Covariate effects in ERGMs

567 Statistical analysis of social networks

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Dutch college data

Friendship ties among 32 college students enrolled in a particular program.

- Relations on a 6 point scale, from "dislike" to "best friends";
- Relations measured at seven time points;
- Sex, smoking status and subprogram category also available.

Questions:

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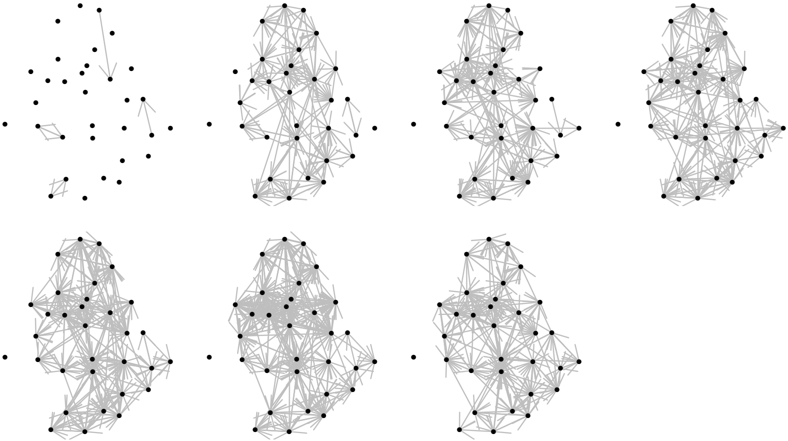

For now, we'll analyze

- the indicator of a positive relation;
- the network at the final timepoint.

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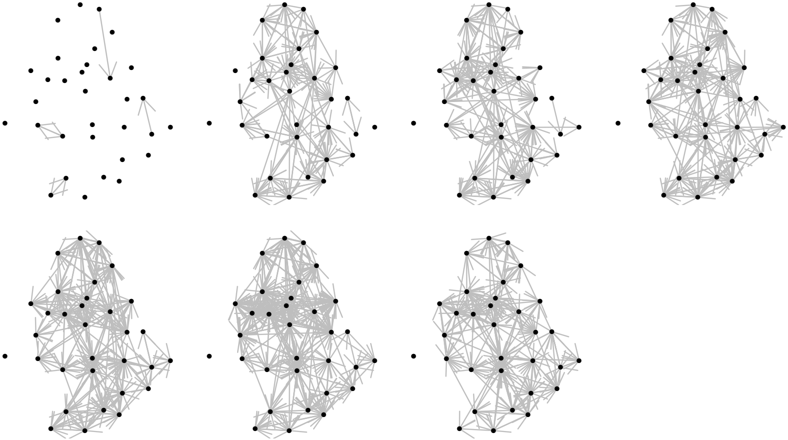

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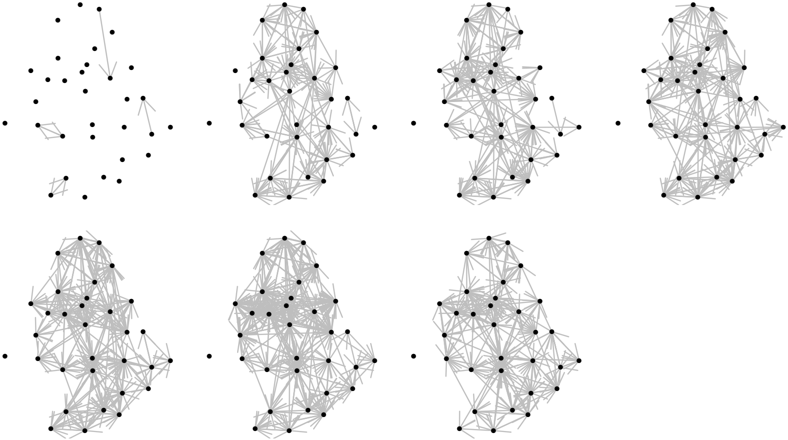

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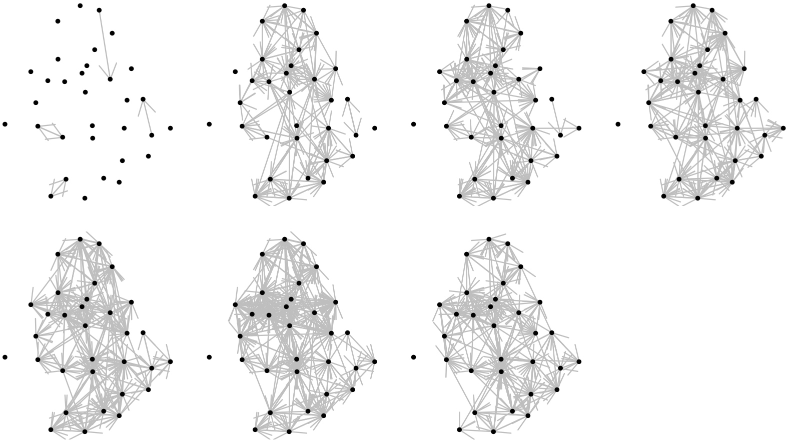

