

Homework 6

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This assignment will need the dolphin network, the invlogit function from the lab, and the mycugtest and myqaptest utilities. These have been packaged in hwk6.zip.

Part I: CUG

For each CUG test, display the summary (print.cug.test) and the probability plot (plot.cug.test), state the null hypothesis, and indicate whether the hypothesis is accepted or rejected.

Loading libraries

```
library(network)
library(igraph)
library(ergm)
library(latticeExtra)
library(intergraph)
library(sand)

# Thanks to Benjamin Lind for the data and examples
```

Setting path and loading utilities and the network

```
setwd("/Users/KevQuant/Desktop/Depaul/csc495/wk7/hwk6")
source("invlogit.R")
source("mycugtest.R")
source("myqaptest.R")
dolphin <- read.graph("dolphin.graphml", format="graphml")
```

assortativity of the network by the Sex attribute

The Null hypothesis is that the assortativity of dolphin network is NOT governed by Sex.

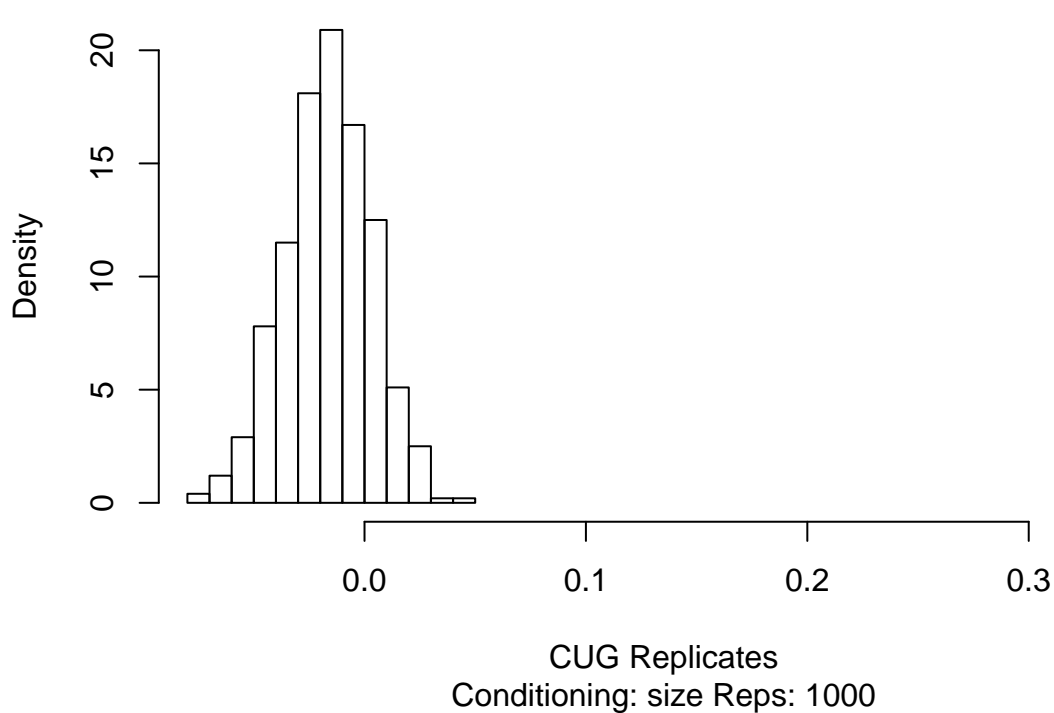
```
set.seed(20170515)
dolphin_cug1 <- mycugtest(dolphin,
                          assortativity.nominal,
                          directed=FALSE,
                          types=as.numeric(factor(V(dolphin)$Sex+1))
)
print.cug.test(dolphin_cug1)
```

```
##
## Univariate Conditional Uniform Graph Test
##
```

```
## Conditioning Method: size
## Graph Type:
## Diagonal Used: FALSE
## Replications: 1000
##
## Observed Value: 0.3463393
## Pr(X>=Obs): 0
## Pr(X<=Obs): 1
```

```
plot.cug.test(dophin_cug1)
```

Univariate CUG Test



Based on the above result, We can reject the NULL hypothesis and we could conclude that the assortativity of dophin network is most likely governed by Sex. The reason is that 100% of our graphs being less than our observed values.

assortativity of the network by degree (assortativity.degree)

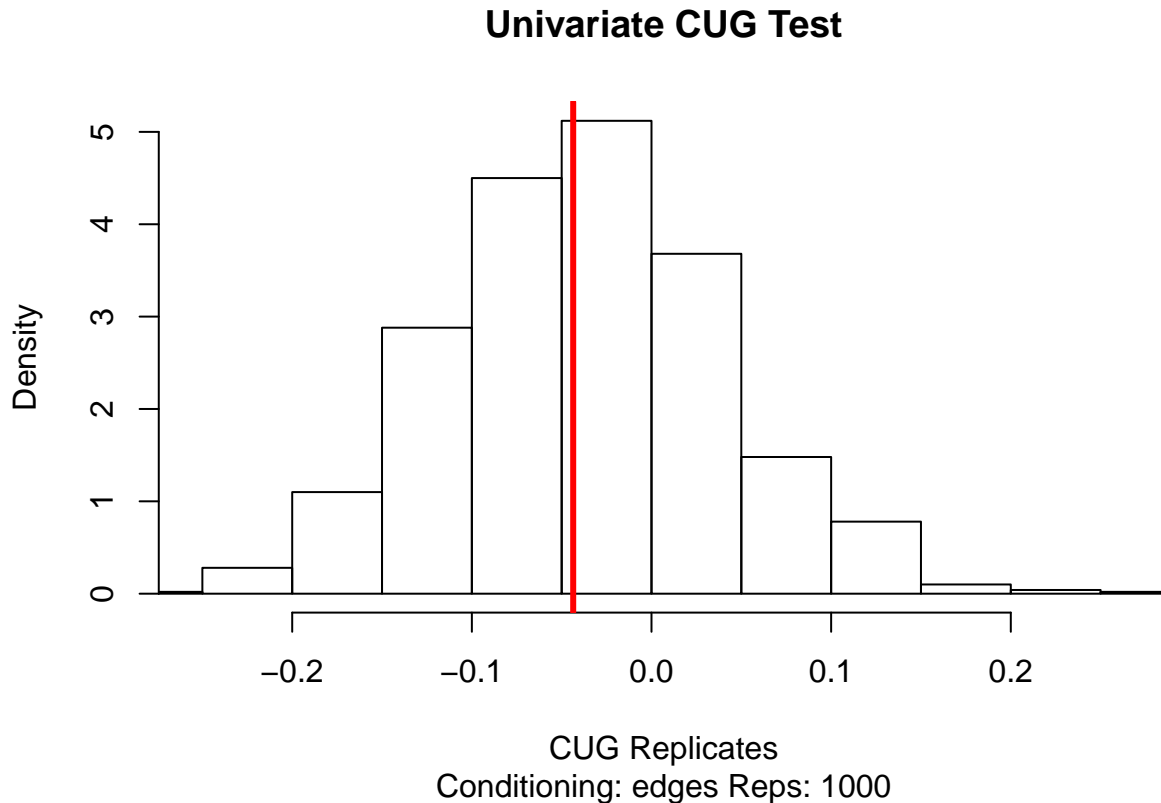
The Null hypothesis is that the assortativity in degree of dophin network is NOT governed by their edges forming

```
dophin_cug2 <-mycugtest(dophin,
                        assortativity.degree,
                        directed=FALSE,
                        cmode="edges"
                      )
print.cug.test(dophin_cug2)
```

```
##
## Univariate Conditional Uniform Graph Test
```

```
##
## Conditioning Method: edges
## Graph Type:
## Diagonal Used: FALSE
## Replications: 1000
##
## Observed Value: -0.04359403
## Pr(X>Obs): 0.529
## Pr(X<=Obs): 0.471
```

```
plot.cug.test(dophin_cug2)
```



