Bayesian Model Determination for Multivariate Ordinal and Binary Data

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Abstract

We consider how to compare different conditional independence specifications for ordinal categorical data, by calculating a posterior distribution over classes of graphical models. The approach is based on the multivariate ordinal probit model (Chib and Greenberg, 1998) where the data are considered to have arisen as truncated multivariate normal random vectors. By parameterising the precision matrix of the associated multivariate normal in Cholesky form (e.g. as Smith and Kohn, 2002) ordinal data models corresponding to directed acyclic conditional independence graphs for the latent variables can be specified and conveniently computed. Where one or more of the variables is binary this parameterisation is particularly compelling, as necessary constraints on the latent variable distribution can be imposed in such a way that a standard, fully normalised, prior can still be adopted. For comparing different directed graphical models we propose a reversible jump MCMC approach. Where interest is focussed on undirected graphical models, this approach is augmented to allow switches in the orderings of variables of associated directed graphs, hence allowing the posterior distribution over decomposable undirected graphical models to be computed. The approach is illustrated with several examples, involving both binary and ordinal variables, and directed and undirected graphical model classes.

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1 Introduction

Suppose that individuals $i = 1, \ldots, n$ are classified by variables $Y_1, \ldots, Y_p$, where variable $Y_j$ has $k_j$ ordered categories. Independent ordered categorical response vectors $y_i = (y_{i1}, y_{i2}, \ldots, y_{ip})$ are observed, where individual $i$ takes level $y_{ij} \in \{1, \ldots, k_j\}$ for the variable $Y_j$. The multivariate ordinal probit model supposes each $Y_j$ can be considered as having arisen as a continuously distributed random variable $Z_j$, which has been subsequently categorised by comparing its value on the continuous scale with a set of thresholds dividing the categories. Hence, for each individual $y_i$, we assume the existence of a latent multivariate continuous variable $z_i \in \mathbb{R}^p$. For each $y_{ij}$, the value taken on the ordinal scale is determined by which of the $k_j$ contiguous regions, defined by the thresholds, contains $z_{ij}$. In a probit model, the latent distribution of the $z_i$ is assumed to be multivariate normal with mean $\beta$ and variance-covariance matrix $\Sigma$.

Threshold models for multivariate ordinal data are not a recent phenomenon. Ashford and Sowden (1970) and Anderson and Pemberton (1985) used this type of model for multivariate binary and ordinal data respectively. However, these type of models have become much more popular in recent years, largely due to the fact that they admit convenient Bayesian computation. Albert and Chib (1993) showed that, for univariate probit models and for models based on an underlying $t$ distribution, computation of posterior distributions in a Bayesian analysis was particularly straightforward using a Gibbs sampler as, by including the latent continuous observations $z_i$ as part of the updating process, all conditional distributions required for sampling were of standard form. Chib and Greenberg (1998) extended this approach to analyse multivariate binary data. Further developments have included latent multivariate $t$ distributions for binary (Chen and Dey, 1998) or ordinal (Chen and Shao, 1999) data and latent normal mixture distributions (Kottas et al., 2005). A Bayesian approach based on logistic models is described by O’Brien and Dunson (2004).

Multivariate categorical data is often expressed in the form of a contingency table, with a cell representing each combination of levels of the categorical variables. Commonly, the main focus of interest when analysing such data is the structure of the association between the classifying variables. Log-linear models provide a convenient way of describing the structure in a multiway contingency table. In particular, a subclass of loglinear interaction models are the undirected graphical models which describe conditional
independences among the variables (see, for example, Edwards, 2000; Whit-uptaker, 1990). Such models have been successfully used in numerous areas of application, both to learn about relationships between variables, and to obtain efficient estimates and predictions related to a table.

Standard log-linear models can be, and frequently are, used to analyse contingency tables with ordinal variables. An obvious drawback of this approach is that it ignores the information provided by the ordinal nature of the variables. For example, equivalent results would be obtained under any permutation of the levels of any of the variables. In this paper we propose an approach which explicitly acknowledges that the variables are ordinal, by adopting a multivariate probit model, while at the same time exploring the association structure of the data by considering models that constrain the precision (inverse covariance) matrix $\Sigma^{-1}$ of the latent normal variables. Graphical models correspond to constraints on $\Sigma^{-1}$, as $[\Sigma^{-1}]_{jk} = 0$ represents conditional independence of $Z_j$ and $Z_k$ given the remaining latent variables.

Our approach throughout is Bayesian. Hence, for model determination, we calculate posterior model probabilities using

$$f(m|y) \propto f(m)f(y|m)$$

where $m \in M$ indexes models and $f(y|m)$ is the marginal likelihood of model $m$, defined as

$$f(y|m) = \int f(y|m, \theta_m)f(\theta_m|m)d\theta_m \quad (1)$$

and $\theta_m$ are the parameters for model $m$. Note that the marginal likelihood requires the prior density $f(\theta_m|m)$ to be normalised. For the multivariate probit models we want to consider, the marginal likelihood is intractable. We shall use a Reversible Jump Markov chain Monte Carlo (RJMC MC) method (Green, 1995) to calculate posterior probabilities.

Critical to the implementation of our approach is the parameterisation of the precision matrix $\Sigma^{-1}$ in Cholesky form. This will be described in more detail in the next Section, and it brings three clear benefits. Firstly, the conditional independence constraints in the reparameterisation can be incorporated while using standard, fully normalised, prior densities, which is essential for marginal likelihood computation. Furthermore, additional constraints which need to be imposed when binary variables are present can
also be incorporated without affecting this facility. Finally, such a specification is important for the development of efficient RJMCMC computation. A drawback is that not all graphical models can be specified using a given Cholesky parameterisation. This, however, can be largely mitigated by further development of the RJMCMC approach, as described in Section 4.

The paper is structured as follows: In Section 2, we describe the modelling approach with the parameterisation in terms of the Cholesky decomposition, and the posterior simulation of the full model. In Section 3, we define the Reversible Jump Markov chain Monte Carlo procedure used to find posterior model probabilities for a given Cholesky parameterisation, and in Section 4 we define the extra RJMCMC step required to move between alternative parameterisations. Finally, in Section 5, we discuss the choice of prior parameters and provide four examples of our approach.

2 The Model

2.1 Model specification

For each individual \( y_i \), we assume a corresponding latent multivariate continuous variable \( z_i \in \mathbb{R}^p \). Each \( z_i \) is assumed to be independently normally distributed with common mean \( \beta \) and variance-covariance matrix \( \Sigma \),

\[
z_i = (z_{i1}, z_{i2}, \ldots, z_{ip})^T \sim N(\beta, \Sigma) \quad i = 1, \ldots, n.
\]

If covariate information about individuals was available then we would relax the assumption of common mean, but here we focus on modelling the association structure through the covariance matrix \( \Sigma \).

We assume the existence of ordered thresholds which, for each classifying variable, divide the real line (the sample space for each \( z_{ij} \)) into intervals corresponding to the ordered categories. Let \( \alpha(j, c) \) denote the threshold which separates levels \( c \) and \( c + 1 \) for variable \( j \). Then, for each \( c \in \{1, \ldots, k_j\} \),

\[
y_{ij} = c \quad \text{if and only if} \quad \alpha(j, c - 1) \leq z_{ij} < \alpha(j, c).
\]  

By definition, \( \alpha(j, 0) = -\infty \) and \( \alpha(j, k_j) = \infty \) respectively.

The mapping between parameters \( \beta, \Sigma \) and \( \alpha = \{\alpha(j, c), j = 1, \ldots, p, c = 1, \ldots, k_j - 1\} \) and cell probabilities in the corresponding multiway contingency table is many-to-one, as any transformation of location or scale in \( \mathbb{R}^p \)
leads to the same distribution for $y_i$. Hence, it is common to impose two identifiability constraints for each component of $z_i$. For ordinal variables with at least three levels, it is most computationally convenient to constrain the lowest and highest thresholds, $\alpha(j, 1)$ and $\alpha(j, k_j - 1)$ to prespecified values. Here, we choose to constrain these values so that, under a standard normal marginal latent distribution for $z_{ij}$, the probability of $y_{ij}$ taking the highest or lowest level are both equal to $1/k_j$. Hence, the constraints applied are

$$
\alpha(j, 1) = \Phi^{-1}(1/k_j) \quad \alpha(j, k_j - 1) = -\Phi^{-1}(1/k_j)
$$

(3)

where $\Phi$ is the standard normal distribution function.

