Auto-Logistic Actor Attribute Models (ALAAMs) INSNA Sunbelt XLV Paris 2025

Johan Koskinen

Department of Statistics Stockholm University University of Melbourne

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Koskinen Sunbelt XLV ALAAM June 22, 2025 1/83

Preamble

 All material is on the workshop repository https://github.com/johankoskinen/ALAAM

- Download the RMarkdown file CHDH-SNA-2025-2.Rmd rename ALAAM-INSNA-XVL and update
- Download the (proto) manual https: //github.com/johankoskinen/ALAAM/blob/main/alaam_effects.pdf
- ► This afternoon CHDH-SNA-2025-3.Rmd and a selection of other examples maybe merge ALAAMINSNAXVL
- In order to run the Markdown you need
 - ▶ The R-package ■
 - ► The RStudio interface R Studio
- We will predominantly use the packages
 - sna
 - network
- as well as balaam. R from GitHub



2 / 83

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What is new

If you have used BayesALAAM before

- Entirely new
 - ► MultivarALAAM.R ⇒ balaam.R
 - ▶ Documentation: alaam_effects.pdf
- Define and estimate the model using
 - ▶ Standard formula agree \sim odegree + mood + sex + simple
 - ▶ Main function estimate.alaam returns estimate.alaam.obj
- The object prevBayes
 - ▶ Continue previous estimation estimate.alaam.obj
 - recalibrate the proposal variance-covariance matrix
- Model selection
 - ▶ Obtain posterior deviance from post.deviance.alaam applied on estimate.alaam.obj
 - Calculate DIC using alaam.dic directly on object returned by post.deviance.alaam
- ... and a lot of other tweaks that may or may not have broken the functionality

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Agenda



- Data
- Homophily
- ALAAM
- Contagion
- Estimation
 - Monitoring performance
- GOF
- 5 Model selection
- 6 Missing data

 - Interactions
 - SBC
 - Fully Bayesian
- 9 HALAAM
- 10 Further topics



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Data structure and homophily

Data structure and homophily



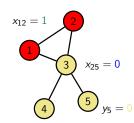
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Data - binary outcomes

Tie-variables:

$$X_{ij} = \begin{cases} 1, & \text{if tie from } i \text{ to } j \\ 0, & \text{else} \end{cases}$$

$$y_2 = 1$$



Adjacency matrix

$$\mathbf{X} = (X_{ij})_{ij \in V \times V} = \begin{vmatrix} \cdot & 1 & 1 & 0 & 0 \\ 1 & \cdot & 1 & 0 & 0 \\ 1 & 1 & \cdot & 1 & 1 \\ 0 & 0 & 1 & \cdot & 0 \\ 0 & 0 & 1 & 0 & \cdot \end{vmatrix}$$

Nodes: $V = \{1, 2, \dots, n\}$ Attribute vector

$$oldsymbol{y} = egin{bmatrix} \mathbf{1} & \mathbf{1} & \mathbf{0} & \mathbf{0} & \mathbf{0} \end{bmatrix}^{ op}$$



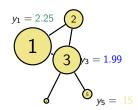
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Data - Continuous outcomes

Tie-variables:

$$X_{ij} = \begin{cases} 1, & \text{if tie from } i \text{ to } j \\ 0, & \text{else} \end{cases}$$

$y_2 = 1$



Adjacency matrix

$$\mathbf{X} = = egin{bmatrix} \cdot & 1 & 1 & 0 & 0 \ 1 & \cdot & 1 & 0 & 0 \ 1 & 1 & \cdot & 1 & 1 \ 0 & 0 & 1 & \cdot & 0 \ 0 & 0 & 1 & 0 & \cdot \end{bmatrix}$$

Nodes: $V = \{1, 2, ..., n\}$

Attribute vector

$$y = \begin{bmatrix} 2.25 & 1 & 1.99 & .05 & .15 \end{bmatrix}^{\mathsf{T}}$$



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Homophily





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Homophily - empirical evidence

We repeatedly **observe** that people that are *similar* hang together





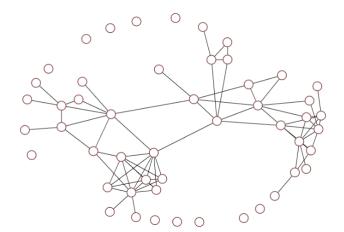






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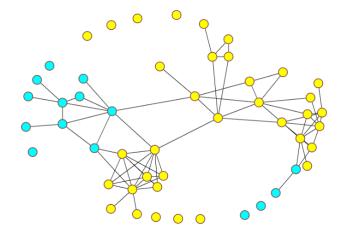
Yuval Kalish - school kids Israel (1)





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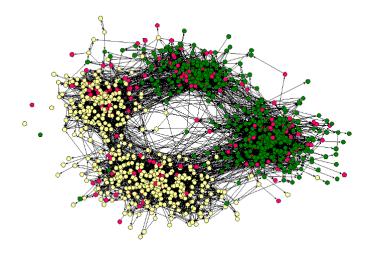
Yuval Kalish - school kids Israel (2)





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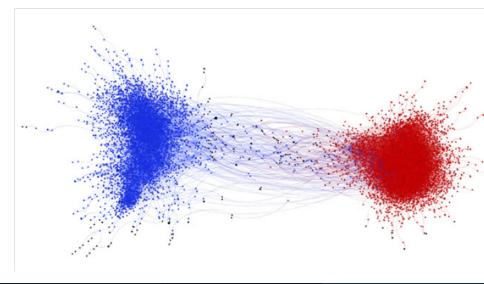
Ad Health - school kids of different races (Moody et al)





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Democrats and Republicans on twitter (Brady et al., 2017)

