The Universal model and prior: multinomial GLMs

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Abstract

This paper generalises the exponential family GLM to allow arbitrary distributions for the response variable. This is achieved by combining the model-assisted regression approach from survey sampling with the GLM scoring algorithm, weighted by random draws from the posterior Dirichlet distribution of the support point probabilities of the multinomial distribution. The generalisation provides fully Bayesian analyses from the posterior sampling, without MCMC. Several examples are given, of published GLM data sets. The approach can be extended widely: an example of a GLMM extension is given.

Keywords: GLM, model-assisted inference, IWLS, Bayesian bootstrap.

1 Introduction

Discussions of the foundations of survey sampling were extensive in the 1960s and 70s, from many points of view. The following quotes are particularly relevant to the contribution of this paper.
The basic question to ask is why should finite population inference be different from inferences made in the rest of statistics? I have yet to find a satisfactory answer. My view is that survey statisticians should accept their responsibility for providing stochastic models for finite populations in the same way as statisticians in the experimental sciences. These models can then be treated within the framework of conventional theories of inference. The problems with the Neyman approach then disappear to be replaced by disputes between frequentists, Bayesians, empirical Bayesians, fiducialists and so on. But at least these disputes are common to all braches of statistics and sample surveys are no longer seen as an outlier. Smith (1976)

All actual sample spaces are discrete, and all observable random variables have discrete distributions. The continuous distribution is a mathematical construction, suitable for mathematical treatment, but not practically observable. Pitman (1979, p. 1).

The basic feature of our theory is a special parametrization of finite populations of \( N \) units.

... we assume, with essentially no loss of generality, that this characteristic \( y \) is measured on a known scale with a finite set of scale points \( y_t (t = 1, ..., T) \). ... Any finite population can then be completely described by the set of \( T \) non-negative integer parameters \( N_t \), being the number of units in the population having the characteristic \( y_t \) and satisfying the condition \( \sum_{t=1}^{T} N_t = N \).

... If suitable prior information is available, Bayesian concepts can be adjoined to our theory using the complete likelihood. ... It will be seen that with our theory every sample design ... requires the derivation of its appropriate likelihood for the observables \( n_t \). In this paper the only
sampling procedures considered are simple random sampling with equal probabilities with or without replacement. Extensions to multi-stage designs, unequal probability sampling etc., will be considered in subsequent papers. (Hartley and Rao 1968, pp. 548-9)

The model-based and design-based schools of inference have been slowly converging. In the rigid design-based “model-assisted” approach, set out in detail in Särndal, Swensson and Wretman (1992), models had a very limited role, relating only the population mean and variance parameters to “auxiliary” variables. Analysis was through the sample selection probabilities and survey weights from the inverse selection probabilities. Least squares was invoked for optimality in model fitting.

This constraint on the use of models has been relaxed in some modern survey sampling treatments. Chambers, Steel, Wang and Welsh (2012) used explicit probability models for response variables and their maximum likelihood analysis. The survey weights were barely mentioned: analysis was through the “missing information principle”, regarding the unsampled part of the population as missing data, which was effectively imputed from the model and data of the observed sample. With non-informative ignorable survey designs, the sample selection indicators were ancillary and served no inference function.

The early developments in Fisherian model-based analysis, relying heavily on the Central Limit Theorem for asymptotic optimality, were developed much further by the GLM (Nelder and Wedderburn 1972) and EM algorithm (Dempster, Laird and Rubin 1977) inventions. Their reliance on specific probability models required the further development of model evaluation and assessment methods for the exponential family. Quasi-likelihoods (Wedderburn 1974) were an attempt to extend GLM properties to unspecified data distributions. Bayesian MCMC extensions of EM, beginning with the Data Augmentation algorithm
(Tanner and Wong 1987) corrected the optimism of confidence intervals through credible intervals, which accounted for skewness in the likelihoods for models outside the Gaussian (Aitkin 2018 gives simple examples). However they were equally dependent on the validity of the probability model assumption. This placed both Fisherian frequentists and Bayesians in the same difficulty as the survey samplers: the Fisherian sufficiency and optimality of the likelihood for inference depended on the validity of the probability model assumption, but this could never be proved correct – it could at most be consistent with the data.

The possible use of the multinomial distribution and its conjugate Dirichlet prior as a general distribution and prior for data analysis, was begun by Hartley and Rao (1968), Ericson (1969) and Hoadley (1969). These papers were necessarily theoretical, since the computational facilities needed were not then developed for either the profile likelihood analysis for maximum likelihood, or the posterior sampling for Bayesian analysis.