For binary variables, $k_j = 2$ and there is only one free threshold, which is constrained using $\alpha(j, 1) = 0$. Hence an additional constraint is required when binary variables are present. Chib and Greenberg (1998) constrain the marginal variance $\sigma^2_{jj}$ corresponding to a binary variable. This requires specifying a prior distribution and simulating from the posterior distribution of a restricted-covariance matrix. The prior normalising constant for a distribution over covariance matrices restricted in this way is not generally available, which potentially creates difficulties for model determination as this constant is explicitly required in the marginal likelihood (1). For three alternative models for the covariance structure, Chib and Greenberg (1998) evaluate the normalising constant for their restricted priors by a simple simulation. In the approach which we shall describe, all prior normalising constants are explicitly available.

As mentioned above, the focus of the paper, as is often the case in contingency table analysis, is modelling the association amongst the classifying variables. Here, the models we shall consider reflect different association patterns by imposing various constraints on the covariance matrix $\Sigma$. The remaining parameters $\beta$ and $\alpha$ are given noninformative prior distributions. The prior for $\beta$ is normal with a diffuse covariance structure and the thresholds $\alpha(j, c)$ are given uniform prior distributions subject to order restrictions and the identifiability constraints.

The models which we shall consider will be conditional independence (graphical) models for the latent variables. It should be noted that although marginal independence relationships between latent variables apply equivalently to the corresponding observed ordinal variables, conditional independence relationships do not. For example, $Z_1 \perp\!\!\!\!\perp Z_2 | Z_3$ implies $Y_1 \perp\!\!\!\!\perp Y_2 | Z_3$ but not $Y_1 \perp\!\!\!\!\perp Y_2 | Y_3$. Hence the models we shall consider will not represent
exact conditional independences between classifying variables but do still represent interesting hypotheses concerning associations between the variables of interest. Indeed, we argue that modelling conditional independences between the latent variables is more natural and more satisfying than modelling conditional independences amongst the observed ordinal variables. The reason for this is that the models are invariant to the way in which the ordinal variables are coded. For example, consider an example with three variables, generated by the model $Z_1 \perp\!\!\!\!\!\!\perp Z_2 | Z_3$, where $Y_3$ has four ordinal levels ($k_3 = 4$). Now suppose that $Y_3$ is recoded by combining levels 3 and 4 into a single level. The conditional independence part of the model is unaffected by this – we merely remove the uppermost threshold for the third variable. However, if we were considering conditional independence models for the observed variables, the way in which the variables are coded is critical and, for example, the model $Y_1 \perp\!\!\!\!\!\!\perp Y_2 | Y_3$ will no longer hold under a recoding of $Y_3$ as this changes the conditioning information.

For multivariate normal variables such as $\mathbf{z}_i$, conditional independence of $Z_j$ and $Z_k$ given the other latent variables is defined by $[\Sigma^{-1}]_{jk} = [\Sigma^{-1}]_{kj} = 0$. Hence, one possible approach would be to consider any conditional independence, or undirected graphical, model for the latent variables by imposing the necessary constraints on the precision matrix $\Sigma^{-1}$. One drawback with this is the requirement to construct prior distributions and simulate posterior distributions over the space of constrained precision matrices. For decomposable graphical models (those which can be represented by an independence graph without chordless cycles of length four or greater; see Lauritzen, 1996), Dawid and Lauritzen (1993) proposed the hyper-inverse Wishart class of prior distributions over covariance matrices consistent with the model. These distributions admit generally straightforward computation. Roverato (2002) and Dellaportas et al. (2003) considered prior distributions for general undirected graphical models, but which require some approximation for the prior normalising constant. One possibility would be to adapt one of these approaches, imposing the additional constraints on the variances $\sigma_{jj}$ of those $Z_j$ corresponding to binary variables, and approximating the prior normalising constant in some way. However, having done this, we would still need to construct a method for simulating the posterior distribution of a constrained distribution.

Instead, we adopt an approach where we can apply all the necessary constraints but still use standard normalised prior distributions. Furthermore, efficient posterior computation for any decomposable graphical model
is straightforward. The precision matrix $\Sigma^{-1}$ is parameterised in terms of its Cholesky decomposition

$$
\Sigma^{-1} = \Phi^T \Phi
$$

where $\Phi$ is an upper triangular matrix, or equivalently as

$$
\Sigma^{-1} = \Psi^T \Lambda \Psi
$$

(4)

where $\Psi$ is an upper triangular matrix with diagonal elements equal to 1 and $\Lambda$ is a diagonal matrix with elements $\lambda_j \equiv \phi_{jj}^2$. The joint distribution for the latent variables $f(z_i) = f(z_{i1}, z_{i2}, ..., z_{ip})$ can now be expressed in the following recursive form.

$$
\begin{align*}
z_{ip} & = N(\beta_p, \lambda_p^{-1}) \\
z_{i,p-1} | z_{ip} & = \beta_{p-1} - \psi_{p-1,p} (z_{ip} - \beta_p) + N\left(0, \lambda_{p-1}^{-1}\right) \\
& \vdots \\
z_{ij} | z_{i,j+1}, ..., z_{ip} & = \beta_j - \psi_{jp} (z_{ip} - \beta_p) - \psi_{j,p-1} (z_{i,p-1} - \beta_{p-1}) - \cdots - \psi_{j,j+1} (z_{i,j+1} - \beta_{j+1}) + N\left(0, \lambda_j^{-1}\right) \\
& \vdots \\
z_{i1} | z_{i2}, ..., z_{ip} & = \beta_1 - \psi_{1p} (z_{ip} - \beta_p) - \psi_{1,p-1} (z_{i,p-1} - \beta_{p-1}) - \cdots - \psi_{12} (z_{i2} - \beta_2) + N\left(0, \lambda_1^{-1}\right).
\end{align*}
$$

(5)

Therefore, $\lambda_j$ can be interpreted as the conditional precision of the latent data for variable $j$ given the latent data for all variables succeeding $j$ in the decomposition. The off-diagonal elements of $\Psi$ can be interpreted as regression coefficients. Where a natural ordering of the variables exists, for example for longitudinal data where the $Y_j$ represent the same variable observed at different points in time, then the decomposition (5), and hence (4), provides a natural way of specifying the distribution of $z_i$. Daniels and Pourahmadi (2002) and Smith and Kohn (2002) both exploit this in the analysis of longitudinal Gaussian data.

With this parameterisation, it is clear from (5) that setting $\psi_{jk} = 0$ implies that $Z_j$ is conditionally independent of $Z_k$ given $\{Z_{j+1}, \ldots, Z_p\} \setminus \{Z_k\}$. Hence, $\psi_{jk} = 0$ implies a missing edge in the directed graphical model where the directions of the edges are implied by the ordering of the variables in the original covariance matrix $\Sigma$. That is, $\psi_{jk} \neq 0$ ($j < k$) implies the
presence of a directed edge from $Z_k$ to $Z_j$ in the directed acyclic graph (DAG) representing the model. Smith and Kohn (2002) propose modelling longitudinal Gaussian data by comparing parsimonious covariance models which allow any combination of $\psi_{jk}$ coefficients to be equal to zero. A similar approach is adopted by Fronk and Giudici (2004), and extended to DAG models for multivariate binary data by Fronk (2002) where, as in the current paper, the conditional independence specifications apply to latent normally distributed variables.

Where no natural ordering of variables exists, we focus on undirected graphical models, where conditional independence of $Z_j$ and $Z_k$ given $\{Z_1, \ldots, Z_p\} \setminus \{Z_j, Z_k\}$ is represented by the absence of an undirected edge between $Z_j$ and $Z_k$ in the graph representing the model. In the multivariate normal distribution such a conditional independence implies $[\Sigma^{-1}]_{jk} = 0$. In our analysis using undirected graphical models we want to take advantage of the benefits offered by the decompositions (4) and (5) for computation. From Theorem 1 of Roverato (2000), originally from Paulsen et al. (1989), for every decomposable graphical model, there exists an ordering of the variables $(Z_1, \ldots, Z_k)$ such that the space of precision matrices satisfying the model (with the relevant off-diagonal elements set to zero) contains exactly those which can be written as (4) with the corresponding $\psi_{jk}$ set equal to zero. This is essentially the well known result that every decomposable undirected graphical model admits a ‘perfect ordering’ of vertices. The edges of the undirected graph can be replaced by directed edges (with the ordering defining the direction) and the resulting model is exactly equivalent in terms of its Markov (conditional independence) properties. Hence, any individual decomposable undirected graphical model can be parameterised using (4) and (5) provided that the variables are ordered appropriately.