Based on the above result, We don't have enough evidence to reject the NULL hypothesis and we could conclude that the assortativity in degree of dophin network is most likely NOT governed by their edge forming. The reason is that 52.9% of our graphs greater than our observed values

transitivity of the network

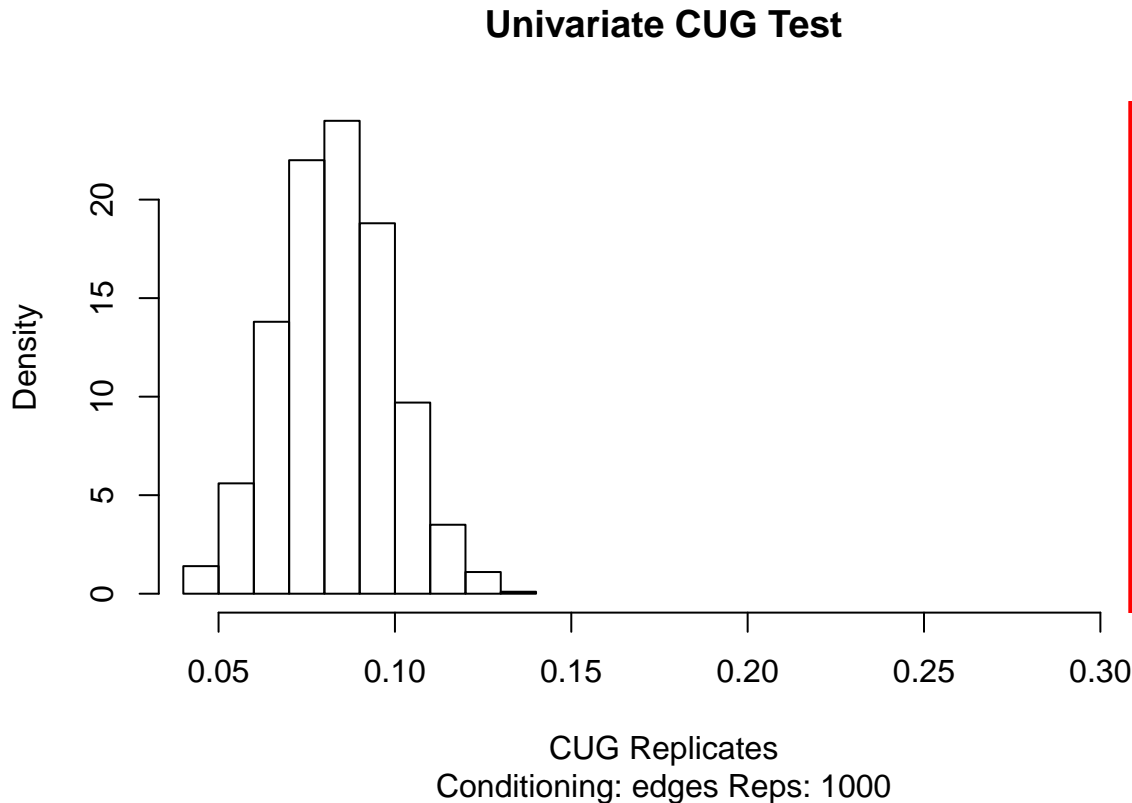
The Null hypothesis is that the transitivity of dophin network is NOT governed by Global mode

```
dophin_cug3<-mycugtest(dophin,
                        transitivity,
                        cmode="edges",
                        type="global"
                      )
print.cug.test(dophin_cug3)
```

```
##
## Univariate Conditional Uniform Graph Test
```

```
##
## Conditioning Method: edges
## Graph Type:
## Diagonal Used: FALSE
## Replications: 1000
##
## Observed Value: 0.3087757
## Pr(X>=Obs): 0
## Pr(X<=Obs): 1
```

```
plot.cug.test(dolphin_cug3)
```



Based on the above result, We can reject the NULL hypothesis and we could conclude that the the transitivity of dolphin network is most likely governed by Global Mode. The reason is that 100% of our graphs being less than our observed values.

Part II: QAP

assortativity of the network by Sex

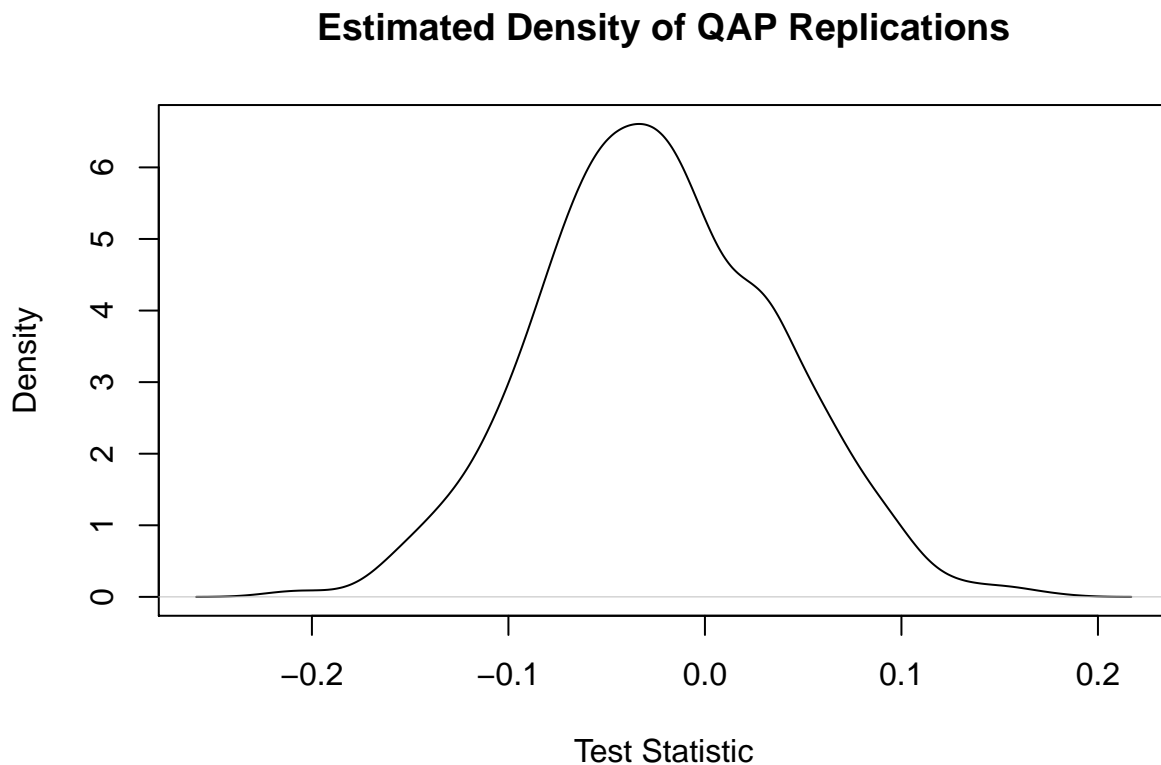
The Null hypothesis is that the assortativity of dolphin network is NOT governed by Sex.

```
dolphin.qap<-myqaptest(dolphin,
                      assortativity_nominal,
                      directed=FALSE,
                      types=as.numeric(factor(V(dolphin)$Sex)))
summary.qaptest(dolphin.qap)
```

```
##
```

```
## QAP Test Results
##
## Estimated p-values:
## p(f(perm) >= f(d)): 0
## p(f(perm) <= f(d)): 1
##
## Test Diagnostics:
## Test Value (f(d)): 0.3463393
## Replications: 1000
## Distribution Summary:
##   Min:      -0.2177566
##   1stQ:     -0.06520471
##   Med:      -0.02656603
##   Mean:     -0.02405249
##   3rdQ:      0.01828202
##   Max:       0.1758204
```

```
plot.qaptest(dolphin.qap)
```



Based on the above result, We can reject the NULL hypothesis and we could conclude that the assortativity of dolphin network is most likely governed by Sex. The reason is that 100% of our graphs being less than our observed values.

Part III: ERGM - Create four models of the dolphin network.

For each model, display the model summary, the MCMC diagnostics, the model goodness-of-fit ($GOF \sim model$) with plot, and the network goodness-of-fit with plots. For the MCMC models (all except #1), save the model fit in an Rdata file and load it when running knitr, include the call to `ergm` as a non-executing code block as we did in lab.