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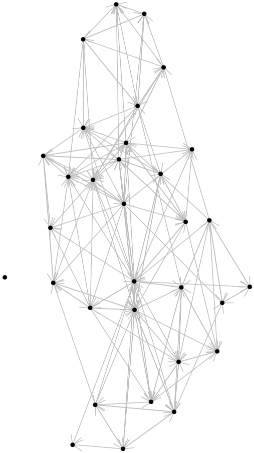

```
mean( Y7,na.rm=TRUE)

## [1] 0.1693548

mean( Y7[ X$male==1, X$male==1 ],na.rm=TRUE )

## [1] 0.3571429

mean( Y7[ X$male==0, X$male==0 ],na.rm=TRUE )

## [1] 0.1956522

mean( Y7[ X$smoke==1, X$smoke==1 ],na.rm=TRUE )

## [1] 0.2692308

mean( Y7[ X$smoke==0, X$smoke==0 ],na.rm=TRUE )

## [1] 0.2017544

SP<-outer(X$prog,X$prog,"==")
mean( Y7[SP], na.rm=TRUE)

## [1] 0.2861111
```

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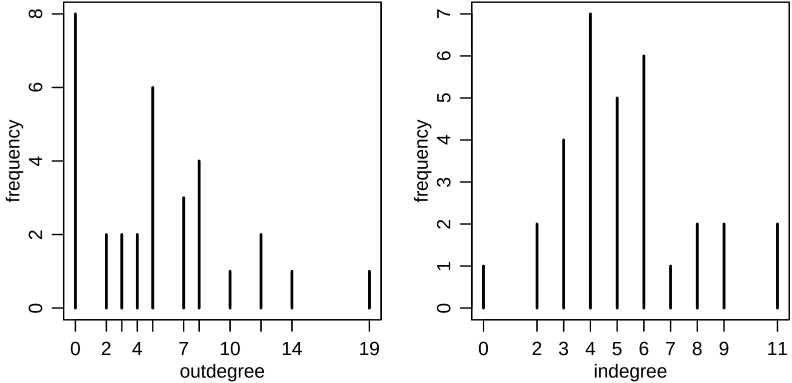

```
mean(outdegree[X$smoker==1])  - mean(outdegree[X$smoker==0])

## [1] 0.3562753

mean(indegree[X$smoker==1])  - mean(indegree[X$smoker==0])

## [1] 0.2267206
```

Degree heterogeneity and Reciprocity

```
#### degree analysis
sd(outdegree)

## [1] 4.662825

sd(indegree)

## [1] 2.514474

cor(outdegree, indegree)

## [1] 0.1705822

#### dyad census
M<-sum(Y7*t(Y7),na.rm=TRUE)/2
A<-sum(Y7,na.rm=TRUE) - 2*M
N<- choose(nrow(Y7),2) - M - A

p11<-2*M/(2*M+A)
p10<-A/(A+2*N)
log( p11 * (1-p10) /( (1-p11) * p10) )

## [1] 2.250258
```

Preliminary analysis

Some preliminary findings:

- Covariate effects:
  - homophily by sex, smoking behavior and program;
  - smokers seem more outgoing and popular.
- Network patterns:
  - positive reciprocity;
  - outdegree variance is larger than indegree variance, and little correlation betwen the two.

To summarize covariate effects, some researchers employ "network regression:"

- convert sociomatrix and covariate matrices to vectors;
- perform ordinary regression (OLS, logistic regression, Poisson regression).

Such a procedure should **not** be called network regression:

- it is just regression;
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Logistic regression

Nevertheless, regression with appropriate covariates might be adequate.

In particular, network patterns could be explained by covariates:

- degree heterogeneity could be explained by one or more nodal covariates;
- reciprocity could be explained by a group comembership variable.