Lindsey (1971, 1974a, 1974b, 1997), Lindsey and Mersch (1992) took the multinomial in a different direction, as a basis for modelling the underlying density or mass function, by expressing the multinomial as a set of constrained Poisson counts, and using the log-linear Poisson model to fit functions of the response variable as model terms.

Rubin (1981) extended the Bayesian analysis to the non-informative Haldane (1948) Dirichlet prior, and gave it the name Bayesian bootstrap. Maximum likelihood analysis was stimulated by the work of Owen (1988) on empirical likelihood. Maximising the likelihood over the multinomial parameters, constrained by the fixed population mean, generated the profile empirical likelihood. Owen’s book (2001) emphasised the frequentist applications of profile empirical likelihoods for the population mean, while recognising the Bayesian extension with the conjugate Dirichlet prior. Gutiérrez-Pena and Walker (2005) and Walker and
Gutiérrez-Pena (2007) argued for the multinomial/Dirichlet as the fundamental inference model and prior. The difficulty was extending it to the common useful models, like GLMs and their extensions, and to survey designs more complex than the simple random sample.

Aitkin (2008) extended the Bayesian bootstrap to both multiple regression models and stratified and clustered survey designs. A further extension was given there to the regression model parameters in a two-level survey design. It was unclear how to deal with GLMs, since the usual parameters of interest are in the linear predictor, whose ML estimates are not linear functions of the observations.

J. Rao and his colleagues (for example Wu and Rao 2010 and Yi, Rao and Li 2016) combined the empirical profile likelihood with a flat prior on the mean to produce a composite or pseudo likelihood, analysed in the conventional survey sampling framework.

Huang (2014, Zhang and Huang 2018) extended the profile empirical likelihood to regression models. The computations were complex, and implemented only in MATLAB. The extension did not include more general sample designs.

The present paper provides a way to express the population parameters of interest through the converged scoring algorithm of the GLM analysis, and to combine this with the extended Bayesian bootstrap. This provides a full Bayesian analysis of the GLM, without the usual probability model assumption, and without the need for MCMC analysis: simple simulations from the Dirichlet posterior distribution are all that is needed.

The paper describes the procedure in Section 2, and subsequent sections give examples of increasingly complex GLMs and their analyses. Section 6 gives discussion of the approach.
2 Summary of the procedure

The procedure involves:

- a non-informative ignorable survey design;
- a structural model specification of the population parameters of interest (the fixed part of the GLM);
- a multinomial distribution for the response variable with population proportion parameters on the distinct joint support points of the population response and covariates;
- the non-informative Haldane Dirichlet prior on the multinomial parameters;
- a maximum likelihood (ML) algorithm based on a tentative specification of the random part of the GLM which allows for weighting of the observations.

The structural model is fitted by the ML algorithm with a sequence of random weights drawn from the posterior Dirichlet distribution of the multinomial parameters. The random weights induce random values of the parameter MLEs, which define the posterior distribution of the model parameters.

3 Example 1: a population mean

We use an example from Aitkin (2010 Chs 1 and 4) of a simple random sample of size 40 from a population of 648, given in Table 1. The question of interest is the population mean family income.
Table 1: Family income data, in units of 1000 dollars

| Income | 26  | 35  | 38  | 39  | 42  | 46  | 47  | 47  | 47  | 52  |
|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 53     | 55  | 55  | 56  | 58  | 60  | 60  | 60  | 60  | 60  |     |
| 65     | 65  | 67  | 67  | 69  | 70  | 71  | 72  | 75  | 77  |     |
| 80     | 81  | 85  | 93  | 96  | 104 | 104 | 107 | 119 | 120 |     |

3.1 Multinomial analysis

For the multinomial analysis, the income population consists of $N$ values $Y_i$. We tabulate them conceptually into the $D$ distinct values $Y_J$ with frequency $N_J$. The probability that a randomly drawn sample value gives the value $Y_J$ is $p_J = N_J/N$. Our interest is not in the $p_J$ but in the population mean $\mu = \sum_{J=1}^{D} p_J Y_J$.

The likelihood of the sample is (omitting the known constant)

$$L(p) = \prod_{J=1}^{D} p_J^{n_J}.$$  

We tabulate the sample values correspondingly, obtaining $d$ distinct values $y_j$ with frequencies $n_j$ in Table 2.

