Network Data Homework 5

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Part A

Introduction

For the part A, we are going to fit the ERGMs model. For the ERGMs model, also called exponential random graph models. This is a statistical model for the network. This is a very useful, flexible and powerful modeling approach for building and testing statistical models of networks. In order to construct the ERGMs model, we use the dataset of "coevolve".

Model 1

From the model 1, we change the network to an undirected one. And to make sure the result is the same, we set a seed =40. So, we have the result of change models in the following.

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

Formula:   m1 ~ edges

Iterations:  5 out of 20

Monte Carlo MLE Results:
      Estimate Std. Error MCMC % z value Pr(>|z|)
edges -1.46511    0.09924      0  -14.76   <1e-04 ***
---
Signif. codes:  0 ?**?0.001 ?*?0.01 ??0.05 ??0.1 ??1

     Null Deviance: 923.3  on 666  degrees of freedom
 Residual Deviance: 643.2  on 665  degrees of freedom

AIC: 645.2    BIC: 649.7    (Smaller is better.)
```

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

Formula:   m2 ~ edges

Iterations:  5 out of 20

Monte Carlo MLE Results:
      Estimate Std. Error MCMC % z value Pr(>|z|)
edges -1.44553    0.09864      0  -14.65   <1e-04 ***
---
Signif. codes:  0 ?**?0.001 ?*?0.01 ??0.05 ??0.1 ??1

     Null Deviance: 923.3  on 666  degrees of freedom
 Residual Deviance: 649.0  on 665  degrees of freedom

AIC: 651    BIC: 655.5    (Smaller is better.)
```

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

Formula:   m3 ~ edges

Iterations:  5 out of 20

Monte Carlo MLE Results:
      Estimate Std. Error MCMC % z value Pr(>|z|)
edges -1.41660    0.09776      0  -14.49   <1e-04 ***
---
Signif. codes:  0 ?**?0.001 ?*?0.01 ??0.05 ??0.1 ??1

     Null Deviance: 923.3  on 666  degrees of freedom
 Residual Deviance: 657.6  on 665  degrees of freedom

AIC: 659.6    BIC: 664.1    (Smaller is better.)
```

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

Formula:   m4 ~ edges

Iterations:  5 out of 20

Monte Carlo MLE Results:
      Estimate Std. Error MCMC % z value Pr(>|z|)
edges -1.38817    0.09693      0  -14.32   <1e-04 ***
---
Signif. codes:  0 ?**?0.001 ?*?0.01 ??0.05 ??0.1 ??1

     Null Deviance: 923.3  on 666  degrees of freedom
 Residual Deviance: 666.0  on 665  degrees of freedom

AIC: 668    BIC: 672.5    (Smaller is better.)
```

From above result, we can see that the model with only variable of edge is significant. The pvalue of edges variable are smaller than 0.05. So, we can consider that it is significant. Also, we calculate the plogis for the coefficient of model, we have

Model	Fit1	Fit2	Fit3	Fit4
Value	0.1876877	0.1906907	0.1951952	0.1996997

Model 2

For the model 2, different from the previews one, we add more variables into the model. In this model, we add the gender, smoke effect.

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

Formula:   m1 ~ edges + nodefactor("gender") + nodefactor("smoke") +
    nodematch("gender", diff = TRUE) + nodematch("smoke",
    diff = TRUE)

Iterations:  5 out of 20

Monte Carlo MLE Results:
                    Estimate Std. Error MCMC % z value Pr(>|z|)
edges                -9.5827     1.3677      0  -7.007   <1e-04 ***
nodefactor.gender.2   4.5252     0.6124      0   7.390   <1e-04 ***
nodefactor.smoke.1    0.2256     0.5960      0   0.379    0.705
nodematch.gender.1    8.4736     1.1850      0   7.151   <1e-04 ***
nodematch.gender.2        NA     0.0000      0      NA       NA
nodematch.smoke.0     0.4289     0.6970      0   0.615    0.538
nodematch.smoke.1         NA     0.0000      0      NA       NA
---
Signif. codes:  0 ?**?0.001 ?*?0.01 ??0.05 ??0.1 ??1

     Null Deviance: 923.3  on 666  degrees of freedom
 Residual Deviance: 467.9  on 659  degrees of freedom