Let's do an ordinary logistic regression and evaluate the fit.

```
XM<-array(dim=c(n,n,5) )

XM[,,1]<-matrix( X[,2] ,n,n)

XM[,,2]<-t(XM[,,1])

XM[,,3]<-outer( X[,1],X[,1],"==")

XM[,,4]<-outer( X[,2],X[,2],"==")

XM[,,5]<-outer( X[,3],X[,3],"==")


y7<-c(Y7)

x<-apply(XM,3,"c")

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fit.glm<-glm( y7 ~ x ,family=binomial)
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Logistic regression fit

```
summary(fit.glm)

##
## Call:
## glm(formula = y7 ~ x, family = binomial)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.1144  -0.6909  -0.4446  -0.3119   2.4689
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -3.2122     0.2671 -12.027  < 2e-16 ***
## xrsmoke       0.2548     0.1882   1.354 0.175716
## xcsmoke       0.2130     0.1881   1.132 0.257500
## xssex         0.6930     0.2079   3.334 0.000857 ***
## xssmoke       0.7983     0.1863   4.285 1.83e-05 ***
## xsprog        1.1030     0.1800   6.127 8.94e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 902.45  on 991  degrees of freedom
## Residual deviance: 819.39  on 986  degrees of freedom
##   (32 observations deleted due to missingness)
## AIC: 831.39
##
## Number of Fisher Scoring iterations: 5
```

Fitting logistic regression in `ergm`

Logistic regression is an ERGM with independent relations.

Suppose our model is

$$\log \text{odds}(y_{i,j} = 1) = \beta_0 + \beta_r x_{r,i} + \beta_c x_{c,j} + \beta_d x_{d,i,j}$$

Then

$$\begin{aligned}\Pr(\mathbf{Y} = \mathbf{y} | \mathbf{X}, \beta) &= \prod_{i \neq j} \left(\frac{e^{(\beta_0 + \beta_r x_{r,i} + \beta_c x_{c,j} + \beta_d x_{d,i,j}) y_{i,j}}}{1 + e^{\beta_0 + \beta_r x_{r,i} + \beta_c x_{c,j} + \beta_d x_{d,i,j}}} \right) \\ &= c(\mathbf{X}, \beta) \times \exp \left(\beta_0 \sum_{i \neq j} y_{i,j} + \beta_r \sum_{i \neq j} x_{r,i} y_{i,j} + \right. \\ &\qquad \left. \beta_c \sum_{i \neq j} x_{c,j} y_{i,j} + \beta_d \sum_{i \neq j} x_{d,i,j} y_{i,j} \right)\end{aligned}$$

The sufficient statistics simplify to the four-dimensional vector

$$\mathbf{t}(\mathbf{y}) = \left(y_{\cdot\cdot}, \sum_{i=1}^{n} x_{r,i} y_{i\cdot}, \sum_{j=1}^{n} x_{c,j} y_{\cdot j}, \sum_{i \neq j} x_{d,i,j} y_{i,j} \right).$$

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&= c(\mathbf{X}, \boldsymbol{\beta}) \times \exp \left(\beta_0 \sum_{i \neq j} y_{i,j} + \beta_r \sum_{i \neq j} x_{r,i} y_{i,j} + \right. \\
&\qquad \left. \beta_c \sum_{i \neq j} x_{c,j} y_{i,j} + \beta_d \sum_{i \neq j} x_{d,i,j} y_{i,j} \right)
\end{aligned}$$

The sufficient statistics simplify to the four-dimensional vector

$$\mathbf{t}(\mathbf{y}) = \left(y_{\cdot\cdot}, \sum_{i=1}^{n} x_{r,i} y_{i\cdot}, \sum_{j=1}^{n} x_{c,j} y_{\cdot j}, \sum_{i \neq j} x_{d,i,j} y_{i,j} \right).$$

Fitting logistic regression in `ergm`

As logistic regression is an ERGM, we should be able to fit it with `ergm`.

We first need to convert the data to a `network` object:

```
library(ergm)
netdat<-network(Y7,vertex.attr=X)
```

Sometimes you want to add vertex attributes one at a time:

```
netdat<-network(Y7)
set.vertex.attribute(netdat,"male",X[,1])
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Fitting logistic regression in ergm

The model is then fit, as before, by specifying sufficient statistics:

```
fit.ergm<-ergm( netdat ~ edges + nodeocov("smoker")  + nodeicov("smoker") +
                nodematch("male") + nodematch("smoker") + nodematch("program") )
```

The terms `nodeicov`, `nodeocov` and `nodematch` create sufficient statistics out of nodal covariates:

- `nodeocov` creates a row regression effect;
- `nodeicov` creates a column regression effect;
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See the ergm manual for more details.

