Relational and network data analysis with `amen`

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May 20, 2015

Abstract

Relational data often exhibit strong statistical dependencies. Certain types of second-order dependencies, such as degree heterogeneity and reciprocity, can be well represented with additive random effects models. Higher-order dependencies, such as transitivity and stochastic equivalence, can often be represented with multiplicative effects. The `amen` package provides estimation and inference for a class of additive and multiplicative random effects models for network and relational data of a variety of types, including binary, ordinal and continuous relations. The package also provides methods for missing, censored and fixed-rank nomination data, as well as longitudinal relational data. This vignette illustrates the use of the `amen` package via analyses of several of these different types of relational data.

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1 The Gaussian AME model

A variable that is measured or observed on pairs of objects, individuals or nodes is called a *relational variable*. Data on a relational variable for a population of n nodes may be represented as a *sociomatrix*, an $n \times n$ square matrix $\mathbf{Y}$ with an undefined diagonal. The i,jth entry of $\mathbf{Y}$, denoted $y_{i,j}$, gives the value of the relation between nodes i and j from the perspective of node i, or in the direction from i to j. For example, in a relational dataset describing friendships, $y_{i,j}$ might represent a quantification of how much person i likes person j. A running example in this section will be an analysis of international trade data, where $y_{i,j}$ is the (log) dollar-value of exports from country i to country j. These data can be obtained from the `IR90s` dataset included with the `amen` package. Specifically, we will analyze trade data between the 30 countries having the highest GDPs:

```
#### ---- obtain trade data from top 30 countries in terms of GDP
data(IR90s)

gdp<-IR90s$nodevars[,2]
topgdp<-which(gdp>=sort(gdp,decreasing=TRUE)[30] )
Y<-log( IR90s$dyadvars[topgdp,topgdp,2] + 1 )

Y[1:5,1:5]

          ARG        AUL       BEL        BNG        BRA
ARG        NA 0.05826891 0.2468601 0.03922071 1.76473080
AUL 0.0861777         NA 0.3784364 0.10436002 0.21511138
```

```
BEL 0.2700271 0.35065687        NA 0.01980263 0.39877612
BNG 0.0000000 0.01980263 0.1222176         NA 0.01980263
BRA 1.6937791 0.23901690 0.6205765 0.03922071         NA
```

1.1 The social relations model

Relational data often exhibit certain types of statistical dependencies. For example, it is often the case that observations in a given row of the sociomatrix are similar to or correlated with each other. This should not be too surprising, as these observations all share a common "sender," or row index. If a sender i_1 is more "sociable" than sender i_2, we would expect the relational values in row i_1 to be larger than those in row i_2, on average. In this way, heterogeneity of the nodes in terms of their "sociability" corresponds to a large variance of the row means of the sociomatrix. Similarly, nodal heterogeneity in "popularity" corresponds to a large variance in the column means.

A classical approach to evaluating across-row and across-column heterogeneity in a data matrix is the ANOVA decomposition. A model-based version of the ANOVA decomposition posits that the variability of the $y_{i,j}$'s around some overall mean is well-represented by additive row and column effects, that is,

$$y_{i,j} = \mu + a_i + b_j + \epsilon_{i,j}.$$

In this model, heterogeneity among the parameters $\{a_i : i = 1, \ldots, n\}$ and $\{b_j : j = 1, \ldots, n\}$ give rise to observed heterogeneity in the row means and column means of the sociomatrix, respectively. If the $\epsilon_{i,j}$'s are assumed to be i.i.d. from a mean-zero normal distribution, the hypothesis of no row heterogeneity (all a_i's equal to zero) or no row heterogeneity (all b_j's equal to zero) can be evaluated with normal-theory F-tests. For the trade data, this can be done in R as follows:

```
#### ---- ANOVA for trade data

Rowcountry<-matrix(rownames(Y),nrow(Y),ncol(Y))
Colcountry<-t(Rowcountry)

anova(lm( c(Y) ~ c(Rowcountry) + c(Colcountry) ) )

Analysis of Variance Table
```

```
Response: c(Y)
               Df Sum Sq Mean Sq F value    Pr(>F)
c(Rowcountry)  29 202.48  6.9819  29.524 < 2.2e-16 ***
c(Colcountry)  29 206.32  7.1144  30.084 < 2.2e-16 ***
Residuals     811 191.79  0.2365
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The results indicate a large degree of heterogeneity of the countries as both exporters and importers - much more than would be expected if the "true" a_i's were all zero, or the "true" b_j's were all zero (and the $\epsilon_{i,j}$'s were i.i.d.). Based on this result, the next steps in a data analysis might be to compare the row means or the column means, that is, to compare the countries in terms of their total or average imports and exports. This can equivalently be done via comparisons among estimates of the row and column effects:

```
#### ---- comparison of countries in terms of row and column means
rmean<-rowMeans(Y,na.rm=TRUE) ; cmean<-colMeans(Y,na.rm=TRUE)

muhat<-mean(Y,na.rm=TRUE)
ahat<-rmean-muhat
bhat<-cmean-muhat

# additive "exporter" effects
head( sort(ahat,decreasing=TRUE)  )

      USA       JPN       UKG       FRN       ITA       CHN
1.4801300 1.0478834 0.6140597 0.5919777 0.4839285 0.4468015

# additive "importer" effects
head( sort(bhat,decreasing=TRUE)  )

      USA       JPN       UKG       FRN       ITA       NTH
1.5628243 0.8433793 0.6683700 0.5849702 0.4712668 0.3628532
```

We note that these simple estimates here are very close to, but not exactly the same as, the least-squares/maximum likelihood estimates (this is because of the undefined diagonal in the sociomatrix).

While straightforward to implement, this classical ANOVA analysis ignores a fundamental characteristic of relational data: Each node appears in the dataset as both a sender and a receiver of

relations, or equivalently, the row and column labels of the data matrix refer to the same set of objects. In the context of the ANOVA model, this means that each node i has two additive effects - a row effect a_i and a column effect b_i. Often it is of interest to evaluate the extent to which these effects are correlated, for example, to evaluate if sociable nodes in the network are also popular. Additionally, each (unordered) pair of nodes i, j has two outcomes, $y_{i,j}$ and $y_{j,i}$. It is often the case that $y_{i,j}$ and $y_{j,i}$ are correlated, as these two observations come from the same *dyad*, or pair of nodes.

Correlations between the additive effects can be evaluated empirically simply by computing the sample covariance of the row means and column means, or alternatively, the $\hat{a}_i$'s and $\hat{b}_i$'s. Dyadic correlation can be evaluated by computing the correlation between the matrix of residuals from the ANOVA model and its transpose:

```
#### ---- covariance and correlation between row and column effects
cov( cbind(ahat,bhat) )

          ahat      bhat
ahat 0.2407563 0.2290788
bhat 0.2290788 0.2289489

cor( ahat, bhat)

[1] 0.9757237
```

```
#### ---- an estimate of dyadic covariance and correlation
R <- Y - ( muhat + outer(ahat,bhat,"+") )
cov( cbind( c(R),c(t(R)) ),use="complete")

          [,1]      [,2]
[1,] 0.2212591 0.1900891
[2,] 0.1900891 0.2212591

cor( c(R),c(t(R)),use="complete")

[1] 0.8591242
```

As shown by these calculations and in Figure 1, country-level export and import volumes are highly correlated, as are the export and import volumes within country pairs. A foundational

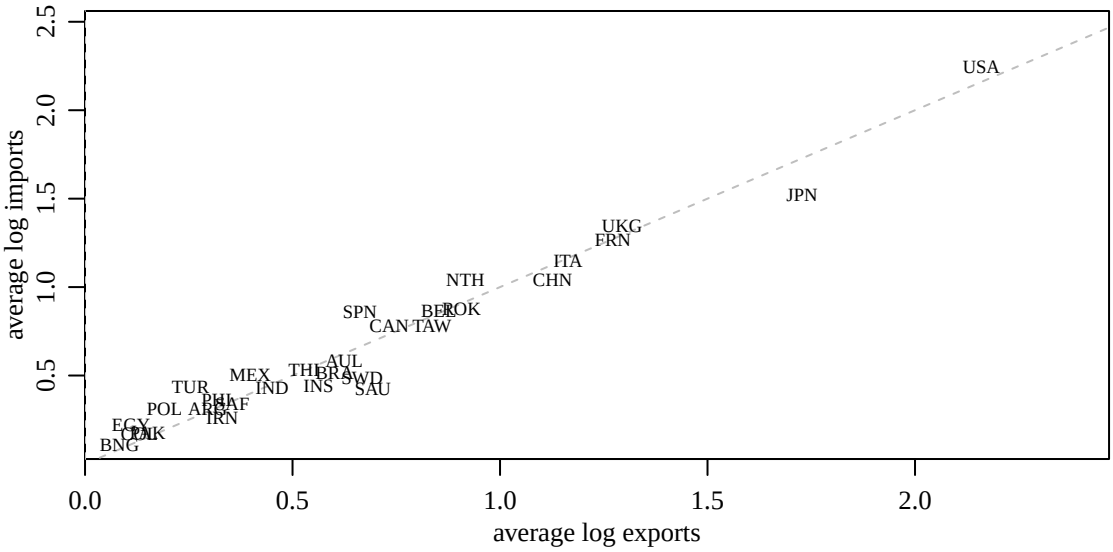


Figure 1: Scatterplot of country-level average imports versus exports.

model for analyzing such within-node and within-dyad dependence is the *social relations model*, or SRM (Warner et al., 1979), a type of ANOVA decomposition that describes variability among the entries of the sociomatrix $\mathbf{Y}$ in terms of within-row, within-column and within-dyad variability. A normal random-effects version of the SRM has been studied by Wong (1982) and Li and Loken (2002), among others, and takes the following form:

$$y_{i,j} = \mu + a_i + b_j + \epsilon_{i,j} \tag{1}$$

$$\{(a_1, b_1), \ldots, (a_n, b_n)\} \sim \text{i.i.d. } N(0, \Sigma_{ab})$$

$$\{(\epsilon_{i,j}, \epsilon_{j,i}) : i \neq j\} \sim \text{i.i.d. } N(0, \Sigma_e),$$

where

$$\Sigma_{ab} = \begin{pmatrix} \sigma_a^2 & \sigma_{ab} \\ \sigma_{ab} & \sigma_b^2 \end{pmatrix} \quad \text{and} \quad \Sigma_\epsilon = \sigma_\epsilon^2 \begin{pmatrix} 1 & \rho \\ \rho & 1 \end{pmatrix}.$$

Note that conditional on the row effects $\{a_1, \ldots, a_n\}$, the mean in the ith row of $\mathbf{Y}$ is given by $\mu + a_i$, and the variability of these row-specific means is given by σ_a^2. In this way, the row effects represent across-row heterogeneity in the sociomatrix, and σ_a^2 is a single-number summary of this heterogeneity. Similarly, the column effects $\{b_1, \ldots, b_n\}$ represent heterogeneity in the column means, and σ_b^2 summarizes this heterogeneity. The covariance σ_{ab} describes the linear association between these row and column effects, or equivalently, the association between the row means and

column means of the sociomatrix. Additional variability across dyads is described by σ_ϵ^2, and within dyad correlation (beyond that described by σ_{ab}) is captured by ρ. More precisely, straightforward calculations show that, under this random effects model,

$$
\begin{aligned}
\text{Var}[y_{i,j}] &= \sigma_a^2 + 2\sigma_{ab} + \sigma_b^2 + \sigma_\epsilon^2 && \text{(across-dyad variance)} \\
\text{Cov}[y_{i,j}, y_{i,k}] &= \sigma_a^2 && \text{(within-row covariance)} \\
\text{Cov}[y_{i,j}, y_{k,j}] &= \sigma_b^2 && \text{(within-column covariance)} \\
\text{Cov}[y_{i,j}, y_{j,k}] &= \sigma_{ab} && \text{(row-column covariance)} \\
\text{Cov}[y_{i,j}, y_{j,i}] &= 2\sigma_{ab} + \rho\sigma_e^2 && \text{(row-column covariance plus reciprocity)} ,
\end{aligned}
\tag{2}
$$

with all other covariances between elements of $\mathbf{Y}$ being zero. We refer to this covariance model as the *social relations covariance model*.

The `amen` package provides model fitting and evaluation tools for the SRM via the default values of the `ame` command:

```
fit_SRM<-ame(Y)
```

The top row of figures provided by the fitting command are traceplots of the parameter values, including covariance parameters on the left and regression parameters on the right. The covariance parameters include Σ_{ab}, ρ, and σ^2, and are stored as the list component VC in the fitted object. The only regression parameter for this model is the intercept μ, which is included by default for the Gaussian SRM. The intercept, and any other regression parameters are stored as BETA in the fitted object. We can compare these estimates obtained from `amen` to the estimates from the ANOVA-style approach as follows:

```
muhat                                  # empirical overall mean

[1] 0.680044

mean(fit_SRM$BETA)                     # model-based estimate

[1] 0.6616449

cov( cbind(ahat,bhat))                 # empirical row/column mean covariance

          ahat      bhat
ahat 0.2407563 0.2290788
bhat 0.2290788 0.2289489
```

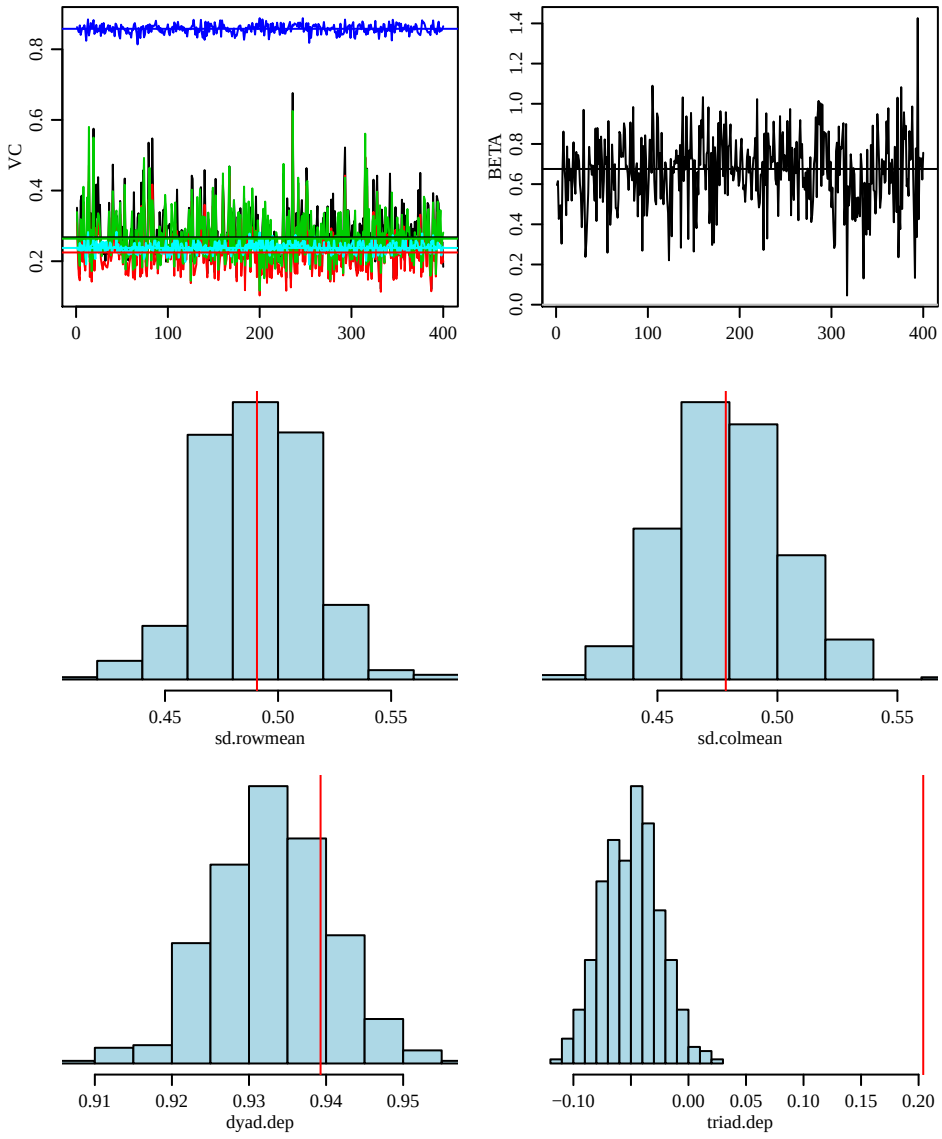
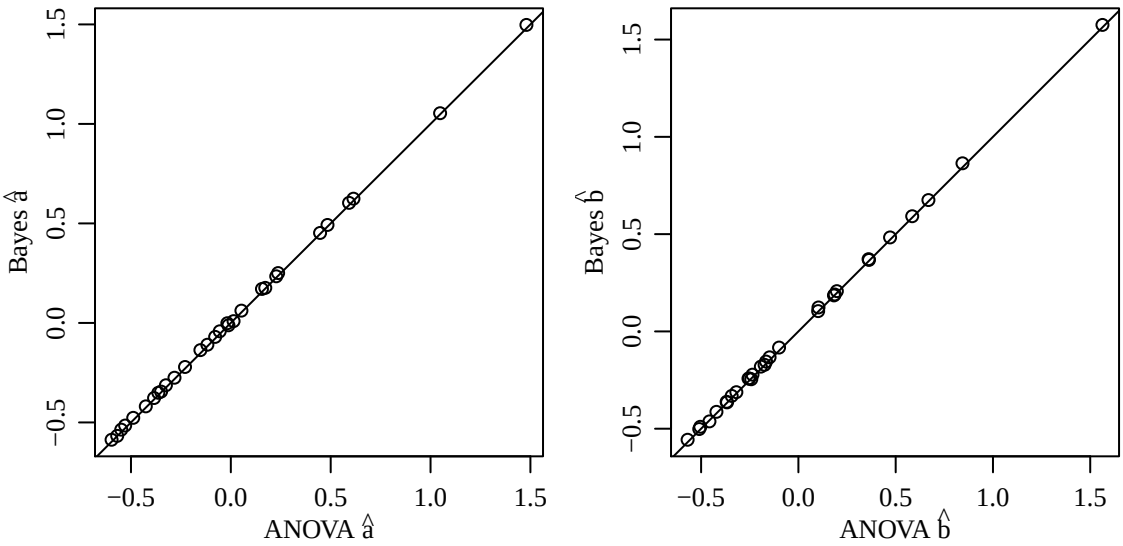


Figure 2: Default plots generated by the ame command.

```
apply(fit_SRM$VC[,1:3],2,mean)      # model-based estimate

       va       cab        vb
0.2811301 0.2368096 0.2728049

cor( c(R), c(t(R)) ,use="complete")  # empirical residual dyadic correlation

[1] 0.8591242

mean(fit_SRM$VC[,4] )               # model-based estimate

[1] 0.857584
```

Posterior mean estimates of the row and column effects can be accessed from `fit_SRM$APM` and `fit_SRM$BPM`, respectively. These estimates are plotted below, against the corresponding ANOVA estimates.



The second two rows of Figure of 2 give posterior predictive goodness of fit summaries for four network statistics: (1) the empirical standard deviation of the row means; (2) the empirical standard deviation of the column means; (3) the empirical within-dyad correlation; (4) a normalized measure of triadic dependence. Details on how these are computed can be obtained by examining the `gofstats` function. The blue histograms represent values of `gofstats(Ysim)`, where `Ysim` is simulated from the posterior predictive distribution. These histograms should be compared to the observed statistics `gofstats(Y)`, which for these data are 0.491, 0.478, 0.939, 0.204, given by vertical red lines in the figure. Generally speaking, large discrepancies between the posterior

predictive distributions (histograms) and the observed statistics (red lines) suggest model lack of fit. For these data, the model does well at representing the data with respect to the first three statistics, but shows a discrepancy with regard to the triadic dependence statistic. This is not too surprising, as the SRM only captures second-order dependencies (variances and covariances).

1.2 Social relations regression modeling

Often we wish to quantify the association between a relational variable and some observed nodal or dyadic characteristics. Useful for such situations is a type of linear mixed effects model we refer to as the *social relations regression model* (SRRM), which combines a linear regression model with the covariance structure of the SRM as follows:

$$y_{i,j} = \beta^T \mathbf{x}_{d,i,j} + \beta_r^T \mathbf{x}_{r,i} + \beta_c^T \mathbf{x}_{c,j} + a_i + b_j + \epsilon_{i,j}, \tag{3}$$

where $\mathbf{x}_{d,i,j}$ is a vector of characteristics of dyad i, j, $\mathbf{x}_{r,i}$ is a vector of characteristics of node i as a sender, and $\mathbf{x}_{c,j}$ is a vector of characteristics of node j as a receiver. We refer to $\mathbf{x}_{d,i,j}$, $\mathbf{x}_{r,i}$ and $\mathbf{x}_{c,i}$ as dyadic, row and column covariates, respectively. In many applications the row and column characteristics are the same so that $\mathbf{x}_{r,i} = \mathbf{x}_{c,i} = \mathbf{x}_i$, in which case they are simply referred to as nodal covariates. However, it can sometimes be useful to distinguish $\mathbf{x}_{r,i}$ from $\mathbf{x}_{c,i}$: In the context of friendships among students, for example, it is conceivable that some characteristic of a person (such as athletic or academic success) may affect their popularity (how much they are liked by others), but not their sociability (how much they like others).

We illustrate parameter estimation for the SRRM by fitting the model to the trade data. Nodal covariates include (log) population, (log) GDP, and polity, a measure of democracy. Dyadic covariates include the number the number of conflicts and (log) geographic distance between countries, the number of shared IGO memberships, and a polity interaction (the product of the nodal polity scores).

```
#### ---- nodal covariates
dimnames(IR90s$nodevars)[[2]]

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

Xn<-IR90s$nodevars[topgdp,]
Xn[,1:2]<-log(Xn[,1:2])
```

```
#### ---- dyadic covariates
dimnames(IR90s$dyadvars)[[3]]

[1] "conflicts"   "exports"     "distance"    "shared_igos" "polity_int"

Xd<-IR90s$dyadvars[topgdp,topgdp,c(1,3,4,5)]
Xd[,,3]<-log(Xd[,,3])
```

Note that dyadic covariates are stored in an $n \times n \times p_d$ array, where n is the number of nodes and p_d is the number of dyadic covariates.

The SRRM can be fit using the `ame` function by just specifying the covariates:

```
fit_srrm<-ame(Y,Xd=Xd,Xr=Xn,Xc=Xn)
```

Posterior mean estimates, standard deviations, nominal z-scores and p-values may be obtained with the `summary` command:

```
summary(fit_srrm)


Regression coefficients:
                  pmean   psd z-stat p-val
intercept        -6.405 1.254 -5.109 0.000
pop.row          -0.330 0.132 -2.502 0.012
gdp.row           0.567 0.150  3.770 0.000
polity.row       -0.015 0.020 -0.788 0.431
pop.col          -0.302 0.126 -2.389 0.017
gdp.col           0.537 0.147  3.650 0.000
polity.col       -0.006 0.019 -0.309 0.757
conflicts.dyad    0.076 0.042  1.829 0.067
distance.dyad    -0.041 0.007 -6.122 0.000
shared_igos.dyad  0.883 0.186  4.756 0.000
polity_int.dyad  -0.001 0.001 -1.662 0.097

Variance parameters:
    pmean   psd
va  0.264 0.105
cab 0.212 0.097
vb  0.250 0.099
```

```
rho 0.785 0.019
ve  0.157 0.011
```

The column `z-stat` is obtained by dividing the posterior means by their posterior standard deviations, and each `p-val` is the the probability that a standard normal random variable exceeds the corresponding `z-stat` in absolute value. Based on these calculations, there appears to be strong evidence for associations between countries' export and import levels with both population and GDP. Additionally, there is evidence that geographic proximity and the number of shared IGOs are both positively associated with trade between country pairs.

It is instructive to compare these results to those that would be obtained under an ordinary linear regression model that assumed i.i.d. residual standard error. Such a model can be fit in the `amen` package by opting to fit a model with no row variance, column variance or dyadic correlation:

```
fit_rm<-ame(Y,Xd=Xd,Xr=Xn,Xc=Xn,rvar=FALSE,cvar=FALSE,dcor=FALSE)
```

```
summary(fit_rm)


