BAYESIAN COHORT MODELS FOR
GENERAL COHORT TABLE ANALYSES

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Summary

New Bayesian cohort models designed to resolve the identification problem in cohort analysis are proposed in this paper. At first, the basic cohort model which represents the statistical structure of time-series social survey data in terms of age, period and cohort effects is explained. The logit cohort model for qualitative data from a binomial distribution and the normal-type cohort model for quantitative data from a normal distribution are considered as two special cases of the basic model. In order to overcome the identification problem in cohort analysis, a Bayesian approach is adopted, based on the assumption that the effect parameters change gradually. A Bayesian information criterion ABIC is introduced for the selection of the optimal model. This approach is so flexible that both the logit and the normal-type cohort models can be made applicable, not only to standard cohort tables but also to general cohort tables in which the range of age group is not equal to the interval between periods. The practical utility of the proposed models is demonstrated by analysing two data sets from the literature on cohort analysis.

1. Introduction

Birth cohort, which may be defined as a set of people who were born within the same time interval, is an important concept in the study of social change (Ryder [13], Glenn [4], Mason and Fienberg [9]). Cohort analysis is concerned with the separation of the age, period and cohort effects from observations of some quantity classified by age group and survey period. It has been pointed out, however, that there exists an identification problem in cohort analysis, that is, the age, period and cohort effects cannot be separated without some prior in-

Key words: Bayesian cohort model, cohort analysis, ABIC, identification problem, logit model, general cohort table.
formation (Mason and others [10], Pullum [12], Fienberg and Mason [3]).

Nakamura [11] proposed a Bayesian logit cohort model for a standard
cohort table in which the range in years covered by each age group
equals the interval in years between successive survey periods, extend-
ing the basic idea of the general Bayesian modeling for linear problems
developed by Akaike [1]. This modeling successfully solved the iden-
tification problem in cohort analysis.

This paper presents Bayesian cohort models for general cohort table
analyses. These models will be applicable to a wide variety of cohort
data sets: quantitative as well as qualitative, and not only sets ar-
ranged in the standard cohort table but also those arranged in the
general cohort table in which the range of each age group does not
equal the interval of survey periods.

First, the basic cohort model is described in Section 2. Next the
likelihood of the cohort model is obtained in Section 3, assuming the
binomial sampling model for qualitative data. In Section 4, a Bayesian
approach to the cohort analysis is adopted and, following Akaike [1],
a Bayesian information criterion ABIC for selecting the optimal model
is defined. The practical utility of the proposed model is demonstrated
in Section 5, by analysing two data sets: the data of homicide rates
and the data of percentages of political independents in the United
States. The sampling model for quantitative data and the correspond-
ing cohort model are also considered in Section 6. The details of the
derivation of ABIC and the parameter estimates, and the APL pro-
grams are shown in the Appendices.

The usefulness of the Bayesian approach is now being verified by
other successful applications by Ishiguro and Akaike [5], Kashiwagi [7],
Ishiguro and Sakamoto [6], and others.

2. The basic cohort model

In the cohort analysis model, we assume that \( y_{ij} \), a parameter
which characterizes the \( \ell \)-th age group in the \( j \)-th survey period, can
be decomposed into the form

\[
(2.1) \quad y_{ij} = \mu + \mu_i + \mu_j + \mu_{ij}, \quad i = 1, \ldots, I; \quad j = 1, \ldots, J; \quad k = 1, \ldots, K;
\]

where \( \mu \) is the grand mean effect, \( \mu_i \) the effect of the age group, \( \mu_j \)
the effect of the survey period, and \( \mu_{ij} \) the effect of the birth cohort.
The \( \mu \)'s in (2.1) are subject to the following constraints:

\[
(2.2) \quad \sum \mu_i = \sum \mu_j = \sum \mu_{ij} = 0.
\]

Note that there is a functional relationship among \( i, j \) and \( k \) due to
the inherent structure of cohorts; for example, \( k = j - i + I \) and \( K = I \)
+J−1 in standard cohort table analysis.

We can rewrite the model (2.1) with the constraints (2.2) in vector and matrix notation as

\[ y = D\mu, \]

where \( y = (y_{11}, y_{21}, \ldots, y_{IJ})', \mu = [\mu, \mu_2', \ldots, \mu_{I-1}', \mu_1, \mu_2', \ldots, \mu_{J-1}', \mu_{I}', \ldots, \mu_{K-1}')', \quad D = [1, D_*], \quad I = (1, \ldots, 1)', \quad D_* \) is an appropriate \( IJ \times L \)

design matrix expressing the relationship among the three demographic factors, and \( L = I + J + K - 3 \). The prime ('') denotes the transpose of a vector or a matrix. For an example of the design matrix, see Section 5.

3. Logit model and the likelihood

Here we consider the binomial sampling model for dichotomous response data. The other sampling model for quantitative data is mentioned in Section 6.

Under the binomial sampling model, it is natural to take \( q \), the vector of logits, for \( y \) in (2.3). Then we can write the model (2.3) as

\[ q = (\log \frac{p_{11}}{1-p_{11}}, \log \frac{p_{21}}{1-p_{21}}, \ldots, \log \frac{p_{IJ}}{1-p_{IJ}})' = D\mu, \]

where \( p_{ij} \) is the cell probability of a positive response for the \((i, j)\) cell of the cohort table, and \( \log \) denotes the natural logarithm. We may call it as the logit cohort model.

