A CLASS OF INVERTIBLE FUNCTIONS FOR ANALYSIS OF CATEGORICAL RESPONSE USING LINEAR MODELS

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ABSTRACT

Assuming an intrinsically linear model of the form \( f(x) = x_0 \), the analysis of categorical response using linear models is readily available through use of the SAS procedure PROCAT. In particular, it will be well if for any vector \( x_0 \) of exogeneous variables, we are able to invert \( f(\cdot) \) in order to predict the expected relative composition \( \pi_1 \) of the underlying multinomial population. A general class of invertible response functions is obtained and tested against two familiar data sets and one relating the composition of freshwater algae samples to water chemistry. The effect of category order on goodness-of-fit is examined.

INTRODUCTION

The following situation is familiar in bioassay and, we think, is recognizable in other contexts, notably statistical ecology and survey research in the social sciences. Suppose a sample is drawn at random from each of \( s \) category multinomial populations, and that with each sample are associated measurements on \( c \) concomitant variables, here denoted by the vector \( x \) of \( (x_1, x_2, \ldots, x_c) \). The resulting data may be displayed as in Table 1:

<table>
<thead>
<tr>
<th>Pop.</th>
<th>Categories of response</th>
<th>Total</th>
<th>Concur.</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>( n_{11} ) ( \ldots ) ( n_{1r} ) ( \pi_{11} ) ( \ldots ) ( \pi_{1r} ) ( x_1' )</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>( n_{21} ) ( \ldots ) ( n_{2r} ) ( \pi_{21} ) ( \ldots ) ( \pi_{2r} ) ( x_2' )</td>
<td></td>
<td></td>
</tr>
<tr>
<td>( \vdots )</td>
<td>( n_{s1} ) ( \ldots ) ( n_{sr} ) ( \pi_{s1} ) ( \ldots ) ( \pi_{sr} ) ( x_s' )</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

where the density function for the \( i \)'th sample is

\[
\frac{\prod_{j=1}^{r} \pi_{ij}^{n_{ij}}}{\prod_{j=1}^{r} \pi_{ij}^{n_{ij}}},
\]

subject to the multinomial constraints \( \pi_{ij} > 0 \)

and \( \sum_{j=1}^{r} \pi_{ij} = 1 \). We shall assume \( n_{ij} \gg 1 \) and a dense sample so that empirical estimates \( \hat{\pi}_{ij} = \frac{n_{ij}}{n_i} \), are well defined. It is presumed that the \( \{\hat{\pi}_{ij}\} \) are functionally related to the concomitant variables so that variation in \( x \) somehow results in variation in the expected relative abundances in the categories of response. The statistical problem is to obtain a more precise understanding of this relationship through specification of an appropriate model.

This paper will be limited to consideration of the following special case of those intrinsically linear models whose general form was described by Grizzle, Starmer, and Koch (1969) and later extended by Amemiya (1976). Define \( s \) 1 x \( r \) vectors \( \pi_{i1}, \pi_{i2}, \ldots, \pi_{ir} \). Let \( \{\pi_{mi}\}; m = 1, 2, \ldots, u \leq r-1 \) be a set of twice differentiable response functions which are assumed to be identical for each of the \( s \) populations, and collect these into \( s \) 1 x \( u \) vectors \( f(\pi_{i1}) = \{f_1(\pi_{i1}), \ldots, f_u(\pi_{i1})\} \). We then postulate that there exists \( f(\cdot) \) such that \( f(\pi_{mi}) = x_{mi} \), for \( i = 1, 2, \ldots, s \), where \( x_i \) is a \( u \times 1 \) design matrix of rank \( v \) consisting of known functions of the elements of \( x_i \), while \( \pi_{mi} \) is a \( v \times 1 \) vector of unknown parameters to be estimated.

Note that our requirement that \( \pi_{mi} \) only be a function of its particular associated \( x_i \) is relaxed in the general formulations previously cited.

As an example, if \( r = 2 \), then \( f(\pi_{mi}) = \Phi(\pi_{mi}) + \beta_0 + \beta_1 x_i \) corresponds to the familiar probit model with \( v = 2 \). Note also that given any \( x_0 \), then \( \pi_{mi} = \Phi(\beta_0 + \beta_1 x_i) \) is uniquely defined so that the usual probit model is invertible in the sense of the following section.