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Fitting logistic regression in ergm

```
summary(fit.ergm)
```

```
##
## ==========================
## Summary of model fit
## ==========================
##
## Formula:   netdat ~ edges + nodeocov("smoker") + nodeicov("smoker") + nodematch("male")
##     nodematch("smoker") + nodematch("program")
##
## Iterations:  5 out of 20
##
## Monte Carlo MLE Results:
##                    Estimate Std. Error MCMC %  p-value
## edges               -3.2122     0.2671      0  < 1e-04 ***
## nodeocov.smoker      0.2548     0.1882      0 0.176026
## nodeicov.smoker      0.2130     0.1881      0 0.257774
## nodematch.male       0.6930     0.2079      0 0.000889 ***
## nodematch.smoker     0.7983     0.1863      0  < 1e-04 ***
## nodematch.program    1.1030     0.1800      0  < 1e-04 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##      Null Deviance: 1375  on 992  degrees of freedom
##  Residual Deviance: 1292  on 986  degrees of freedom
##
## AIC: 1304    BIC: 1334    (Smaller is better.)
```

Goodness of fit

We fit this model without regard to its network structure:

- across sender heterogeneity/within sender correlation;
- across receiver heterogeneity/within receiver correlation;
- reciprocity/within dyad correlation.

It is possible that such patterns could be explained by covariates:

- heterogeneity in smoking leads to heterogeneity in degree;
- homophily for sex, smoking and group leads to reciprocity.

Let's examine this with a goodness of fit evaluation.

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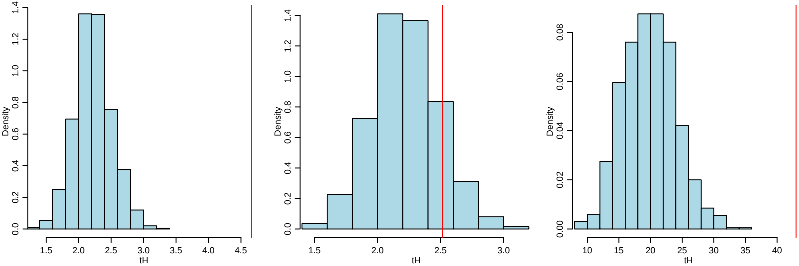
Goodness of fit

```
s.obs<-c(sd(rsum(Y7)),sd(csum(Y7)),mdyad(Y7))

py.hat<-fit.glm$fitted
s.SIM<-NULL
for(s in 1:S)
{
  Ysim<-matrix(NA,nrow(Y7),nrow(Y7))
  Ysim[!is.na(Y7)] <- rbinom(length(py.hat),1,py.hat)
  s.SIM<-rbind(s.SIM, c(sd(rsum(Ysim)),sd(csum(Ysim)),mdyad(Ysim)))

}
```



Goodness of fit

```
mean(s.SIM[,1]>=s.obs[1])

## [1] 0

mean(s.SIM[,2]>=s.obs[2])

## [1] 0.135

mean(s.SIM[,3]>=s.obs[3])

## [1] 0
```

Evaluation: These results indicate

- more outdgree heterogeneity than expected under the MLE;
- more reciprocity than expected;
- indegree heterogeneity is as expected.

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Evaluation: These results indicate

- more outdgree heterogeneity than expected under the MLE;
- more reciprocity than expected;
- indegree heterogeneity is as expected.

p_1 with covariates

This lack of fit can be addressed by adding statistics to the model:

```
fit.p1cov.1<-ergm( netdat ~ edges + sender + receiver + mutual +
             nodeocov("smoker") + nodeicov("smoker") +
             nodematch("male") + nodematch("smoker") + nodematch("program") )
```

```
## Error in which.package.InitFunction(fun):  could not find function
"findFunction"
```

```
summary(fit.p1cov.1)

## Error in summary(fit.p1cov.1):  object 'fit.p1cov.1' not found
```

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```
## Error in which.package.InitFunction(fun):  could not find function
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```

```
summary(fit.p1cov.1)

## Error in summary(fit.p1cov.1):  object 'fit.p1cov.1' not found
```

Regression terms

```
fit.p1cov.1$coef[-(1:(2*n))]

## Error in eval(expr, envir, enclos):  object 'fit.p1cov.1' not found
```

p_1 with alternative term order

```
fit.p1cov.2<-ergm(netdat ~
             nodeocov("smoker") + nodeicov("smoker") +
             nodematch("male") + nodematch("smoker") + nodematch("program") +
             edges + sender + receiver + mutual  )
```

```
## Error in which.package.InitFunction(fun):  could not find function
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```

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summary(fit.p1cov.2)

## Error in summary(fit.p1cov.2):  object ’fit.p1cov.2’ not found
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## Error in which.package.InitFunction(fun):  could not find function
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```

```
summary(fit.p1cov.2)

## Error in summary(fit.p1cov.2):  object 'fit.p1cov.2' not found
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Confounding

The problem is **confounding** between these effects and the sender and receiver effects.