Regression coefficients:
                  pmean   psd  z-stat p-val
intercept        -4.417 0.170 -25.947 0.000
pop.row          -0.318 0.022 -14.621 0.000
gdp.row           0.664 0.024  27.417 0.000
polity.row       -0.007 0.005  -1.335 0.182
pop.col          -0.280 0.023 -12.328 0.000
gdp.col           0.622 0.024  25.590 0.000
polity.col        0.002 0.005   0.509 0.611
conflicts.dyad    0.238 0.057   4.152 0.000
distance.dyad    -0.053 0.004 -14.407 0.000
shared_igos.dyad -0.021 0.028  -0.739 0.460
polity_int.dyad   0.000 0.001   0.280 0.780

Variance parameters:
    pmean   psd
va  0.000 0.000
```

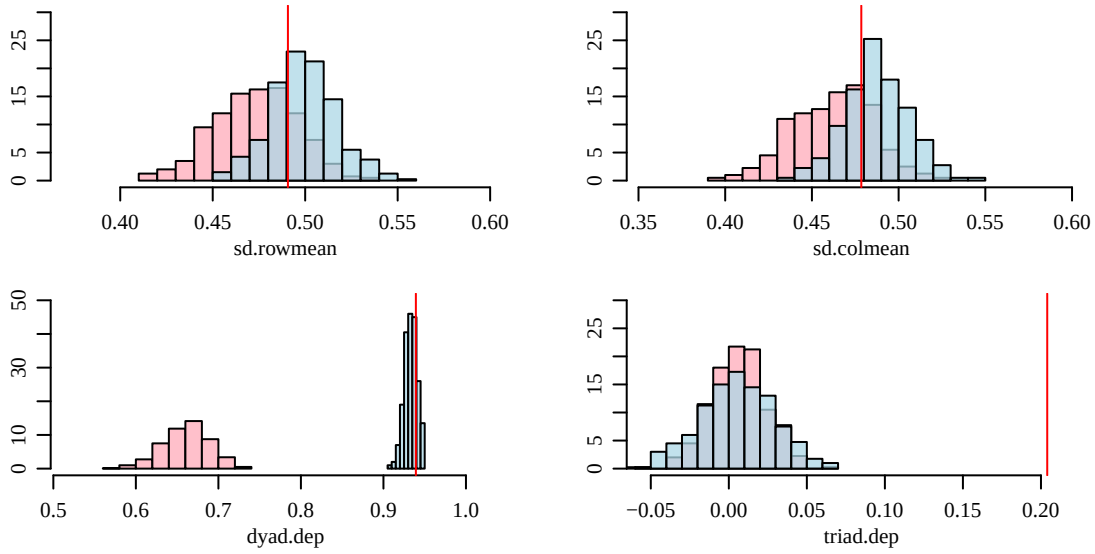


Figure 3: Posterior predictive distributions of goodness of fit statistics for the ordinary regression model (pink) and the SRRM (blue).

```
cab 0.000 0.000
vb  0.000 0.000
rho 0.000 0.000
ve  0.229 0.011
```

The parameter standard deviations (i.e., standard errors) under this i.i.d. model are almost all larger than those under the SRM fit. The explanation for this is that the i.i.d. model wrongly assumes independent observations, and thus overrepresents the amount of precision in the parameter estimates. This can be seen in the posterior predictive goodness of fit plots given in Figure 3. The plots show, in particular, that the data exhibit much more dyadic correlation than can be explained by the i.i.d. model. In contrast, the SRRM does not show such a discrepancy with regard to this statistic. However, both models fail to represent the amount of triadic dependence in the data, as shown in the fourth goodness of fit plot.

1.3 Transitivity and stochastic equivalence via multiplicative effects

It is often observed that the similarity of two nodes i and j in terms of their individual characteristics $\mathbf{x}_i$ and $\mathbf{x}_j$ is associated with the value of the relation $y_{i,j}$ between them. For example, suppose for

each node i that x_i is the indicator that person i is a member of a particular group or organization. Then $x_i x_j$ is the indicator that i and j are co-members of this organization, and this fact may have some effect on their relation $y_{i,j}$. A positive effect of $x_i x_j$ on $y_{i,j}$ is referred to as homophily, and a negative effect as anti-homophily. Measuring homophily on as observed characteristic can be done within the context of the SRRM by creating a dyadic covariate $x_{d,i,j}$ from a nodal covariate x_i through multiplication ($x_{d,i,j} = x_i x_j$) or some other operation. Homophily on nodal characteristics can lead to certain types of patterns often seen in network and relational data, sometimes referred to as transitivity, balance and clustering. For example, in a binary network where people prefer to form ties to others who are similar to them, there tend to be a lot of "transitive triples," that is, triples of indices i, j, k having a link between each pair. One explanation of this is that links from i to j and from i to k occur because i is similar to both j and to k. If this is the case, then j and k must also be somewhat similar, and so there is a high probability of a link between j and k, which would form a triangle of ties among nodes i, j and k. Multiple linked triangles result in visual "clusters" in graphs of social networks.

More generally, in the case of multiple sender and receiver covariates, we are interested in how a person with characteristics $\mathbf{x}_{r,i}$ relates to a person with characteristics $\mathbf{x}_{c,j}$. This can be evaluated in the SRRM by including a set of regression terms equivalent to $\mathbf{x}_{r,i}^T \mathbf{B} \mathbf{x}_{c,i}$ Although this term is multiplicative in the covariates, it is linear in the parameters, as

$$\mathbf{x}_{r,i}^T \mathbf{B} \mathbf{x}_{c,i} = \sum_k \sum_l b_{k,l} x_{r,i,k} x_{c,j,l}$$

and so the matrix of parameters may be estimated within the context of a linear regression model simply by including all products of the elements of $\mathbf{x}_{r,i}$ and $\mathbf{x}_{c,j}$ as dyadic covariates. In practice, if $\mathbf{x}_{r,i}$ and $\mathbf{x}_{c,j}$ are of the same length (for example, if they are the same), then it is common to take $\mathbf{B}$ to be a diagonal matrix, in which case

$$\mathbf{x}_{r,i}^T \mathbf{B} \mathbf{x}_{c,i} = b_1 x_{r,i,1} x_{c,j,1} + \cdots b_p x_{r,i,p} x_{c,j,p}.$$

Such terms in the regression model can often account for network patterns such as transitivity and clustering, as described above. They can also account for another type of network pattern, known as stochastic equivalence, where it is observed that a group of nodes all relate to the other nodes (and each other) in a similar way. If such groups are related to the observed nodal covariates, then often

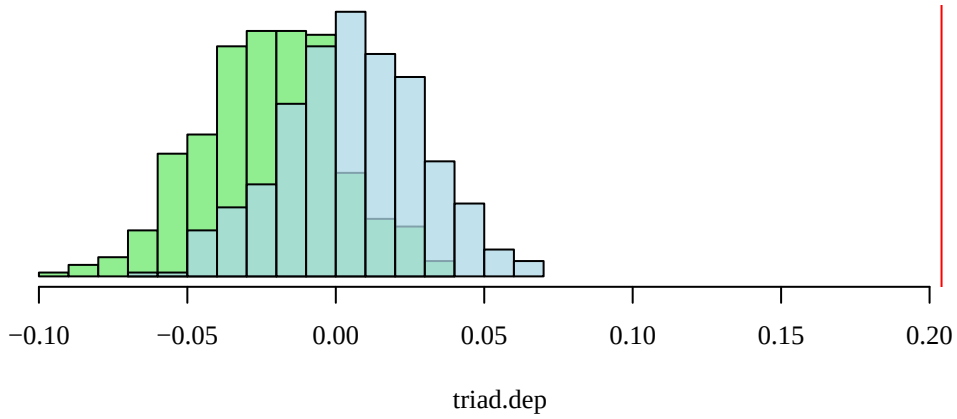


Figure 4: Comparison of the SRRM with (blue) and without (green) nodal interaction effects, in terms of the triadic dependence statistic.

the stochastic equivalence in the data may be estimated and represented by these multiplicative regression terms.

This can be seen to a limited degree in the trade data: Note that the number of shared IGOs and the polity interaction can both be viewed as dyadic covariates obtained by multiplication of nodal covariates. We can fit an SRRM without these effects:

```
fit_srrm0<-ame(Y,Xd[,,1:2],Xn,Xn)
```

Now we compare the resulting posterior predictive distribution of the transitivity statistic to that under the full SRRM that included these multiplicative effects with the histograms in Figure 4: The figure shows that, while both models do not fully represent the triadic dependence in the data, the model that includes the nodal interactions does slightly better. This raises the possibility that there may exist other nodal attributes, not given in the dataset, whose multiplicative interaction might help further describe the triadic dependence observed in the data. In such cases, it can be useful to include *latent* nodal characteristics into the regression model, resulting in the following:

$$y_{i,j} = \beta^T \mathbf{x}_{d,i,j} + \beta_r^T \mathbf{x}_{r,i} + \beta_c^T \mathbf{x}_{c,j} + a_i + b_j + \mathbf{u}_i^T \mathbf{v}_j + \epsilon_{i,j}, \tag{4}$$

Here, $\mathbf{u}_i$ is a vector of latent, unobserved factors or characteristics that describe node i's behavior as a sender, and similarly $\mathbf{v}_j$ describes node j's behavior as a receiver. In this model, the mean

of $y_{i,j}$ depends on how "similar" $\mathbf{u}_i$ and $\mathbf{v}_j$ are (i.e., the extent to which the vectors point in the same direction) as well as the magnitudes of the vectors. Note also that basic results from matrix algebra indicate that any type of network pattern that could be described by a regression term of the form $\mathbf{x}_{r,i}\mathbf{B}\mathbf{x}_{c,j}$ can also be described by the multiplicative effects term $\mathbf{u}_i^T\mathbf{v}_j$.

We call a model of the form (4) an *additive and multiplicative effects* model, or AME model, for network and relational data. An AME model essentially combines an *additive main effects, multiplicative interaction* model, or AMMI model (Gollob, 1968; Bradu and Gabriel, 1974), a class of models developed in the psychometric and agronomy literature, with the SRM covariance structure that recognizes the relational aspect of the data. An AME model, like other latent factor models, requires the specification of the dimension of the latent factors. In the `amen` package, this can be set with the option `R` in the `ame` command The letter `R` here stands for "rank": If $\mathbf{U}$ and $\mathbf{V}$ are $n \times R$ matrices of the latent factors, then $\mathbf{U}\mathbf{V}^T$ has rank `R`. For example, a rank-2 AME model may be fit as follows:

```
fit_ame2<-ame(Y,Xd,Xn,Xn,R=2)
```

The diagnostic plots for the model fit are given in Figure 5. Note that, unlike all previous models considered, this model provides an adequate fit in terms of the triadic dependence statistic. The regression parameter estimates and their standard errors lead to more or less similar conclusions as in the SRRM, except that the number of shared IGOs no longer has a large effect after controlling for the triadic dependence with the latent factors.

