## Higher order patterns via factor models 567 Statistical analysis of social networks

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# Conflict data

Y<-conflict90s\$conflicts											
Xn<-confl	ict90s\$	nodeva	rs								
colnames(	Xn)										
## [1] "p	op"	"gdp"	"po	lity"							
Xn[,1:2]<	-log(Xn	1[,1:2]	)								
<pre>table(Y)</pre>											
## Y											
## 0	1	2	3	4	5	6	7	8			
## 16567	154	22	14	7	2	2	1	1			

# Dichotomized conflict data





#### SRM fit to ordinal data

```
#### nodal covariates only
fit_n<-ame(Y,Xrow=Xn,Xcol=Xn,model="ord",nscan=10000)</pre>
```

summary(fit\_n)

##

## beta:

```
##
         pmean psd z-stat p-val
## pop.row 0.256 0.121 2.114 0.034
## gdp.row -0.430 0.099 -4.334 0.000
## polity.row -0.014 0.017 -0.797 0.425
## pop.col 0.207 0.096 2.151 0.031
## gdp.col -0.371 0.078 -4.774 0.000
## polity.col -0.001 0.014 -0.062 0.950
##
## Sigma_ab pmean:
## a b
## a 1.134 0.801
## b 0.801 0.687
##
## rho pmean:
## 0.804
```

## SRM fit to ordinal data

plot(fit\_n)



```
gofstats
## function (Y)
## {
##
       sd.rowmean <- sd(rowMeans(Y, na.rm = TRUE), na.rm = TRUE)</pre>
##
       sd.colmean <- sd(colMeans(Y, na.rm = TRUE), na.rm = TRUE)</pre>
##
       dyad.dep <- cor(c(Y), c(t(Y)), use = "complete.obs")</pre>
       E <- Y - mean(Y, na.rm = TRUE)
##
##
       D <- 1 * (!is.na(E))
       E[is.na(E)] <- 0
##
       triad.dep <- sum(diag(E %*% E %*% E))/(sum(diag(D %*% D %*%
##
##
           D)) * sd(c(Y), na.rm = TRUE)^3)
       gof <- c(sd.rowmean, sd.colmean, dyad.dep, triad.dep)</pre>
##
##
       names(gof) <- c("sd.rowmean", "sd.colmean", "dyad.dep", "triad.dep")</pre>
##
       gof
## }
## <environment: namespace:amen>
```

Let  $\mathbf{E} = (\mathbf{Y} - \mathbf{11}^T \bar{y}_{..})/s_y$ , that is,  $e_{i,j} = (y_{i,j} - \bar{y}_{..})/s_y$ .

- $\overline{y}_{\cdots}$  is the grand mean;
- $s_y$  is the sample standard deviation of the  $y_{i,j}$ 's
- $e_{i,j}$  is like a "scaled residual" from the simple mean model  $y_{i,j} = \mu + \epsilon_{i,j}$ .

The sum of the diagonal of  $E^3$  gives the scaled third-order moment:

$$\mathsf{trace}(\mathsf{E}^3) = \sum_i \sum_j \sum_k e_{i,j} e_{j,k} e_{k,i}$$

$$t(\mathbf{Y}) = \frac{\sum_{i} \sum_{j} \sum_{k} e_{i,j} e_{j,k} e_{i,j}}{\# \text{ of ordered triads}}$$

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## Triad dependence and transitivity

#### This triadic dependence measure is related to transitivity for binary data:

**Transitive triple:** An ordered triple (i, j, k) is transitive if  $i \rightarrow j \rightarrow k \rightarrow i$   $(y_{i,j} = y_{j,k} = y_{k,i})$ .

$$trans(\mathbf{Y}) = \sum_{i} \sum_{j} \sum_{k} y_{i,j} y_{j,k} y_{k,i}$$

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#### SRM fit to ordinal data with dyadic covariates

##### dyadic and nodal covariates
fit\_dn<-ame(Y,Xdyad=Xd,Xrow=Xn,Xcol=Xn,model="ord",nscan=10000)</pre>

summary(fit\_dn)

##					
##	beta:				
##		pmean	psd	z-stat	p-val
##	pop.row	0.212	0.095	2.230	0.026
##	gdp.row	0.077	0.078	0.992	0.321
##	polity.row	-0.028	0.013	-2.045	0.041
##	pop.col	0.205	0.092	2.232	0.026
##	gdp.col	-0.029	0.078	-0.376	0.707
##	polity.col	0.002	0.012	0.130	0.896
##	<pre>polity_int.dyad</pre>	-0.003	0.001	-2.419	0.016
##	imports.dyad	-0.142	0.100	-1.415	0.157
##	shared_igos.dyad	-0.017	0.005	-3.383	0.001
##	distance.dyad	-1.837	0.101	-18.244	0.000
##					
##	Sigma_ab pmean:				
##	a b				
##	a 0.500 0.332				
##	b 0.332 0.462				
##					
##	rho pmean:				
##	0.566				

