Modeling homophily and stochastic equivalence in symmetric relational data

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- associations among words
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Observed explanatory variables is represented similarly

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To discover the covariation of \( Y \) and \( X \)

- linear predictor \( \beta^T x_{i,j} \),
- node-specific latent variables \( u_i, u_j \in \{u_1, \ldots, u_n\} \),
Homophily and stochastic equivalence

**Homophily**: the relationships between nodes with similar characteristics are stronger than the relationships between nodes having different characteristics.

**Stochastic equivalence**: the nodes can be divided into groups such that members of the same group have similar patterns of relationships.
Hopmophily: by latent distance model

- transitivity: a friend of a friend is a friend
- balance: the enemy of my friend is an enemy
- existence of cohesive subgroups of nodes
- conditional means of $y_{i,j}$ is a function of $\beta'x_{i,j} - |u_i - u_j|$
- strong relationship between $i$ and $j$ suggests small $|u_i - u_j|$
- further implies $|u_i - u_k| \approx |u_j - u_k|$, i.e., nodes $i$ and $j$ are assumed to have similar relationships to other nodes
Cont’d

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**Stochastic Equivalence: by latent class model**

- would require a large number of classes,
- none of which would be particularly cohesive or distinguishable from others
Issue

Two primary features of interest in social network and relational data analysis

- **classes of nodes with similar roles**: identified by latent class model
- **locational properties of the nodes**: identified by latent distance model

However,

- many real networks exhibit combinations of structural equivalence and homophily in varying degrees
- use of either the latent class or distance model would only be representing part of the network structure

Latent eigenmodel: $\beta^T x_{i,j} + u_i \Lambda u_j \{u_1, \ldots, u_n\}$ are node-specific factors and $\Lambda$ is a diagonal matrix.
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**Latent eigenmodel:**

\[ \beta' x_{i,j} + u_i^T \Lambda u_j \]

\{u_1, \ldots, u_n\} are node-specific factors and \( \Lambda \) is a diagonal matrix
Justification of latent variable modeling

- For undirected data, nodes as suggested exchangeable
- For any permutation \( \pi \) of the integers \( \{1, \ldots, n\} \) and any set of sociomatrices \( A \)

\[
Pr(\{y_{i,j} : 1 \leq i < j \leq n\} \in A) = Pr(\{y_{\pi i, \pi j} : 1 \leq i < j \leq n\} \in A)
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- if a model satisfies the above exchangeability condition for each integer $n$,
- a latent variable model can be written in the form of

$$y_{i,j} = h(\mu, u_i, u_j, \epsilon_{i,j})$$

i.i.d. latent variables $\{u_1, \ldots, u_n\}$,

i.i.d. pair-specific effects $\{\epsilon_{i,j} : 1 \leq i < j \leq n\}$,

$h$ that is symmetric in its second and third arguments
A general Probit model for binary network data

Different choice of function $h$ lead to different models for $y$

\[
\{\epsilon_{i,j} : 1 \leq i < j \leq n\} \sim \text{i.i.d. } N(0, 1)
\]
\[
\{u_1, \ldots, u_n\} \sim \text{i.i.d. } f(u|\psi)
\]
\[
y_{i,j} = h(\mu, u_i, u_j, \epsilon_{i,j}) = \delta_{(0,\infty)}(\mu + \alpha(u_i, u_j) + \epsilon_{i,j})
\]

$\mu$ and $\psi$ are parameters to be estimated

$\alpha$ is a symmetric function
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Different choice of function $h$ lead to different models for $y$

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$\mu$ and $\psi$ are parameters to be estimated
$\alpha$ is a symmetric function

- By adding a linear predictor $\beta^T x_{i,j}$ to $\mu$ to represent covariation between $Y$ and $X$
- Integrating over $\epsilon_{i,j}$,
\[ Pr(y_{i,j} = 1|x_{i,j}, u_i, u_j) = \Phi[\mu + \beta^T x_{i,j} + \alpha(u_i, u_j)] \]
Assume $\epsilon_{i,j}$’s independent,

- In the case of binary relational datasets,

$$Pr(y_{i,j} = 1|x_{i,j}, u_i, u_j) \equiv \theta_{i,j} = \Phi[\mu + \beta^T x_{i,j} + \alpha(u_i, u_j)]$$

$$Pr(Y|X, u_1, \ldots, u_n) = \prod_{i<j} \theta_{i,j}^{y_{i,j}} (1 - \theta_{i,j})^{1-y_{i,j}}$$
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\]