To illustrate this issue, consider a simple model with just

- sender effects;
- one sender-specific covariate.

$$\Pr(Y_{i,j} = y_{i,j}) = \frac{e^{(\mu + a_i + \beta x_i) y_{i,j}}}{1 + e^{\mu + a_i + \beta x_i}}$$

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Confounding

The sufficient statistics can be found by summing the exponent over pairs:

$$\sum_{i \neq j} \mu y_{i,j} + a_i y_{i,j} + \beta x_i y_{i,j} = \mu y_{\cdot\cdot} + \sum_i a_i y_{i\cdot} + \beta \sum_i x_i y_{i\cdot}$$

Naively, the parameters and sufficient statistics are

$$\begin{aligned} \boldsymbol{\theta} &= (\mu, a_1, \ldots, a_n, \beta) \\ \mathbf{t}(\mathbf{y}) &= (y_{\cdot\cdot}, y_{1\cdot}, \ldots, y_{n\cdot}, \sum_i x_i y_{i\cdot}) \end{aligned}$$

Note that

1. $y_{\cdot\cdot}$ is a function of $y_{1\cdot}, \ldots, y_{n\cdot}$ (this leads to side conditions on the a_i's);
2. $\sum x_i y_{i\cdot}$ is a function of $y_{1\cdot}, \ldots, y_{n\cdot}$ (the x_i's are treated as "fixed").

This latter phenomenon means that β and the a_i's are not jointly estimable.

Confounding

Let's examine this more explicitly:

$$\begin{aligned}
\mathbf{t}(\mathbf{y}) \cdot \boldsymbol{\theta}(\mu, \mathbf{a}, \beta) &= \mu y_{\cdot\cdot} + \sum_i a_i y_{i\cdot} + \beta \sum_i x_i y_{i\cdot} \\
\mathbf{t}(\mathbf{y}) \cdot \boldsymbol{\theta}(\mu, \mathbf{a} - c\mathbf{x}, \beta + c) &= \mu y_{\cdot\cdot} + \sum (a_i - c x_i) y_{i\cdot} + (\beta + c) \sum x_i y_{i\cdot} \\
&= \mu y_{\cdot\cdot} + \sum a_i y_{i\cdot} + \beta \sum x_i y_{i\cdot} \\
&= \mathbf{t}(\mathbf{y}) \cdot \boldsymbol{\theta}(\mu, \mathbf{a}, \beta).
\end{aligned}$$

Nonidentifiability:

This result implies that for any two values of β, say β_1 and β_2, there are vectors $\mathbf{a}_1$ and $\mathbf{a}_2$ such that

$$l(\mu, \mathbf{a}_1, \beta_1 : \mathbf{y}) = l(\mu, \mathbf{a}_2, \beta_2 : \mathbf{y}).$$

The data information can't distinguish between $(\mu, \mathbf{a}_1, \beta_1)$ and $(\mu, \mathbf{a}_2, \beta_2)$.

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Modeling options

There are three commonly used methods of addressing this issue:

1. fit the model without sender and receiver effects;
2. fit the model without sender and receiver regressors;
3. use a random effects model.

We don't want to do 1 if the logistic regression model has been rejected.

We will fit the model in item 2, but use a two-stage procedure for estimating nodal covariate effects: For example,

- obtain $\hat{\theta} = (\hat{\mu}, \hat{\mathbf{a}})$;
- fit the regression model $\hat{a}_i = \beta x_i + \epsilon_i$.

This is an ad-hoc approximation to the random effects approach:

- Model $y_{i,j}$ as a function of a_i;
- Model a_i as a function of x_i

$$\begin{aligned} a_i &= \beta x_i + \epsilon_i \\ \{\epsilon_1, \ldots, \epsilon_n\} &\sim \text{i.i.d.normal}(0, \sigma_a^2) \end{aligned}$$

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- obtain $\hat{\boldsymbol{\theta}} = (\hat{\mu}, \hat{\mathbf{a}})$;
- fit the regression model $\hat{a}_i = \beta x_i + \epsilon_i$.

This is an ad-hoc approximation to the random effects approach:

- Model $y_{i,j}$ as a function of a_i;
- Model a_i as a function of x_i

$$a_i = \beta x_i + \epsilon_i$$

$$\{\epsilon_1, \ldots, \epsilon_n\} \sim \text{i.i.d.normal}(0, \sigma_a^2)$$

We will cover such models shortly.