## SRM fit to ordinal data with dyadic covariates

plot(fit\_dn)



# GOF comparison



#### Adding these dyadic covariates improved the fit with regard to $t(\mathbf{Y})$ .

Note that each of these dyadic covariates was a function of nodal covariates:

- $x_{i,j,1} = f_1(\text{polity}_i, \text{polity}_j)$
- $x_{i,j,2} = f_2(igo_i, igo_j)$
- $x_{i,j,3} = f_3(\text{location}_i, \text{location}_j)$

This suggests models of the form

$$y_{i,j} \sim \beta_0 + \beta_1 x_{i,j}$$
  
 $x_{i,j} = s(x_i, x_j)$ 

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More generally, let

- $u_i$  be a covariate of *i* as a sender of ties;
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 $y_{i,j} \sim \beta_0 + \beta_1 \times s(u_i, v_j)$ 

Such a model can describe various types of higher-order dependence, including transitivity

stochastic equivalence

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Homophily on covariates can explain transitivity:

$$y_{i,j} \sim \beta_0 + \beta_1 \times s(x_i, x_j)$$

If  $\beta_1 > 0$  and the  $y_{i,j}$ 's are binary, then

- $y_{i,j} = 1 \Rightarrow x_i \approx x_j;$
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- $x_i \approx x_j, \ x_i \approx x_k \Rightarrow x_j \approx x_k.$
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#### Stochastic equivalence

Returning to the more general model:

$$y_{i,j} \sim \beta_0 + \beta_1 \times s(u_i, v_j)$$

If  $u_i = u_k$  then *i* and *j* are equivalent as senders in terms of the model.

**Example:** Logistic regression

$$\Pr(Y_{i,j} = 1) = \frac{e^{\beta_0 + \beta_1 s(u_i, v_j)}}{1 + e^{\beta_0 + \beta_1 s(u_i, v_j)}}$$

If  $u_i = u_k = u$ , then

$$\Pr(Y_{i,j} = 1) = \frac{e^{\beta_0 + \beta_1 s(u_i, v_j)}}{1 + e^{\beta_0 + \beta_1 s(u_i, v_j)}} = \Pr(Y_{k,j} = 1),$$

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# In our hypothetical model of social relations, we've seen how nodal characteristics relate to homophily and stochastic equivalence.

Homophily: Similar nodes link to each other

- "similar" in terms of characteristics (potentially unobserved)
- homophily leads to transitive or clustered social networks
- observed transitivity may be due to exogenous or endogenous factors

(See Shalizi and Thomas 2010 for a more careful discussion

Stochastic equivalence: Similar nodes have similar relational patterns

- similar nodes may or may not link to each other.
- equivalent nodes can be thought of as having the same "role"

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## Visualizing stochastic equivalence



For which network is homophily a plausible explanation?

Which network exhibits a large degree of stochastic equivalence?

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- AddHealth friendships: friendships among 247 12th-graders
- Word neighbors in Genesis: neighboring occurrences among 158 words
- Protein binding interactions: binding patterns among 230 proteins



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Homophily and stochastic equivalence from unobserved variables can be represented with a latent factor model:

$$y_{i,j} \sim \boldsymbol{u}_i^T \boldsymbol{\mathsf{D}} \boldsymbol{v}_j,$$

- **u**<sub>i</sub> is a vector of latent factors describing *i* as a sender of ties;
- $v_i$  is a vector of latent factors describing j as a receiver of ties;
- D is a diagonal matrix of factor weights.

Normal, binomial, ordinal data can be represented with this structure as follows:

$$z_{i,j} = \boldsymbol{u}_i^T \mathbf{D} \boldsymbol{v}_j + \epsilon_{i,j}$$
$$y_{i,j} = g(z_{i,j})$$

- g(z) = z for normal data;
- g(z) = 1(z > 0) for binomial data;
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$$y_{i,j} \sim \boldsymbol{u}_i^T \boldsymbol{\mathsf{D}} \boldsymbol{v}_j,$$

- **u**<sub>i</sub> is a vector of latent factors describing *i* as a sender of ties;
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- D is a diagonal matrix of factor weights.