The reason for using this parameterisation is that we can use a prior distribution which is conditionally conjugate. This makes posterior computation much more straightforward than when using the precision matrix to parameterise the variance of $z_i$. Furthermore, for a binary $Y_j$, we constrain the conditional precision $\lambda_j$ to fix the scale of $Z_j$. Unlike fixing $\sigma^2_{jj}$, this does not create any computational difficulties. Both of these issues are discussed in more detail in Section 2.2.
2.2 Prior and posterior distributions

We start by considering a full (saturated) covariance structure, with no conditional independence constraints. The joint distribution of \((y_i, z_i)\) given the parameters \((\beta, \Psi, \Lambda, \alpha)\) is

\[
f(y_i, z_i | \beta, \Psi, \Lambda, \alpha) = f(y_i | z_i, \alpha) f(z_i | \beta, \Psi, \Lambda)
\]

where \(f(y_i | z_i, \alpha)\) is a degenerate distribution which puts all of its mass on those levels of the categorical variables implied by the thresholds and the corresponding latent variables, as described by (2). The latent variable density \(f(z_i | \beta, \Psi, \Lambda)\) is multivariate normal with mean \(\beta\) and covariance \((\Psi^T \Lambda \Psi)^{-1}\). Hence, the joint posterior density of the unknown parameters \((\beta, \Psi, \Lambda, \alpha)\) together with the unobserved latent variables \(z = \{z_i\}\) given the observed data \(y = \{y_i\}\) is given by

\[
f(z, \beta, \Psi, \Lambda, \alpha | y) = f(\beta, \Psi, \Lambda, \alpha) \prod_{i=1}^{n} f(y_i | z_i, \alpha) f(z_i | \beta, \Psi, \Lambda) \tag{6}
\]

where \(f(\beta, \Psi, \Lambda, \alpha)\) is the joint prior density for \((\beta, \Psi, \Lambda, \alpha)\), which will typically be decomposed as

\[
f(\beta, \Psi, \Lambda, \alpha) = f(\beta | \Psi, \Lambda) f(\Psi | \Lambda) f(\Lambda) f(\alpha)
\]

so that the thresholds \(\alpha\) are a priori independent of the parameters of the latent variable distribution. In practice, it is common for the multivariate normal mean \(\beta\) to also be a priori independent of \((\Psi, \Lambda)\).

Daniels and Pourahmadi (2002) and Smith and Kohn (2002) showed that a conditionally conjugate prior distribution for the full (unconstrained) multivariate normal model for \(z_i\) can be obtained by placing independent gamma prior distributions on the conditional precision parameters \(\lambda_j\) and, conditional on \(\lambda_j\), independent multivariate normal priors on the partial (non-zero) rows \(\Psi_j = (\psi_{j,j+1}, \ldots, \psi_{j,p})\) of the upper triangle of the matrix \(\Psi\). Hence, the prior distribution for \((\Lambda, \Psi)\) is:

\[
\begin{align*}
\lambda_j & \sim \text{Gamma}(q_j/2, 2b_j) \\
\psi_{j,j} | \lambda_j & \sim N(\mu_j, \lambda_j^{-1} A_j^{-1})
\end{align*}
\]

(7) (8)

For a certain choice of hyperparameters, this prior distribution simplifies to the inverse-Wishart distribution, the usual conjugate prior for covariance
matrices. Suppose that $\Sigma$ is assumed to be, \textit{a priori}, inverse-Wishart with parameters $A$ and $q$ (so that $E(\Sigma) = (q-p-1)^{-1}A$). Then this is equivalent to (7) and (8) with

$$q_j = q - j + 1$$

(9)

$$b_j = (a_{jj} - a_j^T A_j^{-1} a_j)^{-1}$$

(10)

$$\mu_j = -A_j^{-1} a_j$$

(11)

where $A$ is partitioned as

$$A = \begin{pmatrix}
\ddots & \ddots & \ddots \\
. & a_{jj} & a_j^T \\
. & a_j & A_j
\end{pmatrix}_{\downarrow}^{j^{\text{th}} \text{ column}} \leftarrow j^{\text{th}} \text{ row.}$$

(12)

Recall that for a binary classifying variable $Y_j$, the location of the corresponding latent variable $Z_j$ is fixed by constraining the single threshold parameter $\alpha(j,1)$ to be equal to zero. An additional constraint is required to fix the scale of $Z_j$. We choose to impose this constraint on $\lambda_j$, the conditional precision of $Z_j$ given $Z_j + 1, \ldots, Z_p$. The only change to the above specification is that these $\lambda_j$ parameters no longer have a gamma prior distribution in (7). In practice, we use the constraint $\lambda_j = 1$. The remaining components of the prior distribution are entirely unaffected and normalised prior densities can be explicitly evaluated.

Convenient priors for the other unknown parameters are $N(\nu, \mathbf{T})$ for $\beta$ and uniform for the thresholds $\alpha(j,c)$ subject to order restrictions and the identifiability constraints.

Substituting these prior densities into (6) yields the posterior distribution
of the unknown parameters:

\[
f(z, \beta, \Phi, \alpha|y) \propto \exp\left[-\frac{1}{2}(\beta - \nu)^T T^{-1}(\beta - \nu)\right] \\
\times \prod_{j=1}^{p} \lambda_j^{q_j+n+p-j} \exp\left[-\frac{\lambda_j}{2} \left\{ (\psi_j - \mu_j)^T A_j (\psi_j - \mu_j) + b_j^{-1} \right\} \right] \\
\times \prod_{i=1}^{n} \exp\left[-\frac{1}{2}(z_i - \beta)^T \Psi^T \Lambda \Psi (z_i - \beta) \right] \\
\times \prod_{i=1}^{n} \prod_{j=1}^{p} I [\alpha(j, y_{ij} - 1) \leq z_{ij} \leq \alpha(j, y_{ij})] \tag{13}
\]

Posterior computation is carried out using Markov Chain Monte Carlo (MCMC) to generate random samples from this distribution. Specifically, we use a Gibbs sampler, which samples iteratively from the conditional posterior distributions of the unknown parameters, including the latent data $z$. The normal-inverse gamma prior for $(\Psi, \Lambda)$ is conditionally conjugate, therefore the posterior distributions of $\psi_j | \lambda_j$ and $\lambda_j | \psi_j$ are multivariate normal and gamma respectively. This is a key advantage of the Cholesky decomposition parameterisation of the model. Given the latent data, these conditional posterior distributions are

\[
\psi_j | \lambda_j, z, \beta \sim N \left( (A_j + G_j)^{-1}(A_j \mu_j - g_j), \lambda_j^{-1}(A_j + G_j)^{-1} \right) \tag{14}
\]

\[
\lambda_j | \psi_j, z, \beta \sim \text{Gamma} \left( \frac{q_j + n + p - j}{2}, 2\delta_j \right) \tag{15}
\]

where

\[
\delta_j^{-1} = b_j^{-1} + (\psi_j - \mu_j)^T A_j (\psi_j - \mu_j) + g_{jj} + 2g_j^T \psi_j + \psi_j^T G_j^{-1} \psi_j \tag{16}
\]

and $G$ is the sums-of-products matrix $\sum_i(z_i - \beta)^T(z_i - \beta)$, partitioned in the same way as $A$. These conditional distributions are exactly those which arise in the equivalent analysis of multivariate normal models using this parameterisation, and are derived, for a particular prior structure, by Smith and Kohn (2002). Similarly, the mean $\beta$ of the latent data distribution has a multivariate normal conditional posterior distribution with mean

\[
E[\beta|z, \Psi, \Lambda] = (n\Psi^T \Lambda \Psi + T^{-1})^{-1} \left( \Psi^T \Lambda \Psi \sum_{i=1}^{n} z_i + T^{-1} \nu \right)
\]
and variance

\[ \text{Var}[\beta|z, \Psi, \Lambda] = \left(n\Psi^T\Lambda\Psi + T^{-1}\right)^{-1}. \]

The remaining conditional distributions required for the Gibbs sampler are for the latent data \(z\) and the thresholds \(\alpha\). Given the observed classification data \(y_i\), the latent data \(z_i\) for individual \(i\) is constrained to the interval \([\alpha(j, y_{ij}) - 1, \alpha(j, y_{ij})]\), for each \(j\). Hence, the posterior conditional distribution for \(z_i\) given the other parameters is \(N(\beta, (\Psi^T\Lambda\Psi)^{-1})\) restricted to the interval \([\alpha(j, y_{ij}) - 1, \alpha(j, y_{ij})]\). To sample from this distribution, we use the approach of Geweke (1991), and sample each component of \(z_i\) from its restricted univariate normal conditional distribution, which is a straightforward sampling task using, for example, the inverse distribution function method (Devroye, 1986). Finally, the threshold parameters are generated from their conditional posterior distributions

\[ \alpha(j, c|z) \sim \text{Uniform}\left(\max_{i:y_{ij}=c} z_{ij}, \min_{i:y_{ij}=c+1} z_{ij}\right) \]

Starting with initial values for all parameters, the sampling scheme proceeds by sampling iteratively from the above conditional posterior distributions.