- In the case of relational datasets have ordinal, non-binary measurements,

\[
Pr(y_{i,j} = y|x_{i,j}, u_i, u_j) \equiv \theta_{i,j}^{(y)}
\]

\[
= \Phi[\mu_y + \beta^T x_{i,j} + \alpha(u_i, u_j)] - \Phi[\mu_{y-1} + \beta^T x_{i,j} + \alpha(u_i, u_j)]
\]

\[
Pr(Y|X, u_1, \ldots, u_n) = \prod_{i<j} \theta_{i,j}^{(y_{i,j})}
\]

where \(\{\mu_y\}\) are parameters to be estimated for all but the lowest value \(y\) in the sample space.
Effects of nodal variation

Latent calss model:

\[ \alpha(u_i, u_j) = m_{u_i, u_j} \]
\[ u_i \in \{1, \ldots, K\}, i \in \{1, \ldots, n\} \]
\[ M \text{ a } K \times K \text{ symmetric matrix} \]

Latent distance model:

\[ \alpha(u_i, u_j) = -|u_i - u_j| \]
\[ u_i \in \mathbb{R}^K, i \in \{1, \ldots, n\} \]

Latent eigenmodel:

\[ \alpha(u_i, u_j) = u_i^T \Lambda u_j \]
\[ u_i \in \mathbb{R}^K, i \in \{1, \ldots, n\} \]
\[ \Lambda \text{ a } K \times K \text{ diagonal matrix} \]
Interpredation of the latent eigenmodel

Latent eigenmodel:

$$\beta' x_{i,j} + u_i^T \Lambda u_j$$

\{u_1, \ldots, u_n\} are node-specific factors and \(\Lambda\) is a diagonal matrix

- Each node \(i\) has a vector of unobserved characteristics
  \(u_i = \{u_{i,1}, \ldots, u_{i,K}\}\),
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- Each node \( i \) has a vector of unobserved characteristics
  \[ u_i = \{u_{i,1}, \ldots, u_{i,K}\}, \]

- Similar values of \( u_{i,k} \) and \( u_{j,k} \) will contribute positively or negatively to the relationship between \( i \) and \( j \), depending on whether \( \lambda_k > 0 \) or \( \lambda_k < 0 \).
Interpretation of the latent eigenmodel

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- The model can represent both positive or negative homophily in varying degrees,
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- the model can represent both positive or negative homophily in varying degrees,

- can also represent that stochastically equivalent nodes may or may not have strong relationship with one another.
Generalization

let $S_n$ be the set of $n \times n$ sociomatrices, and let

$$C_K = \{ C \in S_n : c_{i,j} = m_{u_i,u_j}, u_i \in \{1, \ldots, K\}, M_{K \times K}\}$$

$$D_K = \{ D \in S_n : d_{i,j} = -|u_i - u_j|, u_i \in \mathbb{R}^K\}$$

$$E_K = \{ E \in S_n : e_{i,j} = u_i^T \Lambda u_j, u_i \in \mathbb{R}^K, \Lambda_{K \times K}\}$$

- Latent eigenmodel generalizes the latent class model
- Latent eigenmodel weakly generalizes the latent distance model
- Latent distance model cannot generalizes the latent eigenmodel
Parameter estimation by MCMC

- Include an additional latent variable $z_{i,j}$,

$$z_{i,j} \sim \mathcal{N}(\beta' x_{i,j} + \alpha(u_i, u_j))$$

$$y_{i,j} = y, \text{ if } \mu_y < z_{i,j} < \mu_{y+1}$$

- Using conjugate prior distributions where possible, the MCMC algorithms proceed by generating a new state

$$\phi^{(s+1)} = \{Z^{(s+1)}, \mu^{(s+1)}, \beta^{(s+1)}, u_1^{(s+1)}, \ldots, u_n^{(s+1)}\}$$

from a current state $\phi^{(s)}$
Model comparison on three different datasets

Three data sets:

1. Adolescent health social network - homophily
2. Word neighbors in Genesis - stochastic equivalence
3. Protein-protein interaction data - both

Five-fold cross validation for each combination of data, dimension ($K \in \{3, 5, 10\}$) and model
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Table 1: Cross validation results and area under the ROC curves.