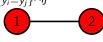


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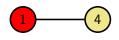
Homophily

Hanging together, being similar



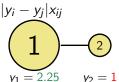


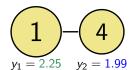
$$y_1 = 1$$
 $y_2 = 1$



$$y_1 = 1$$
 $y_2 = 0$

Continuous Y_i :







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Correlations of continuous outcomes (1)

Correlation for variables U and V:

$$corr(U, V) = \frac{\sum_{i=1}^{n} (u_i - \bar{u})(v_i - \bar{v})}{\sqrt{\sum_{i=1}^{n} (u_i - \bar{u})^2 \sum_{i=1}^{n} (v_i - \bar{v})^2}}$$

For network correlation we only need associations

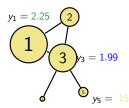
$$(y_i - \bar{y})(y_i - \bar{y})$$

Between i and i that are connected, i.e.

$$x_{ij} = 1$$



$$y_2 = 1$$



Nodes:
$$V = \{1, 2, ..., n\}$$

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Correlations of continuous outcomes (2)

$y_2 = 1$ $y_1 = 2.25$ $y_2 = 1$ $y_3 = 1.99$ $y_5 = .15$

Nodes: $V = \{1, 2, ..., n\}$

Moran's I:

$$I_k = \frac{n \sum_{i=1}^n \sum_{j=1}^n (y_i - \bar{y})(y_j - \bar{y}) x_{ij}^{(k)}}{\sum_{i,j} x_{ij}^{(k)} \sum_{j=1} y_j^2}$$

Where

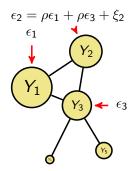
$$x_{ij}^{(1)} = x_{ij}$$

and $x_{ij}^{(2)}$ if i and j are at a distance of 2, etc If I_1, I_2, \ldots are large, neighbouring nodes have similar values



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Network autocorrelation model



The Network autocorrelation model:

$$Y_i = \beta_0 + \beta_1 x_{i1} + \cdots + \beta_k x_{ik} + \epsilon_i$$

assumes a linear model where there is autocorrelation between the errors

$$\epsilon_i = \rho \sum_{i=1}^n w_{ij} \epsilon_j + \xi_i, \ \xi_i \stackrel{iid}{\sim} N(0, \sigma^2)$$

where w_{ii} is either x_{ii} or a scaled version of it **Nodes**: $V = \{1, 2, ..., n\}$ **Note**: if $\rho = 0$, we have regular regression with independent observations



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Network effects model

$Y_2 = \rho Y_1 + \rho Y_2 + \epsilon_2$ Y_1 Y_3 Y_3

Nodes:
$$V = \{1, 2, ..., n\}$$

The **Network effects model**:

$$Y_i = \rho \sum_{j=1}^n w_{ij} Y_j + \beta_0 + \beta_1 x_{i1} + \dots + \beta_k x_{ik} + \epsilon_i$$

where w_{ij} is either x_{ij} or a scaled version of it, assumes a non-linear model where there is autocorrelation between the outcomes. Errors are assumed independent

$$\epsilon_i \stackrel{iid}{\sim} N(0, \sigma^2)$$

Note: if $\rho = 0$, we have regular regression with independent observations

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ALAAM - The basic model

The Model



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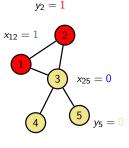
Data - binary outcomes

We want to model binary Attribute vector

$$oldsymbol{y} = egin{bmatrix} \mathbf{1} & \mathbf{1} & \mathbf{0} & \mathbf{0} & \mathbf{0} \end{bmatrix}^{ op}$$

conditional on Adjacency matrix

$$\mathbf{X} = egin{bmatrix} \cdot & 1 & 1 & 0 & 0 \ 1 & \cdot & 1 & 0 & 0 \ 1 & 1 & \cdot & 1 & 1 \ 0 & 0 & 1 & \cdot & 0 \ 0 & 0 & 1 & 0 & \cdot \end{bmatrix}$$



Marginally, we can think of modelling the probabilities

$$p_i = \mathbb{E}(Y_i \mid \mathbf{X}) = \Pr(Y_i = 1 \mid \mathbf{X})$$



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Logit: Log-odds

Odds

For a probability p, we define the odds as

$$\frac{p}{1-p}$$
.

which is always positive, and increases with p (e.g. $\frac{0.9}{0.1} > \frac{0.5}{0.5} > \frac{0.1}{0.9} > 0$)

Logit

The logarithm of the odds, the log odds, is called logit

$$\operatorname{logit}(p) = \log\left(\frac{p}{1-p}\right)$$

which is increases with p but logit(p) takes all values in $\mathbb R$

ln ₽sw^r

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The logit maps probabilities to all values in $\mathbb R$

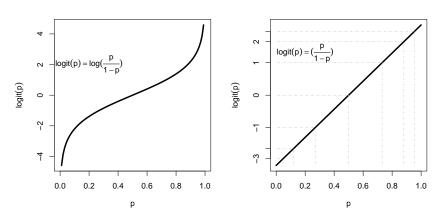


Figure: Probabilities against logit function. Logit scale on vertical axis (right)



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Logit link function and linear predictors