It is now straightforward to see that parameterising the covariance using (4) has a particular advantage for ordinal data models. We have chosen to fix the location and scale of the latent variables \(Z_j\) by fixing two thresholds where the number of categories \(k_j\) of \(Y_j\) is greater than 2. For binary \(Y_j\), we fix the single threshold \(\alpha(j, 1)\) together with the conditional precision \(\lambda_j\). It is straightforward to see that imposing these constraints results in very minor modification of our MCMC sampler. The only changes in the conditional distributions required for sampling are that the conditional distribution for any constrained threshold or \(\lambda_j\) parameter is replaced by a degenerate distribution putting all its mass on the fixed value. The conditional posterior distributions of \(\Psi, \Lambda, \beta\) and \(z\) are entirely unaffected.

### 2.3 Conditional independence models

Adapting the model to allow various conditional independence structures (with certain \(\psi_{jk}\) set to zero) is also straightforward. First, we note that the prior and conditional posterior distributions for \(\beta\) and \(\alpha\), and the conditional posterior distributions for the latent data \(z_i\) are unchanged. The normal-inverse gamma prior for \((\Psi, \Lambda)\) can easily be adapted by taking the
multivariate normal distributions for $\psi_j$ to be over only those components which are not constrained to zero by the model. If the number of such unrestricted components is denoted by $c_j$, we notice that, in the prior, $\mu_j$ now has $c_j$ components and $A_j$ is a $c_j \times c_j$ matrix. Hence, in expressions (13) and (15) we replace $p - j$ in the distribution of $\lambda_j$ by $c_j$. Furthermore, in (14) and (16), $g_j$ and $G_j$ are now defined as submatrices of the sums-of-products matrix $G$ corresponding to those variables $k > j$ with $\psi_{jk}$ not constrained to zero by the model. Smith and Kohn (2002) derived these distributions for a multivariate normal conditional independence model with a particular prior structure.

Roverato (2002) shows that the prior parameters $b_j$, $q_j$, $\mu_j$, and $A_j$ in (7) and (8) can be chosen to make the prior distribution on the corresponding variance matrix $\Sigma$ a hyper-inverse Wishart distribution with parameters $q$ and $A$. This is the natural conjugate prior for the covariance corresponding to a decomposable model. The prior parameters required are $q_j = q - p + 1 + c_j$, with $b_j$ and $\mu_j$ as in (10) and (11) respectively, where $a_j$ and $A_j$ are now submatrices of $A$ restricted to those variables $k > j$ with $\psi_{jk}$ not constrained to zero by the model. As Roverato (2002) observes, this distribution is equivalent to taking an inverse Wishart distribution for the saturated precision matrix $\Sigma^{-1}$ and conditioning on those components of $\Sigma^{-1}$ which are constrained to zero by the model. Note that for any model with at least one binary classifying variable, certain $\lambda_j$ are constrained, so even with the appropriate choice of prior parameters, the exact correspondence between the normal inverse gamma prior for $(\Psi, \Lambda)$ and the inverse Wishart or hyper-inverse Wishart is lost.

3 Model Determination

We now extend our approach to allow uncertainty about the appropriate conditional independence structure for the latent variables $Z_1, \ldots, Z_p$. As described in Section 1, model uncertainty is incorporated by introducing a parameter $m$ indicating the model, together with a prior distribution on $m$. Inference concerning which models are supported by the data and prior distribution is based on the corresponding posterior distribution for $m$. Model uncertainty can then be accounted for in predictive inference by a model-averaged predictive distribution – a mixture of predictive distributions under the various models, weighted according to posterior model probabilities.
The parameter $\theta_m$ associated with model $m$ comprises $(\alpha, \beta, \Lambda, \Psi)$. Here, each model $m$ comprises a different conditional independence structure for $z_i$. Initially, we will consider directed graphical models with respect to a fixed ordering of the variables $Z_1, \ldots, Z_p$ so each $m$ constrains different sets of components of $\Psi$ to zero. Hence, the dimension of $\theta_m$ varies according to the number of free $\psi_{jk}$ parameters. More general conditional independence structures will be considered in Section 4. The prior distribution $f(\theta_m|m)$, when certain components of $\Psi$ are constrained to zero, is as described in Section 2.3.

We use a Reversible Jump Markov chain Monte Carlo (RJMCMC, Green, 1995) approach for posterior inference. This is a general MCMC approach, based on the Metropolis-Hastings algorithm, which is well-suited to model determination problems where different models have parameter spaces of varying dimensionality. An RJMCMC sampler simulates a Markov chain over models and model parameters for which the equilibrium distribution is the required posterior distribution $f(m, \theta_m|y)$. Fronk and Giudici (2004) propose an RJMCMC sampler for directed graphical Gaussian model determination, whereas Smith and Kohn (2002) use a Gibbs sampler. The latter approach could be applied here, but RJMCMC approach allows us to consider undirected models, which are the main focus of our analysis. Further details are given in Section 4.

The basis for our MCMC approach is the collection of conditional posterior distributions presented in Sections 2.2 and 2.3. A ‘null’ move of our RJMCMC sampler preserves the current value for the model $m$, and simply updates the model parameters $\theta_m$ and the latent data $z$, by generating from these posterior conditional distributions. Null moves are mixed with attempted model transitions. We restrict transitions between models to those which involve either adding or subtracting a single directed edge from the current graphical model. The direction of the edge is determined by the pre-specified ordering of variables. An edge is added to the current model by proposing a non-zero value for an element of $\Psi$ which was previously constrained to zero. An edge is removed from the current model by setting to zero a previously non-zero element of $\Psi$.

Formally, the RJMCMC procedure is defined as follows. At each stage of the RJMCMC, there are $\binom{p}{2}$ move types (each corresponding to one of the $\binom{p}{2}$ possible edges in the model, or entries in the upper triangle of $\Psi$) plus the null move. Here, we assume that for any model $m$, edge transitions are proposed with equal probability. The null move generally has a higher
probability to enhance mobility of the chain. Suppose the current state of the Markov chain at time \( t \) is represented by \( (m^t, \theta^t_{m^t}) \). Adding an edge involves a proposed move to a new model \( m' \) and corresponding parameter vector \( \theta_{m'} \), with dimension \( \dim(\theta_{m'}) + 1 \), i.e. there is one extra parameter to generate. Suppose that the extra parameter to be generated is \( \psi_{jk} \). Our implementation of RJMCMC involves proposing a value of \( \psi_{jk} \) directly using a proposal density \( g(\psi_{jk}) \), and leaving all other components of \( \Psi \) unchanged. Hence the proposed \( \Psi' \) is identical to \( \Psi^t \) in all components except \( \psi_{jk} \) where zero is replaced by the value generated from \( g \). The general RJMCMC procedure allows very flexible forms of transition proposal for \( \theta_{m'} \) given \( (m^t, \theta^t_{m^t}) \) but this relatively elementary one seems to work well in the current context.

Our proposal for adding an edge implies that when proposing to remove an edge from model \( m^t \) to move to a model \( m' \) with one fewer parameter, the proposed \( \Psi' \) is obtained from \( \Psi^t \) by setting the corresponding \( \psi_{jk} \) to zero.