Modeling options

There are three commonly used methods of addressing this issue:

1. fit the model without sender and receiver effects;
2. fit the model without sender and receiver regressors;
3. use a random effects model.

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$$\{\epsilon_1, \ldots, \epsilon_n\} \sim \text{i.i.d.normal}(0, \sigma_a^2)$$

We will cover such models shortly.

Dyadic covariates for *p*1

```
fit.p1cov.d<-ergm(netdat ~
       nodematch("male") + nodematch("smoker") + nodematch("program")  +
       edges + mutual + sender + receiver )
```

```
## Error in which.package.InitFunction(fun):  could not find function
"findFunction"
```

```
summary(fit.p1cov.d)

## Error in summary(fit.p1cov.d):  object 'fit.p1cov.d' not found
```

Extracting row and column effects

```
a.hat<-c(0,fit.p1cov.d$coef[4+(2:nrow(Y))] )

## Error in eval(expr, envir, enclos):  object 'fit.p1cov.d' not found

b.hat<-c(0,fit.p1cov.d$coef[4+ nrow(Y)-1 + (2:nrow(Y))]     )

## Error in eval(expr, envir, enclos):  object 'fit.p1cov.d' not found
```

```
## Error in xy.coords(x, y, xlabel, ylabel, log):  object 'a.hat' not found
## Error in xy.coords(x, y, xlabel, ylabel, log):  object 'b.hat' not found
## Error in plot(a.hat, b.hat):  object 'a.hat' not found
```

Nodal covariate effects

How does a covariate $\mathbf{x} = \{x_1, \ldots, x_n\}$ relate to

- outgoingness $(a_1, \ldots, a_n)$?
- popularity $(b_1, \ldots, b_n)$?

```
## Error in eval(expr, envir, enclos):  object 'a.hat' not found
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```
## Error in eval(expr, envir, enclos):  object 'a.hat' not found
## Error in eval(expr, envir, enclos):  object 'b.hat' not found
```

Statistical evaluation

```
lm(a.hat~xsmoke)

## Error in eval(expr, envir, enclos):  object 'a.hat' not found
```

The problem here is that $\hat{a}_i$ is $-\infty$ for nodes with zero outdegree.
What can we do?

0. give up;
1. remove the problematic observations;
2. replace the problematic observations with some large negative value;
3. fit a random effects model.

Item 1 removes information and biases the results:

- Zero degree nodes are highly informative about covariate effects.
- Their removal could bias the estimated effects towards zero.

Item 2 requires we can pick the “right” replacement value.

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Statistical evaluation

```r
lm(a.hat~xsmoke)

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Ad-hoc statistical evaluation

```
a.hat[a.hat == -Inf ] <- NA

## Error in a.hat[a.hat == -Inf] <- NA: object ’a.hat’ not found

b.hat[b.hat == -Inf ] <- NA

## Error in b.hat[b.hat == -Inf] <- NA: object ’b.hat’ not found

summary(glm(a.hat˜xsmoke))$coef

## Error in eval(expr, envir, enclos):  object ’a.hat’ not found

summary(glm(b.hat˜xsmoke))$coef

## Error in eval(expr, envir, enclos):  object ’b.hat’ not found
```

The results suggest that smoking doesn’t have a large effect on sender or receiver effects, and hence on outgoingness or popularity.

Ad-hoc statistical evaluation

However: What if

- all $-\infty$ a_i's corresponded to smokers?
- all $-\infty$ b_j's corresponded to nonsmokers?

Either possibility would suggest a estimating the parameter as further away from zero, making it "more significant."

```
xsmoke[is.na(a.hat)]

## Error in eval(expr, envir, enclos):  object 'a.hat' not found

xsmoke[is.na(b.hat)]

## Error in eval(expr, envir, enclos):  object 'b.hat' not found

mean(xsmoke)

## [1] 0.40625

mean(xsmoke[is.na(a.hat)])