Model1: edges and sex assortativity

```
source("lab2-utils.R")
set.seed(20170515)
dop.net<-asNetwork(dophin)
dop.m1<-ergm(dop.net ~ edges + nodemix("Sex",base=c(1,6)))

## Evaluating log-likelihood at the estimate.
summary(dop.m1)

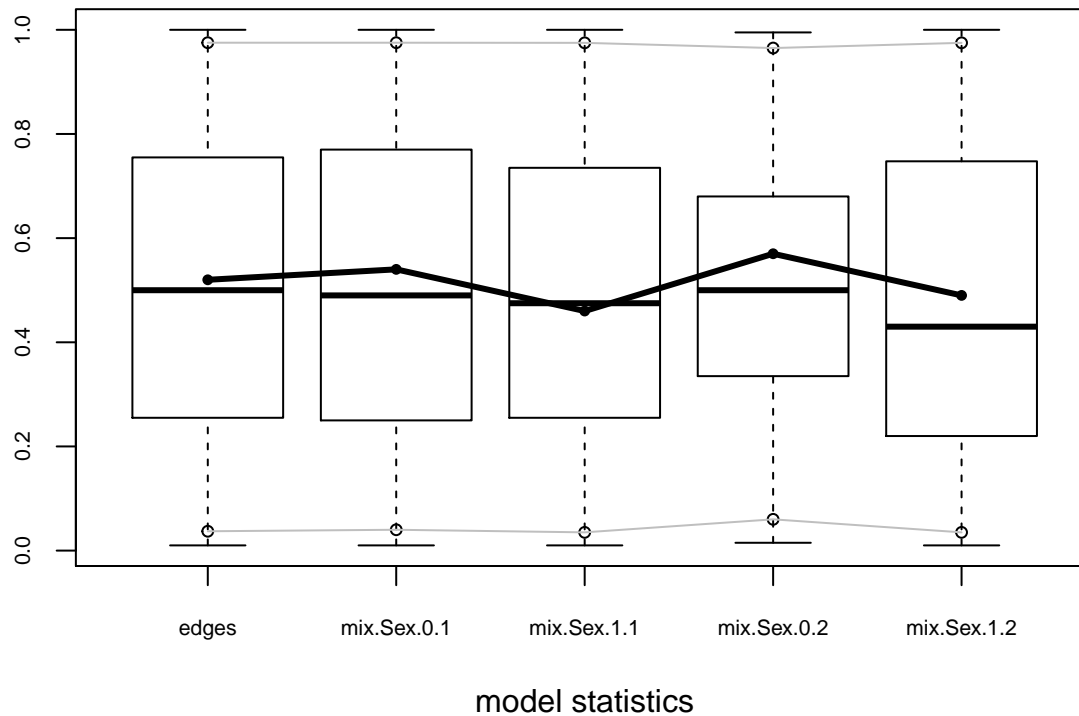
##
## =====
## Summary of model fit
## =====
##
## Formula:    dop.net ~ edges + nodemix("Sex", base = c(1, 6))
##
## Iterations: 6 out of 20
##
## Monte Carlo MLE Results:
##           Estimate Std. Error MCMC % p-value
## edges      -1.7320    0.1600    0 < 1e-04 ***
## mix.Sex.0.1 -1.1443    0.2227    0 < 1e-04 ***
## mix.Sex.1.1 -0.3602    0.2120    0 0.08947 .
## mix.Sex.0.2 -1.4460    0.5348    0 0.00691 **
## mix.Sex.1.2 -1.1504    0.4201    0 0.00623 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##      Null Deviance: 2621  on 1891  degrees of freedom
## Residual Deviance: 1057  on 1886  degrees of freedom
##
## AIC: 1067    BIC: 1094    (Smaller is better.)

#Goodness of Fit
par(mar=c(5,3,3,3))
#Per Instruction, use gof(ergmFitObject, GOF=~model)
dop.m1.gof<-gof(dop.m1, GOF=~model)
dop.m1.gof

##
## Goodness-of-fit for model statistics
##
##           obs min   mean max MC p-value
## edges      159 132 157.98 187      1.00
## mix.Sex.0.1  44  29  44.46  65      1.00
## mix.Sex.1.1  58  37  56.86  74      0.92
## mix.Sex.0.2   4   0   4.08   9      1.00
## mix.Sex.1.2   7   0   6.57  14      0.98

plot(dop.m1.gof)
```

Goodness-of-fit diagnostics



Model 2: Model 1 + degree(1)

```
#dop.m2<-ergm(dop.net ~ edges + nodemix("Sex",base=c(1,6)) + degree(1))
#save(dop.m2, file="dop-m2.Rdata")
load("dop-m2.Rdata")
summary(dop.m2)
```

```
##
## =====
## Summary of model fit
## =====
##
## Formula:   dop.net ~ edges + nodemix("Sex", base = c(1, 6)) + degree(1)
##
## Iterations: 2 out of 20
##
## Monte Carlo MLE Results:
##           Estimate Std. Error MCMC % p-value
## edges       -1.4517    0.1607      0 <1e-04 ***
## mix.Sex.0.1  -1.1203    0.2509      0 <1e-04 ***
## mix.Sex.1.1   -0.2476    0.1653      0 0.1343
## mix.Sex.0.2  -1.1743    0.5706      0 0.0397 *
## mix.Sex.1.2   -0.8058    0.4333      0 0.0631 .
## degree1       2.8671    0.3709      0 <1e-04 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```

##      Null Deviance: 2621   on 1891   degrees of freedom
## Residual Deviance: 1038   on 1885   degrees of freedom
##
## AIC: 1050    BIC: 1084    (Smaller is better.)
#diagnostics
mcmc.diagnostics(dop.m2)

## Sample statistics summary:
##
## Iterations = 16384:4209664
## Thinning interval = 1024
## Number of chains = 1
## Sample size per chain = 4096
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##              Mean      SD Naive SE Time-series SE
## edges          -52.5986 28.162  0.44004      1.53900
## mix.Sex.0.1    -15.0068  9.171  0.14329      0.44071
## mix.Sex.1.1    -22.7795 11.778  0.18404      0.56349
## mix.Sex.0.2     -0.8135  1.994  0.03116      0.05027
## mix.Sex.1.2     -2.2966  2.652  0.04144      0.08240
## degree1         15.1633  8.802  0.13753      0.46652
##
## 2. Quantiles for each variable:
##
##              2.5% 25% 50% 75% 97.5%
## edges          -101 -73 -55 -33    6
## mix.Sex.0.1     -31 -22 -16  -9    4
## mix.Sex.1.1     -41 -32 -24 -15    3
## mix.Sex.0.2      -4  -2  -1   0    4
## mix.Sex.1.2      -6  -4  -3  -1    4
## degree1         -1   9  15  21   33
##
##
## Sample statistics cross-correlations:
##              edges mix.Sex.0.1 mix.Sex.1.1 mix.Sex.0.2 mix.Sex.1.2
## edges          1.0000000  0.8775995  0.8230738  0.3688912  0.4433159
## mix.Sex.0.1    0.8775995  1.0000000  0.6346491  0.2606578  0.3098048
## mix.Sex.1.1    0.8230738  0.6346491  1.0000000  0.1891700  0.3497198
## mix.Sex.0.2    0.3688912  0.2606578  0.1891700  1.0000000  0.2824489
## mix.Sex.1.2    0.4433159  0.3098048  0.3497198  0.2824489  1.0000000
## degree1       -0.9513050 -0.8268356 -0.7956945 -0.3557077 -0.4429567
##              degree1
## edges          -0.9513050
## mix.Sex.0.1    -0.8268356
## mix.Sex.1.1    -0.7956945
## mix.Sex.0.2    -0.3557077
## mix.Sex.1.2    -0.4429567
## degree1         1.0000000
##
## Sample statistics auto-correlation:
## Chain 1