Applying the general results of Green (1995), we accept proposed model transitions, that is we set \( (m^{t+1}, \Psi^{t+1}) := (m', \Psi') \) with probability \( \min\{1, \pi\} \) where

\[
\pi = \frac{f(z^t | \Psi^t, \Lambda^t, \beta^t) f(\Psi^t, \Lambda^t, \beta^t | m^t) f(m^t)}{f(z^t | \Psi', \Lambda^t, \beta^t) f(\Psi', \Lambda^t, \beta^t | m^t) f(m^t) g(\psi_{jk}^t)}
\]

when the proposal involves adding an edge. When the proposal involves removing an edge, \( 1/g(\psi_{jk}^t) \) is replaced by \( g(\psi_{jk}^t) \) in (17). If a proposal is rejected then \( (m^{t+1}, \Psi^{t+1}) := (m^t, \Psi^t) \). Note that in the standard reversible jump acceptance probabilities we would expect to see the product of conditional distributions as in (5) then the only terms in the product which differ in numerator and denominator are \( f(z_{i,j}^t | \psi_{i,j}^t, \lambda_j, \beta) \) for each \( i \), where \( z_{i,j} \equiv (z_{i,j+1}, \ldots, z_{ip}) \), so further simplification is possible. Furthermore, for the prior we use in this paper, \( f(\Psi, \Lambda, \beta | m) \) decomposes as \( f(\beta) \prod_j f(\psi_j | \lambda_j, m) f(\lambda_j | m) \) where \( f(\psi_j | \lambda_j, m) \) and \( f(\lambda_j | m) \) depend on
only through the number of components of \( \psi_j \) which are constrained to zero by \( m \). Hence for proposals involving a single \( \psi_{jk} \) as above, (17) can be written as

\[
\pi = \frac{\left[ \prod_i f(z_{ij}^i|z_{i,j>}^i, \psi^{i}_j, \lambda^i_j, \beta^i_j) \right] f(\psi^i_j|\lambda^i_j, m') f(\lambda^i_j|m) f(m')}{\left[ \prod_i f(z_{ij}^i|z_{i,j>}^i, \psi^{i}_j, \lambda^i_j, \beta^i_j) \right] f(\psi^i_j|\lambda^i_j, m) f(\lambda^i_j|m) f(m)} 1 g(\psi^i_{jk}). \tag{18}
\]

It remains to specify the proposal distribution for generating \( \psi_{jk} \) when it is proposed to add an edge to the current model. A particularly natural choice for this is to use the posterior conditional distribution of \( \psi_{jk} \) given the current values of \( \beta, \lambda_j \), and \( \psi_{j\setminus k} \) (the other components of \( \psi_j \)), as no change is proposed to any of these parameters. Using (14) it can be seen that the posterior conditional (proposal) distribution for \( \psi_{jk} \) is univariate normal with mean \((a_{kk} + g_{kk})^{-1}\xi_{jk}\) and variance \(\lambda_j(a_{kk} + g_{kk})^{-1}\) where

\[
\xi_{jk} = [A_j \mu_j - g_j]_k - \sum_{l>j,l\neq k} [A_j + G_j]_{kl} \psi_{jl}
\]

Here \( \mu_j \) and \( A_j \) are the parameters of the prior distribution for the unconstrained components of \( \psi_j \) under the proposed (extended) model \( m' \), and \( g_j \) and \( G_j \) are submatrices of the sums-of-products matrix, as described in Section 2.3.

Although transitions between nested models differing by a single component are common in RJMCMC samplers, it is relatively rare that the posterior conditional distribution is available as a proposal in this way. This is because calculating the proposal normalising constant often requires a calculation of similar difficulty to evaluating the marginal likelihood so that, if the posterior conditional is available, there are more convenient ways of evaluating the posterior model probabilities. Here, the availability of this type of proposal arises because the Gaussian model determination problem is more straightforward, and hence we might expect to be able to calculate \( f(z|m) \) more directly for a given \( z \). However as we do not observe \( z \), our required marginal likelihood is \( f(y|m) \) and this remains inaccessible by direct methods.
4 RJMCMC with order switching

The RJMCMC algorithm described in Section 3 generates from a Markov chain for which the stationary distribution is the posterior distribution over directed graphical models for \((Z_1, \ldots, Z_k)\), given a prespecified ordering of these variables. In many ordinal data analyses, there is no obvious ordering for the variables, and issues concerning conditional independence are more naturally addressed by considering undirected graphical models. A subset of the DAGs for a given ordering, the perfect DAGs, as described by Lauritzen (1996, p7), are Markov-equivalent (imply exactly the same conditional independence structure) to the corresponding (same edges) undirected graphs. However, not all decomposable undirected graphs are represented for a given ordering. For example, in the ordering \((Z_1, Z_2, Z_3)\) it is not possible to encode the single conditional independence \(Z_3 \perp \perp Z_2 | Z_1\) by constraining elements of \(\Psi\) to zero. Hence, to adapt the algorithm described in Section 3 to generate from the posterior distribution over all undirected graphical models, it is necessary to augment it with another class of transitions permitting the ordering of the variables to be changed.

In our adapted algorithm for decomposable undirected graphical models, we include proposals which switch two adjacent variables in the existing ordering. We also restrict the patterns of zeros in \(\Psi\) to those which correspond exactly to undirected graphical models (or equivalently to perfect DAGs), automatically rejecting any proposed edge additions or deletions which lead to DAGs without this property. It is straightforward to see that any permissible model/ordering combination can be reached from any other via transitions of these two types. [The easiest way to see this is to note that any perfect DAG in a particular ordering can be built up from (or reduced to) the null (no edges) model, one edge at a time via a sequence of perfect DAGs. It remains to note that, within the null model, all orderings are permissible and any ordering can be obtained from any other by a sequence of switches of adjacent variables.]

When a switch of variables \(j\) and \(j+1\) \((j = 1, \ldots, p-1)\) in the ordering is proposed, it is accompanied by a deterministic transformation of parameters in the model, \(\theta' = g(\theta)\). This kind of proposal is straightforward to incorporate within the RJMCMC framework. Assuming that the probability of proposing the switch of variables \(j\) and \(j+1\) is independent of the current ordering, that all orderings are considered equally likely \(a \text{ priori}\), and that no change to the current graphical model \(m\) is proposed, then the proposal
is accepted with probability \( \min\{1, \pi\} \) where

\[
\pi = \frac{f(z' | \Psi', \Lambda', \beta') f(\Psi, \Lambda', \beta|m, \alpha')}{f(z | \Psi', \Lambda', \beta') f(\Psi, \Lambda, \beta|m, \alpha')} \left| \frac{\partial(z', \Psi', \Lambda', \beta')}{\partial(z, \Psi, \Lambda, \beta)} \right|
\]

and \( o \) is used to denote the ordering of the variables. The prior for \((\Psi, \Lambda)\) is allowed to depend on \( o \), as with binary variables different orderings imply different components of \( \Lambda \) subject to identifiability constraint. However, we assume that the prior distribution over \((o, m)\) is such that \( f(o|m) \) is uniform, for any \( m \); see Section 5 for further discussion.

By switching the relevant components of \( z, \mu \) and the precision matrix \( \Sigma^{-1} \), the proposal can be implemented in a way such that the likelihood ratio \( f(z' | \Psi', \Lambda', \beta')/f(z | \Psi, \Lambda, \beta) \) in (19) is equal to one, which is desirable in terms of maximising acceptance probability. The induced transformation on \((\psi, \Lambda)\) is given by

\[
\lambda'_j = \rho^2 \lambda_{j+1}
\]

\[
\lambda'_{j+1} = \lambda_j / \rho^2
\]

\[
\psi'_{j,j+1} = \frac{\lambda_j \psi_{j,j+1}}{(\lambda_j + 1) \rho^2}
\]

\[
\psi'_{j,k} = \psi_{j+1,k} + \lambda_j \psi_{j,j+1} \psi_{j,k} / \lambda_{j+1} / \rho^2 \quad k = j + 2, \ldots, p
\]

\[
\psi'_{j,k} = \psi_{j,j+1} \psi_{j+1,k} \quad k = j + 2, \ldots, p \quad j = 1, \ldots, j - 1
\]

\[
\psi'_{j,1} = \psi_{j,j+1} \psi_{j+1,k} \quad k = j + 2, \ldots, p
\]

\[
\psi'_{1,j+1} = \psi_{j+1,k} \quad k = j + 2, \ldots, p
\]

where

\[
\rho = \left(1 + \frac{\lambda_j \psi^2_{j,j+1}}{\lambda_{j+1}} \right)^{1/2}
\]