While

$$0 \le p \le 1$$

as $logit(p) \in \mathbb{R}$, we write

$$\operatorname{logit}(p_i) = \eta_i$$

where η_i is the linear predictor

$$\eta_i = \beta_0 + \beta_1 x_{i1} + \dots + \beta_k x_{ik}$$

which is a linear regression



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The logit-link function

For any x_{i1}, \ldots, x_{ik} , and parameters $\beta_0, \beta_1, \ldots, \beta_k$, we can calculate

$$\eta_i = \beta_0 + \beta_1 x_{i1} + \dots + \beta_k x_{ik}$$

and use the inverse logit

$$\eta_i = \underbrace{\log\left(rac{p_i}{1-p_i}
ight)}_{logit} \quad \overset{\Rightarrow}{\underset{\mathsf{solve for } p_i}{\Rightarrow}} \quad p_i = \underbrace{rac{e^{\eta_i}}{1+e^{\eta_i}}}_{\mathsf{inverse logit}}$$

to calculate the probability p_i

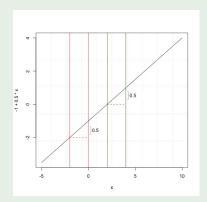


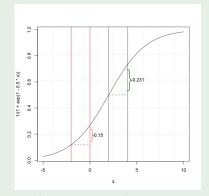
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Probabilities and the linear predictor: non-linearity

Example (Hypothetical example)

Assume logit $[E(Y \mid x)] = \eta$, where $\eta = -1 + 0.5x$





$$\eta_1 - \eta_0 = \beta_1(x_1 - x_0)$$
, but $logit^{-1}(\eta_1) - logit^{-1}(\eta_0)$

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Binary outcomes

We want to model

$$p_i = \Pr(Y_i = 1 \mid \mathbf{X})$$

and if the Y_i are independent

$$p(\mathbf{y} \mid \mathbf{X}) = \prod_{i=1}^{n} \Pr(Y_i = y_i \mid \mathbf{X})$$

where for each $i = 1, \ldots, n$

$$\mathsf{Pr}(Y_i = 1 \mid \mathbf{X}) = \frac{e^{\eta_i}}{1 + e^{\eta_i}}$$



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Auto-Logistic Actor Attribute Model (ALAAM)

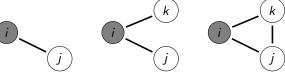
What if we let $Pr(Y_i = 1 | \mathbf{X})$ depend on i's position in the network? For example

$$\eta_i = \beta_0 + \beta_{\text{deg}} \sum_j x_{ij} + \beta_{\text{var}} \sum_{j,k} x_{ij} x_{ik} + \beta_{\text{tri}} \sum_{j,k} x_{ij} x_{ik} x_{jk}$$

which gives us a model

$$p(y \mid \mathbf{X}) = \exp\left\{oldsymbol{eta}^{ op} z(y, \mathbf{X}) - \psi(oldsymbol{eta})
ight\}$$

where $z(y, \mathbf{X}) = (z_1, \dots, z_p)^{\top}$, $z_1 = \sum y_i$, and



$$z_2 = \sum_i y_i x_{i+}$$
 $z_3 = \sum_i y_i \sum_{j,k} x_{ij} x_{ik}$ $z_4 = \sum_i y_i \sum_{j,k} x_{ij} x_{ik} x_{jk}$



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Auto-Logistic Actor Attribute Model (ALAAM)

If $eta_{
m deg}>0$ then nodes with high degree centrality are more likely to have $y_i=1$ than nodes with low degree



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The network activity ALAAM

Frank and Strauss (1986) derived an ERGM for interdependent network ties from a Markov dependence assumption. For attributes:

Markov dependence assumption (Robins et al., 2001)

Considering the collection of variables $\mathbf{M} = (y, \mathbf{X})$ Let variables M_u and M_v be conditionally independent if $u \cap v = \emptyset$

Example (Conditionally dependent variables)

The outcomes Y_i and X_{ij} are conditionally dependent as $\{i\} \cap \{i,j\} = \{i\}$

Example (Conditionally independent variables)

The outcomes Y_i and X_{kj} are conditionally independent as $\{i\} \cap \{i,j\} = \emptyset$



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Deriving model from dependence (as in ERGM)

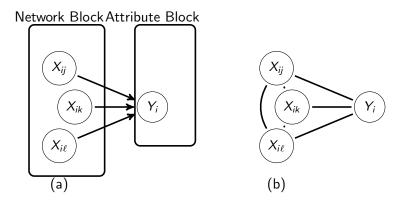


Figure: Dependence graph (a) and Moral graph (b) of network activity dependence model (Robins et al., 2001)

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 June 22, 2025
 30 / 83

The network activity ALAAM

The statistics z_r correspond to cliques in the Moral graph, and includes

- intercept: $\sum y_i$
- degree: $\sum y_i \sum_i x_{ij}$
- stars: $\sum y_i \sum x_{ij_1} \cdots x_{ij_k}$

But crucially, no statistics of the type

$$y_i y_j x_{ij}$$

and thus Y_i and Y_j are independent given **X**

$$\Pr(Y_i = y_i, Y_j = y_j \mid \mathbf{X}, \boldsymbol{y}_{-i,j}) = \Pr(Y_i = y_i \mid \mathbf{X}, \boldsymbol{y}_{-i,j}) \Pr(Y_j = y_j \mid \mathbf{X}, \boldsymbol{y}_{-i,j})$$



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The network activity ALAAM - logistic regression

The network activity ALAAM is equivalent to logistic regression with

$$logit(p_i) = \beta_0 + \beta_1 z_{i1} + \dots + \beta_1 z_{ip}$$

where the statistics z_{ih} are summaries of i's network position



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The network activity ALAAM - logistic regression

Example (Modern contraceptive use in rural Kenya)

	Mean	Description		
mcUse	0.35	Do you use modern contraceptive (MC)		
		techniques?		
Age	34.41	Age (sd:16.04)		
Female	0.60	Female (1) or Male (0)		
HasChildren	0.68	Have one child or more		
relevan Others Approve	0.45	Other people's approval is important		
relevan Others Use	0.67	I care if other people use MC		
mcUseConflict	0.68	The use of MC is contentious and causes		
		conflict		
numFriends	0.88	Tallied: the number of names of people		
		they spend their free time with		