```
summary(fit_ame2)


Regression coefficients:
                  pmean   psd z-stat p-val
intercept        -4.200 0.741 -5.665 0.000
pop.row          -0.286 0.074 -3.869 0.000
gdp.row           0.574 0.097  5.918 0.000
polity.row       -0.001 0.011 -0.084 0.933
pop.col          -0.242 0.072 -3.350 0.001
gdp.col           0.524 0.096  5.432 0.000
polity.col        0.008 0.011  0.730 0.466
conflicts.dyad    0.017 0.038  0.446 0.656
distance.dyad    -0.038 0.004 -8.747 0.000
shared_igos.dyad  0.119 0.087  1.365 0.172
polity_int.dyad  -0.001 0.000 -2.298 0.022
```

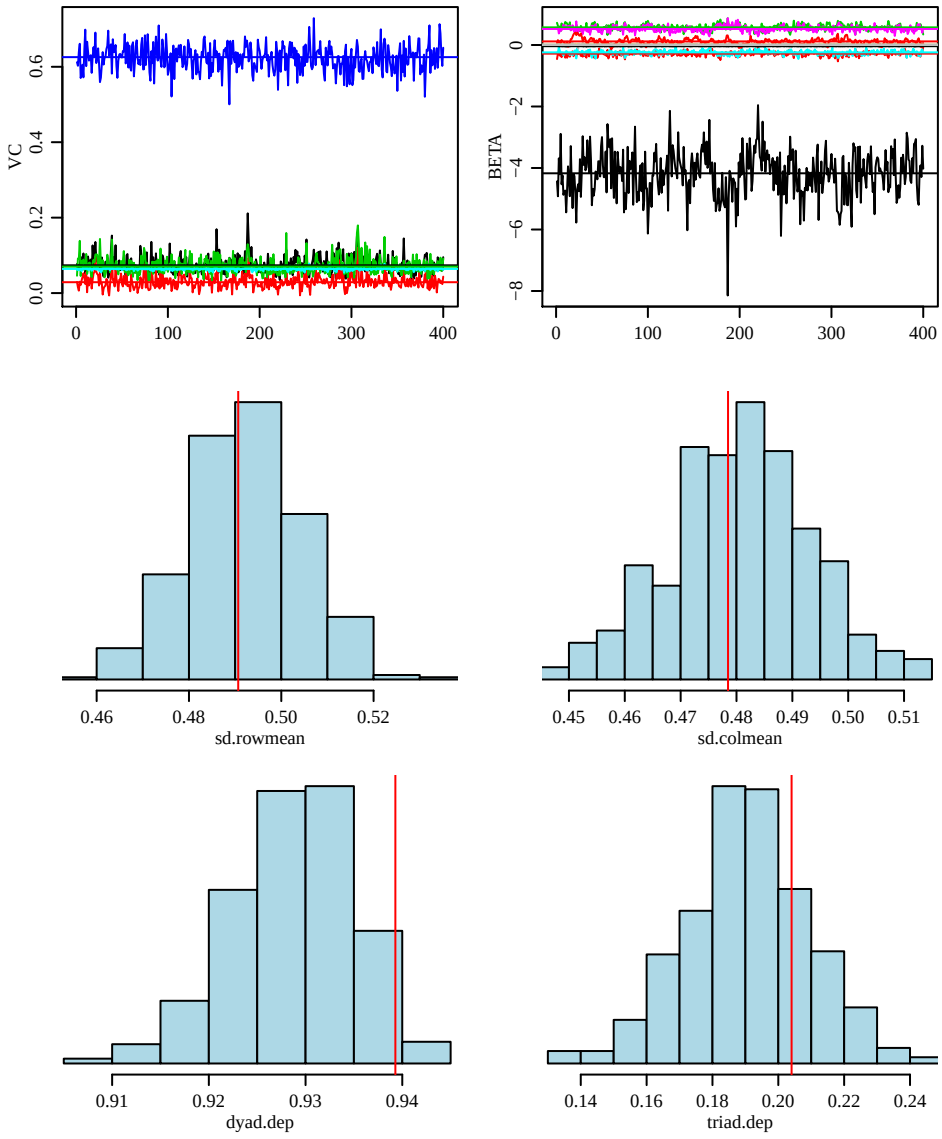


Figure 5: Diagnostic plots for the rank-2 AME model.

```
Variance parameters:
    pmean   psd
va  0.076 0.023
cab 0.031 0.019
vb  0.073 0.023
rho 0.623 0.035
ve  0.064 0.004
```

In some cases it is of interest to examine the estimated latent factors and compare them across nodes. Some ways to do this include clustering the latent factors or simply plotting them. The function `circplot` in the `amen` package provides a plot that can describe the estimated latent factors of a rank-2 model. Such a plot for the trade data is shown graphically in Figure 6. Such a figure can help identify groups of nodes that are similar to each other in terms of exporting and importing behavior, after controlling for regression and additive row and column effects. For example, the plot identifies the high trade volume between countries on the Pacific rim.

2 AME models for ordinal data

Relational datasets often include relational variables that are not well-represented by normal models. In some cases, such as with trade data, the relation of interest can be transformed so that the Gaussian AME model is reasonable. In other cases, such as with binary, ordinal, discrete or sparse relations, no such transformation is available. Examples of such data include measures of friendship that are binary (not friends/friends) or ordinal (dislike/neutral/like), discrete counts of conflictual events between countries, or the amount of time two people spend on the phone with each other (which might be zero for most pairs in a population).

In this section we describe extensions of the Gaussian AME model to accommodate ordinal relational data, where in what follows, ordinal means any outcome for which the possible values can be put in some order. This includes discrete outcomes (such as binary indicators or counts), ordered qualitative outcomes (such as low/medium/high, i.e. the "traditional" definition of ordinal), and even continuous outcomes. The extensions are based on latent variable representations of probit and ordinal probit regression.

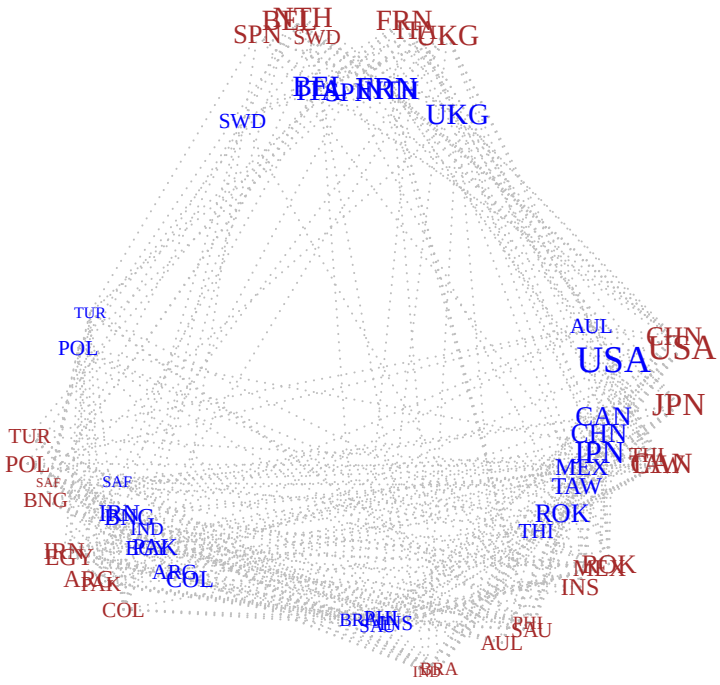


Figure 6: Circle plot of estimated latent factors. Directions of $\hat{\mathbf{u}}_i$'s and $\hat{\mathbf{v}}_i$'s given in red and blue, respectively, with the plotting size a function of the factor magnitudes. Dashed lines between countries indicate greater than expected trade based on the regression terms and additive effects.

2.1 Example: Analysis of a binary outcome

The simplest type of ordinal relation is a binary indicator of some feature of the relationship between i and j, so that $y_{i,j} = 0$ or 1 depending on whether or not the feature is absent or present, respectively. Data on such relations, particularly those indicating a social interaction or friendship, are often called *social networks*. For example, the dataset `lazegalaw` included with the `amen` package includes a social network of friendship ties between 71 members of a law firm, along with two other dyadic relations and several nodal characteristics. The friendship data are displayed as a graph in Figure 7, where the nodes are colored according to which of three offices each lawyer works.

We first consider fitting a probit SRM model to these binary data, without including any explanatory covariates. This model can be written as

$$z_{i,j} = \mu + a_i + b_j + \epsilon_{i,j} \tag{5}$$

$$y_{i,j} = 1(z_{i,j} > 0), \tag{6}$$

where the distributions of the random effects a_i, b_j, and $\epsilon_{i,j}$ follow the Gaussian SRM covariance model as described above. In words, this model expresses the observed binary relation $y_{i,j}$ as the indicator that some continuous latent relation $z_{i,j}$ exceeds zero. Assuming the SRM for the latent relation yields a model for the observed binary data that allows for within row, within column and within dyad dependence. This model can be fit with the `ame` command by specifying that the relation type is binary:

```
fit_SRM<-ame(Y,model="bin")
```

It is instructive to compare the fit of this model to that provided by a reduced model that lacks the SRM terms:

```
fit_SRG<-ame(Y,model="bin",rvar=FALSE,cvar=FALSE,dcor=FALSE)
```

This is a probit model that contains only an intercept, and so is equivalent to the simple random graph model (SRG). The fits of these two models in terms of the four goodness of fit statistics computed by `gofstats` are compared in Figure 8. As might be expected, the SRG fails in terms of all four statistics. In contrast, the SRM model provides a good fit in terms of the three statistics that represent second-order dependencies. Both models fail in terms of representing third-order dependence.

```
data(lazegalaw)

Y<-lazegalaw$Y[,,2]
Xd<-lazegalaw$Y[,,-2]
Xn<-lazegalaw$X

dimnames(Xd)[[3]]

[1] "advice" "cowork"

dimnames(Xn)[[2]]

[1] "status"    "female"    "office"    "seniority" "age"       "practice"
[7] "school"

netplot(lazegalaw$Y[,,2],ncol=Xn[,3])
```

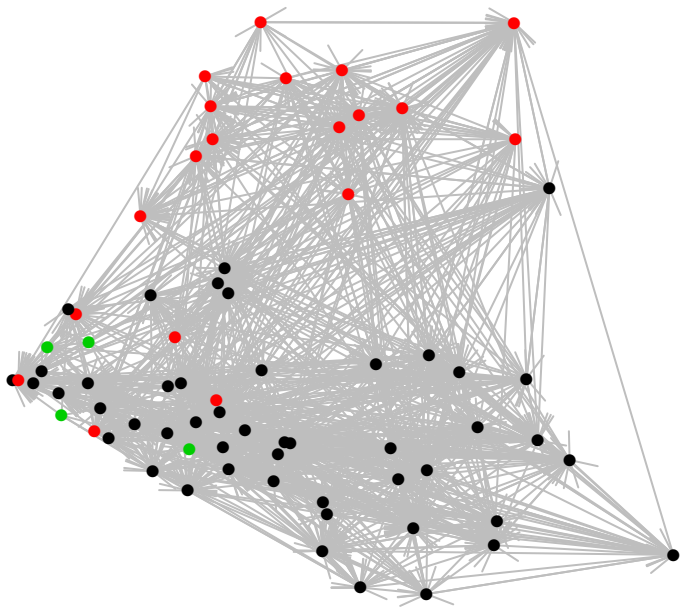


Figure 7: Graph of friendship network between 71 lawyers. Node colors represent at which of the three offices each lawyer works.

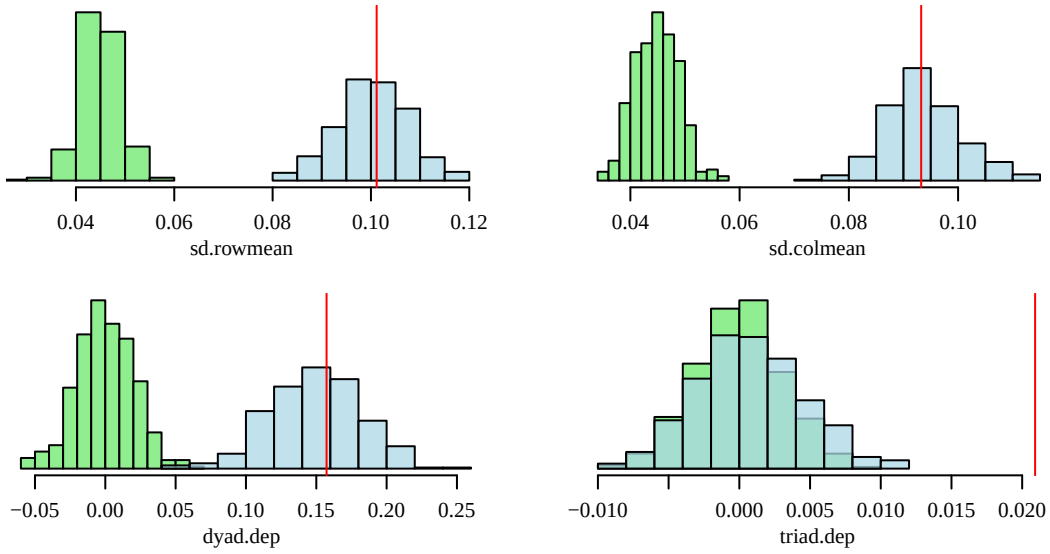


Figure 8: Comparison of SRM (blue) and SRG (green) for the Lazega law friendship network.

A common empirical description of row and column heterogeneity in network data are the row and column sums, typically referred to as the *outdegrees* and *indegrees*. Based on the form of the model in (5), we might expect that the outdegrees and indegrees would be positively associated with the estimates of the a_i's and b_j's respectively. For example, the larger a_i is, the larger the entries of $z_{i,j}$ for each j, thereby making more of the $y_{i,j}$'s equal to one rather than zero. This relationship between the degrees and the parameter estimates is illustrated in Figure 9. The figure does indeed show a strong positive association between these quantities, but note that the relationship is not strictly monotonic. The reason for this can be explained by the fact that it is both the a_i parameters *and* the b_j parameters that are used to describe nodal heterogeneity. For example, suppose two nodes have the same outdegree, but the first links to several nodes that have low indegrees, whereas a second node links to the same number of nodes but ones having high indegrees. The first node will have an a_i estimate that is higher than that of the second, because the b_j's of the nodes that the first links to will be lower than those of the nodes that the second links to.

We next consider a probit SRRM that includes the SRM terms, linear terms for the binary or ordinal nodal covariates, and the other dyadic relations as dyadic covariates. This model is formulated as in the SRM probit model, except that $z_{i,j}$ follows an SRRM rather than an SRM.

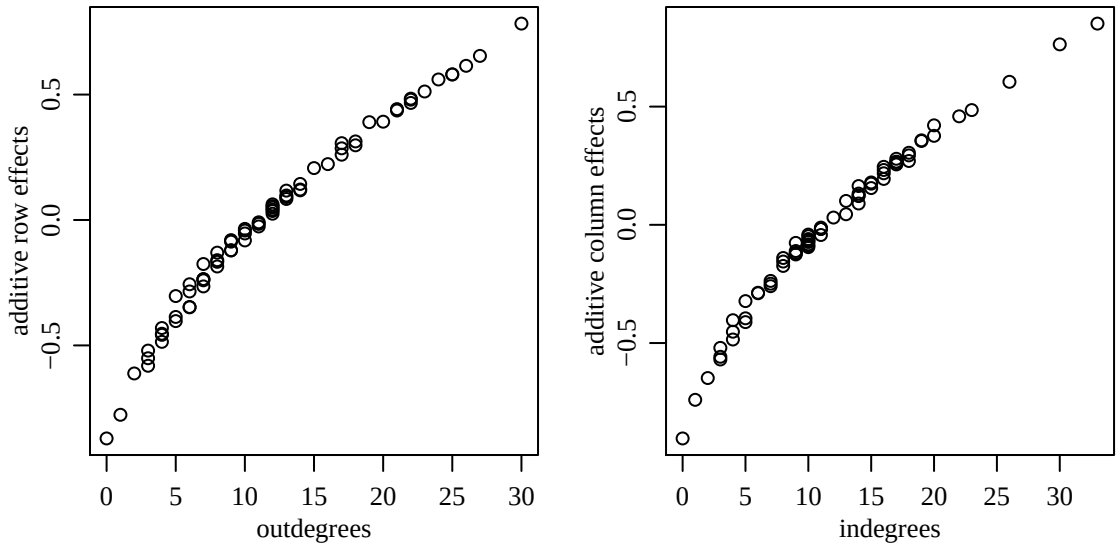


Figure 9: Comparison of SRM (blue) and SRG (green) for the Lazega law friendship network.