All other elements of \( \Psi \) are unchanged. Note that when \( \psi_{j,j+1} = 0 \), the transformation is a simple re-labelling of components. The transformation respects the model, with components of \( \Psi \) constrained to zero being unchanged, provided that the current and proposed orderings are perfect for the current DAG, as required. The transformation is self-inverse, and hence reversibility is assured. However, where one or both of the variables being switched is binary, we have imposed an identifiability constraint on the corresponding component of \( \Lambda \). Therefore the transformation in (20)-(26) is no longer valid. A modification for such transitions, which also involves a deterministic transformation of the latent data \( z \), is described in the Appendix.
The likelihood and prior ratios in (19) are equivalent to those in (17) and for our prior can be simplified in an equivalent way to lead to an expression similar to (18), but including terms corresponding to \((\psi_j, \lambda_j)\) as well as those corresponding to \((\psi_{j+1}, \lambda_{j+1})\). The additional component is the Jacobian term, which for the transformation in (20)-(26) is given by

\[
\left| \frac{\partial (z', \Psi', \Lambda', \beta')}{\partial (z, \Psi, \Lambda, \beta)} \right| = \frac{\lambda_j}{\lambda_j \psi_{j+1}^2 + \lambda_{j+1}} = \frac{\lambda_j}{\lambda_{j+1} \rho^{-2}}
\]

The transformation (20)-(26) has been explicitly constructed so that the likelihood ratio in (19) is equal to one. Furthermore, provided that the prior distribution is symmetric, as it would be if derived from a Wishart prior for \(\Sigma^{-1}\), as suggested in Section 2.2, then the remaining part of the acceptance ratio in (19) is also equal to one, and order switches are always accepted. However, this is not the case for the corresponding order switches described in the Appendix which are required in the presence of binary variables. Nevertheless, our experience is that the modified proposals developed in the Appendix have a high acceptance probability (typically over 0.9).

The full MCMC algorithm for undirected graphical models now proceeds as follows. An initial ordering, model and values for all parameters in this model are specified. The following procedure is then iterated. With some fixed probability we propose a null move, where the new values are generated for the parameters of the current model. Otherwise, a new model is proposed by either adding or subtracting a randomly selected edge from the current model, and accepted with probability \(\min\{1, \pi\}\) as defined in (17) and (18) (or the equivalent expression when the proposal involves removing an edge) but with \(f(m)\) now replaced by \(f(m, o)\). If the proposed model is unavailable in the current ordering the proposal is automatically rejected. At each iteration, a new ordering is also proposed, by randomly selecting a pair of adjacent variables in the current ordering and proposing to switch them. If the current model is not available in the proposed ordering, then the proposal is automatically rejected. Otherwise, the proposed ordering is accepted with probability \(\min\{1, \pi\}\) as defined in (19).
5 Examples

5.1 Introduction and choice of prior parameters

We will present results of our approach applied to four data examples, covering purely ordinal data, mixed binary and ordinal data, and purely binary data, and with model selection focussing both on undirected graphical models, in Examples 1-3, and on directed graphical models in Example 3 and 4, where a variable ordering is specified in advance.

In each example, we are required to specify the prior distribution \( f(m, o) \) of each particular combination of model and ordering. We assume a neutral prior, where \( f(m) \) is uniform over all models under consideration, and \( f(o|m) \) is uniform over all orderings permitted by model \( m \). Hence, \( f(m, o) \) is inversely proportional to \( r(m) \), the number of orderings permitted by model \( m \). Therefore it is necessary, when a new model is proposed, to compute \( r(m) \) in order to compute the acceptance probability for the proposal. An efficient algorithm for performing this computation is given by Chandran et al. (2003), and is implemented within our reversible jump procedure.

We are also required to specify, for each model, the parameters of the prior distribution. As described in Sections 2.2 and 2.3, these are the parameters \( \nu \) and \( T \) of the prior distribution for \( \beta \), the parameters \( (b_j, q_j) \) of the prior distribution for \( \lambda_j \) for each non-binary variable \( j \), and the parameters \( (\mu_j, A_j) \) of the prior distribution for \( \psi_j \) for each variable \( j \). The dimensions of \( \mu_j \) and \( A_j \), will vary with the model under consideration. We choose to reduce this considerable burden of prior specification by deriving the prior parameters from the same inverse-Wishart distribution for all models, in the manner described in Section 2.3. Hence, we are only required to specify a single \( p \times p \) matrix \( A \) and a scalar degrees-of-freedom parameter \( q \). This also provides the required specification of \( (b_j, q_j, \mu_j, A_j) \) for each non-binary variable \( j \). If a more general prior specification for \( (b_j, q_j, \mu_j, A_j) \) was desired, this would not affect the efficiency of our computational procedures.

We assume a diffuse prior for \( \beta \) and choose \( \nu = 0 \) and \( T = tI \) for a large value of \( t \). (In the examples, we use \( t = 50 \), which makes the prior very flat over the scale of the latent variables). We use a neutral prior for \( \Psi \) which assumes that where conditional association is present, there is no prior knowledge as to whether it is likely to be positive or negative. Hence, each element of \( \Psi \) is assumed to have zero prior mean. It follows
from (11) that $A$ is a diagonal matrix and, using the same notation as (12), $A = \text{diag}(a_{11}, \ldots, a_{pp})$.

The choice of $(a_{11}, \ldots, a_{pp})$ and $q$ is critical to the posterior distribution over models, as it is these parameters which control the prior dispersion of $\Psi$, the dimensionality of which changes between models. The magnitude of these parameters depends on the underlying latent scale. For non-binary variables, we have fixed the scale using (2), so that under a standard normal distribution for $Z_j$, the probability of $Y_j$ taking the lowest or highest levels is equal to $1/k_j$. In the absence of strong prior information, it seems reasonable to expect that the prior probability assigned to any of the $k_j$ levels of $Y_j$ would be $1/k_j$. Hence, as $E(\beta_j) = 0$, it remains to set $E(\sigma_{jj}) = 1$ to reflect this. For the inverse-Wishart prior, the means for the variances of the latent $Z_j$ are given by $E(\sigma_{jj}) = a_{jj}(q-p-1)^{-1}$. Therefore, we set $a_{jj} = (q-p-1)$ for all $j$. For binary variables, the conditional precision $\lambda_j$ is fixed at 1, and hence the conditional variance $\lambda_j^{-1}$ is also fixed at this value. As we have chosen to set $a_{jj} = (q-p-1)$, then the constrained value for $\lambda_j^{-1}$, in models where the distribution of $Z_j$ is independent of $\{Z_k, k > j\}$ or when $j = p$, is equal to the prior mean for $\lambda_j^{-1}$, which would be derived from $q$ and $A$, if a constraint was not required. For other models the constrained value for $\lambda_j^{-1}$ exceeds the prior mean derived from $q$ and $A$ by a factor of $(q-p+c_j-1)/(q-p-1)$.

Specification of the prior is completed by choosing a value for $q$. As $A = (q-p-1)I$, we derive, from (7) and (8), that

$$
\text{Var}(\psi_{jk}) = \begin{cases} 
\frac{1}{q-p-1} & k_j = 2 \\
\frac{1}{q-p+c_j-1} & k_j > 2 
\end{cases}
$$

A smaller value of $q$ corresponds to a more diffuse prior distribution for $\Psi$. To fix a value for $q$, we note the correspondence between $A$ in the prior and $A + G$ in the posterior, as displayed in (14) and (16). For $d$ observations, the prior predictive expectation of $g_{jj}$ is $E(g_{jj}) = da_{jj}(q-p-1)^{-1} = d$. Hence, $a_{jj} = q-p-1$ may be interpreted as the weight of the prior, and setting $q = d+p+1$ gives the prior the same expected weight as a sample of $d$ observations. In the subsequent examples, we use $q = p+2$ to represent a prior weight equivalent to a single observation. This ‘unit information’ prior is suitably diffuse, in the absence of strong prior information, but not to the extent of having an undesirable impact on posterior model probabilities.

In each of the examples below, this prior was used. The reversible jump
methodology described in Sections 3 and 4 was used to calculate model probabilities. For each example 500,000 iterations were used, with an order switch attempted at each iteration, and a model transition attempted on 70% of iterations (the remaining 30% being used for null, within-model, transitions). The acceptance rate for proposed model transitions varied from 5% to 15% across the examples we studied. The acceptance rate for order switches (for proposals not automatically rejected because of incompatibility of model and ordering) was much higher, the lowest rate being just under 90% (with a 100% success rate for examples where all variables have at least three levels, as expected). Convergence in model space was assessed by using multiple chains, started from highly dispersed positions in model space, as described in Dellaportas and Forster (1999). On each occasion, we were reassured that the chain converged on the same, most probable, region. In each case, MCMC standard errors were evaluated by the method of batch means (see Geyer, 1992) where the generated sample is divided into a series of subsamples with approximately uncorrelated probability estimates, and then the standard error evaluated as the standard deviation of the subsample means divided by the square root of the number of subsamples. In practice, our chains of 500,000 iterations allowed at least 100 subsamples to be used in every example, which provide sufficiently accurate estimates of MCMC variability.