AIC: 481.9    BIC: 513.5    (Smaller is better.)
```

From the above result, we can see that the gender effect is significant influence of detecting the tie between two people. However, when we check the status of smoke, there are no sign for the significance. Notice that the overall homophily effect only influence the female. While checking the AIC value, we can say this model is better than baseline mode because the AIC value is smaller.

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

Formula:   m2 ~ edges + nodefactor("gender") + nodefactor("smoke") +
    nodematch("gender", diff = TRUE) + nodematch("smoke",
    diff = TRUE)

Iterations:  5 out of 20

Monte Carlo MLE Results:
                    Estimate Std. Error MCMC % z value Pr(>|z|)
edges                -8.9800     1.0856      0  -8.272   <1e-04 ***
nodefactor.gender.2   4.0387     0.4924      0   8.203   <1e-04 ***
nodefactor.smoke.1    0.4176     0.4547      0   0.918   0.3584
nodematch.gender.1    7.4964     0.9348      0   8.020   <1e-04 ***
nodematch.gender.2        NA     0.0000      0      NA       NA
nodematch.smoke.0     0.9531     0.5735      0   1.662   0.0965 .
nodematch.smoke.1         NA     0.0000      0      NA       NA
---
Signif. codes:  0 ?**?0.001 ?*?0.01 ??0.05 ??0.1 ??1

     Null Deviance: 923.3  on 666  degrees of freedom
 Residual Deviance: 479.9  on 659  degrees of freedom

AIC: 493.9    BIC: 525.4    (Smaller is better.)
```

Similar to the preview model (m1), gender effect is significantly influence of detecting the tie between two people. However, when we check the status of smoke, there are no sign for the significance. Notice that the overall homophily effect only influence the female. While checking the AIC value, we can say this model is better than baseline mode because the AIC value is smaller.

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

Formula:   m3 ~ edges + nodefactor("gender") + nodefactor("smoke") +
    nodematch("gender", diff = TRUE) + nodematch("smoke",
    diff = TRUE)

Iterations:  5 out of 20

Monte Carlo MLE Results:
                    Estimate Std. Error MCMC % z value Pr(>|z|)
edges                -9.5376     1.0184      0  -9.365  < 1e-04 ***
nodefactor.gender.2   3.9601     0.4610      0   8.591  < 1e-04 ***
nodefactor.smoke.1    1.0547     0.3859      0   2.733 0.006272 **
nodematch.gender.1    7.2823     0.8647      0   8.422  < 1e-04 ***
nodematch.gender.2        NA     0.0000      0      NA       NA
nodematch.smoke.0     1.8087     0.5203      0   3.476 0.000508 ***
nodematch.smoke.1         NA     0.0000      0      NA       NA
---
Signif. codes:  0 ?**?0.001 ?*?0.01 ??0.05 ??0.1 ??1

     Null Deviance: 923.3  on 666  degrees of freedom
 Residual Deviance: 482.9  on 659  degrees of freedom

AIC: 496.9    BIC: 528.4    (Smaller is better.)
```

When it comes to the m3, different from the previous one, we can see that both gender and smoke effect are significant. Also, the overall homophily effect is seen mainly among female and non-smoker at level 0.05. While checking the AIC value, we can say this model is better than baseline mode because the AIC value is smaller.

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

Formula:   m4 ~ edges + nodefactor("gender") + nodefactor("smoke") +
    nodematch("gender", diff = TRUE) + nodematch("smoke",
    diff = TRUE)

Iterations:  5 out of 20

Monte Carlo MLE Results:
                    Estimate Std. Error MCMC % z value Pr(>|z|)
edges                -9.6876     1.0068      0  -9.623  < 1e-04 ***
nodefactor.gender.2   3.9412     0.4629      0   8.514  < 1e-04 ***
nodefactor.smoke.1    1.2456     0.3366      0   3.701 0.000215 ***
nodematch.gender.1    7.3742     0.8684      0   8.492  < 1e-04 ***
nodematch.gender.2        NA     0.0000      0      NA       NA
nodematch.smoke.0     1.8484     0.4794      0   3.856 0.000115 ***
nodematch.smoke.1         NA     0.0000      0      NA       NA
---
Signif. codes:  0 ?**?0.001 ?*?0.01 ??0.05 ??0.1 ??1

     Null Deviance: 923.3  on 666  degrees of freedom
 Residual Deviance: 485.8  on 659  degrees of freedom

AIC: 499.8    BIC: 531.3    (Smaller is better.)
```

When checking the m4, the result is all the same as m3. Both gender and smoke effect are significant. Also, the overall homophily effect is seen mainly among female and non-smoker at level 0.05. While checking the AIC value, we can say this model is better than baseline mode because the AIC value is smaller.