Let \( N_{ij} \) be the sample size and \( n_{ij} \) be the observed frequency of positive response for the \((i, j)\) cell, then the likelihood of this model (3.1) is given by

\[ f(n|p(\mu)) = \prod_i \prod_j \left( \frac{N_{ij}}{n_{ij}} \right)^{n_{ij}} p_{ij}^{n_{ij}} (1-p_{ij})^{N_{ij} - n_{ij}} \]

where \( n = (n_{11}, n_{21}, \ldots, n_{IJ})' \) and \( p = (p_{11}, p_{12}, \ldots, p_{IJ})' \).

Usually we use the maximum likelihood procedure to obtain the estimate of the parameter \( \mu \), but in the cohort model we cannot uniquely identify the estimate since the column vectors of the design matrix \( D_* \) are linearly dependent. More information on the parameters is necessary in order to completely specify the cohort model.

4. A Bayesian approach to the cohort model

To overcome the difficulty of the identification problem in cohort analysis, we adopt a Bayesian approach discussed by Akaike [1]. As
age, period and cohort effects have the ordinal property, it is natural
to expect that the successive parameters of the age groups, survey
periods, or birth cohorts are not so different, or change gradually. In
other words, the first order differences of the successive effect
parameters,

\[ \mu^i_j - \mu^j_{i+1}, \quad \mu^J_j - \mu^j_{J+1}, \quad \text{and} \quad \mu^K_k - \mu^K_{k+1}, \]

are close to zero for \( i=1, \ldots, I-1; \quad j=1, \ldots, J-1; \quad \text{and} \quad k=1, \ldots, K-1. \)

In order to explicitly describe the expectation stated above, we
assume that the parameter vector \( \mu_* \) has the prior distribution defined by

\[
(4.1) \quad \pi(\mu_* | \sigma^*_A, \sigma^*_P, \sigma^*_C) \propto (2\pi)^{-L/4} |D'_S S^{-1}_D|^{1/2} \exp \left[ -\frac{1}{2} \mu_*' D'_S S^{-1}_D D'_s \mu_* \right]
\]

for the logit cohort model, where \( D_s \) is an \( L \times L \) matrix expressing
the first order differences of the parameters (see Section 5 for an example
of this matrix), and \( S \) is an \( L \times L \) diagonal matrix, the first to the
(\( I-1 \))-th diagonal elements of which are equal to \( \sigma^*_A \), the next \( J-1 \)
diagonal elements are equal to \( \sigma^*_P \), and the last \( K-1 \) diagonal elements
are equal to \( \sigma^*_C \), i.e., \( S=\text{diag} \left( \sigma^*_A, \ldots, \sigma^*_A, \sigma^*_P, \ldots, \sigma^*_P, \sigma^*_C, \ldots, \sigma^*_C \right) \).

If we specify the values of \( \sigma^*_A, \sigma^*_P \) and \( \sigma^*_C \), it is reasonable to de-
fine the estimate of \( \mu \) by the mode of the posterior distribution of \( \mu \),
the distribution which is proportional to \( f(n|\mu) \cdot \pi(\mu_* | \sigma^*_A, \sigma^*_P, \sigma^*_C) \). We
denote this estimate by \( \hat{\mu} \), or, more explicitly, by \( \hat{\mu}(\sigma^*_A, \sigma^*_P, \sigma^*_C) \).

The remaining problem is how to determine the values of \( \sigma^*_A, \sigma^*_P \)
and \( \sigma^*_C \). As a criterion for the determination of \( \sigma^*_A, \sigma^*_P \) and \( \sigma^*_C \), we
adopt ABIC (A Bayesian Information Criterion) proposed by Akaike [1].
ABIC is defined by

\[
(4.2) \quad \text{ABIC} = -2 \log \text{(marginal likelihood)} = -2 \log \int f \cdot \pi \, d\mu_* .
\]

We select the values of \( \sigma^*_A, \sigma^*_P \) and \( \sigma^*_C \) so as to minimize ABIC.

In our Bayesian logit cohort model, the value of ABIC is evaluated
approximately by

\[
(4.3) \quad \text{ABIC} = \sum \sum \left[ n_{ij} \log n_{ij}/\hat{n}_{ij} + (N_{ij} - n_{ij}) \log (N_{ij} - n_{ij})/(N_{ij} - \hat{n}_{ij}) \right] + \hat{\mu}_* D'_S S^{-1}_D D'_s \hat{\mu}_* - \log |D'_S S^{-1}_D D'_s| + \log |D_V V^{-1}_D + D'_S S^{-1}_D D'_s| ,
\]

where \( \hat{n}_{ij} = N_{ij}/(1+\exp(-\hat{q}_{ij})), \quad \hat{q}_i = (\hat{q}_{i1}, \hat{q}_{i2}, \ldots, \hat{q}_{iJ})' = D_s \hat{\mu}, \quad V \text{ is an} \quad IJ \times IJ \text{ diagonal matrix, the (i+j-1)-th diagonal element of which is} \quad [N_{ij}\hat{p}_{ij}(1-\hat{p}_{ij})]^{-1}, \quad \text{and} \quad D_s = D_{ss} - (1'V^{-1})'11'V^{-1}D_s. \)
For further details of the derivation of the estimate \( \hat{\mu} \) and ABIC in this Bayesian
logit cohort model, see Appendix A and B.