Table: Variables in Kenya study on Modern contraception usage (Not exact question wordings)(NSF-CMMI-2005661). Modi, Koskinen, DeChurch, Contractor, 2025, SocNet

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The network activity ALAAM - logistic regression

Example (Modern contraceptive use in rural Kenya (cont.)n = 1303)

Estimated logistic regression

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-0.6340	0.2601	-2.44	0.0148
Age	-0.0554	0.0067	-8.24	0.0000
Female	-1.0232	0.1538	-6.65	0.0000
HasChildren	1.9622	0.2068	9.49	0.0000
relevan Others Approve	1.4696	0.1514	9.70	0.0000
relevan Others Use	0.3415	0.1720	1.99	0.0471
mcUseConflict	-0.3835	0.1474	-2.60	0.0093
numFriends	0.3349	0.0828	4.04	0.0001

How much is the increase in the probability of mcUse if you acquire another friend?

34 / 83

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How account for dependencies through the network

Intuitively¹, we would want the response of i and j not to be independent

$$\Pr(Y_i = 1, Y_j = 1 \mid Y_{-ij}) \neq \Pr(Y_i = 1 \mid Y_{-ij}) \Pr(Y_j = 1 \mid Y_{-ij})$$

If there is a tie from i to j, $x_{ij} = 1$. Suggesting a statistic

$$\sum_{i=1}^{n} \underbrace{y_i}_{\text{your succes}} \underbrace{\sum_{j \neq i} y_j x_{ij}}_{\text{\sharp successful friends}}$$



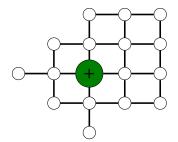
35 / 83

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¹And this is what Robins et al., 2001, did

Ising model (Besag, 1972)

Probability spin $+ \approx \sharp$ neighbours $j \in N(i)$ with spin +



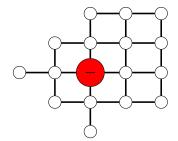
$$\Pr(Y_i = 1 | Y_{N(i)} = y_{N(i)}) \propto \exp\{\theta_1 + \theta_2 \sum_{j \in N(i)} y_j\}$$



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Ising model (Besag, 1972)

Probability spin $+ \approx \sharp$ neighbours $j \in N(i)$ with spin +



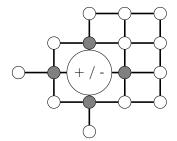
$$\Pr(Y_i = 1 | Y_{N(i)} = y_{N(i)}) \propto \exp\{\theta_1 + \theta_2 \sum_{j \in N(i)} y_j\}$$



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Ising model (Besag, 1972)

Probability spin $+ \approx \sharp$ neighbours $j \in N(i)$ with spin +



$$\Pr(Y_i = 1 | Y_{N(i)} = y_{N(i)}) \propto \exp\{\theta_1 + \theta_2 \sum_{j \in N(i)} y_j\}$$



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Markov random fields for Social Networks

- ppls' networks are not regular lattices
- ppls' attitudes/behaviours also depend on SES, SEX, Education, etc



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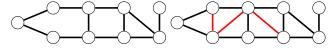
Social dependence is messy

In Graphical models

Conditional independence graph: $i \sim j$ unless

$$X_i \perp X_j | X_{V \setminus \{i,j\}}$$

each node represents one variable (with many observations) some dependence structures are easier than others



not decomposable

decomposable



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Adding dependence between outcomes

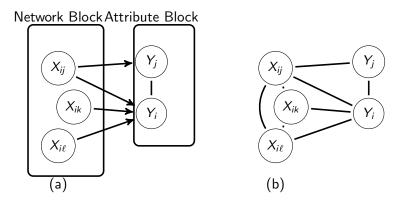


Figure: Dependence graph (a) and Moral graph (b) of model with dependence between attributes that share tie-variables

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Deriving contagion statistics is non-trivial

To derive a non-trivial set of statistics use *realization-dependence* (Baddeley & Möller, 1989).

- Partial dependence graph $Q_{\mathcal{B}}$, is a graph on $\mathcal{V}_{-\mathcal{B}}$
- where $\{i,j\} \in \mathcal{Q}_{\mathcal{B}}$ if
 - \checkmark variables i and j are not conditionally independent conditional on variables $\mathcal{V}_{-\mathcal{B},i,j}$,
 - \checkmark and all variables corresponding to the index set $\mathcal B$ are zero.

In the model, the parameter for the statistic $A\subset\mathcal{V}$ is non-zero only if A is a clique of \mathcal{M} and A is a clique of $\mathcal{Q}_{\mathcal{B}}$ for all \mathcal{B} .

Daraganova (2009) - derived statistics



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Standard ALAAM

From this, and

- Making some Homogeneity assumptions and
- setting some higher-order statistics to zero,

we arrive at the following contagion model

$$\rho_{\theta}(\boldsymbol{y}|\boldsymbol{X}) = \exp\left\{\theta_{0} \sum_{i=1}^{n} y_{i} + \theta_{out} \sum_{i=1}^{n} y_{i} \sum_{j \neq i} x_{ij} + \theta_{in} \sum_{i=1}^{n} y_{i} \sum_{j \neq i} x_{ji} + \theta_{con} \sum_{i,j:i \neq y_{j}} y_{i} y_{j} (x_{ij} + x_{ji}) - \psi(\theta)\right\}$$

This includes an interaction term similar to that of Besag's (1972) classic auto-logistic model but it is subtly different in the definition of the neighbourhood.



