2.6e-59
The log-likelihood improved by 0.0274
Iteration 2 of at most 20:
Convergence test P-value: 1.4e-17
The log-likelihood improved by 0.007127
Iteration 3 of at most 20:
Convergence test P-value: 3e-04
The log-likelihood improved by 0.001976
Iteration 4 of at most 20:
Convergence test P-value: 5e-02
The log-likelihood improved by 0.000819
Iteration 5 of at most 20:
Convergence test P-value: 6.5e-01
Convergence detected. Stopping.
The log-likelihood improved by 0.0002561

This model was fit using MCMC.  To examine model diagnostics and check for degeneracy, use the mcmc.d
```

```
> summary(ego.fit)
```

```
==========================
Summary of model fit
==========================

Formula:   nw ~ edges + nodematch("sex") + degree(0)
<environment: 0xc717e9c>

Iterations:  20

Monte Carlo MLE Results:
              Estimate Std. Error MCMC % p-value
edges          -8.4008     0.2429      1  <1e-04 ***
nodematch.sex   1.5807     0.1839      1  <1e-04 ***
degree0        -0.9605     0.1607      0  <1e-04 ***
---
Signif. codes:  0 âĂŸ***âĂŹ 0.001 âĂŸ**âĂŹ 0.01 âĂŸ*âĂŹ 0.05 âĂŸ.âĂŹ 0.1 âĂŸ âĂŹ 1

     Null Deviance: 172940  on 124750  degrees of freedom
 Residual Deviance:   2903  on 124747  degrees of freedom

AIC: 2909    BIC: 2938    (Smaller is better.)
```

Simulating from this model, the target statistics are again well matched:

```
> ego.sim100 <- simulate(ego.fit, nsim=100,
+    control=control.simulate.ergm(MCMC.interval=10000))
> sim.stats <- attr(ego.sim100,"stats")
> rbind(colMeans(sim.stats), ego.target.stats)
```

```
                  edges nodematch.sex degree0
                 204.56        168.93  180.13
ego.target.stats 205.00        170.00  180.00
```

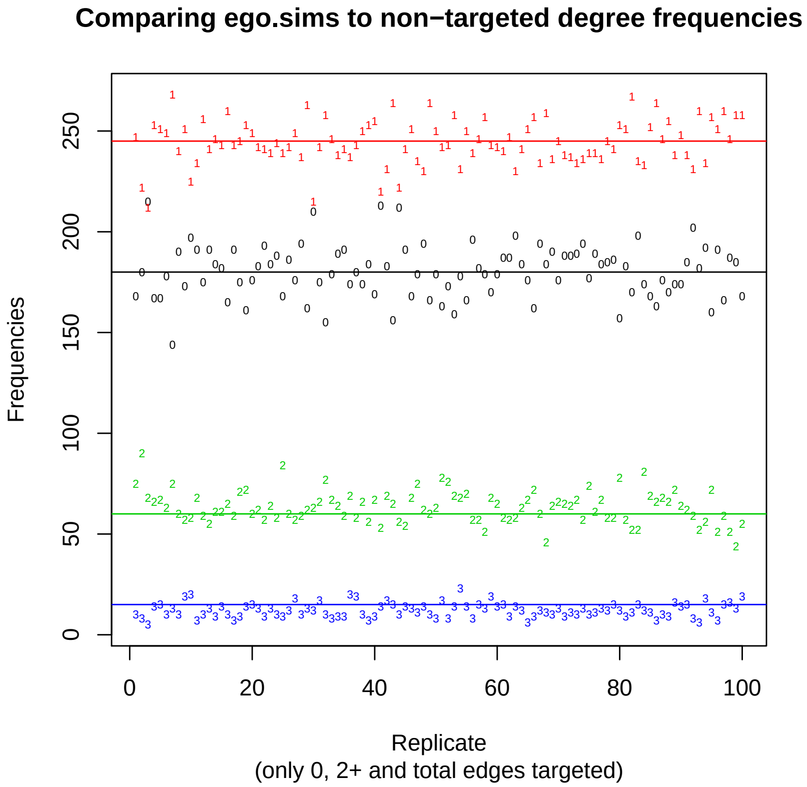
And the full degree frequencies look much better:

```
> sim.fulldeg <- summary(ego.sim100 ~ degree(c(0:10)))
> sim.deg <- cbind(sim.fulldeg[,1:3], apply(sim.fulldeg[,4:11],1,sum))
> colnames(sim.deg) <- c(colnames(sim.fulldeg)[1:3],"degree3+")
> rbind(colMeans(sim.deg),ego.deg)
```

```
        degree0 degree1 degree2 degree3+
         180.13  244.41   63.37    12.09
ego.deg  180.00  245.00   60.00    15.00
```

and finally, plotting the full degree frequencies