<table>
<thead>
<tr>
<th>$K$</th>
<th>Add health</th>
<th>Genesis</th>
<th>Protein interaction</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>dist</td>
<td>class</td>
<td>eigen</td>
</tr>
<tr>
<td>3</td>
<td>0.82</td>
<td>0.64</td>
<td>0.75</td>
</tr>
<tr>
<td>5</td>
<td>0.81</td>
<td>0.70</td>
<td>0.78</td>
</tr>
<tr>
<td>10</td>
<td>0.76</td>
<td>0.69</td>
<td>0.80</td>
</tr>
</tbody>
</table>
Adolescent Health social network
Word neighbors in Genesis
Protein-protein interaction data

[Graph showing protein-protein interactions with a scatter plot and a ROC curve, indicating different methods: distance, class, and vector.]
Conclusion

- Latent distance and latent class models provide concise, easily interpreted descriptions of social networks and relational data.
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- However, neither of these models will provide a complete picture of relational data that exhibit degrees of both homophily and stochastic equivalence.
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- However, neither of these models will provide a complete picture of relational data that exhibit degrees of both homophily and stochastic equivalence.

- In contrast, latent eigenmodel is able to represent datasets with either or both of these data patterns.
Appendix
Eigenmodel generalizes the class and distance model
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To show this statement, let $S_n$ be the set of $n \times n$ sociomatrices, and let

$$C_K = \{ C \in S_n : c_{i,j} = m_{u_i,u_j}, u_i \in \{1, \ldots, K\}, \quad M \text{ is a } K \times K \text{ symmetric matrix}\}$$

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In other words,

- $C_K$ is the set of possible values of $\{ \alpha(u_i, u_j), 1 \leq i < j \leq n \}$ under a $K$-dimensional latent class model,
- similarly for $D_K$ and $E_K$
$\mathcal{E}_K$ generalizes $\mathcal{C}_K$:
\( \mathcal{E}_K \) generalizes \( \mathcal{C}_K \):

- Let \( C \in \mathcal{C}_K \)
- let \( \tilde{C} \) be a completion of \( C \) obtained by setting \( c_{i,j} = m_{u_i,u_i} \)
- At most \( K \) unique rows of \( \tilde{C} \) and so \( \tilde{C} \) is of rank \( K \) at most
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- At most \( K \) unique rows of \( \tilde{C} \) and so \( \tilde{C} \) is of rank \( K \) at most
- Since \( \mathcal{E}_K \) contains all sociomatrices that can be completed as a rank-\( K \) matrix, we have \( \mathcal{C}_K \subset \mathcal{E}_K \)
- Since \( \mathcal{E}_K \) includes matrices with \( n \) unique rows, \( K \subset \mathcal{E} \) unless \( K \geq n \) in which case the two sets are equal
\( \mathcal{E}_{K+1} \) weakly generalizes \( \mathcal{D}_K \):

- Let \( D \in D_K \), generally be of full rank for \( K < n \), it cannot be represented exactly by an \( E \in \mathcal{E}_K \).
$\mathcal{E}_{K+1}$ weakly generalizes $\mathcal{D}_K$:

- Let $D \in D_K$, generally be of full rank for $K < n$, it cannot be represented exactly by an $E \in \mathcal{E}_K$

- What is critical from a modeling perspective is whether or not the order of the entries of each $D$ can be matched by the order of the entries of an $E$. This is because $\{\mu_y : y \in \mathcal{Y}\}$ which can be adjusted to accommodate monotone transformations of $\alpha(u_i, u_j)$
\[ E_{K+1} \] weakly generalizes \( D_K \):

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  This is because \( \{ \mu_y : y \in Y \} \) which can be adjusted to accommodate monotone transformations of \( \alpha(u_i, u_j) \).