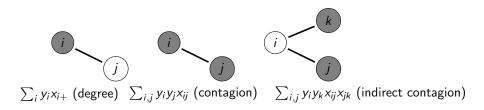
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 43 / 83

Auto-Logistic Actor Attribute Model (ALAAM)

ALAAM defines a distribution on attributes $oldsymbol{y} \in \mathcal{Y} = \{0,1\}^V$

$$p_{ heta}(oldsymbol{y}|oldsymbol{\mathsf{X}}) = \exp\{ heta^{ op}z(oldsymbol{y};oldsymbol{\mathsf{X}}) - \psi(heta)\}$$

ERGM-like model for cross-sectional contagion, e.g.





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The network activity ALAAM - social influence

Example (Modern contraceptive use in rural Kenya (cont.))

Estimated ALAAM

	Poster	rior	95%	6 CI
	Estimate	sd	0.025	0.975
intercept	-0.762	0.291	-1.273	-0.188
contagion	0.457	0.076	0.303	0.592
Age	-0.049	0.007	-0.063	-0.035
Female	-1.091	0.178	-1.461	-0.747
HasChildren	1.710	0.233	1.240	2.154
relevan Others Approve	1.473	0.165	1.140	1.802
relevan Others Use	0.353	0.179	-0.005	0.697
mcUseConflict	-0.359	0.164	-0.678	-0.026

How much is the increase in the probability of mcUse if your friend uses?

45 / 83

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The network activity ALAAM - social influence

A closer look at the pmf

$$p(\boldsymbol{y} \mid \mathbf{X}) = \exp\{\theta^{\top} z(\boldsymbol{y}; \mathbf{X}) - \underbrace{\psi(\theta)}_{\text{norm. const.}}\} = \underbrace{\frac{e^{\theta^{\top} z(\boldsymbol{y}, \mathbf{X})}}{\sum_{\boldsymbol{y} \in \mathcal{X}} e^{\theta^{\top} z(\boldsymbol{y}, \mathbf{X})}}}_{\mathbf{2}^{n} \text{ terms}}$$

We can **only** evaluate *conditional* probabilities

$$\Pr(Y_i = 1 \mid \mathbf{X}, \boldsymbol{y}_{-i}) = \frac{e^{\theta^\top z(\boldsymbol{y}^{i+}, \mathbf{X})}}{e^{\theta^\top z(\boldsymbol{y}^{i+}, \mathbf{X})} + e^{\theta^\top z(\boldsymbol{y}^{i-}, \mathbf{X})}}$$

where y^{i+} is y with $y_i = 1$, and y^{i-} is y with $y_i = 0$



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Estimation

Markov chain Monte Carlo



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Simulating from likelihood

We cannot evaluate likelihood for any θ , but for any θ we can simulate Y_i given $y_1, \ldots, y_{i-1}, y_{i+1}, \cdots, y_n$ using probabilities

$$\mathsf{logit} igg\{ \mathsf{Pr}_{ heta}(Y_i = 1 | oldsymbol{y}_{-i}, oldsymbol{\mathsf{X}}) igg\} = heta^ op \{ z(oldsymbol{y}^{i+}, oldsymbol{\mathsf{X}}) - z(oldsymbol{y}^{i-}, oldsymbol{\mathsf{X}}) \}$$

giving us samples from

$$\boldsymbol{y} \mid \mathbf{X}, \boldsymbol{\theta}$$

We will use this for

- estimation, and
- goodness-of-fit (GOF)

MPNet uses samples in stochastic approximation for MLE



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Simulating from likelihood: Metropolis algorithm

Initialising in vector $y := y_0$, in each iteration t

- Pick $i \in V$ at random
- 2 Propose to set $y_i := 1 y_i$
- **3** Accept and set $y_t := \Delta_i y$, with probability

$$\min\left\{1, \exp\{\theta^\top[z(\Delta_i \boldsymbol{y}, \boldsymbol{\mathsf{X}}) - z(\boldsymbol{y}, \boldsymbol{\mathsf{X}})]\}\right\}$$

lacktriangledown Otherwise set $oldsymbol{y}_t := oldsymbol{y}_{t-1}$

This gives us a sequence

$$y_0,y_1,\ldots,y_k$$
 , $y_{k+1},\ldots,y_{T+1},y_T$ first k will remember y_0

For sufficiently large burnin k, y_{k+1} a draw from model.



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MCMC for un-normalized distributions

MCMC: Sample $\theta^{(0)}, \theta^{(1)}, \ldots$ from $\pi(\theta)$ by

- propose update $\theta^{(t)}$ to $\theta^* q(\theta^*|\theta^{(t)})$
- set $\theta^{(t+1)} := \theta^*$ w.p. $\min\{1, H\}$

$$H = \frac{\pi(\theta^*)}{\pi(\theta^{(t)})} \frac{q(\theta^{(t)}|\theta^*)}{q(\theta^*|\theta^{(t)})}$$

(Works when $\pi(\theta) = f(\theta)/c(\theta)$ and $c(\theta)$ intractable)



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Inference: ALAAM

For our target distribtuion $\pi(\theta|z)$

$$H = \frac{\exp\{\theta^{*\top}z(\boldsymbol{y}; \mathbf{X}) - \psi(\theta^*)\}\pi(\theta^*)}{\exp\{\theta^{(t)\top}z(\boldsymbol{y}; \mathbf{X}) - \psi(\theta^{(t)})\}\pi(\theta^{(t)})} \frac{q(\theta^{(t)}|\theta^*)}{q(\theta^*|\theta^{(t)})}$$

normalising constant $\psi(\cdot)$ of *likelihood* cannot be evaluated (model is doubly intractable)