As ABIC is a non-linear function of \( \sigma^*_A, \sigma^*_P \) and \( \sigma^*_C \), we use the grid
search technique to obtain the smallest ABIC. In practice, we may compare the values of ABIC for every combination of \((\sigma^2_\lambda, \sigma^2_r, \sigma^2_c)\) drawn from, for example, \(\{16\hat{\sigma}^2, 4\hat{\sigma}^2, \hat{\sigma}^2/4, \hat{\sigma}^2/16\}\), where \(\hat{\sigma}^2\) is a geometric mean of \([n_{ij}(N_{ij} - n_{ij})/N_{ij}]^{-1}\)'s for the logit cohort model.

5. Applications

Analysis of homicide rates

The Bayesian estimation procedure for the cohort model proposed in Section 4 is applied first to the data presented in Table 1. The analysis is an example of standard cohort table analyses while it is not clear why the periods of the original table are labeled '1952–1956', etc. The data representing homicide frequencies per 100,000 cross-tabulated by age and period were given by Smith [14] cited in Knoke and Burke ([8], 57–63). Though the assumption of sample size 100,000 for each cell seems to be unrealistic to use the logit cohort model, we will use it temporarily for the purpose of comparing our results with Knoke and Burke's.

| Table 1. Age-period-cohort cross-tabulation of homicide frequencies per 100,000 |
|---------------------------------|-----------------|-----------------|-----------------|-----------------|-----------------|
| 1. 15–19 | 6.2 | 7.5 | 8.6 | 15.1 | 17.1 | 11 |
| 2. 20–24 | 11.8 | 13.6 | 14.2 | 22.9 | 25.5 | 10 |
| 3. 25–29 | 12.4 | 11.9 | 13.6 | 19.3 | 22.2 | 9 |
| 4. 30–34 | 10.8 | 10.6 | 10.9 | 15.5 | 16.9 | 8 |
| 5. 35–39 | 9.4 | 8.8 | 9.1 | 12.5 | 13.4 | 7 |
| 6. 40–44 | 7.7 | 6.8 | 7.1 | 9.6 | 10.2 | 6 |
| 7. 45–49 | 6.1 | 5.7 | 5.5 | 7.3 | 7.4 | 5 |
| Cohort | 1 | 2 | 3 | 4 | 5 |

Source: Smith [14] cited by Knoke and Burke [8].

Figure 1 displays the result of age-period-cohort decomposition of homicide rates per 100,000 by using the ordinary logit model with the identification specification such that the effect of the 40–44 age level is equal to the effect of the 45–49 age level. This model is almost identical to the log-linear model used by Knoke and Burke. Examining the result of their analysis, Knoke and Burke stated: it could be seen that period effects were decreasing over time, contrary to first impressions of the table.

Figure 2 shows the result obtained by the proposed Bayesian logit cohort model. We can see that period effect is increasing over time, as opposed to the result by the ordinal logit model with the identifica-
Figure 1. Estimated effect parameters for homicide rates per 100,000 in the United States presented in Table 1, based on the ordinary logit model with identification specification such that $\mu_{(40-44)} = \mu_{(35-49)}$. 

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<td>30-34</td>
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<td>35-39</td>
<td>3.356</td>
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<td>40-44</td>
<td>3.695</td>
<td></td>
<td></td>
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<td>3.695</td>
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<td>7</td>
<td>0.1834</td>
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<tr>
<td>8</td>
<td>0.3373</td>
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<tr>
<td>9</td>
<td>0.9715</td>
<td></td>
<td></td>
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<td>10</td>
<td>1.3255</td>
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<td>11</td>
<td>1.9056</td>
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* indicates significance at the 0.05 level.
Figure 2. Estimated effect parameters for homicide rates per 100,000 in the United States presented in Table 1, based on the Bayesian logit cohort model.
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-9.0626

( .01 )

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<th>11</th>
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<td></td>
<td>.2066</td>
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* indicates statistical significance.

Figure 3. Estimated effect parameters for homicide rates per 100,000 in the United States presented in Table 1, based on the ordinary logit model with identification specification such that $\mu_\xi = \mu_\eta$. 
tion specification in Figure 1. Age effect starts in the middle, peaks in the 20–24 age level, and then decreases. Cohort effect is almost constant. All these results are consistent to the first impression of the data.

Our procedure proposed here can give us a satisfactory explanation of the data almost automatically without any identification specification, the indefiniteness of which is likely to mislead us. If Knoke and Burke had added the identification specification such that the parameter of cohort 5 is equal to that of cohort 8, they would have obtained the different result with period effect not decreasing (see Figure 3). It is difficult to determine which identification specification should be selected, since the impression of the result depends largely on where the specification is imposed.