Model 3

In the model 3, we can add more limitation for the model. For example in this section, we will add a option name gwesp(). Set the parameter equal to 0.7 and the fixed=true. So we have the result as follow.

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

Formula:   m1 ~ edges + nodefactor("gender") + nodefactor("smoke") +
    nodematch("gender", diff = TRUE) + nodematch("smoke",
    diff = TRUE) + gwesp(0.7, fixed = TRUE)

Iterations:  2 out of 20

Monte Carlo MLE Results:
                      Estimate Std. Error MCMC % z value Pr(>|z|)
edges                  -8.8112         NA     NA      NA       NA
nodefactor.gender.2     3.0314 81754.5765    100   0.000        1
nodefactor.smoke.1      0.4374         NA     NA      NA       NA
nodematch.gender.1      5.2317 82056.8126    100   0.000        1
nodematch.gender.2     -0.4204 81754.5765    100   0.000        1
nodematch.smoke.0       0.5921         NA     NA      NA       NA
nodematch.smoke.1      -0.0896         NA     NA      NA       NA
gwesp.fixed.0.7         0.9204     0.1786      0   5.155   <1e-04 ***
---
Signif. codes:  0 ?**?0.001 ?*?0.01 ??0.05 ??0.1 ??1

     Null Deviance: 923.3  on 666  degrees of freedom
 Residual Deviance: 442.7  on 658  degrees of freedom

AIC: 458.7    BIC: 494.7    (Smaller is better.)
```

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

Formula:   m2 ~ edges + nodefactor("gender") + nodefactor("smoke") +
    nodematch("gender", diff = TRUE) + nodematch("smoke",
    diff = TRUE) + gwesp(0.7, fixed = TRUE)

Iterations:  2 out of 20

Monte Carlo MLE Results:
                      Estimate Std. Error MCMC % z value Pr(>|z|)
edges               -8.280e+00  1.882e+05    100   0.000        1
nodefactor.gender.2  2.268e+00         NA     NA      NA       NA
nodefactor.smoke.1   7.136e-01  2.352e+05    100   0.000        1
nodematch.gender.1   4.099e+00         NA     NA      NA       NA
nodematch.gender.2   2.405e-03         NA     NA      NA       NA
nodematch.smoke.0    1.096e+00  2.352e+05    100   0.000        1
nodematch.smoke.1   -1.618e-01  2.352e+05    100   0.000        1
gwesp.fixed.0.7      1.007e+00  1.910e-01      0   5.273   <1e-04 ***
---
Signif. codes:  0 ?**?0.001 ?*?0.01 ??0.05 ??0.1 ??1

     Null Deviance: 923.3  on 666  degrees of freedom
 Residual Deviance: 447.6  on 658  degrees of freedom

AIC: 463.6    BIC: 499.7    (Smaller is better.)
```

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

Formula:   m3 ~ edges + nodefactor("gender") + nodefactor("smoke") +
    nodematch("gender", diff = TRUE) + nodematch("smoke",
    diff = TRUE) + gwesp(0.7, fixed = TRUE)

Iterations:  2 out of 20

Monte Carlo MLE Results:
                      Estimate Std. Error MCMC % z value Pr(>|z|)
edges               -8.490e+00  4.809e+04    100   0.000        1
nodefactor.gender.2  2.429e+00         NA     NA      NA       NA
nodefactor.smoke.1   7.848e-01         NA     NA      NA       NA
nodematch.gender.1   4.308e+00         NA     NA      NA       NA
nodematch.gender.2  -6.673e-02         NA     NA      NA       NA
nodematch.smoke.0    1.399e+00         NA     NA      NA       NA
nodematch.smoke.1    2.437e-01         NA     NA      NA       NA
gwesp.fixed.0.7      9.063e-01  1.906e-01      0   4.754   <1e-04 ***
---
Signif. codes:  0 ?**?0.001 ?*?0.01 ??0.05 ??0.1 ??1

     Null Deviance: 923.3  on 666  degrees of freedom
 Residual Deviance: 456.5  on 658  degrees of freedom