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Solution to double intractability

Approximate $\hat{\lambda}(\theta, \theta^*) \approx \exp\{\psi(\theta) - \psi(\theta^*)\}$

- off-line importance sample (Koskinen, 2004)
- 'exact' auxiliary variable-based online importance sample with sample size of 1 - (Møller et al., 2006)
- 'exact' online (linked) path sampler auxiliary variable (Koskinen, 2008; Koskinen, 2009)
- online self-tuning auxiliary variable (Murray et al., 2006)
 [Approximate Exchange Algorithm]

ERGO: we can obtain posterior for θ when y is observed



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Monitoring performance of MCMC

Ideally, in our MCMC sample

$$\theta^{(0)}, \theta^{(1)}, \dots, \theta^{(M)}$$

the samples points are independent draws

$$\theta^{(m)} \stackrel{\textit{iid}}{\sim} \pi(\theta|\boldsymbol{y}, \mathbf{X})$$

so that we use Monte Carlo estimators

$$\hat{\mathcal{E}}(\theta|\boldsymbol{y},\mathbf{X}) = \bar{\theta} = \frac{1}{M} \sum_{m=1}^{M} \theta^{(m)}$$
, and $\widehat{Cov}(\theta|\boldsymbol{y},\mathbf{X}) = \frac{1}{M} \sum_{m=1}^{M} (\theta^{(m)} - \bar{\theta})(\theta^{(m)} - \bar{\theta})^{\top}$

as well as approximate probabilities $Pr(\theta \in C)$, for any $C \subset \Theta$



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 53 / 83

Monitoring performance of MCMC - trace plots

In plots, trace plots, of

$$\theta^{(0)}, \theta^{(1)}, \ldots, \theta^{(M)}$$

we should **not** see any

- trend/drift (independence of starting point)
 - > select the number of initial iterations to discard burnin
- serial correlation (good mixing)
 - \triangleright space out sample points $\theta^{(k)}, \theta^{(2k)}, \theta^{(3k)}, \ldots$ thinning of sample



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 54 / 83

Monitoring performance of MCMC - SACF & ESS

The sample autocorrelation function (SACF) measures serial correlation between sample points

$$\theta^{(m-k)}, \theta^{(m)}$$

at different lags k

If SACF at lag k is low, say 30 (SIC?), then taking every k'th sample point will yield an approximately independent sample

The *effective sample size* (**ESS**) tells us roughly how many independent sample points we have

Improving mixing

In our implementation the proposal distribution in each iteration

$$\theta^* \mid \theta^{(t)} \sim N(\theta^{(t)}, \mathbf{\Sigma}_p)$$

SACF can be lowered and mixing improved through improved Σ_p .

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Goodness-of-fit

Goodness-of-fit



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 56 / 83

Goodness-of-fit (GOF)

Once we have a draw

$$\theta^{(0)}, \theta^{(1)}, \dots, \theta^{(M)}$$

from $\pi(\theta|\mathbf{y})$, we can generate draws

$$y^{(0)}, y^{(1)}, \dots, y^{(M)}$$

each from

$$p_{ heta^{(m)}}(oldsymbol{y}^{(m)}|\mathbf{X})$$

GOF evaluation

lf

$$y^{(0)}, y^{(1)}, \dots, y^{(M)}$$

are 'similar' to y, then model has good fit

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57 / 83

Model selection

Picking the 'best' model



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 58 / 83

Posterior deviance

The deviance is defined as minus twice the log likelihood

$$D(\boldsymbol{\theta}) = -2\log[p_{\boldsymbol{\theta}}(\mathbf{y}|\mathbf{X})].$$

Aitkin et al. (2017) graphical comparison of models can be done through comparing the posterior distribution of the deviance Assume a sample

$$\theta_0, \theta_1, \ldots, \theta_T$$

Calculate the deviance $D(\theta_t)$ for the parameters in your posterior.



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Posterior deviance: important

We cannot evaluate log likelihood

$$p_{\theta}(\mathbf{y}|\mathbf{X}),$$

because of $\psi(\theta)$.

But for pairs $\hat{\theta}$ and θ , we can approximate $\hat{\lambda}(\theta, \tilde{\theta}) \approx \exp\{\psi(\theta) - \psi(\tilde{\theta})\}$. Intuition: for bridges $\tilde{\theta} = \theta^{(0)}, \theta^{(1)}, \dots, \theta^{(M)} = \theta$, we draw

$$m{y}_0^{(j)}, m{y}_{2k}^{(j)}, \dots, m{y}_{3k}^{(j)}, m{y}_{4k}^{(j)}, \dots, m{y}_{Tk}^{(j)} \sim m{p}_{ heta^{(j)}}(m{y} \mid m{\mathsf{X}})$$

and use² $\bar{z}^{(j)} = \frac{1}{T} \sum z(y_t^{(j)}, \mathbf{X})$ to get estimate $\hat{\lambda}(\theta, \tilde{\theta}) \approx \exp\{\psi(\theta) - \psi(\tilde{\theta})\}$

NB: Sensitive to T and thinning k - samples $\{y_t^{(j)}\}$ have to be good



60 / 83

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²Requires a bit more thought . . .