Analysis of percentages of political independents

The second application of our procedure is an example of general cohort table analyses. We reanalyse the data of percentages of political independents in the United States presented in Table 2, which is adapted by Glenn ([4], p. 56). As the table is constructed in the form of cohort x period table and the range of age group is not equal to the interval between periods, the situation is a little complicated. We can use, however, the Bayesian logit cohort model by introduction of overlapping age effect parameters involving some hypothetical ones.

Table 2. Percentage of independents in five 10-year birth cohorts, 1945 to 1957 (Ns are in parentheses).

<table>
<thead>
<tr>
<th>Year</th>
<th>1945</th>
<th>1949</th>
<th>1953</th>
<th>1957</th>
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<td>Cohort 1—Ages:</td>
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<td>24-33</td>
<td>28-37</td>
<td>32-41</td>
</tr>
<tr>
<td></td>
<td>25.6</td>
<td>21.4</td>
<td>22.6</td>
<td>23.0</td>
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<tr>
<td></td>
<td>(649)</td>
<td>(1909)</td>
<td>(1520)</td>
<td>(1536)</td>
</tr>
<tr>
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<td>30-39</td>
<td>34-43</td>
<td>38-47</td>
<td>42-51</td>
</tr>
<tr>
<td></td>
<td>17.6</td>
<td>19.4</td>
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<tr>
<td></td>
<td>(666)</td>
<td>(2046)</td>
<td>(1321)</td>
<td>(1287)</td>
</tr>
<tr>
<td>Cohort 3—Ages:</td>
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<td>44-53</td>
<td>48-57</td>
<td>52-61</td>
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<td>19.8</td>
<td>19.7</td>
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<td></td>
<td>(662)</td>
<td>(1727)</td>
<td>(1114)</td>
<td>(943)</td>
</tr>
<tr>
<td>Cohort 4—Ages:</td>
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<td>54-63</td>
<td>58-67</td>
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<tr>
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<td>16.1</td>
<td>17.9</td>
<td>18.1</td>
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<td></td>
<td>(490)</td>
<td>(1209)</td>
<td>(750)</td>
<td>(672)</td>
</tr>
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<td>Cohort 5—Ages:</td>
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<td>68-77</td>
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<td>20.0</td>
<td>13.8</td>
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</tr>
<tr>
<td></td>
<td>(307)</td>
<td>(727)</td>
<td>(382)</td>
<td>(291)</td>
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</tbody>
</table>

Source: American Institute of Public Opinion Surveys, Cited by Glenn ([4], p. 56).
Since the method is not necessarily restricted to age × period tables, we consider the vector \( q \) as \((q_{11}, \ldots, q_{KJ})'\), the \((k+(j-1)K)\)-th element of which is the logit of the expected cell probability for the \((k, j)\) cell of the cohort × period table like Table 2. Let

\[
\boldsymbol{\mu} = (\mu, \mu_{(20-29)}, \mu_{(30-39)}, \mu_{(40-49)}, \ldots, \mu_{(70-79)},
\mu_{(80+)}', \mu_{(90+)}', \mu_{(100+)}', \mu_{(110+)}', \ldots, \mu_{(150+)}')',
\]

\[
D_* = \begin{pmatrix}
1 & 0 & 0 & 0 & \ldots & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & \ldots & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\
0 & 0 & 0 & 0 & \ldots & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\
0 & 0 & 0 & 0 & \ldots & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \\
0 & 0 & 1 & 0 & \ldots & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 1 \\
0 & 0 & 0 & 0 & \ldots & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\
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0 & 0 & 0 & 0 & \ldots & 1 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 1 & 1 & 1 & 1 \\
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0 & 0 & 0 & 0 & \ldots & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 & 1 \\
0 & 0 & 0 & 0 & \ldots & -1 & -1 & -1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 \\
0 & 0 & 0 & 0 & \ldots & -1 & -1 & -1 & 1 & 0 & 0 & 0 & 1 & 1 & 1 & 1 \\
0 & 0 & 0 & 0 & \ldots & -1 & -1 & -1 & 0 & 1 & 0 & 0 & 1 & 1 & 1 & 1 \\
0 & 0 & 0 & 0 & \ldots & -1 & -1 & -1 & 0 & 0 & 1 & 0 & 1 & 1 & 1 & 1 \\
-1 & -1 & -1 & -1 & \ldots & -1 & -1 & -1 & -1 & -1 & -1 & -1 & -1 & -1 & -1 & -1 \\
\end{pmatrix}
\]

and

\[
D_t = \begin{pmatrix}
1 & -1 & 0 & 0 & \ldots & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 1 & -1 & 0 & \ldots & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 1 & -1 & \ldots & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 1 & \ldots & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
\vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\
0 & 0 & 0 & 0 & \ldots & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & \ldots & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & \ldots & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 & 0 & 0 \\
1 & 1 & 1 & 1 & \ldots & 1 & 1 & 1 & 2 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & \ldots & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & \ldots & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & \ldots & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 \\
0 & 0 & 0 & 0 & \ldots & 0 & 0 & 0 & 0 & 0 & 1 & -1 & 0 & 1 & 1 \\
0 & 0 & 0 & 0 & \ldots & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 \\
0 & 0 & 0 & 0 & \ldots & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 \\
0 & 0 & 0 & 0 & \ldots & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & -1 \\
\end{pmatrix}
\]
< HYPER-PARAMETERS AND ABIC >