AIC: 472.5    BIC: 508.5    (Smaller is better.)
```

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

Formula:   m4 ~ edges + nodefactor("gender") + nodefactor("smoke") +
    nodematch("gender", diff = TRUE) + nodematch("smoke",
    diff = TRUE) + gwesp(0.7, fixed = TRUE)

Iterations:  2 out of 20

Monte Carlo MLE Results:
                      Estimate Std. Error MCMC % z value Pr(>|z|)
edges               -8.285e+00         NA     NA      NA       NA
nodefactor.gender.2  1.910e+00  8.365e+05    100   0.000        1
nodefactor.smoke.1   9.191e-01         NA     NA      NA       NA
nodematch.gender.1   3.739e+00  8.365e+05    100   0.000        1
nodematch.gender.2   3.079e-01  8.365e+05    100   0.000        1
nodematch.smoke.0    1.485e+00         NA     NA      NA       NA
nodematch.smoke.1    1.288e-01         NA     NA      NA       NA
gwesp.fixed.0.7      1.034e+00  1.964e-01      0   5.265   <1e-04 ***
---
Signif. codes:  0 ?**?0.001 ?*?0.01 ??0.05 ??0.1 ??1

     Null Deviance: 923.3  on 666  degrees of freedom
 Residual Deviance: 454.9  on 658  degrees of freedom

AIC: 470.9    BIC: 506.9    (Smaller is better.)
```

From above all the result for the four model, we can see that all the models are not good fit the data, there are a lot of NA value for the P-value. Those models are useless.

Part B

Introduction

In this section, we would like to consider the model in the slide #173 and we will add two more effect. To fulfill this requirement, we need to note that for the RSiena data, if it was put into the correct format, then the model specification and building can process. In the first step, we would focus om the model specification with a minimal set of parameters. After that we can add some other effect to further explore the relationship.

Model 0

First specification the model and get the result

	name	effectName	include	fix	test	initialValue	parm
1	fr4wav	constant fr4wav rate (period 1)	TRUE	FALSE	FALSE	2.00405	0
2	fr4wav	constant fr4wav rate (period 2)	TRUE	FALSE	FALSE	2.00405	0
3	fr4wav	constant fr4wav rate (period 3)	TRUE	FALSE	FALSE	2.00405	0
4	fr4wav	outdegree (density)	TRUE	FALSE	FALSE	-0.80750	0
5	fr4wav	reciprocity	TRUE	FALSE	FALSE	0.00000	0
6	fr4wav	transitive triplets	TRUE	FALSE	FALSE	0.00000	0
7	fr4wav	gender alter	TRUE	FALSE	FALSE	0.00000	0
8	fr4wav	gender ego	TRUE	FALSE	FALSE	0.00000	0
9	fr4wav	same gender	TRUE	FALSE	FALSE	0.00000	0
10	fr4wav	smokebeh alter	TRUE	FALSE	FALSE	0.00000	0
11	fr4wav	smokebeh ego	TRUE	FALSE	FALSE	0.00000	0
12	fr4wav	same smokebeh	TRUE	FALSE	FALSE	0.00000	0
13	smokebeh	rate smokebeh (period 1)	TRUE	FALSE	FALSE	0.20811	0
14	smokebeh	rate smokebeh (period 2)	TRUE	FALSE	FALSE	0.20811	0
15	smokebeh	rate smokebeh (period 3)	TRUE	FALSE	FALSE	0.20811	0
16	smokebeh	smokebeh linear shape	TRUE	FALSE	FALSE	0.56173	0
17	smokebeh	smokebeh average similarity	TRUE	FALSE	FALSE	0.00000	0
18	smokebeh	smokebeh total similarity	TRUE	FALSE	FALSE	0.00000	0

And then we simulate the model, after three phases with total of 2399 iteration steps, we get the estimation result.