5.2 Colouring of blackbirds

The first example was used by Anderson and Pemberton (1985) to illustrate a full (no conditional independence) multivariate ordinal probit model. The data are derived from observations of the colouring of 90 blackbirds and consist of three ordinal variables, representing the colouring of the lower mandible ($L$), the upper mandible ($U$) and the orbital ring ($O$), each with three levels. Here, we investigate the evidence for simplifying the model of Anderson and Pemberton (1985) by allowing conditional independence between the latent variables. We note that Anderson and Pemberton (1985) found strong evidence for marginal association for each pair of variables, so we would not expect significant posterior probability on any model with fewer than two edges. Indeed, when we evaluated the posterior distribution over models, it was concentrated on three models, the full model (probability 0.2791, MCMC standard error 0.0037), the model $L \perp\!\!\!\!\perp O|U$ (0.4272, 0.0078) and the model $U \perp\!\!\!\!\perp O|L$ (0.2933, 0.0083).
To assess the benefits of modelling these data using ordinal models, we investigated the extent to which they offer improvements in predictive capability. This was evaluated by predictive cross-validation. In turn, each of the 90 observations was omitted from the data set, and its predictive probability calculated under each of the most probable models above, and by model-averaging using the posterior model probabilities. (In fact, as the 90 observations were all in one of 15 cells of the table, only 15 separate analyses were required). We also calculated the same cross-validation predictive probabilities for non-ordinal graphical models, together with hyper-Dirichlet prior distributions (see Dawid and Lauritzen, 1993), for these data. The non-ordinal models strongly favoured the two simpler structures \(L \perp\!\!\!\!\perp O|U\), \(U \perp\!\!\!\!\perp O|L\) for each of the 15 reduced data sets. Nevertheless, we include the saturated non-ordinal model in our comparisons of predictive probability. Table 1 presents the total logarithmic score for the predictive probabilities,

\[
S = \sum_{i=1}^{90} \log p(y_i | y_{\sim i})
\]

where \(y_{\sim i}\) represents the data \(y\) with \(y_i\) removed. As might be expected from the similarity of their posterior probabilities, there is very little difference between the three ordinal models (or the resulting model average) in terms of predictive capability. However, the ordinal models predict the left-out values with significantly higher probability than the models which do not explicitly account for ordinal structure. The difference, a per-datum average around 0.1 on the logarithmic scale, corresponds to an improvement in predictive probability of about 10% per observation. Hence, considerable gains are possible by using the ordinal data models considered in this paper.

<table>
<thead>
<tr>
<th>Conditional independence structure</th>
<th>Ordinal models</th>
<th>Non-ordinal models</th>
</tr>
</thead>
<tbody>
<tr>
<td>None</td>
<td>-178.4</td>
<td>-197.7</td>
</tr>
<tr>
<td>(L \perp!!!!\perp O</td>
<td>U)</td>
<td>-177.8</td>
</tr>
<tr>
<td>(U \perp!!!!\perp O</td>
<td>L)</td>
<td>-178.3</td>
</tr>
<tr>
<td>model-averaged</td>
<td>-178.4</td>
<td>-190.7</td>
</tr>
</tbody>
</table>

Table 1: Predictive logarithmic scores for cross-validation predictions based on various models

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5.3 Alcohol, obesity and hypertension

Our second example is taken from Knuiman and Speed (1988) and concerns 491 subjects classified according to Hypertension \((H): \text{yes or no})\), Alcohol Intake \((A): 0, 1-2, 3-5, 6+ \text{ drinks per day})\) and Obesity \((O): \text{low, average, high})\). Variables \(O\) and \(A\) are ordinal with 3 and 4 levels respectively and variable \(H\) is binary. Posterior model probabilities are displayed in Table 2.

<table>
<thead>
<tr>
<th>Model</th>
<th>Posterior probability</th>
<th>MCMC standard error</th>
</tr>
</thead>
<tbody>
<tr>
<td>(OH + AH)</td>
<td>0.7254</td>
<td>0.0038</td>
</tr>
<tr>
<td>(A + OH)</td>
<td>0.0913</td>
<td>0.0021</td>
</tr>
<tr>
<td>(AOH)</td>
<td>0.0838</td>
<td>0.0015</td>
</tr>
<tr>
<td>(OH + OA)</td>
<td>0.0526</td>
<td>0.0015</td>
</tr>
<tr>
<td>(O + AH)</td>
<td>0.0266</td>
<td>0.0011</td>
</tr>
<tr>
<td>(OA + AH)</td>
<td>0.0131</td>
<td>0.0007</td>
</tr>
<tr>
<td>(O + A + H)</td>
<td>0.0052</td>
<td>0.0003</td>
</tr>
<tr>
<td>(H + OA)</td>
<td>0.0019</td>
<td>0.0002</td>
</tr>
</tbody>
</table>

Table 2: Posterior Model Probabilities for Alcohol, Obesity and Hypertension Data

The posterior probabilities are dominated by the model which assumes conditional independence of obesity and alcohol intake, given hypertension. (We should make clear that when we refer to a particular variable here, such as ‘obesity’, in the context of conditional independence, we are talking about the corresponding latent variable). Very little posterior probability is given to any model which assumes conditional independence of obesity and hypertension, given alcohol intake. Comparing the posterior probabilities in Table 2 with those evaluated by Dellaportas and Forster (1999) for graphical log-linear models without explicit ordinal structure, significant differences are immediately apparent. The posterior probabilities for the non-ordinal models typically favour models with fewer edges (interactions), with most posterior probability being placed on the mutual independence model and the model \(A + OH\) (typically over 95% for these two models for a wide range of priors). The reason that non-ordinal models do not favour a more complex dependence structure is because incorporating such a structure requires extra model complexity to a degree not warranted by the evidence in the data. For example, to include the edge \(AH\) in a non-ordinal model requires three extra parameters, whereas for the models considered in this
paper, each edge contributes exactly one parameter to the model.

Hence, by considering models which explicitly recognise the ordinal structure, we are able to detect evidence in favour of interactions which are not obvious when non-ordinal models are used. This is consistent with the findings of Dellaportas and Tarantola (2005), who investigate non-ordinal log-linear models for the same data, but allow merging of adjacent levels of certain variables (an explicitly ordinal operation). Their favoured merging collapses alcohol intake to a binary variable and hence they, too, identify more complex dependence structure as, for example, the $AH$ edge is then modelled by a single parameter. As discussed in Section 2.1, our graphical models for the latent variables are invariant under merging of adjacent categories, so we avoid having to consider such operations.

### 5.4 Risk factors for coronary heart disease: a $2^6$ table

For our final two examples, we consider larger tables, and focus on comparison of the conditional independence structures (for latent variables) supported by the data for our ordinal data models, with those identified by previous authors modelling the same data. The first such example is taken from Edwards and Havranek (1985) and concerns 1841 men cross-classified by 6 factors linked to coronary heart disease. The six variables are A, smoking; B, strenuous mental work; C, strenuous physical work; D, systolic blood pressure; E, ratio of $\alpha$ and $\beta$ lipoproteins; F, family anamnesis of coronary heart disease. All six variables are binary.

We considered both directed and undirected models for these data. For directed models, we assumed the variable ordering $FCBAED$, suggested by Madigan and Raftery (1994). The four models with the highest posterior probability (greater than 0.05) are displayed in Figure 1, together with their posterior probabilities (and associated MCMC standard errors). Models (b) and (d) represent the two structures which dominated the posterior distribution reported by Madigan and Raftery (1994). For data containing binary variables only, the main difference between the probit models considered here, and graphical log-linear models is in the modelling of higher-order interactions. For example, the dependence of $D$ on $(A, E)$ identified in all four of our models, is modelled by two conditional regression parameters, whereas in a log-linear structure, it is modelled by three parameters. Hence, the probit models offer more parsimonious ways of modelling association (at
the cost of decreased flexibility in modelling a given association structure). In this example, there was considerable model uncertainty. Only 7 models (with a combined probability of 0.543) have a posterior probability greater than 2%.