HYPER-
PARAMETER

PERIOD = .0039
AGE = .0039
COHORT = 2.0000

ABIC = 39.1325 (SIGMA=0.005799)

< GRAND MEAN >

-1.3518
( 20.56 )

< PERIOD >

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<th>-1.0</th>
<th>.0</th>
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<th>2.0</th>
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<td>1945</td>
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<td></td>
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<td>-.0001</td>
<td></td>
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</tr>
<tr>
<td>1953</td>
<td>.0004</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1957</td>
<td>-.0004</td>
<td></td>
<td></td>
<td></td>
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</tbody>
</table>

< AGE >

| 20-29 | .0024 |    |    |    |
| 22-31 | .0022 |    |    |    |
| 24-33 | .0020 |    |    |    |
| 26-35 | .0022 |    |    |    |
| 28-37 | .0023 |    |    |    |
| 30-39 | .0020 |    |    |    |
| 32-41 | .0012 |    |    |    |
| 34-43 | .0006 |    |    |    |
| 36-45 | .0004 |    |    |    |
| 38-47 | .0003 |    |    |    |
| 40-49 | .0001 |    |    |    |
| 42-51 | .0002 |    |    |    |
| 44-53 | .0002 |    |    |    |
| 46-55 | .0002 |    |    |    |
| 48-57 | .0002 |    |    |    |
| 50-59 | .0000 |    |    |    |
| 52-61 | -.0002 |    |    |    |
| 54-53 | -.0003 |    |    |    |
| 56-55 | -.0006 |    |    |    |
| 58-67 | -.0008 |    |    |    |
| 60-69 | -.0015 |    |    |    |
| 62-71 | -.0020 |    |    |    |
| 64-73 | -.0020 |    |    |    |
| 66-75 | -.0021 |    |    |    |
| 68-77 | -.0022 |    |    |    |
| 70-79 | -.0023 |    |    |    |
| 72-81 | -.0024 |    |    |    |

< COHORT >

| 1916-25 | .2040 |    |    |    |
| 1906-15 | .1151 |    |    |    |
| 1896-05 | -.0632 |    |    |    |
| 1886-95 | -.0756 |    |    |    |
| 1876-85 | -.1803 |    |    |    |

Figure 4. Estimated effect parameters for percentages of political independents in the United States presented in Table 2, based on the Bayesian logit cohort model.
Then the rest of the procedure can be carried out in the same manner as described in Section 4. Note that seven age effect parameters such as \( \mu_{(20,30)} \), \( \mu_{(30,35)} \), \( \mu_{(35,40)} \), \( \mu_{(40,45)} \), \( \mu_{(45,50)} \), \( \mu_{(50,70)} \) and \( \mu_{(70,75)} \) are hypothetical.

Figure 4 shows the result of cohort analysis for the data of percentages of independents by using the Bayesian logit cohort model. Cohort effect is dominant and monotonically decreases. These results are consistent with what Glenn stated on the data earlier. Period and age effect cannot be observed.

6. Normal sampling model

In this section, we consider the other sampling model, the normal one for quantitative data.

Under the normal sampling model, let \( x_{ij} \) be the observed quantity for the \((i, j)\) cell. The likelihood of the model (2.3) is then given by

\[
(6.1) \quad f(x | \mu, \sigma^2) = (2\pi \sigma^2)^{-1/2} \exp \left\{ \frac{-1}{2\sigma^2} (x - D\mu)' W^{-1} (x - D\mu) \right\}
\]

where \( \sigma^2 \) is an unknown constant. \( W \) is a known \( IJ \times IJ \) positive definite diagonal matrix such that \( \det(W) = 1 \), and \( x = (x_{11}, x_{12}, \ldots, x_{IJ})' \). We may call it as the normal-type cohort model. The procedure for estimating parameters is the same as is described for the logit cohort model in Section 3. We assume the prior distribution of \( \mu_* \), defined by

\[
(6.2) \quad \pi(\mu_* | \sigma^2, \sigma^2, \sigma^2, \sigma^2) \\
\propto (2\pi \sigma^2)^{-1/2} |D_0 S^{-1} D_*|^{-1/2} \exp \left\{ -\frac{1}{2\sigma^2} \mu_*' D_0 S^{-1} D_* \mu_* \right\}.
\]

The estimate of \( \mu \) is given by the mode of \( f(x | \mu, \sigma^2) \cdot \pi(\mu_* | \sigma^2, \sigma^2, \sigma^2, \sigma^2) \), the computation of which is easily performed by using the weighted least square method. The value of ABIC is evaluated exactly by

\[
(6.3) \quad \text{ABIC} = (IJ) \log \hat{\sigma}^2 - \log |D_0 S^{-1} D_*| + \log |D_0 W^{-1} D_* + D_0 S^{-1} D_*|,
\]

where \( \hat{\sigma}^2 = [(x - D \hat{\mu})' W^{-1} (x - D \hat{\mu}) + \hat{\mu}_* D_0 S^{-1} D_* \hat{\mu}_*]/(IJ) \), and \( D_w = D_* - (1' W^{-1})^{-1} 1' W^{-1} D_* \). The optimal model which gives the smallest ABIC is selected.