Our point of departure is neither with the linearity assumption nor with the familiar minimum chi-square approach to estimation. Rather, it is to suggest and illustrate the use of a generally invertible, intrinsically linear model which is suitable for polychotomous response. Specifically, we shall want to predict the expected relative composition of a multinomial sample, given the values of \( c \) concomitant variables which are in effect at that time.

INVERTIBILITY

Geometrically, the problem of invertibility must be considered in terms of a two stage mapping \( \Pi \leftrightarrow \Gamma \leftrightarrow \Pi \), where \( \Pi, \Gamma \), and \( \Pi \) are subsets of Euclidean space \( (x_i) \), representing respectively the domain of the concomitant vari-
ables, the response functions, and the multinomial probabilities. We see that \( \Pi = \{(\tau_1, \ldots, \tau_r) \}
\)

\[ 0 < \tau_j < 1, \quad \sum_{j=1}^r \tau_j = 1 \] is an \( r - 1 \) dimensional, bounded set due to the multinomial constraints, so that the problem of finding an invertible class of response functions \( y = f(\tau) \) is equivalent to finding a one-to-one mapping between interior coordinates on the face of an \( r \) dimensional simplex and \( \Gamma \subset E_{r-1} \). In general, however \( \kappa \subset E \) is unbounded, so that \( \Gamma \), which must include all possible linear projections of \( \tau \in \kappa \) into \( E_{r-1} \), must also be unbounded. Hence, \( \Gamma \subset E_{r-1} \) and we may state a definition:

Definition: \( y = f(\tau) \) is an \( r \)-chotomous invertible metametric if \( \tau \in \Pi \rightarrow \Gamma \), where \( \Gamma \subset E_{r-1} \) and \( \tau \in \Pi \) satisfies \( r \)-category, multinomial constraints.

Clearly, the only possible class of single-valued mappings \( \Gamma \rightarrow \kappa \) is provided by \( y = \phi(1 - \tau) \), where \( \tau = (1 - \tau_1, \ldots, 1 - \tau_r) \) is \( 1 \times (r - 1) \). Hence, the requirement of invertibility specifies that the general form of the linear model be restricted to:

\[
\begin{align*}
\gamma_1 &= x_1 + a_1 \\
\gamma_2 &= x_2 + a_2 \\
&\vdots \\
\gamma_m &= x_m + a_m
\end{align*}
\]

where \( y = f(\tau) \) is an \( r \)-chotomous, invertible metametric, and \( x = (x_1, \ldots, x_m) \) for \( i = 1, \ldots, s \).

A GENERAL METAMETRIC

As a preliminary to proposing a general metametric, let us consider two classes of polytomous response functions which have appeared repeatedly in the literature. If the categories of response are ordered, e.g., alive, moribund, or dead, then following Gurian, et al. (1960), let \( \gamma = \Psi(\tau) \) denote any dichotomous, continuous metametric whose range is unbounded on \( E_1 \) (e.g., \( \Psi(\tau) = \Phi^{-1}(\tau) \) defines a probit, \( \Psi(\tau) = \ln \pi/(1 - \pi) \) defines a logit, etc.), and define a set of response functions to be

\[
\Psi_m = f_m(\tau) = \Psi(\sum_{j=1}^r \tau_j), \quad m = 1, 2, \ldots, r-1
\]

where it is assumed that \( \gamma_m = a_1 + \beta^i \tau \) for \( m = 1, 2, \ldots, r-1 \). Typically the logit transformation has been proposed for simplicity. Response functions defined by (2) are unbounded but not invertible, however, since

\[
\tau_m = \Phi^{-1}(\gamma_m) = \Phi^{-1}(\gamma_{m-1}) = \Phi^{-1}(\alpha_m + \beta^i \tau) - \Phi^{-1}(\alpha_{m-1} + \beta^i \tau)
\]

is positive only if an external constraint \( a_m < a_{m-1} \) is imposed.