```
Xno<-Xn[,c(1,2,4,5,6)]
fit_SRRM<-ame(Y, Xd=Xd, Xr=Xno, Xc=Xno, model="bin")
```

```
summary(fit_SRRM)


Regression coefficients:
               pmean   psd z-stat p-val
intercept      0.882 0.659  1.338 0.181
status.row    -0.174 0.175 -0.992 0.321
female.row     0.007 0.143  0.051 0.959
seniority.row -0.008 0.012 -0.675 0.500
age.row       -0.016 0.009 -1.722 0.085
practice.row  -0.227 0.109 -2.089 0.037
status.col    -0.168 0.145 -1.154 0.248
female.col    -0.027 0.123 -0.219 0.827
seniority.col  0.012 0.011  1.056 0.291
age.col       -0.008 0.008 -1.064 0.287
practice.col  -0.286 0.110 -2.602 0.009
advice.dyad   -0.080 0.075 -1.069 0.285
cowork.dyad    1.281 0.063 20.313 0.000
```

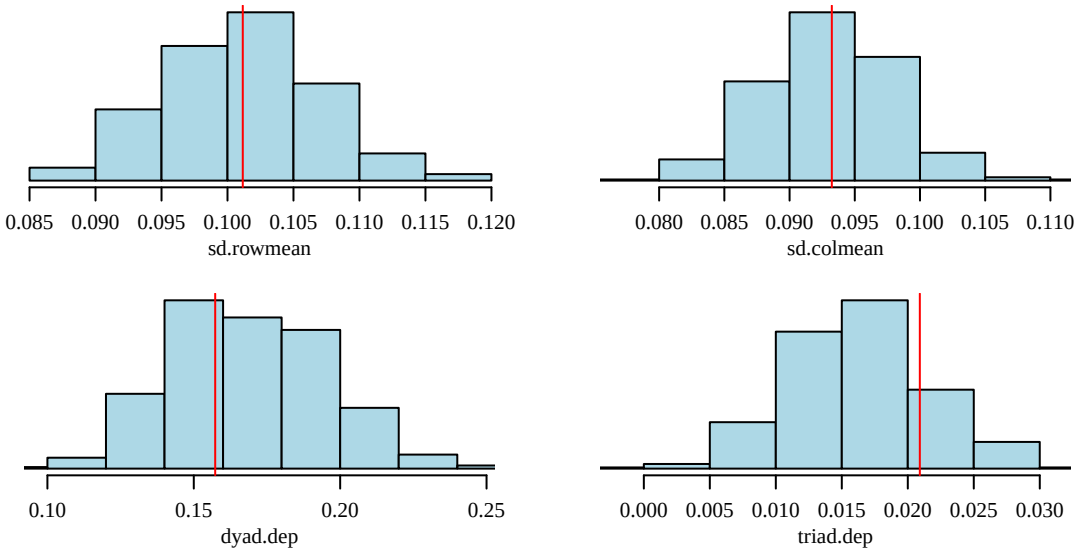


Figure 10: Checks of the fit of the rank-3 AME model to the Lazega law friendship network.

```
Variance parameters:
    pmean   psd
va  0.170 0.037
cab 0.012 0.025
vb  0.134 0.032
rho 0.110 0.048
ve  1.000 0.000
```

There is not much evidence for effects of the nodal characteristics, at least in terms of effects that appear linearly in the SRRM. Additionally, goodness-of-fit plots indicate lack of fit in terms of triadic dependence, as with the SRM model. Thus, we consider instead a model without the "non-significant" regressors from the SRRM removed, and include a rank-3 multiplicative effect.

```
fit_AME<-ame(Y, Xd=Xd[,,2], R=3, model="bin")
```

The goodness-of-fit plots in Figure 10 indicate no strong discrepancy between this model and the data in terms of these statistics. Inference then proceeds via examination of the estimates of regression effects, random effects and covariance parameters. Interpretation of the multiplicative effects can proceed by plotting, looking for clusters, and identification of nodes with large effects. Additionally, it can be useful to try to relate these multiplicative effects to any nodal characteristics

available. For example, we can compute correlations between the multiplicative effects $(\mathbf{u}_i, \mathbf{v}_i)$ and any numerical or ordinal nodal characteristics $\mathbf{x}_i$, and association with categorical variables can be examined via plots.

```
U<-fit_AME$U
V<-fit_AME$V

round(cor(U, Xno),2)

     status female seniority   age practice
[1,]  -0.12  -0.03     -0.19 -0.25    -0.02
[2,]  -0.34  -0.04      0.24  0.25     0.62
[3,]  -0.10   0.26      0.15  0.25     0.22

round(cor(V, Xno),2)

     status female seniority  age practice
[1,]  -0.81  -0.32      0.71 0.62     0.23
[2,]  -0.05   0.11     -0.05 0.00     0.54
[3,]  -0.01   0.23      0.26 0.34     0.27
```

These correlations, and the plots in Figure 11, indicate that these nodal characteristics do play a role in network formation, although in a multiplicative rather than additive manner. If desired, one could use these results to construct multiplicative functions of these nodal attributes for inclusion into a SRRM, or possibly an AME model of lower rank.

2.2 Example: Analysis of an ordinal outcome

The probit AME model for binary data extends in a natural way to accommodate ordinal data with more than two levels. As with binary data, we model the sociomatrix $\mathbf{Y} = \{y_{i,j}\}$ as being a function of a latent sociomatrix $\mathbf{Z}$ that follows a Gaussian AME model. Specifically, our model is

$$\begin{aligned} z_{i,j} &= \beta^T \mathbf{x}_{d,i,j} + \beta_r^T \mathbf{x}_{r,i} + \beta_c^T \mathbf{x}_{c,j} + a_i + b_j + \epsilon_{i,j}, \\ y_{i,j} &= g(z_{i,j}), \end{aligned} \tag{7}$$

where g is some unknown non-decreasing function. The `amen` package takes a semiparametric approach to this model, providing estimation and inference for the parameters in the model (7) for

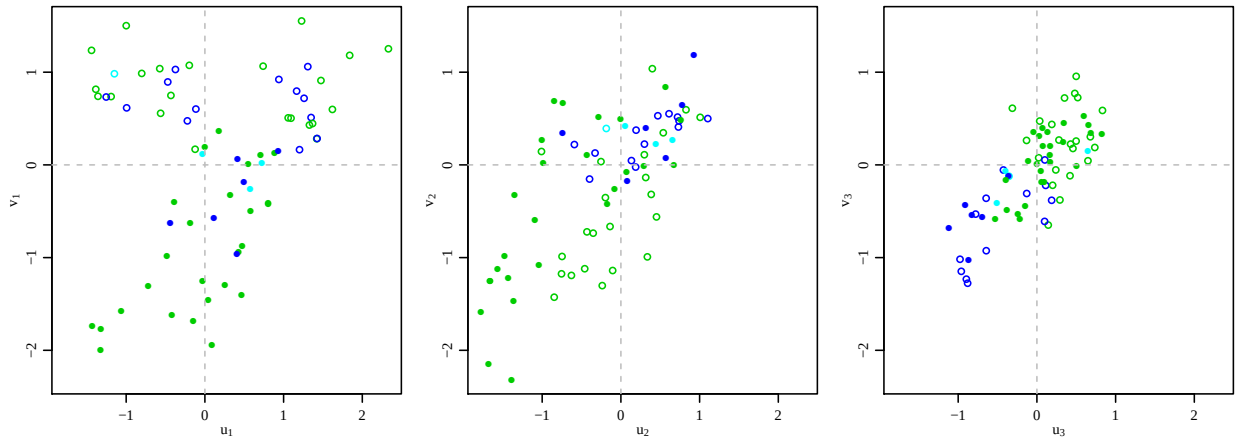


Figure 11: Estimated latent factors plotted in terms of the nodal characteristics `status` (partner=unfilled circle, associate=filled circle) and `office` (Boston=green, Hartford=blue, Providence=light blue).

$\mathbf{Z}$, but treats the function g as a nuisance parameter. This is done using a variant of the extended rank likelihood for ordinal data, described in Hoff (2007) and Hoff (2008). While this approach is somewhat limiting (as estimation of g is specifically provided), it simplifies some aspects of model specification and parameter estimation. In particular, the semiparametric approach allows for modeling of more general types of ordinal relations $y_{i,j}$, such as those that are continuous, have no ties or have a number of levels that is not pre-specified. However, we caution that the computation time required by the MCMC algorithm used by `amen` is increasing in the number of levels of $y_{i,j}$.

We illustrate this model fitting procedure with an analysis of dominance relations between 28 female bighorn sheep, available via the `sheep` dataset included with `amen`. The relational variable $y_{i,j}$ records the number of times sheep i was observed dominating sheep j.