Table 2: Income data tabulation

| $y_j$ | 1   | 2   | 3   | 4   | 5   | 6   | 7   | 8   | 9   | 10  |
|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| $n_j$ | 1   | 1   | 1   | 1   | 1   | 1   | 3   | 1   | 1   | 2   |

We use the Haldane Dirichlet $D(0)$ prior with $a_J = 0$ for all $J$, giving the Dirichlet posterior $D(n)$, now defined on the $d$ distinct values in the observed.
\[ \pi(p_1, \ldots, p_d | y) = \frac{\Gamma(n)}{\prod_{j=1}^{d} \Gamma(n_j)} \prod_{j=1}^{d} p_j^{n_j-1}. \]

Population values unobserved in the sample are given zero posterior probability, and can be omitted from consideration.

![Graph](image)

Figure 1: Posterior cdf, income mean

The posterior distribution from 10,000 draws is shown as a cdf in Figure 1 and as a kernel density, together with the data (unjittered) in Figure 2. It is slightly right-skewed. The 95\% central credible interval is [60.6, 74.2].

The sample mean is \( \bar{y} = 67.1 \) and the (unbiased) variance is \( s^2 = 500.87 \). The survey-sampling large-sample 95\% confidence interval for the mean is \( \bar{y} \pm 1.96s/\sqrt{n} \), which is [60.1, 74.0]; this is nearly identical to the \( t \)-interval [59.9, 74.3] assuming a normal distribution for income. The design-based interval using the finite population correction of \( (1 - 40/648) = 0.938 \) gives the slightly shorter interval [60.6, 73.6]. These intervals are all in close agreement, despite the unusual shape of the population, in Figure 3. It is far from smooth or well-represented by a
gamma or lognormal model.

Figure 2: Posterior density, income mean

Figure 3: Income histogram
4 GLM formulation

An important point for the GLM is that the above analysis can be extended directly to multiple regression models, and can be expressed as a posterior-weighted form of the ML analysis, assuming the structural model for the mean. For a sample \((y^*_i, x^*_i)\) of size \(n\), we model the joint distribution as a multinomial with probabilities \(p_j\) on the distinct population values \((Y_J, X_J)\). With the non-informative Dirichlet prior, we again obtain the posterior on the observed distinct sample support values \((y_j, x_j)\). We define the population parameter of interest as the population value

\[
\mathbf{B} = \mathbf{X}' \mathbf{X}^{-1} \mathbf{X}' \mathbf{Y}
\]

where \(\mathbf{X}\) is the population matrix of covariate values and \(\mathbf{Y}\) the population dependent variate. We make \(M\) draws \(p_j^{(m)}\) for each distinct observation and take them as prior weights in the GLM sense, leading to \(M\) ML estimates of the regression coefficient vector:

\[
\beta^{(m)} = [(X' W^{(m)} X)^{-1} X' W^{(m)} y]
\]

where \(W\) is the diagonal matrix of the Dirichlet posterior draws \(p_j\). These estimates define the posterior distribution of \(\beta\).

We do not need to investigate the residual distribution to check its specification: the population parameters of interest have been defined by the user, and the posterior weighting provides protection against mis-specification of a Gaussian distribution. But this still provides an efficient analysis in the Fisherean sense: we have used the likelihood, and the “nonparametric” multinomial and prior provide the minimal information necessary for a posterior distribution statement.
This approach can be extended to general GLMs with an arbitrary response
distribution: we need only to specify the population model parameters of interest
through the GLM representation.

5 Example 2: vaso constriction

Finney’s data (1947) on vaso constriction in the skin of the digits of the hand are used widely in statistical packages and books (for example Aitkin, Francis, Hinde and Darnell 2009) as an example of logistic regression. The response variable is 39 measures of the presence (1) or absence (0) of the vaso constriction response in subjects; the covariates are the values of volume and rate of air inspired. We fit by ML a logistic regression with variables log volume (LV) and log rate (LR). The estimates and SEs (standard errors) are:

\[ \hat{\beta}_0 = -2.88(1.32), \hat{\beta}_{LV} = 5.18(1.86), \hat{\beta}_{LR} = 4.56(1.84). \]

For the multinomial model, we need to define the population regression parameters of interest. Särndal et al (1992) do not deal with GLMs. We give a general definition of the GLM population model parameters, as population analogues of the IWLS scoring algorithm; in this algorithm we write at the \( r \)-th iteration:

\[ \beta_{r+1} = [X'W_rX]^{-1}X'W_rz_r, \]

where \( W \) is the matrix of iterative weights and \( z \) is the adjusted dependent variate; both are functions of the model parameters. At convergence of the algorithm, we have

\[ \hat{\beta} = [X'\hat{W}X]^{-1}X'\hat{W}\hat{z}, \]

where \( \hat{W} \) is the matrix of converged iterative weights and \( \hat{z} \) is the converged
adjusted dependent variate We define the population regression parameters $B$ by

$$B = [X'WX]^{-1}X'WZ,$$

where $X$ is the population matrix of covariate values, $W$ the population matrix of weights, and $Z$ the population adjusted dependent variate. (Of course these are not observable.)