Cox (1966) proposed a trichotomous logistic model for unordered categorical response which may be extended as follows to form an invertible, polychotomous metametric. Suppose we define the \( m \)th response function to be:

\[
\gamma_m = f_m(\tau) = \ln \pi_m / (1 - \sum_{j=1}^m \pi_j)
\]

for \( m = 1, 2, \ldots, r-1 \), where \( \gamma_m = \beta^i \tau \) to complete the specification of an intrinsically linear model. Thus,

\[
f_m = r - 1 \gamma - 1 + \gamma_1 = 1/(1 + e^{-f})
\]

and it may be verified by induction and use of the identity

\[
\pi_m = e^{f_m} / \Pi \end{array} (1 + e^{f_{m-1}})
\]

for \( m = 1, 2, \ldots, r-1 \). Clearly \( 0 < \pi_m < 1 \), while

\[
\pi_1 = 1 - \sum_{j=1}^r \pi_j = 1 - \sum_{j=1}^r e^{f_j} / \Pi (1 + e^{f_j})
\]

for \( m = 1, 2, \ldots, r-1 \). Clearly \( 0 < \pi_m < 1 \), while

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\pi_1 = 1 - \sum_{j=1}^r \pi_j = 1 - \sum_{j=1}^r e^{f_j} / \Pi (1 + e^{f_j})
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\pi_1 = 1 - \sum_{j=1}^r \pi_j = 1 - \sum_{j=1}^r e^{f_j} / \Pi (1 + e^{f_j})
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\]

for \( m = 1, 2, \ldots, r-1 \). Clearly \( 0 < \pi_m < 1 \), while

\[
\pi_1 = 1 - \sum_{j=1}^r \pi_j = 1 - \sum_{j=1}^r e^{f_j} / \Pi (1 + e^{f_j})
\]
\[ f_m = \ln(\exp(\sum \pi_j)) = \exp(\sum \pi_j) \]
\[ f_m = e^m + \exp(\sum \pi_j), \]
so that

\[ f_m = \ln(\exp(\sum \pi_j)) = \exp(\sum \pi_j) \] (9)

for \( m = 2, 3, \ldots, r-1 \), and these are unbounded. Their inverse is obtained as

\[ f_m = \exp(\sum \pi_j) = e^m + \Sigma e^j \]

while in general for \( m = 2, 3, \ldots, r-1 \),

\[ f_m = \exp(\sum \pi_j) = e^m + \Sigma e^j \]

so that

\[ f_m = \exp(\sum \pi_j) = e^m + \Sigma e^j \] (10)

Clearly, \( f_m > 0 \) for this set, while cancellation in pairs results in

\[ f_m = \exp(\sum \pi_j) = e^m + \Sigma e^j \]

so that

\[ f_m = 1 - \Sigma \pi_m > 0. \] Thus, the multinomial constraints are satisfied.

An immediate question is whether the class defined by equation (7) is exhaustive. However, if we choose the logit transformation \( f_m = \ln(\pi_m/(1-\pi_m)) \) with \( f_m = 1 + \exp(-\gamma) \), then even though equations (3) and (8) match as do (4) and (10), the general term

\[ f_m = \exp(\sum \pi_j) = e^m + \Sigma e^j \]

from equation (9) does not match (3), nor does

\[ f_m = \exp(\sum \pi_j) = e^m + \Sigma e^j \]

from equation (11) agree with equation (6). Hence Cox's metrictic is not contained in the class defined by equation (7).

**ESTIMATION**

Following Grizzle, et al. (op. cit.), a best asymptotic normal (BAN) estimator \( \hat{\psi} \) of \( \psi \) is obtained as the solution of normal equations

\[ S_d = \text{H}(\hat{\psi}) \text{V}(\hat{\psi}) \text{H}(\hat{\psi}) \]

where \( r \)-square variance of \( \hat{\psi} \) is defined by

\[ \text{V}(\hat{\psi}) = \left\{ \begin{array}{ll} \psi_{ij}(1 - \pi_{ij})/n, & \text{if } j = k \\
\pi_{ik}/n_i, & \text{if } j \neq k \end{array} \right. \] (14)

while differentiation of \( \hat{\psi}(\pi) \) with respect to the elements of \( \pi \) yields \( (r-1) \times r \) matrix in the form

\[ \text{H}(\hat{\psi}) \]

and for \( m = 2, 3, \ldots, r-1 \),

An adequacy of the fitted model may be tested as usual by comparing

\[ \chi^2 = \sum_{i=1}^p f(\hat{\psi}_i)/f(\psi) - b \times X'S^{-1}f(\psi) \]

with critical values of the chi-square distribution with \( (r-1)(s-c) \) degrees of freedom.