```

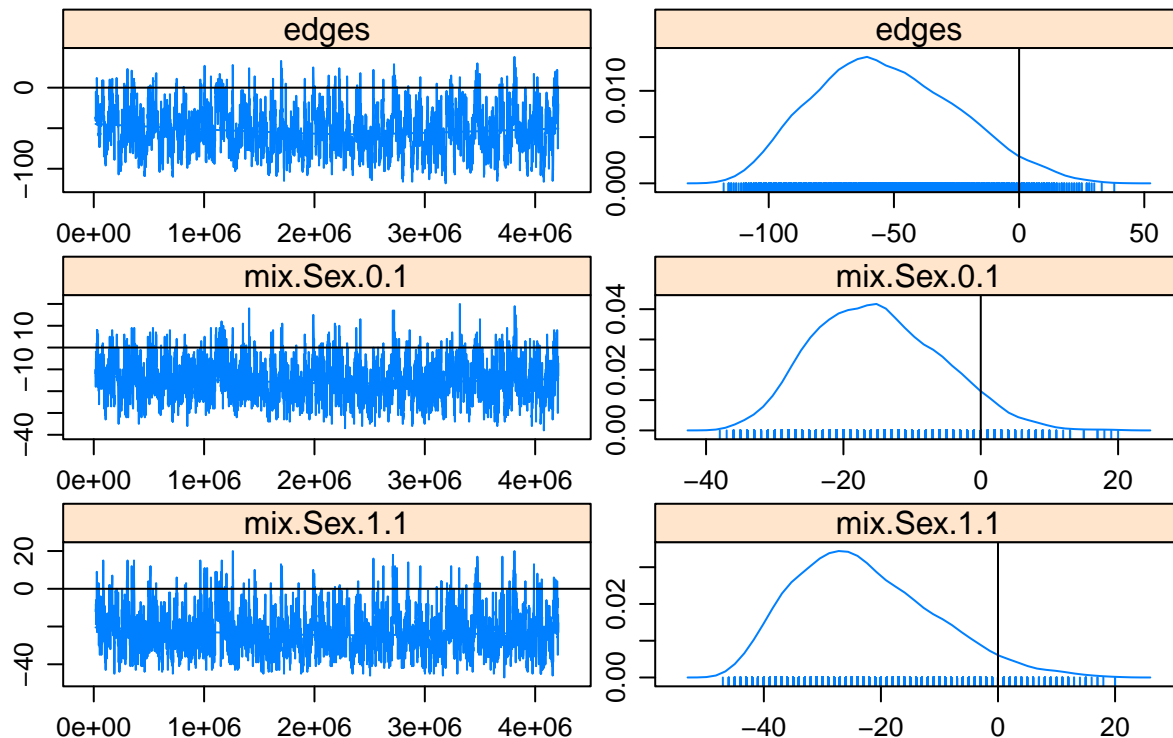


```

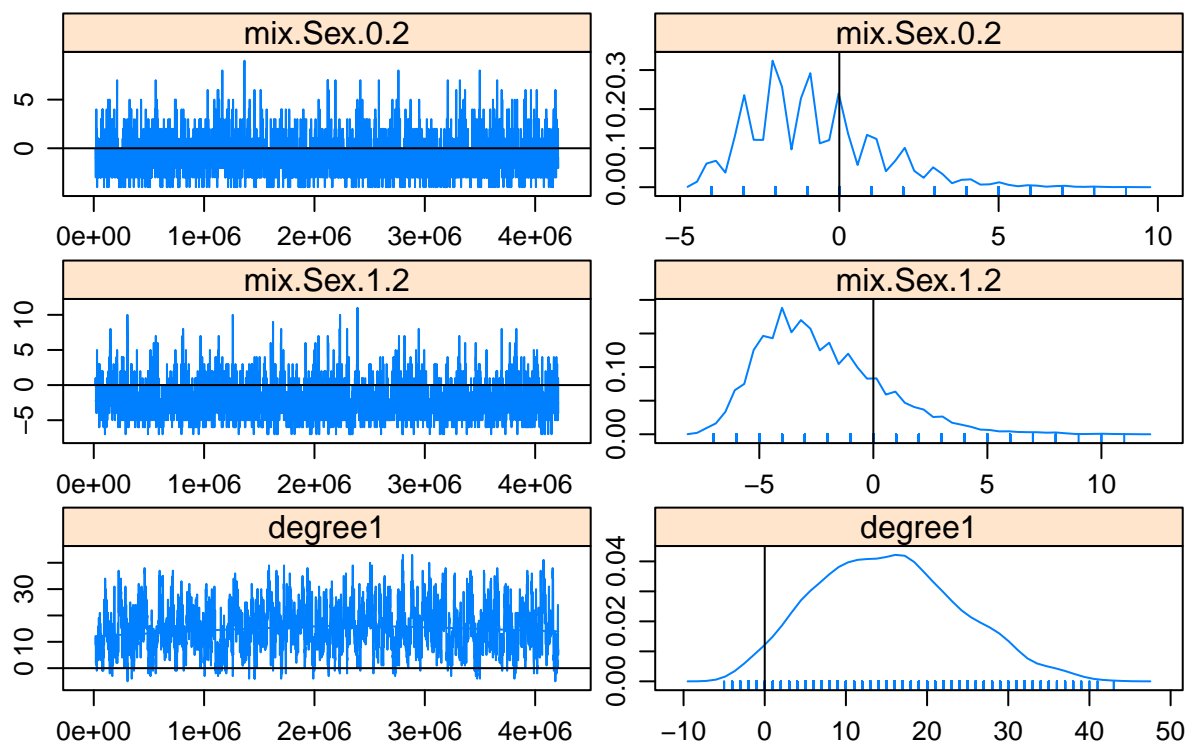
##          edges mix.Sex.0.1 mix.Sex.1.1 mix.Sex.0.2 mix.Sex.1.2
## Lag 0      1.0000000    1.0000000    1.0000000    1.0000000    1.0000000
## Lag 1024  0.8245442    0.6228075    0.7343582    0.28055026   0.40966816
## Lag 2048  0.7057262    0.5107398    0.5785575    0.14449284   0.21424926
## Lag 3072  0.6027898    0.4413146    0.4678744    0.10265658   0.15010326
## Lag 4096  0.5161563    0.3706322    0.3828723    0.09103486   0.10559415
## Lag 5120  0.4425875    0.3172409    0.3294853    0.06755625   0.07327409
##          degree1
## Lag 0      1.0000000
## Lag 1024  0.8108735
## Lag 2048  0.6888242
## Lag 3072  0.5871358
## Lag 4096  0.5040561
## Lag 5120  0.4342127
##
## Sample statistics burn-in diagnostic (Geweke):
## Chain 1
##
## Fraction in 1st window = 0.1
## Fraction in 2nd window = 0.5
##
##          edges mix.Sex.0.1 mix.Sex.1.1 mix.Sex.0.2 mix.Sex.1.2      degree1
##          2.0158      1.5784      1.8217      0.6981      1.6151      -2.0631
##
## Individual P-values (lower = worse):
##          edges mix.Sex.0.1 mix.Sex.1.1 mix.Sex.0.2 mix.Sex.1.2      degree1
##          0.04381845  0.11446777  0.06849988  0.48508508  0.10628127  0.03910220
## Joint P-value (lower = worse):  0.2577637 .

```

Sample statistics



Sample statistics

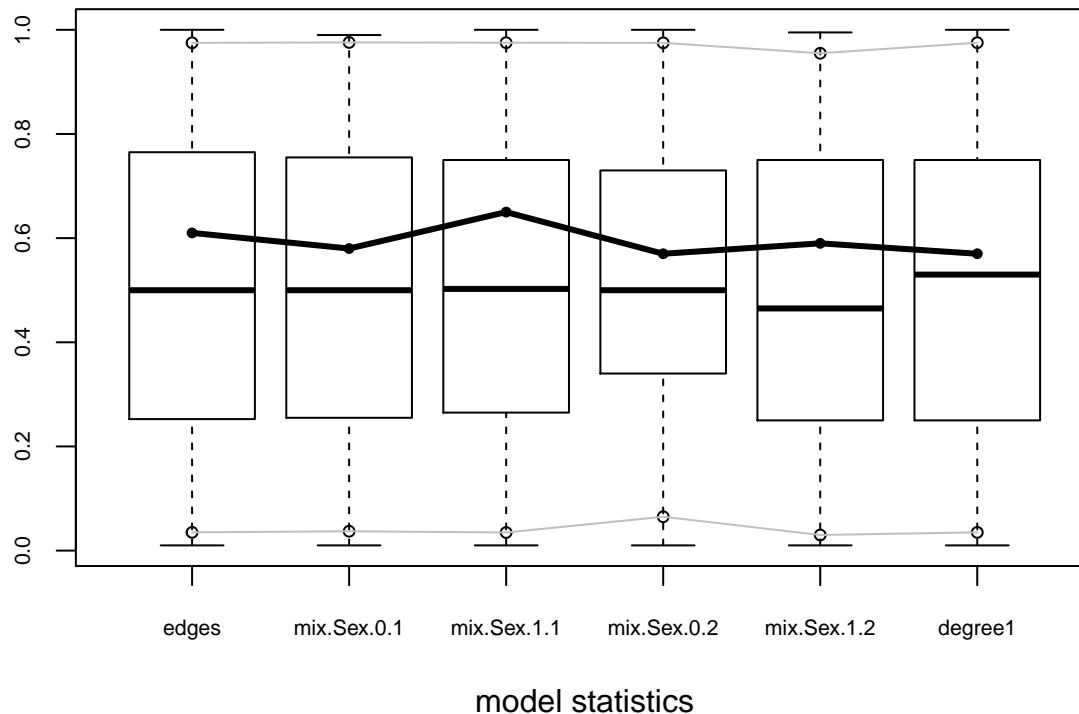


```
##
## MCMC diagnostics shown here are from the last round of simulation, prior to computation of final par
#Goodness of Fit
#Per Instruction, use gof(ergmFitObject, GOF=~model)
par(mar=c(5,3,3,3))
dop.m2.gof<-gof(dop.m2, GOF = ~model)
dop.m2.gof
```

```
##
## Goodness-of-fit for model statistics
##
##      obs min  mean max MC p-value
## edges    159  85 163.93 235      0.82
## mix.Sex.0.1  44  18  44.39  61      0.92
## mix.Sex.1.1  58  28  61.70  89      0.76
## mix.Sex.0.2   4   0   4.40  12      1.00
## mix.Sex.1.2   7   1   7.70  16      1.00
## degree1     9   1  10.34  34      0.98
```

```
plot(dop.m2.gof)
```