We adapt this definition to generalise the ML algorithm above. We use the IWLS algorithm with additional weighting of the weight matrix by the random draws of the Dirichlet posterior probabilities $p_j^{[m]}$ on the observed support. So the IWLS algorithm for the GLM ML estimation is randomly iteratively weighted as in the previous example: we have at convergence and the $m$-th draw

$$\beta^{[m]} = [X'W^{[m]}X]^{-1}X'W^{[m]}Z.$$
The posterior distributions of the parameters from $M=1,000$ draws are shown in Figures 5, 6 and 7. They are very heavily skewed.
The similarity of the two regression coefficients has suggested that they could be equated. To assess the plausibility of this, we show in Figure 7 the posterior cdf of $\beta_{LV} - \beta_{LR}$. The central 95% credible interval includes zero. We proceed with the model of a common regression coefficient $\beta$ on the composite variable $LT = LR + LV$, with intercept $\alpha$. The ML estimates and (SE)s are $\hat{\alpha} = -3.05(1.27)$ and $\hat{\beta} = 4.93(1.72)$.

We compare the fitted models with the composite variable $LV + LR$, and their precisions, by ML and posterior weighted ML. Figure 8 shows the ML fitted model (solid curve) and the 95% confidence region, computed on the logit scale and transformed, based on the information matrix (dashed curves). The confidence region is very wide: the sample of 39 is too small for any precision.

![Figure 7: Vaso-constriction: log volume - log rate posterior](image)

Figures 9 and 10 show the posterior distributions of $\alpha$ and $\beta$. 

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Figure 8: Vaso-constriction: data, ML fitted LT model (solid curve) and 95% confidence region (interior of dashed curves)

Figure 9: Vaso-constriction: posterior distribution of $\alpha$ for common $\beta$
The posterior median and 95% central credible intervals are: for \( \alpha \), \(-3.43\) and \([-9.94, -1.07]\), and for \( \beta \), \(5.46\) and \([2.84, 13.92]\). The posterior medians are larger in magnitude than the MLEs: the Bayesian median curve has moved slightly to the right, and has a slightly steeper slope than the ML curve. The 95% confidence intervals: \([-5.59, -0.51]\) for \( \alpha \) and \([1.49, 8.37]\) for \( \beta \) are much shorter and are mislocated: the covariance matrix of the ML estimates cannot represent or allow for the severe skewness in the parameter posteriors.

Figure 11 shows both the fitted ML logistic regression with the bounds of the 95% confidence region (dashed curves) and the posterior median of the fitted model, with the bounds of the 95% credible region (solid curves) from 10,000 draws. The differences between the two sets of bounds are greater than those between the medians, and these differences increase away from the 50% probability, especially for low values of LT.
6 Example 3: absence from school

A demanding data set on children's absence from school was discussed in Aitkin (1978) and subsequently in Aitkin, Anderson, Francis and Hinde (1989) and in other books and articles (for example Venables and Ripley 2002). The data, from 146 children, are counts of days absent from school and form a 4-way unbalanced cross-classification by culture C, sex S, age group A and normal/slow learner L. There were eight zero values of absence. The full data were given in the discussion of Aitkin (1978 p. 223), and can be found in R.

The analysis in Aitkin (1978) used Gaussian-theory-based ANOVA for the unbalanced cross-classification. The second analysis in Aitkin (1978) using a lognormal distribution of (days+1) established the importance of the three-way CSL interaction, and the irrelevance of the four-way and other three-way interactions.
Aitkin et al (1989) considered a Poisson analysis for the counts; the log-linear Poisson model scale would give similar parameters to the lognormal analysis. They pointed out however the severe overdispersion of values within many cells of the classification, invalidating the Poisson standard errors. They concluded that neither a negative binomial nor a quasi-likelihood analysis was appropriate; as Nelder said in his 1978 discussion

“These data are intrinsically awkward.”