Computationally, it is convenient to note that the elements of \( \text{V}(\hat{\psi}) \) can be evaluated in terms of the c.d.f. \( G(\psi) = \psi(\gamma) \) of the assumed dichotomous metrictic and its associ-
ated density function \( g(\gamma) = G'(\gamma) \). Clearly 
\( \psi(\Sigma_{i,j}) = G^{-1}(\Sigma_{i,j}) \), while for any \( 0 < \pi < 1 \), direct differentiation of the inverse function 
\( \gamma = G^{-1}(\pi) \) with respect to \( \pi \) yields 
\[ \psi(\Sigma_{i,j}) = (g(G^{-1}(\Sigma_{i,j})))^{-1}. \]
Hence, 
\[ \psi(\Sigma_{i,j}) = \left( g(G^{-1}(\Sigma_{i,j})) \right)^{-1}. \]

Occasionally, empirical use of equation (7) will result in an attempt to take the logarithm of zero for the case of an unoccupied cell in Table 1. Following Grizzle, et al., we suggest replacing \( n_{ij} = 0 \) by \( n_{ij} = 1/\alpha \) and adjusting \( \pi_{ij} \) accordingly. Thus \( \pi_{ij} \) is estimated by \( \pi_{ij} = n_{ij}/(n_{i} + \alpha \cdot k_{i}) \), where \( k_{i} \) is the number of empty cells for the sample from the \( i \)th population.

### PERMUTATION EFFECTS

Recalling that our generalized, polychotomous metametric (as well as Cox’s form) applies to unordered categories of response, then choice of a particular form \( \gamma = \psi(\pi) \) only specifies \( \xi(\pi) \) to be a member of a class generated by all possible permutations in order of label assignment for the \( r \) categories of multinomial response. Since choice of order to some extent affects goodness-of-fit, we have prepared three examples which illustrate the effects of this flexibility, as well as suggesting a “rule-of-thumb” for specifying an initial configuration.

Grizzle, et al. (op. cit.) reported data which gives the frequencies of three severities of the 'dumping syndrome' following surgery for duodenal ulcer. The four operations reported at each of four hospitals (\( \alpha \)-effects) were \( \alpha_{1} \equiv \) drainage and vagotomy, \( \alpha_{2} \equiv 25\% \) resection and vagotomy, \( \alpha_{3} \equiv 50\% \) resection and vagotomy, and \( \alpha_{4} \equiv 75\% \) vagotomy. Grizzle, et al. assigned a severity code of 1 to no response, 2 to slight, and 3 to moderate response so that a linear response function of the form \( f(\alpha_{1}) = \alpha_{1} \) could be used. We feel that this arbitrary assignment of scores has little to recommend itself. Instead, we have fitted all 3! permutations of the response categories using our polychotomous logistic given by equations (8) and (12), using a design matrix consisting of the partitions 
\[ X_{k} = \eta_{k} \otimes \eta_{k} \]
where the vector set \( \{\eta_{k}\} \) is defined as follows:

<table>
<thead>
<tr>
<th>Perm.</th>
<th>Order</th>
<th>( X^{2}(18) )</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1,2,3</td>
<td>11.97</td>
<td>0.00734</td>
</tr>
<tr>
<td>2</td>
<td>1,3,2</td>
<td>11.85</td>
<td>0.00105</td>
</tr>
<tr>
<td>3</td>
<td>2,1,3</td>
<td>12.53</td>
<td>0.00629</td>
</tr>
<tr>
<td>4</td>
<td>2,3,1</td>
<td>12.64</td>
<td>0.00105</td>
</tr>
<tr>
<td>5</td>
<td>3,1,2</td>
<td>12.52</td>
<td>0.00629</td>
</tr>
<tr>
<td>6</td>
<td>3,2,1</td>
<td>12.07</td>
<td>0.00734</td>
</tr>
</tbody>
</table>

This may be compared with an identical analysis of similar data which reports the number of mice litters with 0, 1, or 2+ depletions as a function of five litter sizes (\( \tau \)-effects) and two levels of a treatment effect (\( \alpha \)-effects) \( \{ \text{cf. Grizzle, et al. (op. cit.)} \} \).