Goodness-of-fit diagnostics



Model 3: Model 1 + degree(1) + degree(2)

```
#dop.m3<-ergm(dop.net ~ edges + nodemix("Sex",base=c(1,6)) + degree(1) + degree(2))
#save(dop.m3,file="dop-m3.Rdata")
load("dop-m3.Rdata")
summary(dop.m3)
```

```
##
## =====
## Summary of model fit
## =====
##
## Formula:   dop.net ~ edges + nodemix("Sex", base = c(1, 6)) + degree(1) +
##            degree(2)
##
## Iterations: 2 out of 20
##
## Monte Carlo MLE Results:
##           Estimate Std. Error MCMC % p-value
## edges       -1.4184    0.1446    0 <1e-04 ***
## mix.Sex.0.1  -1.1310    0.2140    0 <1e-04 ***
## mix.Sex.1.1  -0.2865    0.1447    0 0.0479 *
## mix.Sex.0.2  -1.2026    0.4950    0 0.0152 *
## mix.Sex.1.2  -0.8497    0.3458    0 0.0141 *
## degree1      2.7169    0.4484    0 <1e-04 ***
## degree2      1.1676    0.4916    0 0.0176 *
## ---
```

```

## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##      Null Deviance: 2621  on 1891  degrees of freedom
## Residual Deviance: 1033  on 1884  degrees of freedom
##
## AIC: 1047    BIC: 1086    (Smaller is better.)

#diagnostics
mcmc.diagnostics(dop.m3)

## Sample statistics summary:
##
## Iterations = 16384:4209664
## Thinning interval = 1024
## Number of chains = 1
## Sample size per chain = 4096
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##              Mean      SD Naive SE Time-series SE
## edges        -3.2610 30.282  0.47316      1.32279
## mix.Sex.0.1  -1.8342  9.919  0.15498      0.35638
## mix.Sex.1.1  -0.7256 13.960  0.21812      0.53856
## mix.Sex.0.2   0.1506  2.319  0.03623      0.05505
## mix.Sex.1.2   0.2043  3.372  0.05268      0.08781
## degree1       0.9226  5.469  0.08545      0.25378
## degree2       0.5696  3.233  0.05051      0.11474
##
## 2. Quantiles for each variable:
##
##              2.5% 25% 50% 75% 97.5%
## edges        -65 -24  -1  19   51
## mix.Sex.0.1  -21  -9  -2   5   17
## mix.Sex.1.1  -28 -10   0   9   25
## mix.Sex.0.2   -4  -2   0   2    5
## mix.Sex.1.2   -5  -2   0   2    8
## degree1       -7  -3   0   4   14
## degree2       -5  -2   0   3    8
##
##
## Sample statistics cross-correlations:
##              edges mix.Sex.0.1 mix.Sex.1.1 mix.Sex.0.2 mix.Sex.1.2
## edges        1.0000000  0.8394709  0.8239083  0.3700236  0.4278837
## mix.Sex.0.1  0.8394709  1.0000000  0.5740000  0.2262342  0.2612545
## mix.Sex.1.1  0.8239083  0.5740000  1.0000000  0.2035508  0.2976526
## mix.Sex.0.2  0.3700236  0.2262342  0.2035508  1.0000000  0.3211488
## mix.Sex.1.2  0.4278837  0.2612545  0.2976526  0.3211488  1.0000000
## degree1     -0.8912960 -0.7265701 -0.7454611 -0.3625585 -0.4230530
## degree2     -0.7208867 -0.6043540 -0.5980571 -0.2497208 -0.3047360
##              degree1 degree2
## edges        -0.8912960 -0.7208867
## mix.Sex.0.1  -0.7265701 -0.6043540
## mix.Sex.1.1  -0.7454611 -0.5980571
## mix.Sex.0.2  -0.3625585 -0.2497208

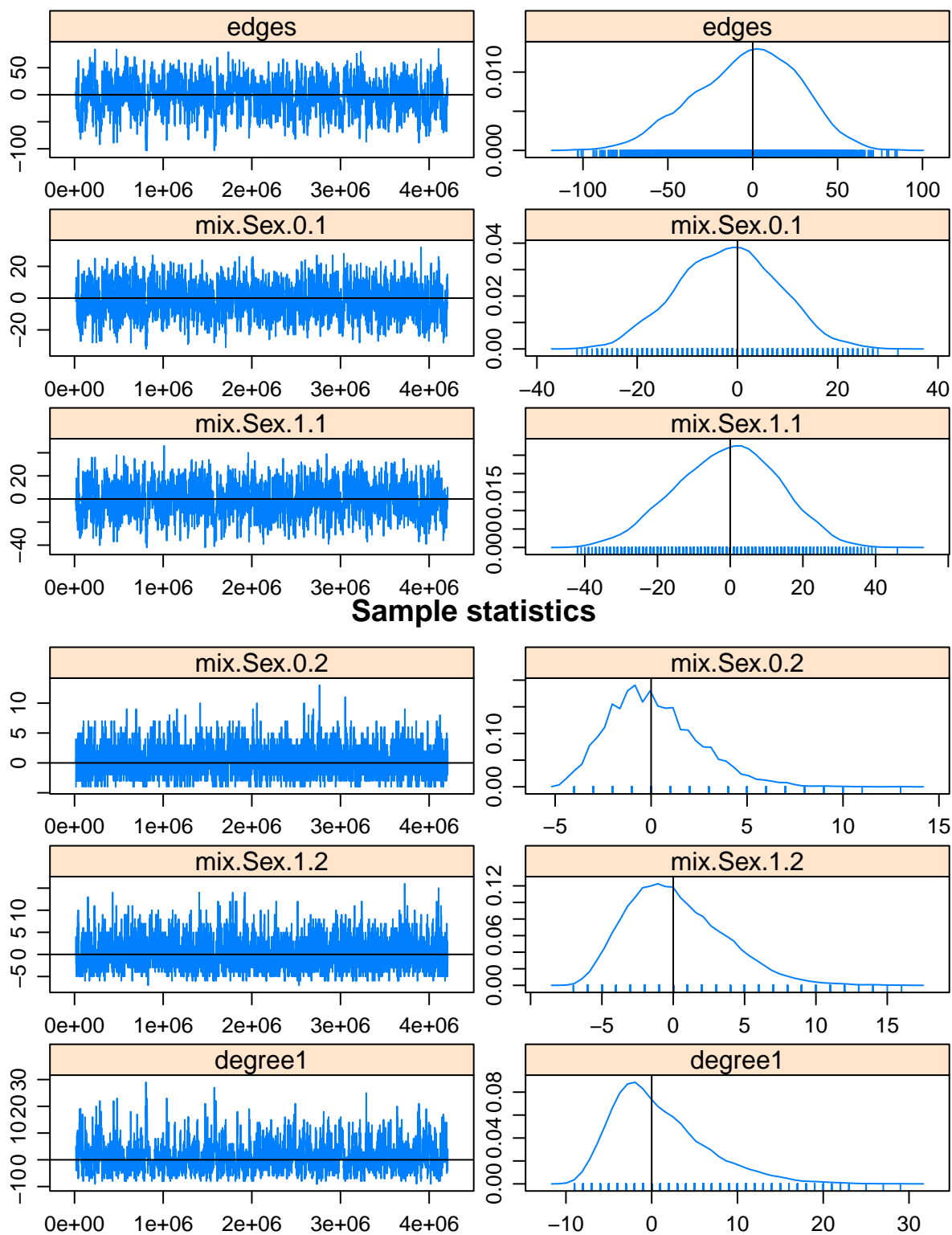
```

```

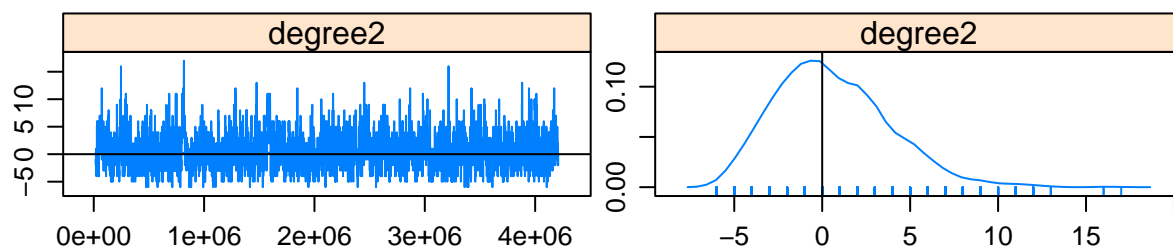
## mix.Sex.1.2 -0.4230530 -0.3047360
## degree1      1.0000000  0.5119594
## degree2      0.5119594  1.0000000
##
## Sample statistics auto-correlation:
## Chain 1
##          edges mix.Sex.0.1 mix.Sex.1.1 mix.Sex.0.2 mix.Sex.1.2
## Lag 0      1.0000000  1.0000000  1.0000000  1.0000000  1.0000000
## Lag 1024  0.7562471  0.5086846  0.6645765  0.20763567  0.31925343
## Lag 2048  0.5892071  0.3629947  0.4730362  0.09284032  0.13771734
## Lag 3072  0.4657453  0.2879074  0.3597760  0.06907238  0.07768737
## Lag 4096  0.3725518  0.2376358  0.2728433  0.06944153  0.06057972
## Lag 5120  0.3085455  0.1886739  0.2121540  0.06531437  0.06561795
##          degree1 degree2
## Lag 0      1.0000000 1.0000000
## Lag 1024  0.6675208 0.4417690
## Lag 2048  0.5229288 0.3368740
## Lag 3072  0.4104187 0.2750557
## Lag 4096  0.3381305 0.2221605
## Lag 5120  0.2779079 0.1791999
##
## Sample statistics burn-in diagnostic (Geweke):
## Chain 1
##
## Fraction in 1st window = 0.1
## Fraction in 2nd window = 0.5
##
##          edges mix.Sex.0.1 mix.Sex.1.1 mix.Sex.0.2 mix.Sex.1.2      degree1
##      -0.02990      0.03409      -0.76819      1.14031      -0.04373      0.16283
##          degree2
##          0.18311
##
## Individual P-values (lower = worse):
##          edges mix.Sex.0.1 mix.Sex.1.1 mix.Sex.0.2 mix.Sex.1.2      degree1
##      0.9761433      0.9728027      0.4423761      0.2541580      0.9651165      0.8706551
##          degree2
##          0.8547126
## Joint P-value (lower = worse):  0.398757 .