## Error in mean(xsmoke[is.na(a.hat)]):  object 'a.hat' not found
```

These results don't give indications of strong relationships between smoking and the tendancy to send or receive ties.

Ad-hoc statistical evaluation

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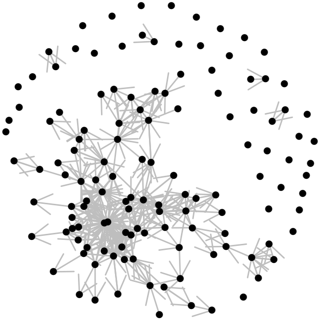
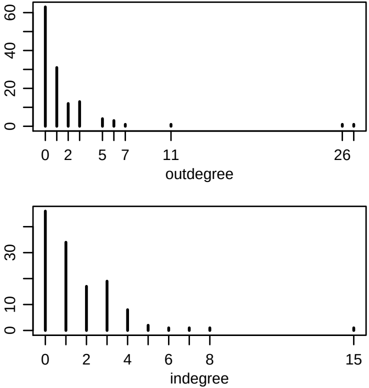
Conflict example





```
mdyad(Y)

## [1] 43

## expected value conditional on outdegree  WF p. 517
(sum(Y,na.rm=TRUE)^2 - sum( rsum(Y)^2) )/(2 *(nrow(Y)-1)^2 )

## [1] 1.178715
```

Network patterns

```
fit.0<-ergm( Y ~ edges  )

## Error in which.package.InitFunction(fun):  could not find function
"findFunction"

s.SIM0<-NULL
for(s in 1:S)
{
  Ysim<-as.matrix(simulate(fit.0))
  diag(Ysim)<-NA
  s.SIM0<-rbind(s.SIM0, c(sd(rsum(Ysim)),sd(csum(Ysim)),mdyad(Ysim)))
}

## Error in simulate(fit.0):  object 'fit.0' not found
```

```
## Error in hist.default(tH, xlim = xlim, main = "", prob = TRUE, col = ncol, :
'x' must be numeric
```

Covariate information

Additionally, we have the following covariates:

- Nodal covariates:
  - population
  - gdp
  - polity
- Dyad covariates:
  - exports
  - shared IGOs
  - geographic distance

Let's see if these covariates account for any of the network patterns.

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Let's see if these covariates account for any of the network patterns.

Coding covariates

It is common to log values of money, population and distance:

```
colnames(Xn)

## [1] "pop"    "gdp"    "polity"

Xn[,1:2]<-log(Xn[,1:2])
colnames(Xn)<-c("lpop","lgdp","polity")
netdat<-network(Y,vertex.attr=as.data.frame(Xn))
```

Dyad covariates enter into ergm via the edgecov function:

```
fit.cov.ergm<-ergm( netdat ~ edges +
   nodeocov("lpop")  +  nodeocov("lgdp")  + nodeocov("polity")  +
   nodeicov("lpop")  +  nodeicov("lgdp")  + nodeicov("polity")  +
 edgecov(Xpol) + edgecov(Xigo) + edgecov(Xldst) + edgecov(Xlexp) + edgecov(Xlimp))
```

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Dyad covariates enter into `ergm` via the `edgecov` function:

```
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 edgecov(Xpol) + edgecov(Xigo) + edgecov(Xldst) + edgecov(Xlexp) + edgecov(Xlimp))
```

Logistic regression fit

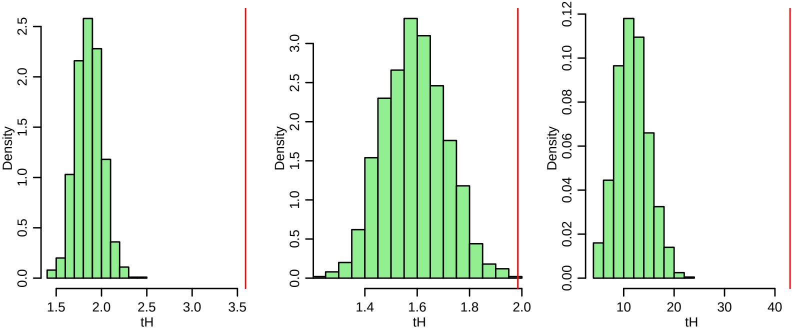
```
summary(fit.cov.ergm)