Normal, binomial, ordinal data can be represented with this structure as follows:

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$$\begin{aligned} f_{i,j} &= \mathbf{u}_i^T \mathbf{D} \mathbf{v}_j + \epsilon_{i,j} \\ &= \sum_{r=1}^R d_r u_{i,r} v_{j,r} + \epsilon_{i,j} \end{aligned}$$

For example, in a 2 factor model, we have

$$z_{i,j} = d_1(u_{i,1} \times v_{j,1}) + d_2(u_{i,2} \times v_{j,2}) + \epsilon_{i,j}$$

- $u_i \approx u_j$ : similarity of latent factors implies approximate stoch equivalence;
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## Matrix decomposition interpretation

Recall from linear algebra:

• Every  $m \times n$  matrix **Z** can be written

## $\bm{Z} = \bm{U}\bm{D}\bm{V}^{T}$

where  $\mathbf{D} = \text{diag}(d_1, \ldots, d_n)$ ,  $\mathbf{U}$  and  $\mathbf{V}$  are orthonormal.

 $\hat{\mathsf{Z}}_k \equiv \mathsf{U}_{[,1:k]}\mathsf{D}_{[1:k,1:k]}\mathsf{V}_{[,1:k]}^T$ 

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# Least squares matrix approximations


Probit version of the symmetric latent factor model:

 $\begin{array}{lll} y_{i,j} &=& g(z_{i,j}) \;, & \text{where } g \text{ is a nondecreasing function} \\ z_{i,j} &=& \mathbf{u}_i^T \Lambda \mathbf{u}_j + \epsilon_{i,j} \;, & \text{where } \mathbf{u}_i \in \mathbb{R}^K \;, \; \Lambda = \text{diag}(\lambda_1, \ldots, \lambda_K) \\ \{\epsilon_{i,j}\} &\stackrel{iid}{\sim} & \text{normal}(0, 1) \end{array}$ 

Writing  $\{z_{i,j}\}$  as a matrix ,

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## Least squares approximations of increasing rank



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$$z_{i,j} = \mathbf{u}_i^T \mathbf{\Lambda} \mathbf{u}_j + \epsilon_{i,j}$$
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For example, in a rank-2 model, we have

$$z_{i,j} = \lambda_1(\mathbf{u}_{i,1} \times \mathbf{u}_{j,1}) + \lambda_2(\mathbf{u}_{i,2} \times \mathbf{u}_{j,2}) + \epsilon_{i,j}$$

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- λ<sub>r</sub> > 0: positive eigenvalues represent homophily;
- λ<sub>r</sub> < 0: negative eigenvalues represent antihomophily.</li>

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$$z_{i,j} = \lambda_1(u_{i,1} \times u_{j,1}) + \lambda_2(u_{i,2} \times u_{j,2}) + \epsilon_{i,j}$$

Interpretation

- $u_{i,r} \approx u_{j,r}$ : equality of latent factors; represents stochastic equivalence;
- $\lambda_r > 0$ : positive eigenvalues represent homophily;

•  $\lambda_r < 0$ : negative eigenvalues represent antihomophily.

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#### Returning to directed relations:

**SRM:** We have motivated the SRM in order to represent 2nd order dependence:

- within row dependence, within column dependence;
- within dyad dependence.

$$z_{i,j} = \beta^T x_{i,j} + a_i + b_j + \epsilon_{i,j}$$
$$y_{i,j} = g(z_{i,j})$$

This model is made up of additive random effects.

**LFM:** We have motivated the LFM to model more complex structures:

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Combining them gives an additive and multiplicative effects model

$$z_{i,j} = \beta^T x_{i,j} + a_i + b_j + \boldsymbol{u}_i^T \mathbf{D} \boldsymbol{v}_j + \epsilon_{i,j}$$
  
$$y_{i,j} = \boldsymbol{g}(z_{i,j})$$

ame(Y, Xdyad=NULL, Xrow=NULL, Xcol=NULL, rvar = !(model=="rrl") , cvar = TRUE, dcor = TRUE, R = 0, model="nrm",...)

Arguments:

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Y: an n x n square relational matrix of relations. See model below for various data types.

Xdyad: an n x n x pd array of covariates

Xrow: an n x pr matrix of nodal row covariates

Xcol: an n x pc matrix of nodal column covariates

rvar: logical: fit row random effects?

cvar: logical: fit column random effects?

dcor: logical: fit a dyadic correlation?

- R: integer: dimension of the multiplicative effects (can be zero)
- model: character: one of "nrm","bin","ord","cbin","frn","rrl" see

#### AME fit to ordinal data with nodal covariates

```
#### nodal covariates and latent factors
fit_nr2<-ame(Y,Xrow=Xn,Xcol=Xn,R=2,model="ord",nscan=10000)</pre>
```

summary(fit\_nr2)

##

## beta:

```
##
         pmean psd z-stat p-val
## pop.row 0.236 0.101 2.329 0.020
## gdp.row -0.092 0.179 -0.516 0.606
## polity.row -0.030 0.015 -2.057 0.040
## pop.col 0.243 0.087 2.783 0.005
## gdp.col -0.173 0.136 -1.267 0.205
## polity.col -0.009 0.013 -0.652 0.515
##
## Sigma_ab pmean:
## a b
## a 0.307 0.167
## b 0.167 0.206
##
## rho pmean:
## 0.838
```

# GOF comparison



### Plots of latent factors

circplot(Y,fit\_nr2\$U,fit\_nr2\$V)



### A blockmodel is

- a partition of the nodes into classes;
- an estimation of the rate of ties between and within classes.