```

Sample statistics



Sample statistics



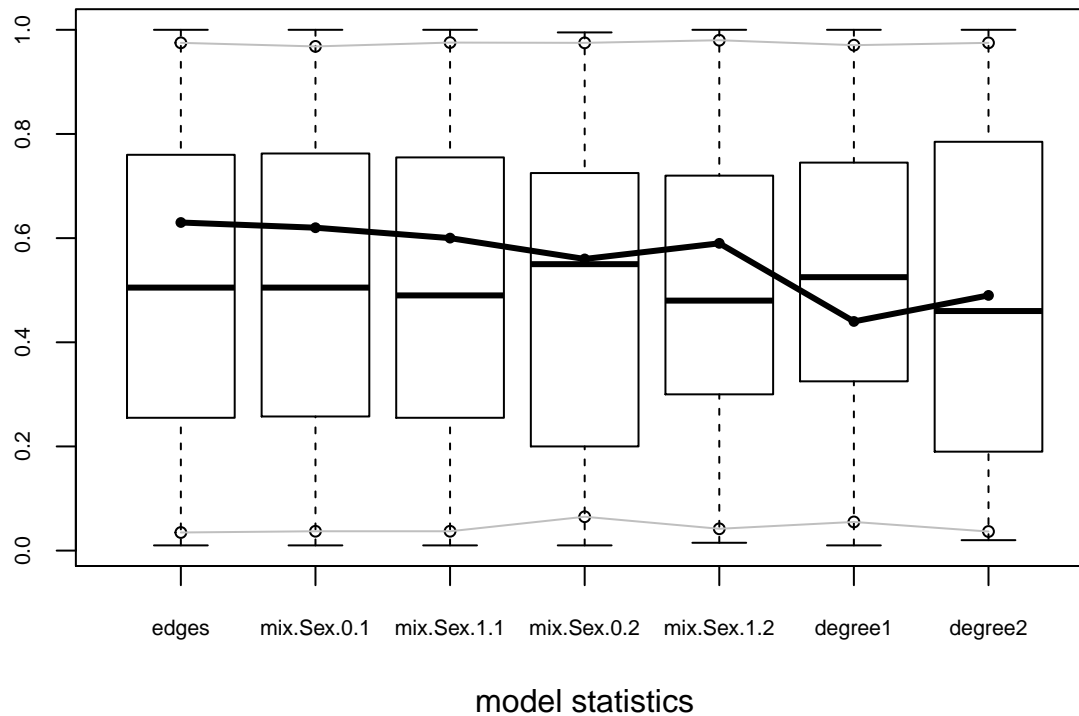
```
##
## MCMC diagnostics shown here are from the last round of simulation, prior to computation of final par
```

```
#Goodness of Fit
#Per Instruction, use gof(ergmFitObject, GOF=~model)
par(mar=c(5,3,3,3))
dop.m3.gof<-gof(dop.m3, GOF =~model)
dop.m3.gof
```

```
##
## Goodness-of-fit for model statistics
##
##          obs min  mean max MC p-value
## edges      159  63 162.25 236      0.74
## mix.Sex.0.1  44  19  44.76  77      0.90
## mix.Sex.1.1  58  17  60.23  87      0.82
## mix.Sex.0.2   4   0   4.09  12      1.00
## mix.Sex.1.2   7   0   7.15  15      1.00
## degree1       9   1   8.86  36      0.88
## degree2       6   0   5.81  17      0.98
```

```
plot(dop.m3.gof)
```