		Estimate	Standard Error	Convergence t-ratio
Network Dynamics				
1.	rate constant fr4wav rate (period 1)	1.1546	(0.7353)	-0.0052
2.	rate constant fr4wav rate (period 2)	1.1398	(3.1203)	-0.0294
3.	rate constant fr4wav rate (period 3)	1.1315	(7.2649)	0.0004
4.	eval outdegree (density)	-3.1658	(3.2318)	-0.0445
5.	eval reciprocity	0.7976	(0.2520)	-0.0229
6.	eval transitive triplets	0.0930	(0.4455)	-0.0243
7.	eval gender alter	-0.3524	(2.6532)	0.0318
8.	eval gender ego	0.3443	(0.7480)	0.0179
9.	eval same gender	1.2691	(4.1219)	-0.0204
10.	eval smokebeh alter	0.7202	(6.6208)	-0.0164
11.	eval smokebeh ego	-0.0552	(0.3140)	0.0393
12.	eval same smokebeh	1.1998	(9.6929)	-0.0058
Behavior Dynamics				
13.	rate rate smokebeh (period 1)	0.2859	(0.6399)	-0.0160
14.	rate rate smokebeh (period 2)	0.3178	(4.6132)	0.0559
15.	rate rate smokebeh (period 3)	0.3220	(4.0871)	0.0332
16.	eval smokebeh linear shape	14.6608	(22907.5335)	0.0935
17.	eval smokebeh average similarity	132.8899	(332929.2533)	-0.2890
18.	eval smokebeh total similarity	-16.5891	(43855.7446)	-0.1140
Overall maximum convergence ratio:		1.4216		

And get the simulation result of new network. We can see that for this new network, the modularity is 0.169 compared with the old model with modularity 0.129. The different is not that big. So, we can say that the new simulation network is similar with original network

```
IGRAPH 39e0d22 DN-- 37 177 --
+ attr: name (v/c), smoke (v/n), gender (v/n), V3 (e/n)
+ edges from 39e0d22 (vertex names):
  [1] 1 ->7  1 ->8  1 ->34 2 ->7  2 ->17 2 ->21 2 ->30 2 ->32 3 ->20 3 ->21 3 ->33 4 ->7
 [13] 4 ->19 4 ->21 4 ->27 5 ->10 5 ->12 5 ->22 5 ->29 6 ->7  6 ->8  6 ->9  6 ->11 6 ->34
 [25] 7 ->1  7 ->8  7 ->9  7 ->13 7 ->18 8 ->1  8 ->4  8 ->7  8 ->17 8 ->19 8 ->21 8 ->30
 [37] 8 ->32 9 ->6  9 ->7  9 ->11 9 ->13 9 ->34 10->5  10->25 10->28 10->29 10->31 11->1
 [49] 11->4  11->6  11->7  11->9  12->10 12->22 12->28 12->29 12->31 13->4  13->7  13->9
 [61] 13->11 13->34 14->16 14->22 14->25 14->31 15->16 15->24 15->31 16->15 16->22 16->24
 [73] 16->25 16->31 16->36 17->4  17->8  17->21 17->27 17->31 17->33 18->2  18->17 18->21
 [85] 19->21 19->30 19->32 19->33 20->3  20->7  20->17 20->21 20->30 20->33 20->35 21->4
+ ... omitted several edges
```

Model 1

Next, create the new network for simulate dataset and repeat the process above to estimate a new model, so we have the result

```
Estimates, standard errors and convergence t-ratios

                                              Estimate   Standard   Convergence
                                                           Error      t-ratio
Network Dynamics
   1. rate constant sim3wav3 rate (period 1)   1.4471  (  0.2773  )    0.0107
   2. rate constant sim3wav3 rate (period 2)   3.9204  (  0.4841  )    0.0029
   3. rate constant sim3wav3 rate (period 3)   3.4639  (  0.4546  )    0.0054
   4. eval outdegree (density)                -3.0235  (  0.2933  )   -0.0284
   5. eval reciprocity                         0.7623  (  0.1627  )   -0.0538
   6. eval transitive triplets                 0.2030  (  0.0418  )   -0.0307
   7. eval gender alter                       -0.3007  (  0.2657  )   -0.0527
   8. eval gender ego                          0.4119  (  0.2666  )   -0.0306
   9. eval same gender                         1.4690  (  0.2870  )   -0.0278
  10. eval smokebehave alter                   0.0515  (  0.1944  )   -0.0564
  11. eval smokebehave ego                    -0.0272  (  0.1981  )   -0.0443
  12. eval same smokebehave                    0.2897  (  0.2474  )   -0.0219

Behavior Dynamics
  13. rate rate smokebehave (period 1)         0.2683  (  0.2260  )   -0.0006
  14. rate rate smokebehave (period 2)         0.3110  (  0.1849  )   -0.0084
  15. rate rate smokebehave (period 3)         0.7220  (  0.3737  )    0.0318
  16. eval smokebehave linear shape            0.6669  (  1.5641  )    0.0440
  17. eval smokebehave average similarity     22.8696  ( 84.7335  )   -0.0483
  18. eval smokebehave total similarity       -3.3770  ( 13.7553  )   -0.0384

Overall maximum convergence ratio:    0.1531
```