Deviance information criterion

Using the posterior distribution of the deviance, we can calculate

$$DIC = E[D(\theta)] + V(D(\theta))/2$$

Models with smaller DIC prefered to models with LARGER DIC



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Missing data

Missing outcomes



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 62 / 83

Missing data (cp Bayesian data augmentation for ERGM)

Under assumption of Missing at Random (MAR) Define the missing data mechanism $f(I|y,\phi)$, where

$$I_i = \begin{cases} 1, & \text{if response } y_i \text{ is unobserved for } i \\ 0, & \text{else} \end{cases}$$

update (impute) missing response by toggling and accepting w.p.

$$\min \left[1, \exp\{\theta^\top (z(\Delta_i y, x) - z(y, x))\} \frac{f(I|\Delta_i y, \phi)}{f(I|y, \phi)}\right]$$

where $\Delta_i y$ is y with element i toggled and set to $1 - y_i$. Update ϕ , with MH-updating and Hastings ratio

$$\min \Big\{1, \frac{f(I|y, \phi^*)\pi(\phi^*)}{f(I|y, \phi)\pi(\phi)}\Big\}.$$



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Missing data (cp Bayesian data augmentation for ERGM)

In the actual estimation, simply define

$$y_i = \left\{ egin{array}{ll} 1, & \mbox{if response } y_i = 1 \mbox{ is unobserved for } i \ 0, & \mbox{if response } y_i = 0 \mbox{ is unobserved for } i \ NA, & \mbox{if response is missing for } i \end{array}
ight.$$

Sampling will return draws

$$(\theta^{(0)}, y_{miss}^{(0)}), (\theta^{(1)}, y_{miss}^{(1)}), \dots, (\theta^{(M)}, y_{miss}^{(M)})$$



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 64 / 83

Interactions with contagion

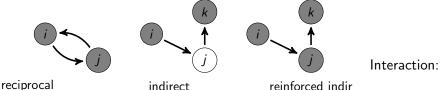
More complicated contagion effects



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More elaborate effects

A number of more elaborate forms of contagion/influence are admissible





influence from some nodes can be θ and for others $\theta + \alpha$



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 66 / 83

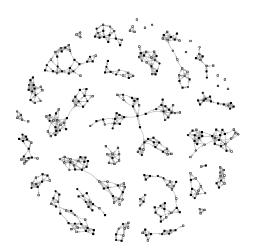
SBC (Koskinen and Daraganova, 2022)

Stockholm Birth Cohort (SBC) cohort study, Stockholm Metropolitan area (Stenberg et al., 2006; Stenberg et al. 2007).

- best-friend network with a cap of three nominations (May 1966)
- Let y be indicators $y_i = 1$ of whether pupils i said that they intended to proceed to higher secondary school, and $y_i = 0$ otherwise (see Koskinen and Stenberg, 2012)
- Here: 19 school classes, six of which are from a school in a suburb in the south of Stockholm and the rest are from three inner-city schools
- The proportion of missing entries range from 0 to 0.286



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 June 22, 2025
 67 / 83





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More elaborate effects - interaction example

Example (Simple contagion of intention to go to higher secondary school)

	mean	sd	ESS	SACF 10	SACF 30	2.5 perc	97.5 perc
intercept	-9.67	1.11	178.03	0.68	0.32	-11.83	-7.51
contagion	0.16	0.10	183.10	0.68	0.32	-0.04	0.35
indegree	-0.07	0.11	183.55	0.67	0.32	-0.29	0.13
sex	-0.09	0.29	134.35	0.70	0.39	-0.66	0.47
family attitude	0.48	0.09	164.22	0.70	0.32	0.33	0.65
marks	0.99	0.15	168.66	0.68	0.32	0.69	1.28
social class 1	0.59	0.32	198.40	0.66	0.24	-0.06	1.19

Table: Posterior summaries for model with controls estimated for contagion-model for progression to upper-secondary school in SBC (thinned sample of 10,000 iterations, taking every 20th iteration, with burnin of 1000)



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More elaborate effects - interaction example

Example (Contextual contagion of intention to go to higher secondary school)

	mean	sd	ESS	SACF 10	SACF 30	2.5 perc	97.5 perc
intercept	-10.13	1.19	168.32	0.76	0.44	-12.81	-8.04
contagion	0.24	0.12	143.31	0.72	0.39	0.02	0.48
indegree	-0.08	0.12	122.80	0.75	0.41	-0.33	0.13
sex	-0.09	0.28	126.04	0.76	0.45	-0.69	0.47
family attitude	0.48	0.08	140.26	0.72	0.38	0.34	0.65
marks	1.01	0.14	265.08	0.72	0.40	0.76	1.31
composition	0.91	0.55	137.33	0.74	0.39	-0.25	1.97
social class 1	0.57	0.34	143.59	0.73	0.37	-0.07	1.21
contagion int	-0.21	0.16	152.15	0.72	0.37	-0.51	0.11

Table: Posterior summaries for model with controls estimated for contagion-model for progression to upper-secondary school in SBC (thinned sample of 10,000 iterations, taking every 20th iteration, with burnin of 1000) with social class interacted with contagion



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 70 / 83

Fully Bayesian

Specifying proper priors



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 71 / 83

Fully Bayesian: what priors?

Assuming

$$y \mid \mathbf{X} \sim ALAAM(\theta, \mathbf{X})$$

The model is

$$P(y \mid \mathbf{X}, \boldsymbol{\theta}) = \exp\{\boldsymbol{\theta}^{\top} \boldsymbol{z}(\boldsymbol{y}, \mathbf{X}) - \psi(\boldsymbol{\theta})\}$$

The aim of the Bayesian inference scheme is to obtain the posterior

$$\pi(\boldsymbol{\theta} \mid \boldsymbol{y}) \propto P(\boldsymbol{y} \mid \mathbf{X}, \boldsymbol{\theta}) \pi(\boldsymbol{\theta})$$

where

$$\pi(\boldsymbol{\theta})$$

is the **prior distribution** for the parameters that *quantify our uncertainty* about the parameter values prior to observing data.

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Fully Bayesian: what priors?