Such a model includes

- a classification function c : {1,...,n} → {1,...,K},
   i.e. c<sub>i</sub> = k means i is in block/group k.
- a between-group tie density matrix:

$$\boldsymbol{\vartheta} = \begin{pmatrix} \theta_{11} & \cdots & \theta_{1K} \\ \vdots & \vdots & \vdots \\ \theta_{K1} & \cdots & \theta_{KK} \end{pmatrix}$$

Under this model,

$$\Pr(Y_{i,j}=1) = \theta_{c_i,c_j}$$

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The blockmodel is a model of the form we've been discussing:

$$y_{i,j} \sim \beta_0 + \beta_1 s(x_i, x_j)$$

#### Let

- $\beta_0 = 0$ ,  $\beta_1 = 1$ ;
- $x_i = c_i, x_j = c_j;$
- $s(x_i, x_j) = \theta_{c_i, c_j}$

#### Stochastic equivalence:

All nodes within the same block are stochastically equivalent, under this model.

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#### Consider the task of identifying stochastically equivalent classes from the data.

In the simplest case of an undirected binary relation, we want to find latent classes  $c_1, \ldots, c_n \in \{1, \ldots, K\}$ ; between-class rates  $\Theta = \{\theta_{k,l} : 1 \le k, l \le K\}$ 

that make the probability of our data large:

$$\mathsf{Pr}(\mathbf{Y} = \mathbf{y} | \boldsymbol{c}, \Theta) = \prod_{i \neq j} heta_{c_i, c_j}^{y_{i, j}} (1 - heta_{c_i, c_j})^{1 - y_{i, j}}$$
 $= \prod_{k=1}^{K} \prod_{l=1}^{K} heta_{k, l}^{s_{k, l}} (1 - heta_{k, l})^{n_{k, l} - s_{k, l}},$ 

where

•  $n_{k,l}$  = number of pairs (i, j) for which  $c_i = k$  and  $c_i = l$ 

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- EM algorithm
- Gibbs sampling/MCMC

The basic model can be extended in various ways:

- covariates/regressors;
- directed data
  - dyadic correlation;
  - separate sender and receiver classes.

Much of this was done in Nowicki and Snijders (2001).

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## Stochastic blockmodel for Cold War data

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A three-class model gives the following inferred classes:

```
rownames(Y)[latentclass==1]
## [1] "CHN" "IRN" "IRQ" "PRK" "USR"
rownames(Y)[latentclass==2]
## [1] "AUL" "CAN" "GFR" "ITA" "NEW" "NOR" "NTH" "PHI" "ROK" "THI" "TUR"
## [12] "UKG" "USA"
```

and everyone else in class 3, with the following between-class means:

round(M,2) ## [,1] [,2] [,3] ## [1,] 0.02 -0.89 0.50 ## [2,] -0.89 4.47 1.07 ## [3,] 0.50 1.07 0.86

These rates are on the probit scale (recall the data are ordinal).

Latent class for Cold War data



#### The essential feature of the blockmodel is the representation

 $y_{i,j} \sim \theta_{c_i,c_j}$ 

#### where

- c<sub>i</sub>, c<sub>j</sub> are unobserved latent class variables;
- Θ is a matrix of between-class intensities.

This model structure can be expressed in matrix form as follows:

$$\theta_{c_i,c_j} = \boldsymbol{u}_i^T \boldsymbol{\Theta} \boldsymbol{u}_j,$$

where

- $u_i$  is a  $K \times 1$  vector of all 0s except  $u_i[c_i] = 1$ ;
- $\Theta$  is the  $K \times K$  matrix of between class intensities.

$$\begin{pmatrix} 0 & 0 & 1 \end{pmatrix} \begin{pmatrix} \theta_{11} & \theta_{12} & \theta_{13} \\ \theta_{21} & \theta_{22} & \theta_{23} \\ \theta_{31} & \theta_{32} & \theta_{33} \end{pmatrix} \begin{pmatrix} 1 \\ 0 \\ 0 \end{pmatrix} = \theta_{31}$$

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### Features of real datasets:

- third-order triadic dependence;
- groups of nodes with similar roles.

# **Explanations of features:**

- homophily on covariates can generate triadic dependence;
- stochastic equivalence can generate groups of similar nodes;
- both features can be represented by the "model"  $y_{i,j} \sim \beta_0 + \beta_1 imes s(u_i, v_j)$

- Generate derived dyadic variables  $s(u_i, v_j)$  from nodal covariates  $u_i, v_j$ .
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