##
## ==========================
## Summary of model fit
## ==========================
##
## Formula:   netdat ~ edges + nodeocov("lpop") + nodeocov("lgdp") + nodeocov("polity") +
##     nodeicov("lpop") + nodeicov("lgdp") + nodeicov("polity") +
##     edgecov(Xpol) + edgecov(Xigo) + edgecov(Xldst) + edgecov(Xlexp) +
##     edgecov(Xlimp)
##
## Iterations:  9 out of 20
##
## Monte Carlo MLE Results:
##                   Estimate Std. Error MCMC %  p-value
## edges             -2.548601   0.362832      0  < 1e-04 ***
## nodeocov.lpop      0.204650   0.083405      0 0.014150 *
## nodeocov.lgdp      0.277993   0.080569      0 0.000561 ***
## nodeocov.polity   -0.081600   0.012262      0  < 1e-04 ***
## nodeicov.lpop      0.193615   0.083862      0 0.020970 *
## nodeicov.lgdp      0.171160   0.079843      0 0.032071 *
## nodeicov.polity   -0.037818   0.012390      0 0.002274 **
## edgecov.Xpol      -0.004510   0.001659      0 0.006551 **
## edgecov.Xigo      -0.011437   0.005592      0 0.040844 *
## edgecov.Xldst     -2.663417   0.142696      0  < 1e-04 ***
## edgecov.Xlexp      0.058343   0.426599      0 0.891219
## edgecov.Xlimp     -0.035318   0.428694      0 0.934341
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Goodness of fit evaluation

```
s.SIM<-NULL

for(s in 1:S)
{
  Ysim<-as.matrix(simulate(fit.cov.ergm))
  diag(Ysim)<-NA
  s.SIM<-rbind(s.SIM, c(sd(rsum(Ysim)),sd(csum(Ysim)),mdyad(Ysim)))
}
```



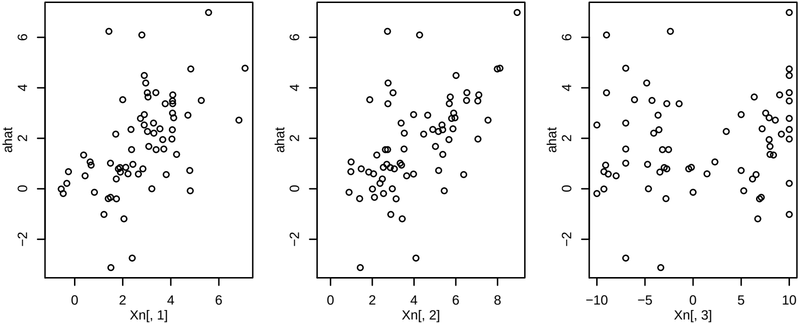
Improvement via covariates

```
## Error in hist.default(tH, xlim = xlim, main = "", prob = TRUE, col = ncol, :
'x' must be numeric
```

```r
fit.cov.ergm<-ergm( netdat ~ edges +
#   nodeocov("lpop")  +  nodeocov("lgdp")  + nodeocov("polity")  +
#   nodeicov("lpop")  +  nodeicov("lgdp")  + nodeicov("polity")  +
 sender + receiver + mutual +
 edgecov(Xpol) + edgecov(Xigo) + edgecov(Xldst) + edgecov(Xlexp) + edgecov(Xlimp))
```

```
## Observed statistic(s) sender2, sender3, sender7, sender9, sender10, sender11, sender12,
## Iteration 1 of at most 20:
## The log-likelihood improved by 0.9757
## Iteration 2 of at most 20:
## The log-likelihood improved by 1.004
## Iteration 3 of at most 20:
## The log-likelihood improved by 1.049
## Iteration 4 of at most 20:
## The log-likelihood improved by 0.9582
## Iteration 5 of at most 20:
## The log-likelihood improved by 0.9893
## Iteration 6 of at most 20:
## The log-likelihood improved by 0.8685
## Iteration 7 of at most 20:
## The log-likelihood improved by 1.025
## Iteration 8 of at most 20:
## The log-likelihood improved by 0.8937
## Iteration 9 of at most 20:
## The log-likelihood improved by 0.9246
## Iteration 10 of at most 20:
## The log-likelihood improved by 0.9991
## Iteration 11 of at most 20:
## The log-likelihood improved by 0.9405
## Iteration 12 of at most 20:
## The log-likelihood improved by 0.985
## Iteration 13 of at most 20:
```

```
ahat<-c(0,fit.cov.ergm$coef[1+(1:(nrow(Y)-1) )]  )
bhat<-c(0,fit.cov.ergm$coef[nrow(Y)+(1:(nrow(Y)-1) )] )
```



```
summary(lm(ahat[ahat> -Inf]~Xn[ahat> -Inf,]) )

##
## Call:
## lm(formula = ahat[ahat > -Inf] ~ Xn[ahat > -Inf, ])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.8238 -0.6376 -0.0533  0.5625  5.2171
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
```

Summary

- Covariates can be included in the ERGMs.
  - dyad level covariates: `nodematch`, `edgecov` and others;
  - node level covariates: `nodeocov`, `nodeicov` and others.
- Covariates can often partially explain degree heterogeneity and reciprocity.
- Node-level parameters are confounded with node-level covariate effects.
  - two stage approach: fit node-level parameters, and then relate to covariates;
  - random effects model: next lecture.

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