### Table 3: Effects of order on goodness-of-fit for the mice depletion data.

<table>
<thead>
<tr>
<th>Perm.</th>
<th>Order</th>
<th>( X^{2}(8) )</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1,2,3</td>
<td>3.51</td>
<td>0.02357</td>
</tr>
<tr>
<td>2</td>
<td>1,3,2</td>
<td>4.07</td>
<td>0.02918</td>
</tr>
<tr>
<td>3</td>
<td>2,1,3</td>
<td>3.61</td>
<td>0.00581</td>
</tr>
<tr>
<td>4</td>
<td>2,3,1</td>
<td>3.39</td>
<td>0.02918</td>
</tr>
<tr>
<td>5</td>
<td>3,1,2</td>
<td>2.70</td>
<td>0.00581</td>
</tr>
<tr>
<td>6</td>
<td>3,2,1</td>
<td>3.61</td>
<td>0.02357</td>
</tr>
</tbody>
</table>

Even though every permutation results in a satisfactory fit for both data sets, still the individual chi-squares are sufficiently distinguishable to suggest a preferred order. Noting from equation (7) that \( \Sigma_{i,j} \) is an integral part of the generalized metametric, let us define \( s_{m}^{2} \) to be the sample variance of the set 
\[ \{ \pi_{ij} ; i = 1,2,\ldots,a \} \] for \( m = 1,2,\ldots,r-1 \).
and finally define $\hat{\sigma}^2$ to be the sample variance of $(a^2_j; m = 1, 2, \ldots, r-1)$. Then from Tables 2 and 3, we see that a permutation which corresponds to minimum chi-square seems to be found in (or near) a class of permutations defined by $\min \hat{\sigma}^2$. Unfortunately, the $\min \hat{\sigma}^2$ class will always contain two permutations due to the symmetry of

$$
\text{var}[\Sigma p_j^r] = \text{var}[1 \cdot \Sigma p_j^r] = \text{var}[\Sigma p_j^{r-1}],
$$

and in $\hat{\sigma}^2$ measure. However, computation of the chi-square values for this pair seems a small price to pay for a good initial configuration, compared to computing goodness-of-fit for all possible permutations. Doubtless, a more analytic attack on the ordering problem for $r >> 3$ should be made in light of the following example.

**ECOLOGICAL EXAMPLE**

Poppe (1976) reported $s = 48$ weeks of algal counts, sampled from a small Arkansas lake and identified into $r = 6$ taxonomic classes

- Chlorophyceae (CHL - green algae)
- Euglenophyceae (E - euglenoids)
- Cyanophyceae (CY - blue green algae)
- Cryptophyceae (CRY - brown flagellates)
- Bacillariophyceae (B - diatoms)
- Cryptophyceae (CRY - brown algae).

Biomass was determined, as well as water chemistry variables consisting of dissolved oxygen (DO), temperature (T), pH, alkalinity (ALK), turbidity, silica, orthophosphate, nitrate (NIT), and ammonia (AM). For the analysis reported here, counts of organisms were pooled across seven samples taken uniformly from 0-3 meters (0.88 ml. total aliquot), while the remaining variables were averaged over this same depth. The biological problem is to approximate a transfer function which relates biomass and the exogenous water chemistry variables to the relative composition of the algal population.

Additional generated variables included a constant intercept, sines and cosines of both 2πt/365 and 4πt/365 ($t =$ Julian date) to account for both an annual cycle and for two population peaks per year which are known for some classes, and the interactions DO $\times$ T, pH $\times$ ALK, and NIT $\times$ AM at the local phycologist's suggestion. After some preliminary testing, all predictors with the exception of the periodic functions of $t$ were lagged to a maximum of four weeks. An initial order consisting of E, CRY, CY, B, CHL, CHR was selected on the basis of $\min \bar{u} = 0.03335$.