Goodness-of-fit diagnostics



Model 4: Model 3 increasing burnin to 20000 and increasing interval to 5000

```
#dop.m4<-ergm(dop.net ~ edges + nodemix("Sex",base=c(1,6)) + degree(1) + degree(2),
#             control=control.ergm(MCMC.burnin = 20000,MCMC.interval = 5000))
#save(dop.m4,file="dop-m4.Rdata")
load("dop-m4.Rdata")
summary(dop.m4)
```

```
##
## =====
## Summary of model fit
## =====
##
## Formula:   dop.net ~ edges + nodemix("Sex", base = c(1, 6)) + degree(1) +
##            degree(2)
##
## Iterations: 2 out of 20
##
## Monte Carlo MLE Results:
##           Estimate Std. Error MCMC % p-value
## edges       -1.4195    0.1452    0 <1e-04 ***
## mix.Sex.0.1  -1.1363    0.2131    0 <1e-04 ***
## mix.Sex.1.1  -0.2845    0.1454    0 0.0506 .
## mix.Sex.0.2  -1.1846    0.4890    0 0.0155 *
## mix.Sex.1.2  -0.8648    0.3408    0 0.0113 *
## degree1      2.7129    0.4540    0 <1e-04 ***
## degree2      1.1460    0.4981    0 0.0215 *
```



```

## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##      Null Deviance: 2621   on 1891   degrees of freedom
## Residual Deviance: 1033   on 1884   degrees of freedom
##
## AIC: 1047    BIC: 1086    (Smaller is better.)
#diagnostics
mcmc.diagnostics(dop.m4)

## Sample statistics summary:
##
## Iterations = 2e+05:20675000
## Thinning interval = 5000
## Number of chains = 1
## Sample size per chain = 4096
##
## 1. Empirical mean and standard deviation for each variable,
##    plus standard error of the mean:
##
##              Mean      SD Naive SE Time-series SE
## edges          0.54517 29.606  0.46260      0.60772
## mix.Sex.0.1    -0.83765  9.967  0.15573      0.18319
## mix.Sex.1.1     1.71509 13.913  0.21740      0.26790
## mix.Sex.0.2     0.01929  2.315  0.03617      0.03617
## mix.Sex.1.2     0.31812  3.421  0.05346      0.05571
## degree1         0.38208  5.241  0.08190      0.10713
## degree2         0.24829  3.141  0.04907      0.05698
##
## 2. Quantiles for each variable:
##
##              2.5% 25% 50% 75% 97.5%
## edges          -63 -18  3  21  53
## mix.Sex.0.1    -21  -8  0   6  18
## mix.Sex.1.1    -26  -8  2  11  28
## mix.Sex.0.2     -4  -2  0   1   5
## mix.Sex.1.2     -5  -2  0   2   8
## degree1        -7  -3 -1   3  13
## degree2        -5  -2  0   2   7
##
##
## Sample statistics cross-correlations:
##              edges mix.Sex.0.1 mix.Sex.1.1 mix.Sex.0.2 mix.Sex.1.2
## edges          1.0000000  0.8382421  0.8208496  0.3349658  0.4211388
## mix.Sex.0.1    0.8382421  1.0000000  0.5668208  0.1977894  0.2574770
## mix.Sex.1.1    0.8208496  0.5668208  1.0000000  0.1673771  0.2777843
## mix.Sex.0.2    0.3349658  0.1977894  0.1673771  1.0000000  0.3062916
## mix.Sex.1.2    0.4211388  0.2574770  0.2777843  0.3062916  1.0000000
## degree1       -0.8829675 -0.7306797 -0.7261157 -0.3272739 -0.4106252
## degree2       -0.7041704 -0.5931346 -0.5754290 -0.2237038 -0.2992225
##              degree1 degree2
## edges          -0.8829675 -0.7041704
## mix.Sex.0.1    -0.7306797 -0.5931346
## mix.Sex.1.1    -0.7261157 -0.5754290

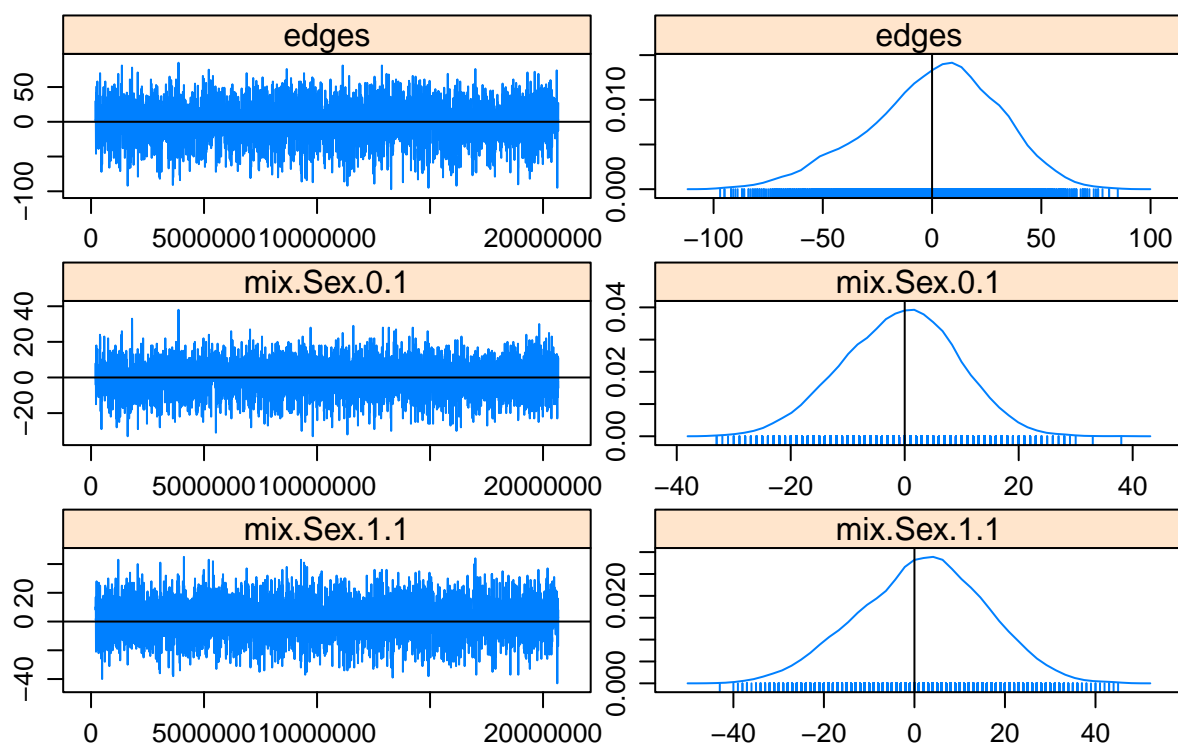
```

```

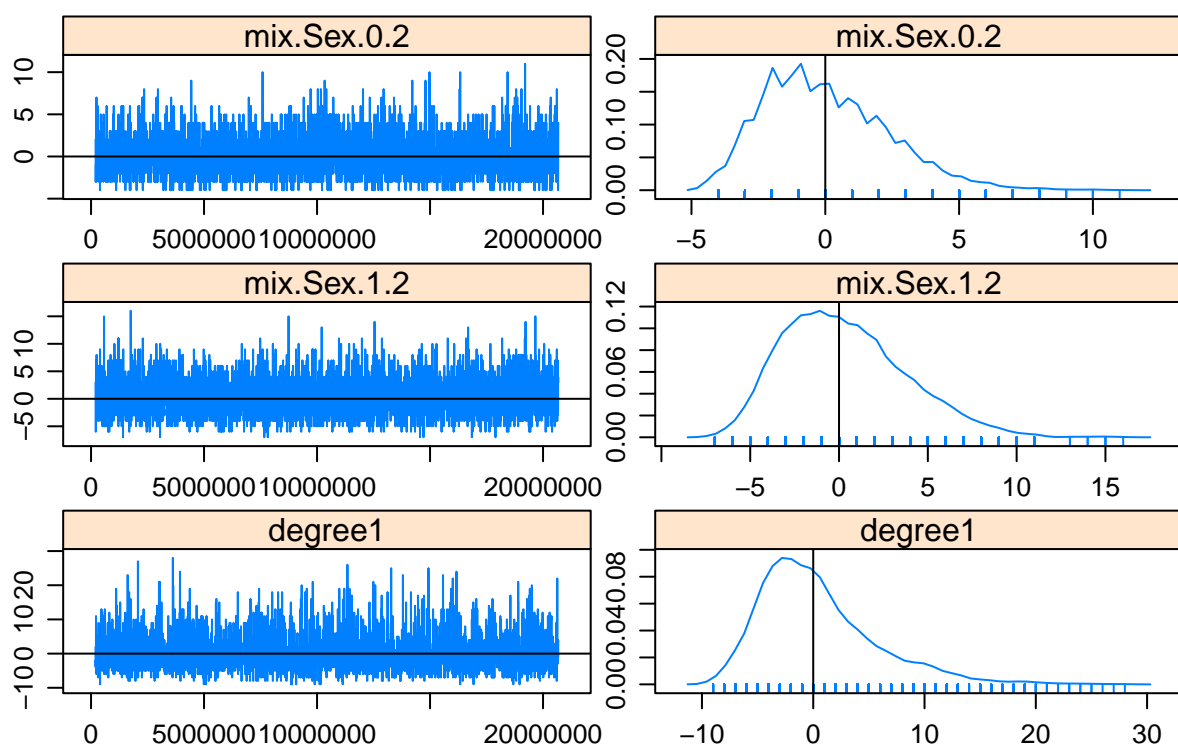
## mix.Sex.0.2 -0.3272739 -0.2237038
## mix.Sex.1.2 -0.4106252 -0.2992225
## degree1      1.0000000  0.4775318
## degree2      0.4775318  1.0000000
##
## Sample statistics auto-correlation:
## Chain 1
##          edges mix.Sex.0.1 mix.Sex.1.1 mix.Sex.0.2 mix.Sex.1.2
## Lag 0      1.000000000 1.000000000 1.000000000 1.000000000 1.000000000
## Lag 5000   0.266159071 0.160855774 0.205799145 0.008819876 0.041210108
## Lag 10000  0.069070825 0.023863776 0.042464742 -0.004852286 0.020114882
## Lag 15000  0.032231365 0.032846652 0.008033016 0.004892967 0.008501756
## Lag 20000 -0.002519302 -0.005360379 0.014089227 -0.013925625 -0.001708839
## Lag 25000  0.018394520 0.015518878 0.006711503 0.021834794 -0.009653945
##          degree1 degree2
## Lag 0      1.000000000 1.000000000
## Lag 5000   0.229671584 0.14818405
## Lag 10000  0.085363081 0.03734657
## Lag 15000  0.035309008 0.01157037
## Lag 20000 -0.008998009 0.01091878
## Lag 25000  0.012685306 0.02658389
##
## Sample statistics burn-in diagnostic (Geweke):
## Chain 1
##
## Fraction in 1st window = 0.1
## Fraction in 2nd window = 0.5
##
##          edges mix.Sex.0.1 mix.Sex.1.1 mix.Sex.0.2 mix.Sex.1.2 degree1
##      0.51022      0.82801      -0.02201      -0.24962      0.89047      0.18151
##      degree2
##      -1.29854
##
## Individual P-values (lower = worse):
##          edges mix.Sex.0.1 mix.Sex.1.1 mix.Sex.0.2 mix.Sex.1.2 degree1
##      0.6098948      0.4076634      0.9824378      0.8028842      0.3732118      0.8559650
##      degree2
##      0.1941021
## Joint P-value (lower = worse): 0.5653145 .