```
data(sheep)

Y<-sheep$dom

gofstats(Y)

 sd.rowmean  sd.colmean    dyad.dep   triad.dep
 0.70037477  0.67209344 -0.19797403 -0.05826448
```

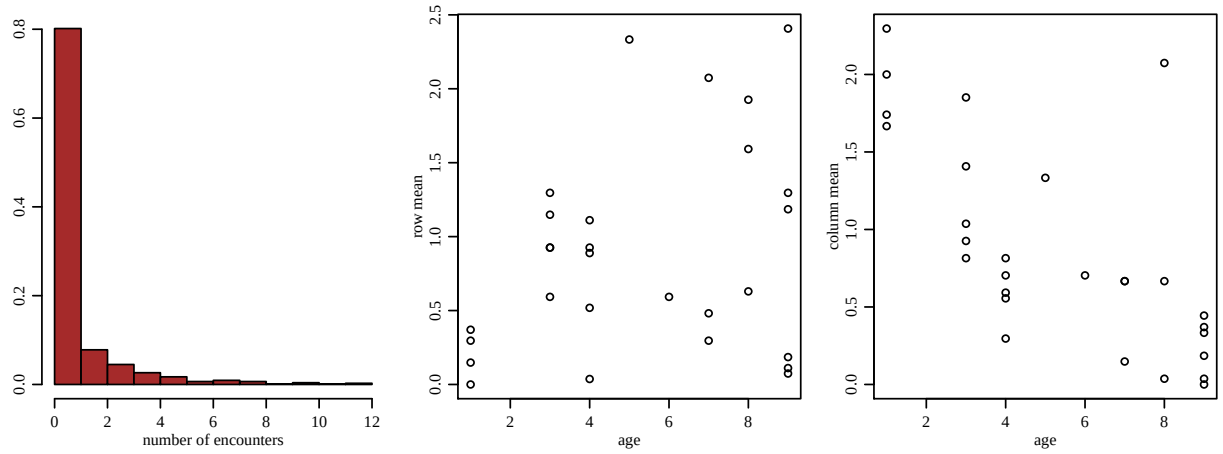


Figure 12: Plot of sheep dominance data. From left to right, a histogram of the number of dominance encounters, age versus row mean, and age versus column mean.

Note that the dyadic dependence and triadic dependence statistics are negative. This makes sense in light of the nature of the relation: Heterogeneity among the sheep in terms of strength or assertiveness would lead to powerful sheep dominating others and not being dominated themselves, which in turn would lead to negative reciprocity. Additionally, under this scenario, if sheep i dominated j, and j dominated k, then it is unlikely that k would be able to dominate i, leading to a negative triadic dependence.

Data on the ages of the sheep are also available. Plots of row and column means versus age are given in Figure 12, and indicate some evidence of an age effect. Particularly, the average number of times that a sheep is dominated is decreasing on average with age. We examine this effect more fully with a ordinal probit regression, fitting a second-degree polynomial in the ages of the sheep:

```
x<-sheep$age - mean(sheep$age)

Xd<-outer(x,x)

Xn<-cbind(x,x^2) ; colnames(Xn)<-c("age","age2")

fit<-ame(Y, Xd, Xn, Xn, model="ord")
```

```
summary(fit)
```

```
Regression coefficients:
          pmean   psd z-stat p-val
age.row   0.158 0.051  3.101 0.002
age2.row -0.086 0.019 -4.454 0.000
age.col  -0.241 0.039 -6.136 0.000
age2.col -0.008 0.015 -0.561 0.575
.dyad     0.043 0.008  5.370 0.000

Variance parameters:
     pmean   psd
va   0.433 0.153
cab  0.039 0.073
vb   0.215 0.084
rho -0.399 0.091
ve   1.000 0.000
```

The results indicate evidence for a positive effect of age on dominance - older sheep are more likely to dominate and less likely to be dominated. The dyadic effect reflects some residual effect of homophily by age: A young sheep's dominance encounters are typically with other young sheep, and older sheep are more likely to be dominated by another older sheep than a younger sheep.

Also note that the summary of the model fit does not include an intercept. This is becuase the intercept is not identifiable using the rank likelihood approach used to obtainthe parameter estimates. Specifically, an intercept term can be thought of as part of the transformation function g, which is being treated as a nuisance parameter.

3 Censored and fixed rank nomination data

Data on human social networks are often obtained by asking members of the study population to name up to a certain number of friends, and possibly rank them. Such a survey method is called a *fixed rank nomination* (FRN) scheme, and is commonly used in studies of institutions such as schools or businesses. For example, the National Longitudinal Study of Adolescent Health (AddHealth, Harris et al. (2009)) asked middle and high-school students to nominate and rank up to five members of the same sex as friends, and five members of the opposite sex as friends.

Data obtained from FRN schemes are similar to ordinal data, in that the ranks of a person's

friends may be viewed as an ordinal response. However, FRN data are also censored in a complicated way. Consider a study where people were asked to name and rank up to and including their top five friends. If person i nominates five people but doesn't nominate person j, then $y_{i,j}$ is censored: The data cannot tell us whether j is i's sixth best friend, or whether j is not liked by i at all. On the other hand, if person i nominates four people as friends but could have nominated five, then person i's data are not censored - the absence of a nomination by i of j indicates that i does not consider j a friend.

A likelihood-based approach to modeling FRN data was developed in Hoff et al. (2013). Similar to the approach for ordinal relational data described above, this methodology treats the observed ranked relational outcomes $\mathbf{Y}$ as a function of an underlying continuous sociomatrix $\mathbf{Z}$ that is generated from an AME model. Letting m be the maximum number of nominations allowed, and coding $y_{i,j} \in \{m, m-1, \ldots, 1, 0\}$ so that $y_{i,j} = m$ indicates that j is i's most liked friend, the FRN likelihood is dervived from the following constraints that the observed ranks $\mathbf{Y}$ tell us about the underlying relations $\mathbf{Z}$:

$$y_{i,j} > 0 \quad \Rightarrow \quad z_{i,j} > 0 \tag{8}$$

$$y_{i,j} > y_{i,k} \quad \Rightarrow \quad z_{i,j} > z_{i,k} \tag{9}$$

$$y_{i,j} = 0 \text{ and } d_i < m \quad \Rightarrow \quad z_{i,j} \leq 0. \tag{10}$$

Constraint (8) indicates that if i ranks j then they have a positive relation with j ($z_{i,j} > 0$), and constraint (9) indicates that a higher rank corresponds to a more positive relation. Letting $d_i \in \{0, \ldots, m\}$ be the number of people that i ranks, constraint (10) indicates that if i could have made additional friendship nominations but chose not to nominate j, they then must not consider j a friend. On the other hand, if $y_{i,j} = 0$ but $d_i = m$ then person i's unranked relationships are censored, and so $z_{i,j}$ could be positive even though $y_{i,j} = 0$. In this case, all that is known about $z_{i,j}$ is that it is less than $z_{i,k}$ for any person k that is ranked by i.

3.1 Example: Analysis of fixed rank nomination data

The `amen` package implements a Bayesian model fitting algorithm based on the FRN likelihood. We illustrate its use with an analysis of data from the classic study on relations between monks described in Sampson (1969), in which each monk was asked to rank up to three other monks in terms of a variety of relations.

```
Y<-sampsonmonks[,,3]

apply(Y>0,1,sum,na.rm=T)

  ROMUL BONAVEN AMBROSE   BERTH   PETER   LOUIS  VICTOR    WINF    JOHN
      3       3       4       3       3       3       3       3       3
   GREG    HUGH    BONI    MARK  ALBERT   AMAND   BASIL   ELIAS    SIMP
      4       3       3       3       3       3       3       3       3
```

Notice that two of the monks didn't follow the survey instructions, and nominated more than three other monks. We treat the maximum number of nominations for these two monks as four. This can be done using the `ame` fitting function, and specifying the FRN likelihood and the number of maximum nominations as follows:

```
odmax<-rep(3,nrow(Y))
odmax[ apply(Y>0,1,sum,na.rm=T)>3 ]<-4

fit<-ame(Y,R=2,model="frn",odmax=odmax)
```

```
summary(fit)


Regression coefficients:
          pmean psd z-stat p-val
intercept 0.594 0.7  0.848 0.397

Variance parameters:
    pmean   psd
va  0.519 0.486
cab 0.002 0.140
vb  0.224 0.121
rho 0.725 0.202
ve  1.000 0.000
```

Goodness of fit plots for these data appear in Figure 13. Notice that the fit in terms of row heterogeneity is very good. This is not too surprising: The simulated sociomatrices used to produce this plot are generated to satisfy the constraint imposed the outdegree constraint imposed by `odmax`, which greatly limits the possible amount of outdegree hetergeneity.

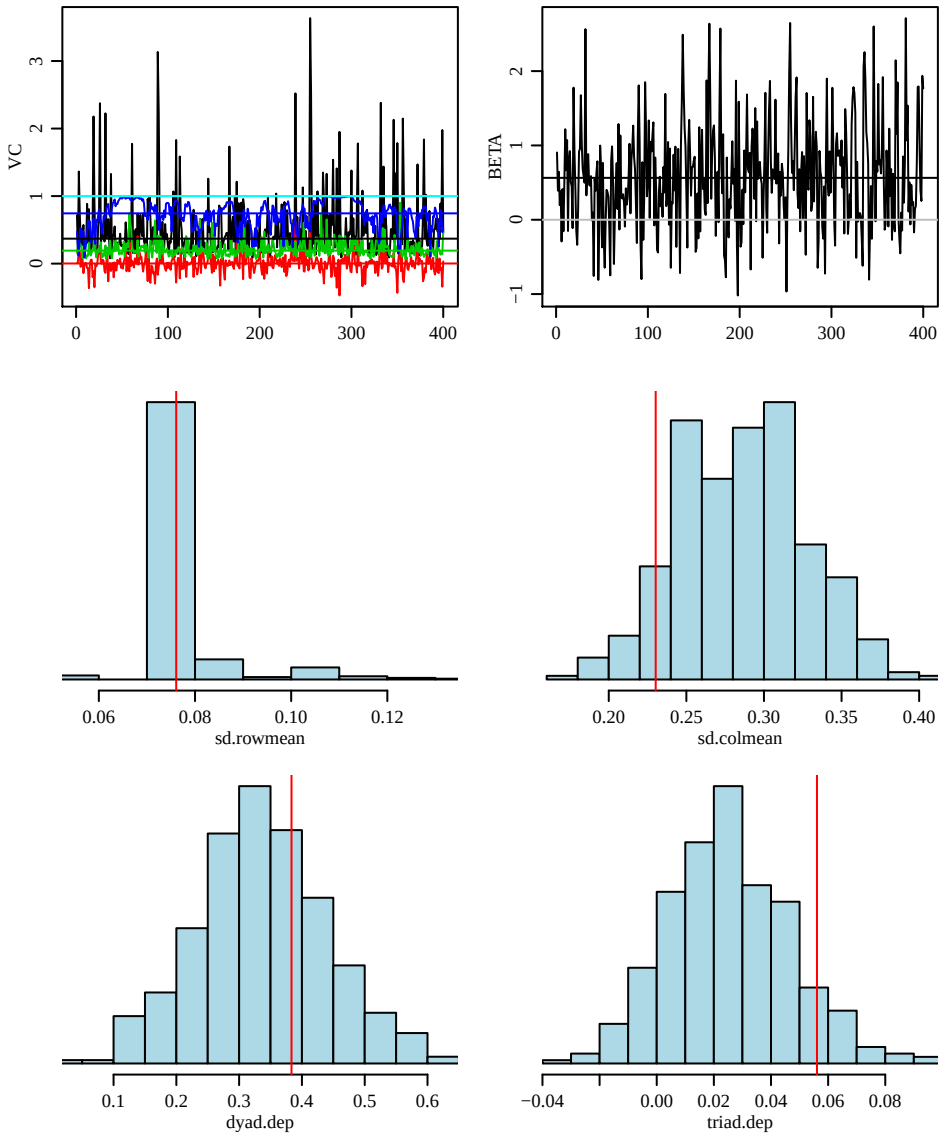


Figure 13: Model fitting plots for Sampson's monk data.

3.2 Other approaches to censored or ranked data

Some relational survey designs ask participants to nominate up to a certain number of friends, but not rank them. Such relational data are binary, but censored in the same way as are data from an FRN survey: Observing that $y_{i,j} = 0$ indicates that i is not friends with j only if person i has made less than the maximum number of nominations. A likelihood-based approach to analyzing such censored binary data is described in Hoff et al. (2013) and is also implemented in the `amen` package using the `model="cbin"` option in the `ame` command.

In other situations the relational outcomes in each row are ordinal, but on completely different scales. In such cases, we may wish to treat the heterogeneity of ties across rows in a semiparametric way, and only estimate the parameters in the AME model based on the ranks of the outcomes within each row. This can be done by using a likelihood for which the ordinal relational data $\mathbf{Y}$ only imposes constraint (9) on the unobserved underlying relations $\mathbf{Z}$. This "relative rank likelihood" is described more fully in Hoff et al. (2013), and can be implemented in `amen` using the `model="rrl"` option in the `ame` command.

4 Sampled or missing relational data

Some relational datasets are only partially observed, in that the value of the relation $y_{i,j}$ is not observed for all pairs i, j. This can happen unintentionally or by design. For example, to avoid the cost of measuring $y_{i,j}$ for all $n(n-1)$ pairs of nodes, some researchers will use multi-stage link-tracing designs, in which nodes are selected into the study in one stage of the design based on their links to nodes included in previous stages.

Given a nodeset, partially observed relational data can be represented by a sociomatrix in which the pairs for which data are not observed are distinguished from pairs for which data are observed. In R, this is done by filling each entry of the socimatrix corresponding to a missing value with an "`NA`". Doing so distinguishes pairs i, j for which we do not know the relational value ($y_{i,j} =$ `NA`) from those, for example, for which we know there is no link ($y_{i,j} = 0$).

When some (non-diagonal) entries of the sociomatrix $\mathbf{Y}$ are missing, the MCMC approximation algorithm used by `amen` proceeds by iteratively simulating model parameters along with values for the missing relations in a way that apporixmates their joint posterior distribution. Roughly

speaking, at each iteration of the MCMC algorithm, values for the missing relations are simulated from their probability distribution conditional on the observed relations and the current values of the model parameters. Such a procedure is appropriate if the missing values are *missing at random*, or more specifically, if the study design is *ignorable*. A study design is ignorable if the probability that a relational value is missing is independent of the model parameters and missing values, conditional on the observed data values. Many types of link tracing designs, such as egocentric and snowball sampling, are ignorable (Thompson and Frank, 2000).

4.1 Example: Egocentric sampling

One popular and relatively inexpensive design for gathering relational data is with an egocentric sample, in which nodes (or "egos") are randomly sampled from a population and then asked about their ties and the ties between their friends. For example, one type of egocentric study design might ask participants "whom are you friends with" and "which of your friends are friends with each other." Data from such a design can be sufficient to estimate parameters in an AME model.

We illustrate this with an example analysis of the effect of sex (male/female) on friendships among a small group of Dutch college students, available in `amen` from the `dutchcollege` dataset.