How can a human quantify their uncertainty about the parameter values prior to observing data?

ullet Default prior: constant $\pi(oldsymbol{ heta}) \propto 1$

For ALAAM this is really hard! Possible choices

- Convenient: Multivariate normal distribution $\mathcal{N}_p(\mu, \mathbf{\Sigma})$
 - ▶ Diagonal: $\Sigma = \lambda I$
 - ▶ Scaling: $\mathbf{\Sigma} = \lambda (\mathbf{X}^{\top} \mathbf{X})^{-1}$
- ullet Caution: setting $oldsymbol{\mu}=\mathbf{0}$ pulls posteriors towards 0 bad for e.g. intercept if $ar{y}$ small
- Experiemental: use a prior to 'fix' a nuisance parameter



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Hierarchical ALAAM

A multilevel version of ALAAM



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Hierarchical ALAAM: preamble

The routines for analysing outcomes

$$y^{(1)}, y^{(2)}, \dots, y^{(G)}$$

for *G* independently observed networks

$$\mathbf{X}^{(1)}, \mathbf{X}^{(2)}, \dots, \mathbf{X}^{(G)}$$

is implemented in very old code in MultivarALAAMalt.R



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Hierarchical ALAAM: principle

Following Koskinen and Snijders' (2023) work on SAOMs, we assume that independently for each group $g=1,\ldots,G$,

$$y^{(g)} \mid \mathbf{X}^{(g)}, \mathbf{\theta}^{(g)} \sim ALAAM(\mathbf{\theta}^{(g)}, \mathbf{X}^{(g)})$$

where parameters are partitioned

$$oldsymbol{ heta}^{[oldsymbol{g}]} = \left(egin{array}{c} oldsymbol{\gamma}^{[oldsymbol{g}]} \ oldsymbol{\eta} \end{array}
ight),$$

into a set of group-specific parameters $\gamma^{[g]} \in \Gamma \subset \mathbb{R}^q$, and a common parameter $\eta \in \mathbf{H} \subset \mathbb{R}^r$, q+r=p.



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 76 / 83

Hierarchical ALAAM: 'fixed' effects

The common parameter, η , can be used to parse out **group-level** effects,e.g. Public/private school,gender composition of school class, etc. We may assume that η , are independent of $\gamma^{[1]}, \gamma^{[2]}, \ldots, \gamma^{[G]}$, with prior

$$\pi(\boldsymbol{\eta} \mid \boldsymbol{\mu}_{\boldsymbol{\eta}}, \boldsymbol{\Sigma}_{\boldsymbol{\eta}}, \boldsymbol{\gamma}^{[1]}, \boldsymbol{\gamma}^{[2]}, \dots, \boldsymbol{\gamma}^{[G]}) = \pi(\boldsymbol{\eta} \mid \boldsymbol{\mu}_{\boldsymbol{\eta}}, \boldsymbol{\Sigma}_{\boldsymbol{\eta}})$$

which for convenience may be assumed to be $\mathcal{N}_r(\mu_n, \Sigma_n)$.



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Hierarchical ALAAM: 'random' effects

The group-level parameters allow, e.g. the intercept and the contagion effect to vary across groups.

We assume

$$\gamma^{[g]} \stackrel{\textit{iid}}{\sim} \mathcal{N}_r(\mu_{\gamma}, \mathbf{\Sigma}_{\gamma}).$$

Assuming that $\gamma^{[g]}$ follow a multivariate normal, it is common (cp Gelman et al., 1995) to assume a Normal-inverse-Wishard prior for the parameters μ_γ and Σ_γ

$$\mu_{\gamma} \mid \mathbf{\Sigma}_{\gamma} \sim \mathcal{N}_q(\mu_0, \mathbf{\Sigma}_{\gamma}/\kappa_0)$$
, and $\mathbf{\Sigma}_{\gamma} \sim \mathcal{IW}_r(\mathbf{\Lambda}_0, \nu_0)$



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Hierarchical ALAAM: the DAG

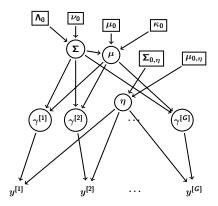


Figure: Dependence structure of hierarchical network model for $\mathbf{Y}^{[g]}$, $g=1,2,\ldots,G$.

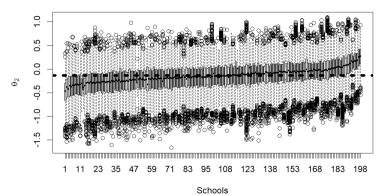


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Hierarchical ALAAM: example (1)

Acke Arvidsson (Master's thesis) analysed hundreds of school classes in SBC

Outcome is leader $(y_i = 1)$ or not $(y_i = 0)$; Network BFF



Posteriors for group-level contagion $\gamma_2^{(g)}$

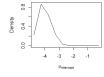


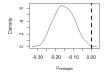
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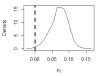
Hierarchical ALAAM: example (2)

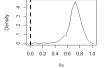
Acke Arvidsson (Master's thesis) analysed hundreds of school classes in SBC

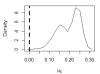
Outcome is leader $(y_i = 1)$ or not $(y_i = 0)$; Network BFF

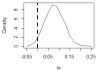












Posteriors for μ



81 / 83

C: indegree; D: sex; E: average test score; F: communication

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Further topics

Further complications



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Further topics: topics

- Missing NOT at random (implemented; also, plug for MNAR ERGM, Januar, Gallagher, Koskinen, Friday 27 8.20AM - OS-65)
- Missing network ties
- Marginal effects: Titanic
- Multivariate ALAAM
- Snowball sample or outlier nodes canchange



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