```
> matplot(1:nrow(sim.deg), sim.deg, pch=as.character(0:3), cex=.5,
+    main="Comparing ego.sims to non-targeted degree frequencies",
+    sub = "(only 0, 2+ and total edges targeted)",
+    xlab = "Replicate", ylab = "Frequencies")
> abline(h=c(180, 245, 60, 15), col=c(1:4))
```



The degree frequencies in these simulated networks are now well centered on the observed frequencies. So adding the one additional parameter to capture the lower than expected number of isolates did a good job of capturing how our observed network deviates from a random network with this density.

The fraction of nodes with 3+ partners produced by our new model might still be a bit low.

**Moral**: We can use ERGMs to estimate network models using target statistics from egocentrically sampled data. The fact that the target statistics are reproduced by this model does not guarantee that additional features of the network would also be reproduced. But starting with simple models can help to identify whether and how the aggregate statistics we observe from an egocentric sample deviate from those we would expect from the model. If we fit all of the observed statistics without a saturated model, we cannot reject the hypothesis that this model produced the network we sampled from.

We can also use this approach to explore network statistics that are not visible at all from the egocentric data, e.g., the geodesic distribution, betweenness, etc., but it must always be remembered that the distributions we will produce are based on our model. They faithfully reproduce the model, but that does not mean that the model faithfully represents the population.

In the STERGM workshop, we show how complete dynamic networks also can be simulated over time on the basis of egocentric data like these, with the minimal addition of a single estimate of partnership duration. For a movie of an example dynamic simulation used to explore the impact of network structure on HIV transmission, see statnet.org/movies.

# 8 Additional functionality in the statnet family of packages

## 8.1 Additional functionality

The statnet suite of packages currently contains many additional features not covered in this tutorial:

- tools for fitting dynamic network models (`stergm`, in the ergm base package)
- tools for fitting relational event models (`relevent` package)
- curved exponential family estimation and simulation (`ergm` base package)
- latent space and latent cluster analysis (`latentnet` package)
- network permutation models (`netperm` package)
- MLE estimation for degree distributions (negative binomial, Poisson, scale-free, etc.) (`degreenet` package)
- analysis of bipartite networks (`network` package)
- simulation of bipartite networks with given degree distributions (`networksis` package)
- hierarchical ERGMs (`hergm` package)

Any of these not in the ergm base package are in stand-alone packages that can be downloaded either from CRAN, or from the `statnet` website. For more detailed information, please visit the `statnet` webpage (http://statnet.org).

## 8.2 Additional functionality in development:

- ERGMs for valued ties – expected later 2012
- Temporal ERGMs (TERGMs) for longitudinal network panel data, and other temporal extensions – expected later 2012
- Temporally extended (vertex and edge) attributes for TERGMS – expected later 2012
- Network movie maker: ndTV – functionality previewed in STERGM workshop this year, CRAN release expected later 2012

## 8.3 Statnet Commons: The development group

Mark S. Handcock <handcock@stat.ucla.edu> David R. Hunter <dhunter@stat.psu.edu> Carter T. Butts <buttsc@uci.edu> Steven M. Goodreau <goodreau@u.washington.edu> Skye Bender-deMoll <skyebend@skyeome.net> Martina Morris <morrism@u.washington.edu> Pavel N. Krivitsky <krivitsky@stat.psu.edu>

# Appendix A: Clarifying the terms – ergm and network

You will see the terms ergm and network used in multiple contexts throughout the documentation. This is common in R, but often confusing to newcomers. To clarify: **ergm**

- **ERGM**: the acronym for an Exponential Random Graph Model; a statistical model for relational data that takes a generalized exponential family form.

- **ergm package**: one of the packages within the `statnet` suite
- **ergm function**: a function within the ergm package; fits an ERGM to a network object, creating an ergm object in the process.
- **ergm object**: a class of objects produced by a call to the ergm function, representing the results of an ERGM fit to a network.

**network**

- **network**: a set of actors and the relations among them. Used interchangeably with the term graph.
- **network package**: one of the packages within the `statnet` suite; used to create, store, modify and plot the information found in network objects.
- **network object**: a class of object in `R` used to represent a network.

# References

Goodreau, S., J. Kitts and M. Morris (2009). Birds of a Feather, or Friend of a Friend? Using Statistical Network Analysis to Investigate Adolescent Social Networks. *Demography 46(1)*: 103-125.

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).*

Krivitsky, P.N.(2009). PhD thesis. *University of Washington, Seattle, WA*

Krivitsky, P. N., M. S. Handcock and M. Morris (2011). Network Size and Composition Effects in Exponential-Family Random Graph Models. *Statistical Methodology, forthcoming*

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/`.