Proceeding as in stepwise regression, the set of 24 predictor variables listed in Table 4 were obtained. The ransacking critical value $\chi^2_{(0,10)}$ of Goodman (1969), where $\bar{u}$ equals the number of regression coefficients being estimated, appeared to be useful both for forward selection of new predictors and for backward examination of any already obtained. For example with $\alpha = 0.10$, significant predictors were declared in Table 4 by comparing absolute values of standardized $\bar{u}$-estimates with $\chi^2_{(0.10)} = 11.8$, based on 120 degrees of freedom. Examination of Table 4 suggests that increasing phosphorous levels tips the balance in favor of the brown algae (CRY) at the expense of the blue-green (CT). Both classes profit from increasing nitrogen levels. Also, as variable selection proceeded, it was interesting to note that the significant effects of both the sine and cosine of $\pi t/365$ were replaced by lagged nitrate and ammonia variables. Thus, the observed phenomenon of two population surges per year seems attributable to changes in the inorganic nitrogen balance.

### Table 4: Standardized estimates of significant regression coefficients ($\alpha = 0.10$) for the order $E$, CRY, CY, B, CHL, CHR.

<table>
<thead>
<tr>
<th>Predictor</th>
<th>CRY</th>
<th>CY</th>
<th>B</th>
</tr>
</thead>
<tbody>
<tr>
<td>Oxygen (lag 2)</td>
<td>-20.6</td>
<td>0.6</td>
<td>-7.7</td>
</tr>
<tr>
<td>Temp. (lag 1)</td>
<td>25.4</td>
<td>22.4</td>
<td></td>
</tr>
<tr>
<td>Temp. (lag 2)</td>
<td>12.2</td>
<td>20.4</td>
<td></td>
</tr>
<tr>
<td>Oxy. x Temp. (lag 2)</td>
<td>14.4</td>
<td>12.3</td>
<td></td>
</tr>
<tr>
<td>pH (lag 2)</td>
<td>26.7</td>
<td>-26.0</td>
<td></td>
</tr>
<tr>
<td>pH x Alk. (lag 2)</td>
<td>-11.8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Turbidity (lag 2)</td>
<td>-19.5</td>
<td>-17.8</td>
<td></td>
</tr>
<tr>
<td>Silica (lag 3)</td>
<td>-30.6</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Phosphates (lag 0)</td>
<td>-11.2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Phosphates (lag 1)</td>
<td>-11.9</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Phosphates (lag 3)</td>
<td>14.2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Nitrate (lag 0)</td>
<td>25.0</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Nitrate (lag 1)</td>
<td>22.8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Nitrate (lag 2)</td>
<td>12.4</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Nitrate (lag 4)</td>
<td>-12.3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ammonia (lag 1)</td>
<td>22.9</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ammonia (lag 3)</td>
<td>-15.0</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Nit. x Am (lag 3)</td>
<td>14.4</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Biomass (lag 0)</td>
<td>21.5</td>
<td>-25.6</td>
<td></td>
</tr>
<tr>
<td>Biomass (lag 2)</td>
<td>-27.1</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

In retrospect, the goodness-of-fit statistic for the original order was $\chi^2 = 1967$ with 100 d.f., while reversing the order of CRY and E resulted in $\chi^2 = 1893$ using the same predictors even though $\bar{u} = 0.03792$ ($> 0.03335$) for the latter case. Hence, our proposed ordering rule, though not optimum, did produce an order at least close to the optimum. In order to more clearly demonstrate the magnitude of the ordering problem, we obtained an extreme $\chi^2 = 3041$ corresponding to the order CRY, CY, CHL, E, B, CHR with associated $\bar{u} = 0.04778$. 

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† Available from the authors as a SAS macro called CAT. Unfortunately, the SAS supplementary procedure FNSCAT was not yet available to accomplish the transformations presented here.

‡ The actual cell counts reported by Poppe were reduced to approximate organism counts using the following average conversions: CHL, 4 cells/c colony; CY, 43 cells/strand; CHR, 16 cells/c colony; B, 8 cells/c colony.

REFERENCES


