Bayesian Methods for Multivariate Categorical Data

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Table 1: Alcohol intake, hypertension and obesity (Knuiman and Speed, 1988)

<table>
<thead>
<tr>
<th>Obesity</th>
<th>Hypertension</th>
<th>Alcohol intake (drinks/day)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>0</td>
</tr>
<tr>
<td>Low</td>
<td>Yes</td>
<td>5</td>
</tr>
<tr>
<td></td>
<td>No</td>
<td>40</td>
</tr>
<tr>
<td>Average</td>
<td>Yes</td>
<td>6</td>
</tr>
<tr>
<td></td>
<td>No</td>
<td>33</td>
</tr>
<tr>
<td>High</td>
<td>Yes</td>
<td>9</td>
</tr>
<tr>
<td></td>
<td>No</td>
<td>24</td>
</tr>
</tbody>
</table>
Table 2: Risk factors for coronary heart disease (Edwards and Havránek, 1985)

A $2^6$ table (not displayed)

1841 men cross-classified by six risk factors for coronary heart disease

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
Table 3: Disclosure risk estimation - Large and sparse

Six potential key variables from the 3% Individual SAR for the 2001 UK Census (http://www.ccsr.ac.uk/sars/2001).

Restricted to 154295 individuals living in South West England

Sex (2 categories)
Age (coded into 11 categories)
Accomodation type (8 categories)
Number of cars owned or available for use (5 categories)
Occupation type (11 categories)
Family type (10 categories)

The full table has 96800 cells of which 3796 are uniques.
The data

Sample data consists of values of categorical variables, recorded for each individual in the sample, expressed as a multiway contingency table.

Individuals $i = 1, \ldots, n$ are classified by variables $j = 1, \ldots, p$, where variable $j$ has $k_j$ (potentially ordered) categories.

Independent categorical response vectors $\mathbf{y}_i = (y_{i1}, y_{i2}, \ldots, y_{ip})$ are observed.

The contingency table $\mathbf{y}$, derived from $\{\mathbf{y}_i, i = 1, \ldots, n\}$ has $k = \prod_{1}^{p} k_i$ cells.
Multinomial models

$y$ has a multinomial($n, \pi$) distribution.

[or $y$ is drawn as a $n/N$ sample from a finite population $Y$ which has a multinomial($N, \pi$) prior distribution, Ericson, 1969]

$$\pi \in S_{p-1} = \left\{ \pi_j > 0, j = 1, \ldots, p : \sum_{j=1}^{p} \pi_j = 1 \right\}$$

typically constrained by a model

e.g. assume a graphical or log-linear model for $\pi$,

$$\log \pi = X_m \beta_m$$
Modelling association

Undirected graphical models

Directed graphical models

General log-linear models
Bayesian inference

The posterior for the model parameters $\beta$ is obtained using

$$ p(\beta|y) \propto p(y|\beta)p(\beta) $$

Posterior $\propto$ likelihood $\times$ prior

This is Bayes theorem.
Bayesian inference for the unconstrained model

For the unconstrained model $\beta = \pi$ and a natural prior for $\pi$ is the Dirichlet with hyperparameters $\alpha = (\alpha_1, \ldots, \alpha_p)$.

$$E(\pi_j) = \frac{\alpha_j}{\sum_{\ell=1}^{p} \alpha_\ell} \quad \text{Var}(\pi_j) = \frac{E(\pi_j)[1 - E(\pi_j)]}{1 + \sum_{\ell=1}^{p} \alpha_\ell}$$

This prior distribution is *conjugate*, leading to a Dirichlet posterior with

$$\alpha \rightarrow \alpha + y.$$ 

Possible diffuse priors have $\alpha = (1, \ldots, 1)$, $\alpha = (\frac{1}{2}, \ldots, \frac{1}{2})$, $\alpha = \left(\frac{1}{p}, \ldots, \frac{1}{p}\right)$. 
### Treatment regimes for cancer of the larynx (from Agresti, 1990)

<table>
<thead>
<tr>
<th>Cancer controlled after treatment?</th>
<th>Yes</th>
<th>No</th>
</tr>
</thead>
<tbody>
<tr>
<td>Surgery</td>
<td>21</td>
<td>2</td>
</tr>
<tr>
<td>Radiation Therapy</td>
<td>15</td>
<td>3</td>
</tr>
</tbody>
</table>