Model 2

Similar process as above and we have the result as follow

```
Estimates, standard errors and convergence t-ratios

                                              Estimate   Standard   Convergence
                                                           Error      t-ratio
Network Dynamics
   1. rate constant sim3wav3 rate (period 1)   1.4467  (   0.2491 )   -0.0139
   2. rate constant sim3wav3 rate (period 2)   3.9101  (   0.5275 )    0.0441
   3. rate constant sim3wav3 rate (period 3)   3.4424  (   0.4375 )   -0.0540
   4. eval outdegree (density)                -3.0324  (   0.3165 )    0.0020
   5. eval reciprocity                         0.7589  (   0.1543 )   -0.0046
   6. eval transitive triplets                 0.2034  (   0.0444 )    0.0213
   7. eval gender alter                       -0.2994  (   0.2631 )    0.0637
   8. eval gender ego                          0.4103  (   0.2662 )    0.0472
   9. eval same gender                         1.4741  (   0.2893 )    0.0192
  10. eval smokebehave alter                   0.0551  (   0.2052 )   -0.0568
  11. eval smokebehave ego                    -0.0168  (   0.2048 )    0.0555
  12. eval same smokebehave                    0.2932  (   0.2474 )    0.0051

Behavior Dynamics
  13. rate rate smokebehave (period 1)         0.2719  (   0.2554 )   -0.0901
  14. rate rate smokebehave (period 2)         0.3182  (   0.2005 )    0.0369
  15. rate rate smokebehave (period 3)         0.7392  (   0.3738 )    0.0888
  16. eval smokebehave linear shape            0.6186  (   1.5459 )    0.0503
  17. eval smokebehave average similarity     23.1453  ( 108.6290 )   -0.0481
  18. eval smokebehave total similarity       -3.4141  (  17.7185 )   -0.0396

Overall maximum convergence ratio:    0.2187
```

Model Comparison

Tow mode estimation are similar, so we can focus on the sign of estimator to find out the effect of different influence. We know that for the rate estimation. It represents the estimated number of likelihoods for change per actor for each period. The eval reveal the attractiveness of a particular network state for actor. For the gender effect, we can see the same gender and gender ego is positive effects, but the gender alter is negative effect. Actor are more like to form a tie based on their own gender rather than opposite gender. For the smoking effect, we can see actor is more likely to make a tie with people who have the same smoking behavior because the same smoke behave estimator is positive. Actor are less likely to make friend with people have opposite smoking habit. From the behavior dynamics, we can find that with the time change, the smoking status become more and more important in the effect of forming a tie.

To test the significant, we can use the Wald Test to test the Zw score and compare it to the significant score.

$$\text{Zw} = \left|\frac{Bestimate}{SE}\right| > Z_{1-\frac{a}{2}}$$

After we are calculating all the result, we find that only same gender is significant at 0.05 significance level. So, we reject the hypothesis which is the likelihood of an ego forming a new friendship tie is higher with an alter who has the same gender. Outdegree, reciprocity and transitivity variables are significant. Notice that since the smokebehave-average-similairyt and eval-smokebehave total similarity are not significant, so we cannot reject the null hypothesis, which is the possibility of changing behavior is related to the average similarity of smoking status across all tied alters.

T-ratios can be used to test the lack of convergence for each estimate. With the small value, it means that the model converges perfectly. We can see both model 1 and model 2 are excellent converge because of the small value of T-ratios. .