7. Discussions

In order to get over the difficulties of the identification problem in cohort analysis, we have developed Bayesian cohort models, which can be classified by sampling model and type of cohort tables into the following four typologies:
<table>
<thead>
<tr>
<th>Sampling Model</th>
<th>Type of Cohort Table</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Standard</td>
</tr>
<tr>
<td>Binomial</td>
<td>BLS</td>
</tr>
<tr>
<td>Normal</td>
<td>BNS</td>
</tr>
</tbody>
</table>

where B stands for a Bayesian cohort model, L for Logit, N for Normal, S for a Standard table, and G for a General one.

As to the sampling models, the binomial one is for the data with a qualitative dependent variable, and the normal one for the data with a quantitative dependent variable. Therefore, the two sampling models are considered to cover the wide range of data we usually analyse. We can also suppose the other sampling models and easily develop the corresponding cohort models.

As to the type of cohort tables, there is essentially no difference between the standard one and the general one. In order to deal with the general cohort table, we have only to arrange the design matrix appropriately. In addition, our Bayesian procedure is so flexible that we can analyse the cohort tables with some missing observations by only eliminating the missing cell quantities from the dependent vector and the corresponding rows from the design matrix.

The assumption that the successive parameters change gradually is considered a kind of the principle of parsimony. Adopting the Bayesian modeling with this assumption, not only can we overcome the identification problem in cohort analysis, but we may also analyse various kinds of cohort data as well.

Acknowledgement

The author would like to thank Professor Yosiyuki Sakamoto for his suggestions and encouragement, and the referees for their useful comments on the earlier version of this paper.

The Institute of Statistical Mathematics
Appendix A

Computational algorithm for the Bayesian logit cohort model

The following steps describe the computational algorithm for estimating the effect parameters of the Bayesian logit cohort model. Concrete procedure by APL program can be seen in Appendix C. As for the normal-type model, it is not necessary to perform an iteration process.

Step 0. Compute the initial value of $\hat{\mu}$.
Set $\hat{n}^{(0)} = n$. Compute $\hat{p} = [\hat{p}_i] = [n_i/N_i]$ and $\hat{q} = [\hat{q}_i] = [\log \hat{p}_i/(1 - \hat{p}_i)]$. Obtain the diagonal matrix $V$ whose diagonal element is $v_{ii} = N_i\hat{p}_i(1 - \hat{p}_i)^{-1}$, and then compute $D_s$. Solve the equation $[D_s'V^{-1}D_s + D_sS^{-1}D_s]\hat{\mu}^{(0)} = D_s\hat{q}$ and compute $\hat{\mu}^{(1)} = [1'V^{-1}\hat{q} - (1'V^{-1}D_s + 1'S^{-1}D_s)\hat{\mu}^{(0)}]/(1'V^{-1})$. Then set the initial value $\hat{\mu}^{(1)}$ and compute $\hat{n}^{(1)}$ through $\hat{q} = D\hat{\mu}^{(1)}$ Set $t = 1$.

Step 1. Check the convergence.
If $\hat{n}^{(t)}$ and $\hat{n}^{(t-1)}$ are sufficiently close, complete the algorithm. Otherwise continue to the next step.

Step 2. Update the $\hat{\mu}$.
Update $V$ and $D_s$ in the same way as in Step 0, and solve equation $[D_s'V^{-1}D_s + D_sS^{-1}D_s]d\mu = D_s'[n - \hat{n}^{(t)}] - D_sS^{-1}D_s\hat{\mu}^{(t)}$ to determine the step size $\Delta \mu$. Then update the estimate $\hat{\mu}_*^{(t+1)} = \hat{\mu}_*^{(t)} + \Delta \mu$, compute $\hat{\mu}^{(t+1)}$, and set $\hat{\mu}^{(t+1)}$. Increment $t$ and return to Step 1. The determination of $\Delta \mu$ is based on the equivalence of maximum likelihood and weighted least squares estimates in the exponential family (see Bradley [2]).

Appendix B

Derivation of ABIC for the Bayesian logit cohort model

Using the fact that $x_i = \log n_i/(N_i - n_i)$ has an approximate normal distribution with mean $q_i = \log p_i/(1 - p_i)$ and variance $v_{ii} = [N_i\hat{p}_i(1 - \hat{p}_i)]^{-1}$, we can replace $f$ in (3.2) with the normal distribution:

(B.1) \[ f \sim (2\pi)^{-L/2}|V|^{-1/2} \exp \left\{ -\frac{1}{2} (x - q)'V^{-1}(x - q) \right\}. \]