Posterior distributions for $P(\text{Yes}|\text{Surgery})$, $P(\text{Yes}|\text{Radiation})$. 

\[
\text{alpha}=(1/4,1/4,1/4,1/4) \quad \text{alpha}=(1,1,1,1)
\]
Decomposable graphical models and the hyper-Dirichlet

\[ A \] \[ B \] \[ C \]

\( A \) is independent of \( B \) given \( C \), so that

\[ p(A = i \text{ and } B = j | C = k) = P(A = i | C = k) P(B = j | C = k) \]

or

\[ \pi_{ijk} = \beta_i^{A} \beta_j^{B} \beta_k^{C} \]

Independent Dirichlet priors for \( \{\beta_i^{A}\} \), \( \{\beta_j^{B}\} \), for each \( k \), and for \( \{\beta_k^{C}\} \).

Conjugate prior leads to tractable computation.
Bayesian inference under model uncertainty

Allows model uncertainty to be coherently incorporated.

Multiple models indexed by $m \in M$.

Joint prior uncertainty about $(m, \beta_m)$ is encapsulated by

$$p(m, \beta_m) = p(m)p(\beta_m|m)$$

where $p(m)$ is a discrete prior distribution over $M$.

By Bayes theorem

$$p(\beta_m|y, m) = \frac{p(y|m, \beta_m)p(\beta_m|m)}{p(y|m)}$$

and

...
\[ p(m|y) = \frac{p(m)p(y|m)}{\sum_{m \in M} P(m)P(y|m)} \]

where \( p(y|m) = \int p(y|m, \beta_m) p(\beta_m|m) d\beta_m. \)

Note that, for any two models, say \( m = 1 \) and \( m = 2 \)

\[
\frac{p(m = 1|y)}{p(m = 2|y)} = \frac{p(m = 1) p(y|m = 1)}{p(m = 2) p(y|m = 2)}
\]

posterior odds = prior odds \( \times \) Bayes factor

The *Bayes factor* quantifies how belief about the two models is moderated in light of the observed data.
Model averaging

Model search and uncertainty is incorporated through the discrete prior [posterior] distribution \( p(m) \) \([p(m|y)]\) over the models \( m \in M \).

Then, posterior predictive expectations of any function of \( Y \) will be a model average

\[
E[g(Y)|y] = \sum_{m \in M} p(m|y)E[g(Y)|y, m].
\]

The posterior model probabilities may not be of interest in themselves – interpret them as weights.
Model uncertainty for laryngeal cancer data

<table>
<thead>
<tr>
<th>Treatment</th>
<th>Cancer controlled after treatment?</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Yes</td>
</tr>
<tr>
<td>Surgery</td>
<td>21</td>
</tr>
<tr>
<td>Radiation Therapy</td>
<td>15</td>
</tr>
</tbody>
</table>

$m = 1$: Independence of Outcome and Treatment; $\pi_{jk} = \beta_j^T \beta_k^O$

$m = 2$: Dependence of Outcome on Treatment; $\pi$ unconstrained

Prior when $m = 1$: Independent Dirichlets on marginal probabilities, $\beta_j^T$, $\beta_k^O$

Prior when $m = 2$: Dirichlet on $\pi$

Bayes factor (for independence) = \[
\begin{cases}
2.11 & \alpha = (1, 1, 1, 1) \\
3.17 & \alpha = (\frac{1}{2}, \frac{1}{2}, \frac{1}{2}, \frac{1}{2}) \\
5.33 & \alpha = (\frac{1}{4}, \frac{1}{4}, \frac{1}{4}, \frac{1}{4})
\end{cases}
\]
Computation for more complex data

Potential computational difficulties

1. Evaluating integrals – may be mathematically intractable

2. Number of models is large.

For decomposable models and hyper-Dirichlet prior distributions, most of the calculations (e.g. Bayes factors) can be performed exactly, and easily.

Otherwise MCMC or approximation such as BIC will be required.