Code

```
library(statnet)
library(intergraph)
library("UserNetR")
library(igraph)
data(Coevolve)
fr_w1 <- Coevolve$fr_w1
fr_w2 <- Coevolve$fr_w2
fr_w3 <- Coevolve$fr_w3
fr_w4 <- Coevolve$fr_w4
m1<- asNetwork(as.undirected(fr_w1))
```

```
m2<- asNetwork(as.undirected(fr_w2))
m3<- asNetwork(as.undirected(fr_w3))
m4<- asNetwork(as.undirected(fr_w4))

#model 1
fit1 <- ergm(m1 ~ edges,control=control.ergm(seed=40))
fit2 <- ergm(m2 ~ edges,control=control.ergm(seed=40))
fit3 <- ergm(m3 ~ edges,control=control.ergm(seed=40))
fit4 <- ergm(m4 ~ edges,control=control.ergm(seed=40))
summary(fit1)
summary(fit2)
summary(fit3)
summary(fit4)
class(fit1)
plogis(coef(fit1))
class(fit2)
plogis(coef(fit2))
class(fit3)
plogis(coef(fit3))
class(fit4)
plogis(coef(fit4))

#model 2
f1 <- ergm(m1 ~ edges + nodefactor('gender') + nodefactor('smoke') +
              nodematch('gender',diff=TRUE) + nodematch('smoke',diff=TRUE),
            control=control.ergm(seed=40))
f2 <- ergm(m2 ~ edges + nodefactor('gender') + nodefactor('smoke') +
              nodematch('gender',diff=TRUE) + nodematch('smoke',diff=TRUE),
            control=control.ergm(seed=40))
f3 <- ergm(m3 ~ edges + nodefactor('gender') + nodefactor('smoke') +
              nodematch('gender',diff=TRUE) + nodematch('smoke',diff=TRUE),
            control=control.ergm(seed=40))
f4 <- ergm(m4 ~ edges + nodefactor('gender') + nodefactor('smoke') +
              nodematch('gender',diff=TRUE) + nodematch('smoke',diff=TRUE),
            control=control.ergm(seed=40))
summary(f1)
summary(f2)
summary(f3)
summary(f4)

#model 3
f1 <- ergm(m1 ~ edges + nodefactor('gender') + nodefactor('smoke') +
              nodematch('gender',diff=TRUE) + nodematch('smoke',diff=TRUE) +
              gwesp(0.7, fixed=TRUE), control=control.ergm(seed=40))
```

```
f2 <- ergm(m2 ~ edges + nodefactor('gender') + nodefactor('smoke') +
                nodematch('gender',diff=TRUE) + nodematch('smoke',diff=TRUE) +
                gwesp(0.7, fixed=TRUE), control=control.ergm(seed=40))
f3 <- ergm(m3 ~ edges + nodefactor('gender') + nodefactor('smoke') +
                nodematch('gender',diff=TRUE) + nodematch('smoke',diff=TRUE) +
                gwesp(0.7, fixed=TRUE), control=control.ergm(seed=40))
f4 <- ergm(m4 ~ edges + nodefactor('gender') + nodefactor('smoke') +
                nodematch('gender',diff=TRUE) + nodematch('smoke',diff=TRUE) +
                gwesp(0.7, fixed=TRUE), control=control.ergm(seed=40))
summary(f1)
summary(f2)
summary(f3)
summary(f4)

#Part B:
library(RSiena)
library(Matrix)
w1 <- cbind(get.edgelist(fr_w1), 1)
w2 <- cbind(get.edgelist(fr_w2), 1)
w3 <- cbind(get.edgelist(fr_w3), 1)
w4 <- cbind(get.edgelist(fr_w4), 1)
w1s <- spMatrix(37, 37, w1[,1], w1[,2], w1[,3])
w2s <- spMatrix(37, 37, w2[,1], w2[,2], w2[,3])
w3s <- spMatrix(37, 37, w3[,1], w3[,2], w3[,3])
w4s <- spMatrix(37, 37, w4[,1], w4[,2], w4[,3])
fr4wav <- sienaDependent(list(w1s,w2s,w3s,w4s))
fr4wav

#coVariate object
gender_vect <- V(fr_w1)$gender
table(gender_vect)

gender <- coCovar(gender_vect)
gender

#Behaviour object
smoke <- array(
  c(V(fr_w1)$smoke, V(fr_w2)$smoke,
    V(fr_w3)$smoke, V(fr_w4)$smoke),
  dim=c(37,4))
smokebehave <- sienaDependent(smoke,type = "behavior")
smokebehave

#Build dynamic model
```

```
friend <- sienaDataCreate(fr4wav,smokebeh,gender)
friend

frndeff <- getEffects(friend)
frndeff1 <- includeEffects(frndeff,sameX,
                          interaction1="gender",name="fr4wav")

frndeff1 <- includeEffects(frndeff1,sameX,
                          interaction1="smokebeh",name="fr4wav")