We define the population parameters of interest as those from the population version of the converged Poisson log-linear model. The previous analyses used the full set of degrees of freedom in each model term. To allow for the possibility of one or more cells departing in mean absence from a simple model for the others, we convert the classification variables to dummies, and regard all the cross-product terms constructed from these as potential candidates for omission from the “full” model. This approach allows for the omission of “main effect” dummies while retaining “interactions” between the dummies.

We fit a sequence of models, beginning with the “full model” of CSL and its marginal main effects and interactions, and all main effects and two-way interactions of the other three factor dummy variables. We use model reduction by backward elimination, dropping from each model the dummy variable with the smallest ratio of posterior mean to posterior standard deviation – the equivalent of a $t$-statistic in ML variable elimination. (The parameter posterior distributions in all the models considered were symmetric and close to Gaussian.) Model reduction is speeded-up by recycling the fitted values from each model fit as the starting values for the next model fit.

We generate 1000 random draws from the posterior Dirichlet distribution on the observed support, and weight the ML parameter estimation by these draws, generating 1000 random draws of the posteriors of all the parameters in each
Variable elimination proceeds as it would for the Poisson model assuming the standard errors were correct, but continues further, as the weighted parameter ML estimates are similar, but the standard errors from the Poisson model understate the posterior standard deviations by factors of 2–3, different for each variable.

Reduction terminates with 11 model variables, by a criterion of ratio of mean to standard deviation greater than 2 (the smallest remaining was 2.65, the next 3.47). The final model posterior means (pmeans) and standard deviations (psd) are given in Table 3.

| variable  | 1   | C   | S   | CS  | CL  | CSL |
|-----------|-----|-----|-----|-----|-----|-----|
| pmean     | 2.17| 1.01| 0.78| -1.20| -1.13| 1.35|
| psd       | 0.17| 0.34| 0.22| 0.30 | 0.32 | 0.35|

| variable  | A3  | A4  | CA2 | CA3 | SA3 | SA4 |
|-----------|-----|-----|-----|-----|-----|-----|
| pmean     | 1.29| 1.17| -0.99| -1.25| -0.85| -1.53|
| psd       | 0.21| 0.21| 0.29 | 0.33 | 0.32 | 0.32|

Table 3: Final model parameters

This 11-parameter model is both more and less complex than that given in the discussion of Aitkin (1978). It is more complex, in having important components of the CA interaction as well as of the CSL and SA interactions, but it is less complex in omitting unimportant components of the latter interactions.

The following tables give the posterior median values (to 1 dp, upper value) and the observed means (rounded) and sample sizes (lower values in parentheses) of days absent by school level for each cell in the cross-classification.

**Primary, slow learners**

| Aboriginal | White |
|------------|-------|
| Girls      | Boys  | Girls | Boys |
| 8.8        | 19.1  | 24.0  | 14.9 |
| (9.3)      | (3.1) | (30.3)| (25.1)|
Primary, average learners

|          | Aboriginal | White |
|----------|------------|-------|
|          | Girls      | Boys  | Girls | Boys |
|          | 8.8        | 19.1  | 7.8   | 19.7 |
|          | (13,5)     | (21,4)| (5,6) | (18,4)|

For average learners, white and Aboriginal children have the same pattern of absence – boys are absent more than twice as often as girls. This is also true for Aboriginal slow learning girls, but white slow learning girls are absent nearly twice as often as boys.

Secondary 1, slow learners

|          | Aboriginal | White |
|----------|------------|-------|
|          | Girls      | Boys  | Girls | Boys |
|          | 8.8        | 19.1  | 8.9   | 5.5  |
|          | (9,3)      | (23,10)| (6,7) | (6,11)|

Secondary 1, average learners

|          | Aboriginal | White |
|----------|------------|-------|
|          | Girls      | Boys  | Girls | Boys |
|          | 8.8        | 19.1  | 2.9   | 7.3  |
|          | (10,2)     | (11,5)| (3,2) | (11,6)|

The pattern of absence in first year for Aboriginal children is the same as for those in the last primary year. For white children, slow learning girls are absent as often as Aboriginal girls, and three times as often as average learning girls, while absence for white boys is nearly the same for slow and average learners.
Secondary 2, slow learners

|            | Aboriginal | White |
|------------|------------|-------|
|            | Girls      | Boys  | Girls | Boys |
| Girls      | 31.8       | 13.6  | 25.0  | 10.7 |
| (37.4)     | (36.8)     | (29.3)| (6.9) |

Secondary 2, average learners

|            | Aboriginal | White |
|------------|------------|-------|
|            | Girls      | Boys  | Girls | Boys |
| Girls      | 31.8       | 13.6  | 25.0  | 10.7 |
| (27.7)     | (2.1)      | (9.7) | (1.1) |

Slow and average learners have the same pattern of absence. Girls are absent 2.5 times as often as boys, and Aboriginal children are absent 25% more often than white children.