For more than a few (3 or 4) cross-classifying variables, number of models gets large and some kind of approximation will be required. (e.g. Monte Carlo – Madigan and York, 1996)

We adopt a search strategy to identify a set of most probable models.
<table>
<thead>
<tr>
<th>Models</th>
<th>HO+HA</th>
<th>O+HA</th>
<th>A+HO</th>
<th>H+O+A</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hyper-Dirichlet (Jeffreys)</td>
<td>0.0360</td>
<td>0.0170</td>
<td>0.6428</td>
<td>0.3042</td>
</tr>
<tr>
<td>Hyper-Dirichlet (Perks)</td>
<td>0.0000</td>
<td>0.0001</td>
<td>0.0290</td>
<td>0.9709</td>
</tr>
</tbody>
</table>
Table 2: Analysis

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

\begin{table}
\centering
\begin{tabular}{|c|}
\hline
\end{tabular}
\end{table}

(a) 0.3565 (0.0081) \hspace{2cm} (b) 0.1032 (0.0042)
Table 3: Analysis

Six potential key variables from the 3% Individual SAR for the 2001 UK Census (http://www.ccsr.ac.uk/sars/2001).

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Family type (10 categories)

The full table has 96800 cells of which 3796 are uniques.

This is our ‘population’, from which we took a 3% subsample.

Most probable model, based on sample data, is SO+OAg+AgF+FN+NAc
**Sample data** contains 4761 individuals in 2330 cells.

1543 (32%) are uniques, of which 114 (7%) are population uniques. Average population total in a sample unique cell is 17.

<table>
<thead>
<tr>
<th>Population</th>
<th>0</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5-9</th>
<th>10-19</th>
<th>20+</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>84867</td>
<td>3682</td>
<td>1694</td>
<td>967</td>
<td>631</td>
<td>1482</td>
<td>757</td>
<td>390</td>
<td>94470</td>
</tr>
<tr>
<td>1</td>
<td>—</td>
<td>114</td>
<td>110</td>
<td>118</td>
<td>104</td>
<td>313</td>
<td>322</td>
<td>462</td>
<td>1543</td>
</tr>
<tr>
<td>2</td>
<td>—</td>
<td>—</td>
<td>0</td>
<td>2</td>
<td>5</td>
<td>28</td>
<td>67</td>
<td>266</td>
<td>368</td>
</tr>
<tr>
<td>Sample</td>
<td>3</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>15</td>
<td>140</td>
</tr>
<tr>
<td>4</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>76</td>
</tr>
<tr>
<td>5-9</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>0</td>
<td>0</td>
<td>125</td>
</tr>
<tr>
<td>10-19</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>0</td>
<td>48</td>
</tr>
<tr>
<td>20+</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>14</td>
</tr>
<tr>
<td>Total</td>
<td>84867</td>
<td>3796</td>
<td>1804</td>
<td>1087</td>
<td>740</td>
<td>1824</td>
<td>1161</td>
<td>1521</td>
<td>96800</td>
</tr>
</tbody>
</table>
Record-level measures of disclosure risk

If $E_j$ represents disclosure event in (sample non-empty) cell $j$

$$P(E_j|Y) = \frac{1}{Y_j}$$

(Benedetti and Franconi, 1998)

Alternatively,

$$P(Y_j = 1|Y) = I[Y_j = 1]$$

is the probability of uniqueness.
Bayesian disclosure risk assessment

We calculate Bayesian predictive probabilities as the posterior expectations

\[ P(\text{event}|\mathbf{y}) = E[P(\text{event}|\mathbf{Y})|\mathbf{y}] \]

Hence our risk measures become

\[ P(E_j|\mathbf{y}) = E[1/Y_j|\mathbf{y}] \]

and

\[ P(Y_j = 1|\mathbf{y}). \]

which are calculated using \( P(\mathbf{Y} - \mathbf{y}|\mathbf{y}) \).
Estimated v. True Disclosure Risk

\[ \log_{10} \left( \frac{1}{F} \right) \]

\[ \log_{10} E \left[ \frac{1}{F} \right] \]
True v. Estimated Probability of Uniqueness

Estimated P(F=1|f) for sample uniques
Proportion population unique

Estimated P(F=1|f) for sample uniques
Proportion population unique
ROC curve for uniqueness detection

Proportion true positive

Proportion false positive