frndeff1 <- includeEffects(frndeff1,egoX,
                          interaction1="smokebeh",name="fr4wav")

frndeff1 <- includeEffects(frndeff1,altX,
                          interaction1="smokebeh",name="fr4wav")

frndeff1 <- includeEffects(frndeff1,avSim,
                          interaction1="fr4wav",name="smokebeh")

frndeff1 <- includeEffects(frndeff1,totSim,
                          interaction1="fr4wav",name="smokebeh")

frndeff1 <- includeEffects(frndeff1,recip,transTrip,
                          name="fr4wav")
#new effects
frndeff1 <- includeEffects(frndeff1,egoX,
                          interaction1="gender",name="fr4wav")

frndeff1 <- includeEffects(frndeff1,altX,
                          interaction1="gender",name="fr4wav")

frndeff1

myalgorithm <- sienaAlgorithmCreate(projname='coevolve')

#simulation
set.seed(999)
RSmod1 <- siena07(myalgorithm, data = friend,
                effects = frndeff1,batch=TRUE,
                verbose=FALSE,useCluster=TRUE,
                initC=TRUE,nbrNodes=3,returnDeps=TRUE)
summary(RSmod1)

#New Model
```

```
library(igraph)
m1 <- RSmod1$sims[[1]][[1]][[1]][[1]]
m2 <- RSmod1$sims[[1]][[1]][[1]][[2]]
m3 <- RSmod1$sims[[1]][[1]][[1]][[3]]
#smokebehaviour
ms1 <- RSmod1$sims[[1]][[1]][[2]][[1]]
ms2 <- RSmod1$sims[[1]][[1]][[2]][[2]]
ms3 <- RSmod1$sims[[1]][[1]][[2]][[3]]
#sparse
m1s <- spMatrix(37, 37, m1[,1], m1[,2], m1[,3])
m2s <- spMatrix(37, 37, m2[,1], m2[,2], m2[,3])
m3s <- spMatrix(37, 37, m3[,1], m3[,2], m3[,3])

sim3wav3 <- sienaDependent(list(w1s,m1s,m2s,m3s))
sim3wav3


#Behaviour object
smoke1 <- array(c(V(fr_w1)$smoke,ms1,ms2,ms3),dim=c(37,4))
smokebehave <- sienaDependent(smoke1,type = "behavior")
smokebehave

#Build dynamic model
friend1 <- sienaDataCreate(fr4wav3,smokebehave,gender)
friend1

#model2
frndeff2 <- getEffects(friend1)
frndeff3 <- includeEffects(frndeff2,sameX,
                          interaction1="gender",name="sim3wav3")

frndeff3 <- includeEffects(frndeff3,sameX,
                          interaction1="smokebehave",name="sim3wav3")

myalgorithm <- sienaAlgorithmCreate(projname='coevolve')

set.seed(999)
RSmod2 <- siena07(myalgorithm, data = friend1,
                 effects = frndeff3,batch=TRUE,
                 verbose=FALSE,useCluster=TRUE,
                 initC=TRUE,nbrNodes=3)
summary(RSmod2)
#model1
frndeff4 <- includeEffects(frndeff3,egoX,
```

```
                                        interaction1="smokebehave",name="sim3wav3")

frndeff4 <- includeEffects(frndeff4,altX,
                                        interaction1="smokebehave",name="sim3wav3")

frndeff4 <- includeEffects(frndeff4,avSim,
                                        interaction1="sim3wav3",name="smokebehave")

frndeff4 <- includeEffects(frndeff4,totSim,
                                        interaction1="sim3wav3",name="smokebehave")

frndeff4 <- includeEffects(frndeff4,recip,transTrip,
                                        name="sim3wav3")

frndeff4 <- includeEffects(frndeff4,egoX,
                                        interaction1="gender",name="sim3wav3")

frndeff4 <- includeEffects(frndeff4,altX,
                                        interaction1="gender",name="sim3wav3")

frndeff4

myalgorithm <- sienaAlgorithmCreate(projname='coevolve')

set.seed(999)
RSmod3 <- siena07(myalgorithm, data = sim_frined,
                          effects = frndeff4,batch=TRUE,
                          verbose=FALSE,useCluster=TRUE,
                          initC=TRUE,nbrNodes=3)
summary(RSmod3)
```