The two most probable undirected graphical models (probability greater than 0.05) are displayed in Figure 2. The most probable model has identical structure to the most probable model identified by Madigan and Raftery (1994) and Dellaportas and Forster (1999) for these data, and is one of the models selected by Edwards and Havranek (1985). Interestingly, the association between variables E and F identified here, was not identified by any of the other approaches.

5.5 Influences on political attitude

Wermuth and Cox (1998) analyse a five way table from a study to determine the influences on political attitude in Germany. The first four variables are A: political attitude (4 levels), B: type of formal schooling (3), C: age group (5), and D: year of study (2 levels). The final variable represented region
(East or West Germany) and as part of their analysis Wermuth and Cox (1998) present models for these two subgroups separately. Here, we analysed the two subgroups entirely separately, and hence we have two four-way tables, each with three ordinal variables and one binary variable. Wermuth and Cox (1998) consider directed graphical models where the variables are ordered $DCBA$. They use log-linear models, but parameterised in a way which makes it straightforward to identify common effects in adjacent factor levels, hence allowing more parsimonious modelling of association structure than would be possible with standard, unconstrained, log-linear interaction models. As discussed in Section 5.3, our graphical models for the latent variables are invariant under merging of adjacent categories. Given this similarity of approach, it is not surprising that, for each region, our most probable directed graphical models for the latent variables, displayed in Figure 3 has identical structure to the models identified by Wermuth and Cox (1998). For the East German data, there was also some support for the inclusion of an association between $A$ and $C$ (probability of edge present around 0.5) and between $A$ and $B$ (0.3). For the West German data, the only other model with non-negligible posterior probability contained the extra edge between $C$ and $D$. 

Figure 2: Most probable undirected graphical models for latent variables underlying risk factors for coronary heart disease. Also presented are corresponding posterior model probabilities (MCMC standard errors in brackets).
Figure 3: Most probable directed graphical model for latent variables underlying ordinal variables in the political attitude data, for each of the two regions (East and West Germany). Also presented are corresponding posterior model probabilities (MCMC standard errors in brackets).

6 Discussion

The examples presented in Section 5 illustrate that modelling conditional independence using the methods described in this paper is feasible across a wide range of data structures, involving ordinal data, binary data or mixed ordinal and binary data. Furthermore, there are significant potential gains in adopting this approach as the more parsimonious parameterisation of association allows interactions to be identified which are less likely to be detected using models which do not explicitly allow for ordinal structure.

The parameterisation of the models, using a Cholesky factorisation, allows fully normalised prior distributions to be used which makes Bayesian model determination feasible. Furthermore, the resulting conditional conjugacy suggests a natural form of the proposal distribution when model transitions are attempted. Therefore, we can finesse what is, typically, most difficult aspect of efficiently implementing a RJMCMC strategy. No initial exploration of the posterior distribution using ‘pilot chains’ is required. Consequently, the acceptance rates for such proposals are high, where the proposed model is supported by the data. This fact is somewhat obscured in the overall acceptance rates of 5% to 15% described in Section 5.1, as these rates also include large numbers of attempted transitions to models with low posterior probability. Of course, using the Cholesky factorisation comes at a price, namely the requirement to involve variable orderings, even when we are considering undirected graphical models. However, the efficiency of our order-switching proposals is such that this is not a significant drawback.
In this paper, we have restricted consideration to contingency tables. However, with relatively straightforward modification, our approach can be extended to analyse multivariate ordinal and binary data with covariates, including longitudinal data, or a mixture of ordinal/binary and continuous variables. Furthermore, the model class can be extended to include graphical chain models. These types of analysis are the subject of ongoing research.

Appendix: Order switches involving binary variables

The transformation described in (20)-(26) cannot be applied when either of the variables to be switched is binary, as it does not preserve the necessary constraint(s) on $\Lambda$. One possible solution to this would be simply to apply (20)-(26) for the unconstrained parameters, and then set the constrained component(s) of $\Lambda$ equal to the required value(s). However, in our experience such proposals can have low acceptance probabilities. To see this, consider the case where $p = 2$, and of the two classifying variables, $Y_1 \equiv A$ is binary, but $Y_2 \equiv B$ has more than two levels. When $A$ precedes $B$ in the ordering then $\lambda_A$ is the conditional precision of $A$ given $B$, but when $B$ precedes $A$, this parameter is the marginal precision. If there is a high level of association (large value of $|\psi_{12}|$) then the conditional precision is usually very much larger than the marginal precision. In other words, by constraining $\lambda_A$ to the same value, independent of the position of $A$ in the ordering, we are effectively imposing a different scale on the latent $z_A$ values for each different model and ordering. There is no problem with this, except that it leads to low acceptance probabilities for proposed transitions which change orderings and unconstrained parameter values, but preserve $z$. Our solution to this is to propose a scale transformation of $z_A$ whenever $A$ is involved in a proposed order switch.

The magnitude of the scale transformation required is clear from (20)-(21). We note that, if the variables being switched are denoted by $A$ (currently in position $j$) and $B$ ($j+1$), then (20) and (21) can be thought of as $\lambda_B' = \rho^2 \lambda_B$ and $\lambda_A' = \rho^{-2} \lambda_A$ respectively. Hence, for a binary variable $C$ where $\lambda_C$ is fixed and cannot be transformed, this immediately suggests that the latent $z_C$ should be rescaled by $\rho^{-1}$ if $C$ is the variable currently in position $j$ and by $\rho$ if $C$ is the variable currently in position $j+1$. Clearly $\beta_C$ needs to be rescaled in the same way. There are consequent modifications
required to (22)-(24) and in particular to (25)-(26) to preserve the conditional means of \( z_1, \ldots, z_{j-1} \). When both variables to be switched are binary, the resulting transformation is

\[
\psi'_{j,j+1} = \frac{\psi_{j,j+1}}{\lambda_{j+1}} \\
\psi'_{jk} = \frac{\psi_{j,k} + \lambda_j \psi_{j,j+1} \psi_{j,k}}{\rho} \\
\psi'_{j+1,k} = \frac{\psi_{j,k} - \psi_{j,j+1} \psi_{j+1,k}}{\rho} \\
\psi'_{kj} = \frac{\psi_{k,j+1}}{\rho} \\
\psi'_{k,j+1} = \rho \psi_{kj}
\]

where \( \rho \) is given by (27). The transformation remains entirely deterministic, and self-inverse. The Jacobian is given by

\[
\left| \frac{\partial (z', \Psi', \Lambda', \beta')} {\partial (z, \Psi, \Lambda, \beta)} \right| = \frac{\lambda_j}{\lambda_{j+1}} \frac{\rho^{d_j - d_{j+1} + 1}}
\]

where \( d_l \) is the number of variables \( k < l \) with \( \psi_{kl} \neq 0 \).

When one of the variables to be switched is binary, and the other has more than two levels, then the precise form of the transformation depends on whether the binary variable is currently in position \( j \) (call this the forward transformation) or in position \( j + 1 \) (its inverse). For the forward transformation, \( \lambda'_j = \rho^2 \lambda_{j+1} \), as in (20), and for its inverse \( \lambda'_{j+1} = \lambda_j / \rho^2 \), as in (21). In both cases, \( \psi'_{j,j+1} = \frac{\lambda_j \psi_{j,j+1}}{\rho \lambda_{j+1}} \), as in (22). The proposals \((\psi'_{jk}, \psi'_{j+1,k})\) in (23)-(24) are modified by multiplying the right hand side of (24) by \( \rho^{-1} \) for the forward transformation, and the right hand side of (23) by \( \rho \) for its inverse. Similarly, the proposals \((\psi'_{kj}, \psi'_{k,j+1})\) in (25)-(26) are modified by multiplying the right hand side of (26) by \( \rho \) for the forward transformation, and the right hand side of (25) by \( \rho^{-1} \) for its inverse. The latent data and relevant component of \( \beta \) are rescaled for the binary variable only. The resulting Jacobian is

\[
\left| \frac{\partial (z', \Psi', \Lambda', \beta')} {\partial (z, \Psi, \Lambda, \beta)} \right| = \frac{\lambda_j}{\lambda_{j+1}} \frac{\rho^{d_j - c_j - n + 1}}
\]

for the forward transformation and

\[
\left| \frac{\partial (z', \Psi', \Lambda', \beta')} {\partial (z, \Psi, \Lambda, \beta)} \right| = \frac{\lambda_j}{\lambda_{j+1}} \frac{\rho^{c_j + 1 - d_{j+1} + n - 1}}
\]

for the inverse.
References