```

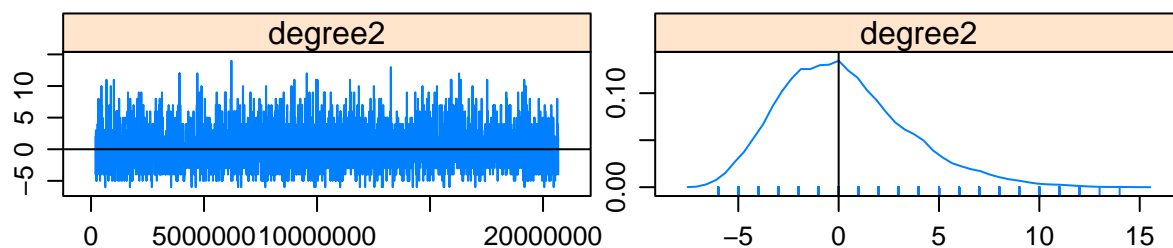
Sample statistics



Sample statistics



Sample statistics



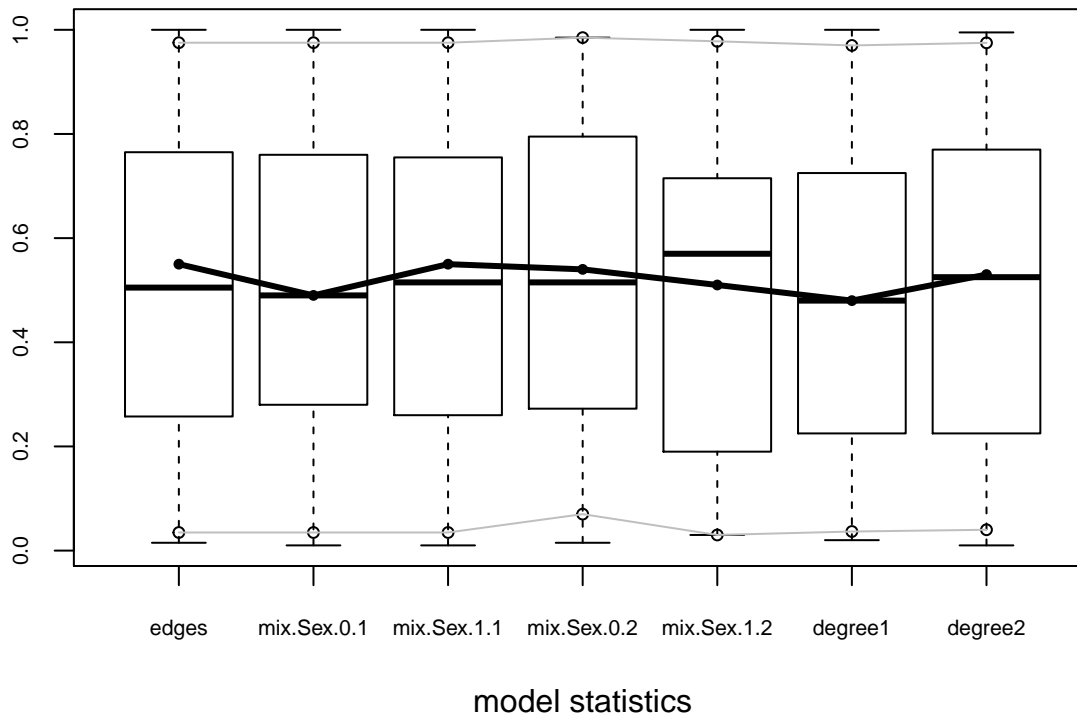
```
##
## MCMC diagnostics shown here are from the last round of simulation, prior to computation of final par:
```

```
#Goodness of Fit
#Per Instruction, use gof(ergmFitObject, GOF=~model)
par(mar=c(5,3,3,3))
dop.m4.gof<-gof(dop.m4, GOF =~model)
dop.m4.gof
```

```
##
## Goodness-of-fit for model statistics
##
##          obs min   mean max MC p-value
## edges      159  94 158.55 219      0.94
## mix.Sex.0.1  44  17  42.91  69      0.98
## mix.Sex.1.1  58  30  58.47  90      0.96
## mix.Sex.0.2   4   0   4.15   9      1.00
## mix.Sex.1.2   7   3   7.22  18      1.00
## degree1       9   2   8.76  22      0.96
## degree2       6   0   6.11  14      1.00
```

```
plot(dop.m4.gof)
```

Goodness-of-fit diagnostics



Part IV: ERGM Interpretation

Compare the probability of a non-assortative (male-female) edge versus an assortative one (male-male, female-female). (Ignore dolphins of unknown sex for now.)

#In the dolphin network, the case of female-female not exist:

#Non-assortative (male-female) = coefficient[2]

```
lst_m.f<-c(dop.m4$coef[2],-dop.m4$coef[2],0)
```

#Assortative (male-male) = coefficient[3]

```
lst_m.m<-c(dop.m4$coef[3],-dop.m4$coef[3],0)
```

#Melting into matrix

```
mat.assort<-outer(lst_m.f,lst_m.m,"+")
```

#Setting column names and row names to the matrix

```
colnames(mat.assort)<-c("MM0","MM1","MM2+")
```

```
rownames(mat.assort)<-c("MF0","MF1","MF2+")
```

#Add first coef

```
mat.lo<-mat.assort+dop.m4$coef[1]
```

#probability

```
mat.pro<-invlogit(mat.lo)
```

```
mat.pro
```

```
##           MM0           MM1           MM2+
## MF0  0.05518579 0.09353219 0.07204005
## MF1  0.36175081 0.50031495 0.42965554
## MF2+ 0.15393992 0.24324047 0.19473817
```

Based on the above result, we could probably conclude that same sex (assortative) are not quite creating connection with other sex(non-assortative). In other words, the same sex would be have the higher chance to

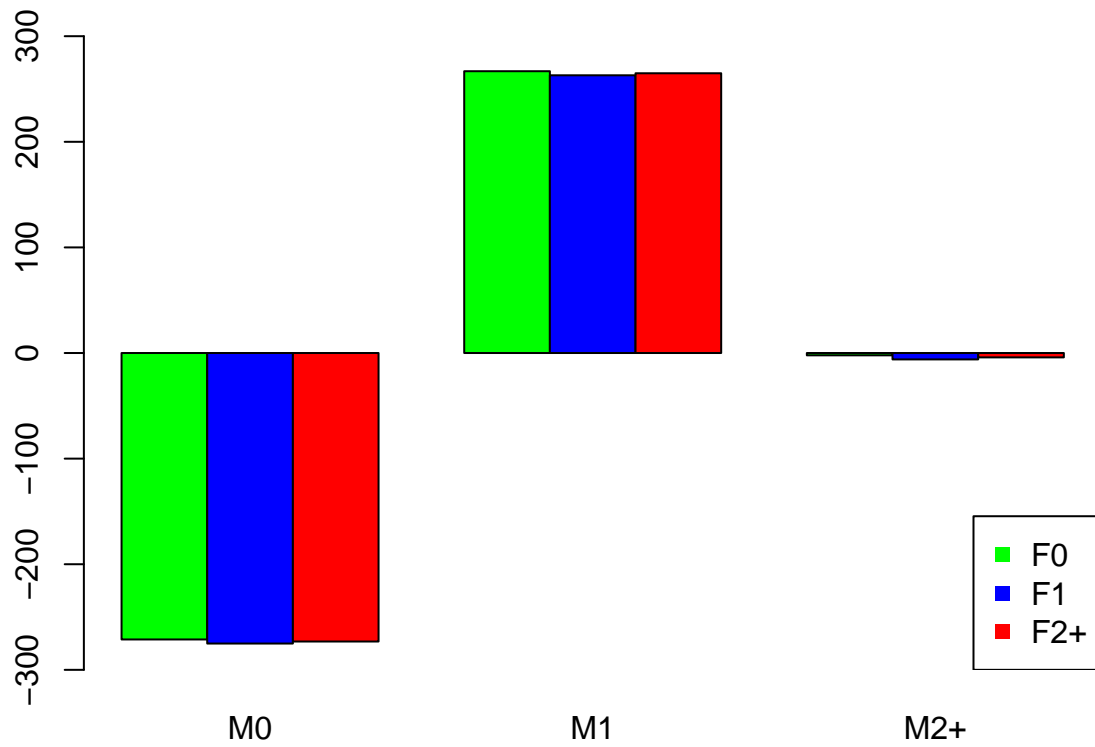
associate new connection with same sex. This result actually prove the result of the CUG and QAP test that the assortativity is most likely governed by sex.

Compare the probability of a second edge being added to a male dolphin versus a female dolphin. Note that it could be an edge to any other dolphin, including one of unknown sex.

```
#dop.m5<-ergm(dop.net ~ edges + nodemix("Sex",base=c(1,6)) +degree(1,by="Sex"),control=control.ergm(MCMC))
#save(dop.m5,file="dop-m5.Rdata")
load("dop-m5.Rdata")
#Female with Coefficient[6]
lst_f<-c(dop.m5$coef[6],-dop.m5$coef[6],0)
#Male with Coefficient[7]
lst_m<-c(dop.m5$coef[7],-dop.m5$coef[7],0)
#Melting into matrix
mat<-outer(lst_f,lst_m,"+")
#Setting column names and row names to the matrix
rownames(mat)<-c("F0","F1","F2+")
colnames(mat)<-c("M0","M1","M2+")
#Add all the possibilities coef including unknown sex coefficient
mat.lo2<-mat+
  dop.m5$coef[1]+
  dop.m5$coef[2]+
  dop.m5$coef[3]+
  dop.m5$coef[4]+
  dop.m5$coef[5]+
  dop.m5$coef[8] #includes the unknow sex coefficient
#Probability
mat.pro<-invlogit(mat.lo2)
mat.pro

##           M0 M1           M2+
## F0  1.589401e-118  1 0.099381130
## F1  3.351266e-120  1 0.002321287
## F2+ 2.307923e-119  1 0.015770551

par(mar=c(3,3,3,3))
barplot(mat.lo2, beside=T,col=c("green","blue", "red"), ylim=c(-300,300))
legend("bottomright",c("F0","F1","F2+"),pch=15,col=c("green","blue", "red"))
```



Based on the above, it shows that Male with degree 1 most likely connects with Female (any degrees). Male with degree 2+ seems not very likely to have more connection with Female (any degrees)