- Note that the matrix of squared distances among a set of \( K \)-dimensional vectors \( \{z_1, \ldots, z_n\} \) is a monotonic transformation of the distances, is a of rank \( K + 2 \) or less, (since

\[
D^2 = [z'_1 z_1, \ldots, z'_n]T 1^T + 1[z'_1 z_1, \ldots, z'_n z_n] - 2ZZ^T
\]

so is in \( E_{K+2} \).
\[ u_i = (z_i, \sqrt{r^2 - z_i^T z_i}) \in \mathbb{R}^{K+1} \forall i \in \{1, \ldots, n\} \]

\[ u_i' u_j = z_i' z_j + \sqrt{(r^2 - |z_i|^2)(r^2 - |z_j|^2)} \]

- For large \( r \), this is approximately \( r^2 - |z_i - z_j|^2/2 \), which is an increasing function of the negative distance \( d_{i,j} \)

- For large enough \( r \) the numerical order of the entries of this \( E \in \mathcal{E}_{K+1} \) is the same as that of \( D \in \mathcal{D}_K \).
$D_K$ does not weakly generalize $\mathcal{E}_1$:

- Consider $E \in \mathcal{E}_1$ generated by $\Lambda = 1, u_1 = 1$ and $u_i = r < 1$ for $i > 1$
  \[ r = e_{1,i_1} = e_{1,i_2} > e_{i_1,i_2} = r^2, \forall i_1, i_2 \neq 1. \]

- For which $K$ is such an ordering of the elements of $D \in D_K$ possible?
  If $K = 1$ then such an ordering is possible only if $n = 3$.
  If $K = 2$ such an ordering is possible for $n \leq 6$. (kissing spheres)

- Increasing $n$ increases the necessary dimension of the Euclidean space, and so for any $K$ there are $n$ and $E \in \mathcal{E}_1$ that have entry orderings that cannot be matched by those of any $D \in D_K$
MCMC cont’d

1. $\forall\{i, j\}$, sample $z_{i,j}$
2. $\forall y \in \mathcal{Y}$, sample $\mu_y$
3. Sample $\beta$
4. Sample $u_1, \ldots, u_n$ and their associated parameters
MCMC cont’d

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2. $\forall y \in Y$, sample $\mu_y$
3. Sample $\beta$
4. Sample $u_1, \ldots, u_n$ and their associated parameters
   - For latent distance model
     - propose and accept or reject new values of $u_i$ with Metropolis algorithms
     - sample the population variances of $u_i$ from (inverse-gamma) full conditional distributions
   - For latent class model
     - Update $u_i$ from multinomial conditional distribution given current $Z$, $\{u_j : j \neq i\}$ and the variance of the elements of $M$
     - sample the elements of $M$ from their normal full conditional distributions and the variance of the entries of $M$ from its (inverse-gamma) full conditional distribution
   - For latent vector model
     - sample $u_i$ from its multivariate normal full conditional distribution
     - sample the mean of $u_i$’s from their normal full conditional distributions
     - sample $\Lambda$ from its multivariate normal full conditional distribution
MCMC cont’d

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   - for latent vector model
     - sample \( u_i \) from its multivariate normal full conditional distribution
     - sample the mean of \( u_i \)'s from their normal full conditional distributions
Model comparison on three different datasets

Three data sets:
- Adolescent health social network - homophily
- Word neighbors in genesis - stochastic equivalence
- Protein-protein interaction data - both

Five-fold cross validation for each combination of data, dimension \( K \in \{3, 5, 10\} \) and model

Randomly divide \( \binom{n}{2} \) data values into 5 sets of roughly equal size, letting \( s_{i,j} \) be the set to which pair \( \{i,j\} \) is assigned.

For each \( s \in \{1, \ldots, 5\} \):
- Obtain posterior distributions of the model parameter conditional on \( \{y_{i,j} : s_{i,j} \neq s\} \), the data on pairs not in set \( s \).
- For pairs \( \{k,l\} \) in set \( s \), let \( \hat{y}_{k,l} = E(y_{k,l} | \{y_{i,j} : s_{i,j} \neq s\}) \), the posterior predictive mean of \( y_{k,l} \) obtained using data not in set \( s \).
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- For each $s \in \{1, \ldots, 5\}$:
  - obtain posterior distributions of the model parameter conditional on $\{y_{i,j} : s_{i,j} \neq s\}$, the data on pairs not in set $s$.
  - for pairs $\{k, l\}$ in set $s$, let $\hat{y}_{k,l} = E(y_{k,l}|\{y_{i,j} : s_{i,j} \neq s\})$, the posterior predictive mean of $y_{k,l}$ obtained using data not in set $s$. 