Therefore, we have

(B.2) \[ f \cdot \pi \sim C_i|V|^{-1/2}|D_s\hat{\mu}_* S^{-1}D_s|^{1/2} \exp \left\{ -\frac{1}{2} \begin{pmatrix} x - D\mu \\ D_s\hat{\mu}_* \end{pmatrix}' \begin{pmatrix} V & 0 \\ 0 & S \end{pmatrix}^{-1} \begin{pmatrix} x - D\mu \\ D_s\hat{\mu}_* \end{pmatrix} \right\} \]
\[ = C_1 \cdot B \exp \left\{ -\frac{1}{2} (y - \tilde{D} \mu)^\top \tilde{\Sigma}^{-1} (y - \tilde{D} \mu) \right\}, \]

where

\[ \tilde{\Sigma} = \begin{bmatrix} V & 0 \\ 0 & S \end{bmatrix}, \quad \tilde{D} = \begin{bmatrix} 1 & D_* \\ 0 & D_t \end{bmatrix}, \quad y = \begin{bmatrix} x \\ 0 \end{bmatrix}, \quad \mu = \begin{bmatrix} \mu \\ \mu_* \end{bmatrix}, \]

\[ B = |V|^{-1/2} |D_t S^{-1} D_t|^{1/2}, \]

and \( C_1, \ C_2, \ \cdots \) are properly chosen constants.

Applying the maximum likelihood estimate \( \hat{\mu} \) (taken for the weighted least square estimate) to the above equation, we can write

\[ f \cdot \pi \sim C_1 \cdot B \exp \left[ -\frac{1}{2} \left\{ (y - \tilde{D} \hat{\mu})^\top \tilde{\Sigma}^{-1} (y - \tilde{D} \hat{\mu}) \right\} \right. \]

\[ \left. + (\tilde{D} \mu - \tilde{D} \hat{\mu})^\top \tilde{\Sigma}^{-1} (\tilde{D} \mu - \tilde{D} \hat{\mu}) \right], \]

and hence

\[ f \cdot \pi d\mu_* \sim C_1 \cdot B \exp \left[ -\frac{1}{2} \left\{ (y - \tilde{D} \hat{\mu})^\top \tilde{\Sigma}^{-1} (y - \tilde{D} \hat{\mu}) \right\} \right. \]

\[ \times \frac{1}{C_2} |(\tilde{D}^\top \tilde{\Sigma}^{-1} \tilde{D})^{-1}|^{1/2} \]

\[ \times \int C_2 |(\tilde{D}^\top \tilde{\Sigma}^{-1} \tilde{D})^{-1}|^{1/2} \exp \left\{ -\frac{1}{2} (\mu - \hat{\mu})^\top \tilde{D}^\top \tilde{\Sigma}^{-1} \tilde{D} (\mu - \hat{\mu}) \right\} d\mu_* \]

\[ = C_s \cdot B \exp \left\{ -\frac{1}{2} (y - \tilde{D} \hat{\mu})^\top \tilde{\Sigma}^{-1} (y - \tilde{D} \hat{\mu}) \right\} \]

\[ \times |\tilde{D}^\top \tilde{\Sigma}^{-1} \tilde{D}|^{-1/2} \cdot |D_t^\top V^{-1} D_t|^{1/2} \exp \left\{ -\frac{(1^\top V^{-1} 1)}{2} (\mu - \hat{\mu})^2 \right\}. \]

Here we set \( \mu = \hat{\mu} \) so as to maximize (B.4), that is, to minimize ABIC, and use \( |\tilde{D}^\top \tilde{\Sigma}^{-1} \tilde{D}| = |1^\top V^{-1} 1| \cdot |D_t^\top V^{-1} D_t + D_t^\top S^{-1} D_t| \). From (B.4), we have

\[ f \cdot \pi d\mu_* \sim C_s \cdot B |D_t^\top V^{-1} D_t + D_t^\top S^{-1} D_t|^{-1/2} \exp \left\{ -\frac{1}{2} (y - \tilde{D} \hat{\mu})^\top \tilde{\Sigma}^{-1} (y - \tilde{D} \hat{\mu}) \right\}. \]

According to the definition of ABIC in (4.2), we have

\[ \text{ABIC} = -2 \log \int f \cdot \pi d\mu_* \]

\[ \sim -2 \log B + \log |D_t^\top V^{-1} D_t + D_t^\top S^{-1} D_t| \]

\[ + (y - \tilde{D} \hat{\mu})^\top \tilde{\Sigma}^{-1} (y - \tilde{D} \hat{\mu}) - 2 \log C_s. \]
\begin{align*}
= \log |V| - \log |D_i S^{-1} D_i| + \log |D_e V^{-1} D_e + D_i S^{-1} D_i| \\
+ (x - D \hat{\mu})^T V^{-1}(x - D \hat{\mu}) + \hat{\mu} D_e S^{-1} D_i \hat{\mu} + C_i.
\end{align*}

Setting \( \hat{\mu}_i = \hat{n}_i / N_i \) and \( \hat{\mu}_i = D \hat{\mu}, \) and taking the logarithm on the both sides of (B.1), we have the following correspondence

\begin{align}
\sum n_i \log \frac{n_i}{\hat{n}_i} + \sum (N_i - n_i) \log \frac{(N_i - n_i)}{(N_i - \hat{n}_i)} + C_i \\
\sim - \frac{1}{2} \log |V| - \frac{1}{2} (x - D \hat{\mu})^T V^{-1}(x - D \hat{\mu}).
\end{align}

Applying this to (B.5), then we have

\begin{align}
\text{ABIC} \sim 2 \sum \{ n_i \log \frac{n_i}{\hat{n}_i} + (N_i - n_i) \log \frac{(N_i - n_i)}{(N_i - \hat{n}_i)} \\
+ \hat{\mu}_i D_i S^{-1} D_i \hat{\mu}_i \\
- \log |D_i S^{-1} D_i| + \log |D_e V^{-1} D_e + D_i S^{-1} D_i| + C_i.
\end{align}

When comparing ABICs for different combinations of hyper parameters, we can ignore the constant term in (B.8). Therefore, we have ABIC for the logit cohort model in (4.3).