```
data(dutchcollege)

Y<-1*( dutchcollege$Y[,,7] > 1 ) # indicator of positive relationship at the last timepoint

Xn<-dutchcollege$X[,1]           # nodal indicator of male sex
Xd<-1*(outer(Xn,Xn,"=="))        # dyadic indicator of same sex
```

We will fit a simple SRRM to these data, and then compare the resulting parameter estimates to those based on data obtained from the egocentric design described above. In our design, we first randomly sample several nodes (egos), record their relational values to the other nodes, and then record the relations between alters having a common ego. R-code that generates such a design is as follows:

```
n<-nrow(Y)
Ys<-matrix(NA,n,n)      # sociomatrix for sampled data
```

```
egos<-sort(sample(n,5)) # ego sample
Ys[egos,]<-Y[egos,]     # relations of egos are observed

for(i in egos)
{
  ai<-which(Ys[i,]==1)  # alters of i
  Ys[ai,ai]<-Y[ai,ai]   # relations between alters of i are observed
}

mean(is.na(Ys))

[1] 0.7314453
```

This particular instance of the design results in a sociomatrix where about 73 percent of the entries are missing (note that the diagonal is already "missing" by definition). Under this design, relations between alters and non-alters are missing, as are relations between alters that do not share an ego.

```
egos

[1]  6 10 12 17 26

Ys[1:10,1:10]

      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
 [1,]   NA   NA   NA   NA   NA   NA   NA   NA   NA    NA
 [2,]   NA   NA    0   NA   NA   NA    0    0   NA     1
 [3,]   NA    0   NA   NA   NA   NA    1    0   NA    NA
 [4,]   NA   NA   NA   NA   NA   NA   NA   NA   NA    NA
 [5,]   NA   NA   NA   NA   NA   NA   NA   NA   NA    NA
 [6,]    0    0    0    0    0   NA    0    0    0     0
 [7,]   NA    0    1   NA   NA   NA   NA    1   NA    NA
 [8,]   NA    0    0   NA   NA   NA    0   NA   NA     1
 [9,]   NA   NA   NA   NA   NA   NA   NA   NA   NA    NA
[10,]    0    1    1    0    0    0    1    1    0    NA
```

We now fit an SRRM model to the complete data and the subsampled data, and compare parameter estimates.

```
fit_pop<-ame(Y,Xd,Xn,Xn,model="bin")   # fit based on full data (population)

fit_ess<-ame(Ys,Xd,Xn,Xn,model="bin")  # fit based on egocentric subsample
```

```
apply(fit_pop$BETA,2,mean)

 intercept       .row       .col      .dyad
-1.8662999  0.3172635  0.3824924  0.7365514

apply(fit_ess$BETA,2,mean)

 intercept       .row       .col      .dyad
-2.1561520  0.3172207  1.1966069  0.9929780
```

The coefficients are similar, even though the second fit is from a dataset with 73 missing values.

The `ame` fitting procedure generates a posterior predictive mean for all entries of the sociomatrix $\mathbf{Y}$, including those entries for which the data are missing. This sociomatrix of fitted values can be used for prediction or imputation of relational data from incomplete datasets. In our example on modeling friendship relations from the `dutchcollege` dataset, we can use this sociomatrix of fitted values to evaluate how well the parameter estimates obtained from the sampled dataset compare to those obtained from the full dataset, in terms of prediction:

```
miss<-which(is.na(Ys))

mean( ( fit_pop$YPM[miss] - Y[miss] )^2, na.rm=TRUE )

[1] 0.09428416

mean( ( fit_ess$YPM[miss] - Y[miss] )^2, na.rm=TRUE )

[1] 0.1350285
```

The first and second numbers reflects "within-sample" and "out-of-sample" goodness of fit, respectively. The small discrepancy between these numbers indicates that reasonable parameter estimates for this model (in terms of out-of-sample predictive squared error) can be obtained from this egocentric sample.

Finally, we consider the variability of the parameter estimates across egocentric samples with a small simulation study: For each of 100 egocentric samples generated above, we obtained parameter

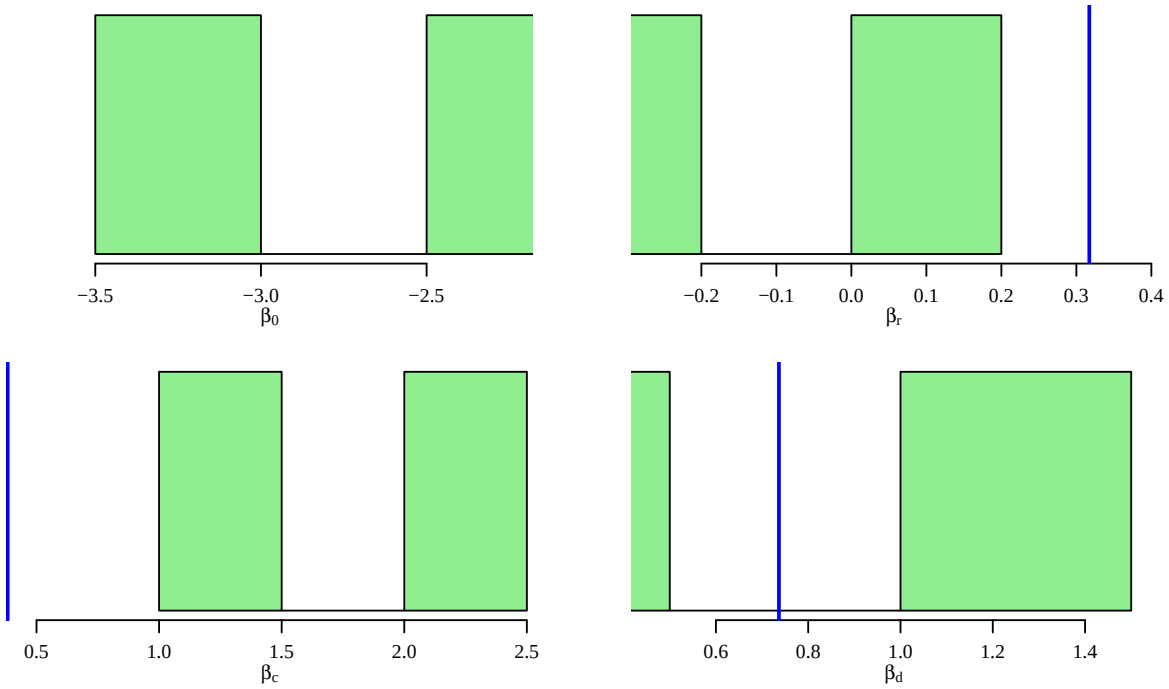


Figure 14: Variability of probit SRRM regression estimates across egocentric samples. Vertical blue lines indicate the estimates obtained from the full (population) dataset.

estimates for the probit SRRM,

$$z_{i,j} = \beta_0 + \beta_r x_i + \beta_c x_j + \beta_d x_{i,j} + \epsilon_{i,j}$$
$$y_{i,j} = 1(z_{i,j} > 0),$$

where x_i is a binary indicator that node i is male, and $x_{i,j}$ is the indicator that i and j are of the same sex. The variability of the parameter estimates across egocentric samples are illustrated with histograms in Figure 14. An illustrative exercise would be to see how increasing or decreasing the amount of missing data in the samples (by increasing or decreasing the number of egos sampled) would affect the concentration of the egocentric estimates around the population estimates.

5 Repeated measures data

Some types of dynamic relational datasets include repeated measurements of dyadic and nodal variables at discrete points in time. The `amen` package provides a rudimentary method of analyzing

such data, based on the following simple extension of the AME model to accommodate replicated relational measurements: For (latent) sociomatrices $\mathbf{Z}_1, \ldots, \mathbf{Z}_T$, the model expresses $z_{i,j,t}$, the (i,j)th element of the tth sociomatrix, as

$$z_{i,j,t} = \beta^T \mathbf{x}_{d,i,j,t} + \beta_r^T \mathbf{x}_{r,i,j,t} + \beta_c^T \mathbf{x}_{c,i,j,t} + a_i + b_j + \mathbf{u}_i^T \mathbf{v}_j + \epsilon_{i,j,t}. \tag{11}$$

Across nodes, dyads and time points, this model extension further assumes the same covariance model for the random effects $\{(a_i, b_i)\}$ as before, allows for dyadic correlation between $\epsilon_{i,j,t}$ and $\epsilon_{j,i,t}$ as before, but assumes $\epsilon_{i,j,t}$'s that involve different dyads *or* different time points as independent. In other words, the data under this model are treated as independent observations from a common AME distribution.

At first glance it may seem that such a model is inappropriate for dynamic relational data, as it doesn't seem to allow for the possibility of dependence over time. However, certain types of dependence can be incorporated into this model via the time-dependent regression terms. Specifically, autoregressive dependence can be modeled by including lagged values of the sociomatrix as regressors. Additionally, time-varying regression parameters can be included in the model by construction of interactions.

We illustrate these possibilities with an analysis of data from the longitudinal study of friendship relations among a small group of Dutch college students, available in `amen` via the `dutchcollege` dataset. Our response $y_{i,j,t}$ is the indicator that person i reports being friendly (or having friendship) with person j at time point t. The graphs of this relation for each of the seven different time points in the dataset are given in Figure 15. The figure reflects the fact that the students were mostly unknown to each other before the study period, and so not surpisingly, the density of the graphs increase over time.

The data also include (static) information on the sex and smoking status of the students, as well as which one of three programs each student was a member. We will examine the effects of these nodal attributes on frienship in using a probit SRRM, where $y_{i,j,t}$ is modeled as the indicator that the latent affinity $z_{i,j,t}$ exceeds zero, where $z_{i,j,t}$ follows model (11). Our analysis will include the binary indicators of male sex and smoking status as row and column regressors, products of these variables as dyadic regressors, and a dyadic binary indicator of whether or not members of a dyad belong to the same program. Finally, we will also include lagged values $y_{i,j,t-1}$ and $y_{j,i,t-1}$ as dyadic predictors of $z_{i,j,t}$ to reflect the possibility of temporal dependence among relations within

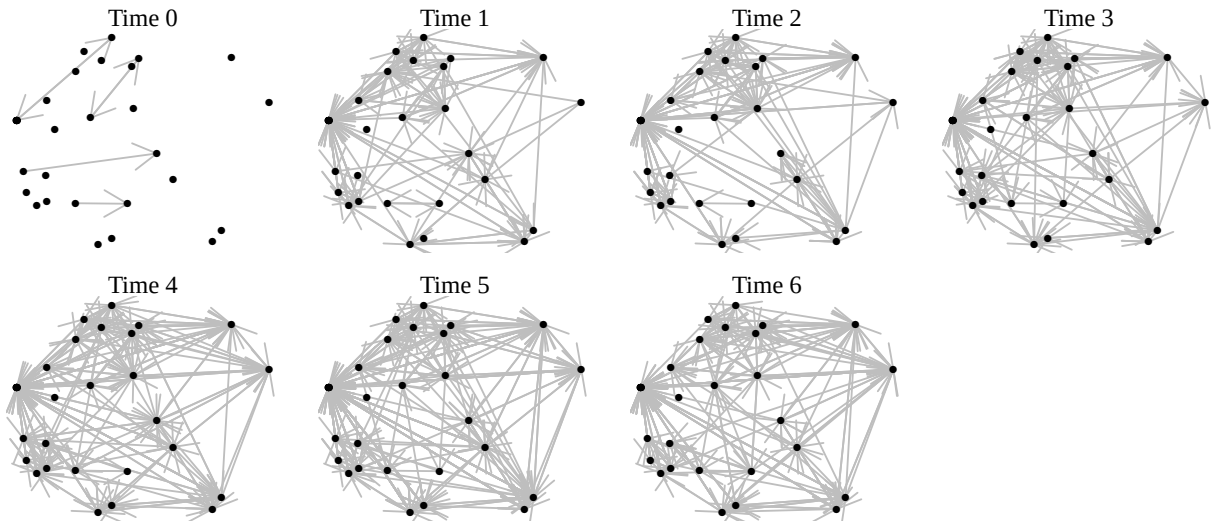


Figure 15: Friendliness network of the Dutch college students, across seven time points.

a dyad. To summarize, our model for the $z_{i,j,t}$'s is as follows:

$$
\begin{aligned}
z_{i,j,t} = & \beta_0 + \\
& \beta_{r,1}\text{male}_i + \beta_{r,2}\text{smoke}_i + \\
& \beta_{c,1}\text{male}_j + \beta_{c,2}\text{smoke}_j + \\
& \beta_{d_1} y_{i,j,t-1} + \beta_{d_2} y_{j,i,t-1} + \\
& \beta_{d_3}\text{male}_i\text{male}_j + \beta_{d_4}\text{smoke}_i\text{smoke}_j + \beta_{d_5}\text{sameprogram}_{i,j} + \\
& a_i + b_j + \epsilon_{i,j,t}
\end{aligned}
$$

The `ame_rep` function in the `amen` package provides parameter estimation and inference for this model using a similar syntax as the `ame` function, except now the nodal attributes `Xrow` and `Xcol` are three-dimensional arrays, with dimensions corresponding to nodes, variables and time points, respectively, and the dyadic regressor array `Xdyad` is now four-dimensional, with dimensions corresponding to nodes, nodes, variables and time points. These arrays for this data analysis can be set up as follows:

```
# outcome
Y<-1*( dutchcollege$Y >= 2 )[,,2:7]
n<-dim(Y)[1] ; t<-dim(Y)[3]


# nodal covariates
```

```
Xnode<-dutchcollege$X[,1:2]                                    # sex and smoking status
Xnode<-array(Xnode,dim=c(n,ncol(Xnode),t))
dimnames(Xnode)[[2]]<-c("male","smoker")

# dyadic covariates
Xdyad<-array(dim=c(n,n,5,t))
Xdyad[,,1,]<-1*( dutchcollege$Y >= 2 )[,,1:6]                  # lagged relation
Xdyad[,,2,]<-array(apply(Xdyad[,,1,],3,t),dim=c(n,n,t))        # lagged reciprocal relation
Xdyad[,,3,]<-tcrossprod(Xnode[,1,1])                           # both male
Xdyad[,,4,]<-tcrossprod(Xnode[,2,1])                           # both smokers
Xdyad[,,5,]<-outer( dutchcollege$X[,3],dutchcollege$X[,3],"==")  # same program
dimnames(Xdyad)[[3]]<-c("Ylag","tYlag","bothmale","bothsmoke","sameprog")
```

The model can be fit using the same syntax as the `ame` command discussed previsouly, and results can summarized before with the `summary` function:

```
fit_ar1<-ame_rep(Y,Xdyad,Xnode,Xnode,model="bin",plot=FALSE)
```

```
summary(fit_ar1)


Regression coefficients:
               pmean   psd z-stat p-val
intercept     -1.612 0.170 -9.457 0.000
male.row      -0.170 0.220 -0.772 0.440
smoker.row    -0.458 0.182 -2.516 0.012
male.col      -0.038 0.162 -0.236 0.813
smoker.col    -0.236 0.145 -1.627 0.104
Ylag.dyad      1.201 0.063 19.146 0.000
tYlag.dyad     0.860 0.062 13.796 0.000
bothmale.dyad  0.740 0.145  5.090 0.000
bothsmoke.dyad 0.661 0.122  5.424 0.000
sameprog.dyad  0.432 0.063  6.880 0.000

Variance parameters:
    pmean   psd
va  0.223 0.073
cab 0.033 0.034
```

```
vb  0.119 0.038
rho 0.641 0.038
ve  1.000 0.000
```

The parameter estimates and standard deviations for $\beta_{d,1}$ and $\beta_{d,2}$ (`Ylag.dyad` and `tYlag.dyad` in the output) indicate strong evidence of large temporal correlation. There also appear to be strong homophily effects in terms of sex, smoking status and program. The nodal effect parameters indicate some evidence that smokers are a bit less social than non-smokers.

Finally, we note that the time interval between the first four measurements was three weeks, whereas the interval between the last three measurements was six weeks. As such, we may want to consider whether or not the effects of the regressors might vary depending on the measurement. Such a possibility can be evaluated simply by adding interaction terms to the regressors. For example, to evaluate whether or not the effect of $y_{i,j,t-1}$ on $z_{i,j,t}$ varies with measurment interval, we can create a new dyadic covariate $y_{i,j,t-1}w_t$ where w_t is a binary indicator that t is in the among the last three measurements. Adding such terms for all of our regressors can be done as follows:

```
Wnode<-Xnode
Wnode[,,1:3]<-0

XWnode<-array( dim=dim(Xnode)+c(0,2,0))
XWnode[,1:2,]<-Xnode ; XWnode[,3:4,]<-Wnode
dimnames(XWnode)[[2]]<-c(dimnames(Xnode)[[2]],paste0(dimnames(Xnode)[[2]],".w"))



Wdyad<-Xdyad
Wdyad[,,,1:3]<-0
XWdyad<-array( dim=dim(Xdyad)+c(0,0,5,0) )
XWdyad[,,1:5,]<-Xdyad ; XWdyad[,,6:10,]<-Wdyad
dimnames(XWdyad)[[3]]<-c(dimnames(Xdyad)[[3]],paste0(dimnames(Xdyad)[[3]],".w"))
```

```
fit_ar1_vb<-ame_rep(Y,XWdyad,XWnode,XWnode,model="bin")
```

```
summary(fit_ar1_vb)



Regression coefficients:
```

```
                  pmean   psd z-stat p-val
intercept        -1.606 0.167 -9.625 0.000
male.row         -0.313 0.238 -1.311 0.190
smoker.row       -0.374 0.204 -1.833 0.067
male.w.row        0.240 0.141  1.696 0.090
smoker.w.row     -0.156 0.137 -1.134 0.257
male.col         -0.068 0.171 -0.395 0.693
smoker.col       -0.208 0.148 -1.402 0.161
male.w.col        0.036 0.133  0.268 0.788
smoker.w.col     -0.048 0.120 -0.403 0.687
Ylag.dyad         1.400 0.101 13.797 0.000
tYlag.dyad        0.855 0.109  7.839 0.000
bothmale.dyad     1.009 0.209  4.831 0.000
bothsmoke.dyad    0.558 0.165  3.373 0.001
sameprog.dyad     0.334 0.080  4.169 0.000
Ylag.w.dyad      -0.296 0.122 -2.432 0.015
tYlag.w.dyad     -0.008 0.131 -0.059 0.953
bothmale.w.dyad  -0.520 0.277 -1.875 0.061
bothsmoke.w.dyad  0.194 0.225  0.864 0.387
sameprog.w.dyad   0.187 0.097  1.924 0.054

Variance parameters:
    pmean   psd
va  0.224 0.075
cab 0.032 0.036
vb  0.116 0.038
rho 0.650 0.037
ve  1.000 0.000
```

These results do not indicate much evidence that the regression coefficients should vary by time period, except possibly the effect on the lagged dyadic variable $y_{i,j,t}$. The negative estimate of this coefficient (corresponding to `Ylag.w.dyad` in the output) makes sense, as it indicates that the effect of the lagged variable is decreased when the interval between times points is longer.

6 Symmetric data

It is sometimes the case that relational observations are *symmetric* or *undirected* by design, in that there is only one relational value $y_{i,j}$ for the dyad (i, j). Such observations can be represented by a symmetric sociomatrix $\mathbf{Y}$, so that $y_{i,j} = y_{j,i}$ for all dyads (i, j). In this case, a natural simplification of the AME model (4) is given by

$$y_{i,j} = \beta_d^T \mathbf{x}_{i,j} + \beta_n^T (\mathbf{x}_i + \mathbf{x}_j) + a_i + a_j + \mathbf{u}_i^T \mathbf{\Lambda} \mathbf{u}_j + \epsilon_{i,j}, \tag{12}$$

$$a_1, \ldots, a_n \sim \text{i.i.d. } N(0, \sigma_a^2) \tag{13}$$

$$\{\epsilon_{i,j}\} \sim \text{i.i.d. } N(0, \sigma_e^2), \tag{14}$$

for $i < j$, with $y_{j,i} = y_{i,j}$ by design. Most of the simplifications leading to this symmetric case are easy to understand, with the possible exception of the change from $\mathbf{u}_i^T \mathbf{v}_j$ in the asymmetric case to $\mathbf{u}_i^T \mathbf{\Lambda} \mathbf{u}_j$. here. In the former case, this representation can justified by the singular value decomposition theorem, which states that any $n \times n$ rank-R matrix $\mathbf{M}$ can be expressed as $\mathbf{U}\mathbf{V}^T$, where $\mathbf{U}$ and $\mathbf{V}$ are $n \times R$ matrices. This means that $m_{i,j}$, the i, jth entry of $\mathbf{M}$ can be expressed as $m_{i,j} = \mathbf{u}_i^T \mathbf{v}_j$, where $\mathbf{u}_i$ and $\mathbf{v}_j$ are the ith and jth rows of $\mathbf{U}$ and $\mathbf{V}$, respectively. In other words, the $\mathbf{u}_i^T \mathbf{v}_j$ in the asymmetric AME model can represent any residual low-rank patterns $\mathbf{M}$ in the sociomatrix $\mathbf{Y}$ that aren't explained by the known regressors. Similarly, in the symmetric case the term $\mathbf{u}_i^T \mathbf{\Lambda} \mathbf{u}_j$ in (14) can represent any residual low-rank patterns $\mathbf{M}$ in the symmetric sociomatrix $\mathbf{Y}$. This follows from the eigenvalue decomposition theorem, which states that any symmetric rank-$\mathbf{R}$ matrix $\mathbf{M}$ can be expressed as $\mathbf{U}\mathbf{\Lambda}\mathbf{U}^T$, or equivalently, the elements $m_{i,j}$ of $\mathbf{M}$ can be expressed as $m_{i,j} = \mathbf{u}_i^T \mathbf{\Lambda} \mathbf{u}_j$.

6.1 Example:

Symmetric versions of the normal, probit and other AME models discussed in the previous sections can be fit using the `ame` command by simply specifiying the option `symmetric=TRUE`.

7 Discussion

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