Secondary 3, average learners

|            | Aboriginal | White |
|------------|------------|-------|
|            | Girls      | Boys  | Girls | Boys |
| Girls      | 28.2       | 6.1   | 25.0  | 5.4  |
| (27.7)     | (15.9)     | (27.7)| (13.10)|

Absence is nearly the same for Aboriginal and white children, but girls are absent nearly five times as often as boys.

The overall conclusions are similar to those in Aitkin (1978), but there are several differences, due to both the different final models and the extended variable elimination from the much larger variabilities of the parameters.

7 Discussion

Bayesian applications of empirical likelihood are few. Most of the applications in Owen (2000) are frequentist, and recent work by Huang (2017) and Zhang and
Huang (2018) follows the same path. Applications to GLMs are complicated by the optimisation problem, and few general-purpose algorithms are available.

A few Bayesians, notably Gutiérrez-Pena and Walker, have argued for the multinomial/Dirichlet combination as a general model and prior for data analysis. Rao and his survey colleagues (Rao and Wu 2010a and 2010b, Wu and Rao 2010, and Datta, Rao and Torabi 2010) have combined the empirical profile likelihood with a flat prior on the mean to develop a composite “Bayesian pseudo-empirical likelihood” approach.

The Bayesian bootstrap posterior weighting approach makes a valuable contribution to all three schools of statistical inference. Each school is effective within its box, but we are now able to look outside the boxes.

• The Bayesian bootstrap posterior weighting approach resolves the very long-term argument over the role of models in the design-based approach. The old argument that official statistics reporting is too important to rely on possibly (or inevitably) incorrect probability models can now be inverted. The multinomial model provides an always true model with efficient inference through the likelihood and posterior distribution of the user’s specified model parameters. The ancillary sample selection indicators are no longer needed for inference with non-informative survey designs. The new argument is that official statistics reporting is too important to rely on possibly (or inevitably) incorrect precision statements from standard errors, robust or not.

• The skewness of likelihoods outside the Gaussian, ignored in the classical asymptotic ML theory, is fully recognised and allowed for: the understatement of variability and location in symmetric confidence intervals is corrected. At the same time the computational value of maximum likelihood in inference is increased: ML estimates, for example from the EM
algorithm, are sufficient. We do not need their standard errors.

- The “nonparametric” Bayesian bootstrap is fully generalised to handle any non-informative survey design and any specific structural model. Model-dependent MCMC methods are not needed, and would not in any case account for departures from the probability model assumption.

Several Bayesian commentators have argued –

The discrete nature of the multinomial/Dirichlet is limiting, outdated and unnatural. Why not use the Dirichlet process? It can represent any distribution by an infinite mixture of whatever kernel mass or density functions you specify. It is now straightforward to fit by MCMC.

What is natural or unnatural is in the eye of the beholder. I follow Pitman’s 1979 eye. The user of the Dirichlet process has to specify a prior “concentration” parameter – essentially the density of the number of mixture components – as well as the prior kernel density, and the resulting distribution is sensitive to the choice of the concentration parameter. (A good example of this sensitivity is given in Lunn, Jackson, Best, Thomas and Spiegelhalter 2013 pp. 293-296, of the number of mixture components in the well-known galaxy data. Two different settings of the concentration parameter lead to posterior distributions with monotonically decreasing probabilities of up to 6 or up to 11 components.)

The Bayesian bootstrap approach depends only on the non-informative Dirichlet prior, which avoids having to specify anything about the population proportions of unobserved values. The kernel density of the Dirichlet process implies such a specification.
8 Extensions

The posterior weighting can be extended straightforwardly to more complex models. Aitkin (2008 and 2010 §4.8) described a two-level model with posterior weighting independently within each upper-level unit. Extensions to more than two levels will require weighting at each level above the lowest, but no new features occur. Multilevel models for large-scale national and international surveys of educational attainment, for example the US National Assessment of Educational Progress – the NAEP – discussed in Aitkin and Aitkin (2011), can be generalised in this way. These and other applications will be described elsewhere.

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