\section*{Appendix C}

\textbf{APL program for solving the Bayesian logit cohort model}

The following APL function \textit{`BLOGIT'}, which computes the estimates of the parameters and ABIC, is the main part of the functions for the Bayesian logit cohort model discussed in this paper.

The calling syntax is

\[ O \leftarrow Z \text{BLOGIT } X, \]

where the first column of the right-hand argument array \( X \) is the vector of observed frequencies \( n \), the second column of \( X \) is the vector of sample sizes \( (N_i) \), and from the third to the last columns of \( X \) give the design matrix \( D \) less its first column; the first column of the left-hand argument array \( Z \) is the vector of the diagonal elements of \( S \), and from the second to the last columns of \( Z \) give the difference matrix \( D \) less its first column; the first element of the output vector \( O \) is ABIC, and from the second to the last elements of the vector \( O \) give the estimated parameter vector \( \hat{\mu} \).

This function needs two functions \textit{`LOGDET'} and \textit{`LRCHISQ'}. The former computes the natural logarithm of the determinant of a matrix \( A \), and the latter the likelihood-ratio chi-square statistic for the observed frequency vector \( N \) and the corresponding expected frequency vector \( M \).
\[ V 0+DS BLOGIT D; ITER; RL; AB; K; T; V; N; S; DMB; DSD; MN; U0; U; Y \]
\[ ; \{W; G; E; DU; A; CONV \}
\[ [1] \]
\[ IHET+(RL+0.00001), (AB+0.001), (K+10), CONV+0 \]
\[ [2] \]
\[ MN+N+D[1;1] \]
\[ [3] \]
\[ V++T+D[1;2] \]
\[ [4] \]
\[ D+ 0 2 +D \]
\[ [5] \]
\[ S++D[1;1] \]
\[ [6] \]
\[ DS++ 0 1 +DS \]
\[ [7] \]
\[ U+(1+pD)pU0+0 \]
\[ [8] \]
\[ Y++(W+V+M+Y)*M+Y+T-M+0.5\lfloor NL-0.5\rfloor; (pS)p0 \]
\[ [9] \]
\[ DSD=(\phi DSD+)\cdot DS\times\phi; (\phi DS)pS \]
\[ [10] \]
\[ LO:N+MM \]
\[ [11] \]
\[ DNE+(D-(pD)pE++(+D\times\phi; (\phi D)pW)*G++/W) \]
\[ [12] \]
\[ A+=(\phi DME)(\phi DME+pW)+.\times DNE+DSD \]
\[ [13] \]
\[ \rightarrow CONV/L1 \]
\[ [14] \]
\[ U+U+DU++(Y+\times DME,[1] DS)\otimes A \]
\[ [15] \]
\[ U0+U0++((G++)/(pT)+Y)--/(E\times DU) \]
\[ [16] \]
\[ Y+=(N-MM+T+1+*U+D+..+U), -S\times DS+.+X \]
\[ [17] \]
\[ W+V+MM\times T-MM \]
\[ [18] \]
\[ \rightarrow LO, CONV+(0\geq K+1)\vee(\vee RL>M+MM)\vee(\vee AB>N+1M-MM) \]
\[ [19] \]
\[ L1:0+(N LRCISQ MM++)+(T-N) LRCISQ T-MM++)/U\times DSD+.+X \]
\[ [20] \]
\[ \rightarrow (O++(G)+1+LOGDET A)-1+LOGDET DSD), U0, U \]
\[ \rightarrow \]

\[ V T-LOGDET A; N; K; B; L; SIGN \]
\[ [1] \]
\[ SIGN+=1+T+(K=N+)+A \]
\[ [2] \]
\[ L0:=(1-I-([B];[B-1,A[1;1]])/L1 \]
\[ [3] \]
\[ SIGN+=SIGN, 0; A[1;1]+B, 0; A[1;1]+A[1;1], 0; B+A[1;1] \]
\[ [4] \]
\[ L1:=(N[X+K+1,0; T-T+\otimes A[1;1], 0; SIGN+SIGN\times \otimes A[1;1]])/L2 \]
\[ [5] \]
\[ L0, pA+(1+1)+A[1;1]+A[1;1], 0; A[1;1]+1+pA)A[1;1] \]
\[ [6] \]
\[ L2: T-SIGN, T \]
\[ \rightarrow \]

\[ V X2L+N LRCISQ M \]
\[ [1] \]
\[ X2L+X2++((N>0)/N)\times (N>0)/N+M \]
\[ \rightarrow \]

REFERENCES


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