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David D. Hanagal
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Applied Statistical Methods

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Preface

The vast applications of statistics through its various dimensions including data science, data mining, stochastic and reliability modelling, sampling and estimation techniques, decision-making, etc., have been developed in recent times. The applications of statistics are increased as the newly methods are being adopted by the researchers who involved in the multidisciplinary areas, viz. astronomy, forensic studies, clinical trials, agriculture, forestry and environment, epidemiology and finance, and even in the business administration in order to take correct decision about the policy and other interventions. In addition, statistics is emerged as a powerful tool in the successful governmental development and industrial progress through tackling difficult challenges. Applied statistics has become an indispensable discipline.

This book is a collection of recent developments in several areas of statistics in the form of chapters (18 in total) written by eminent statistician in their areas of expertise. We tried our best to invite those authors who could capture new developments in statistical methodology and their possible use in important diversified disciplines. The real applications of a wide range of key topics, including small area estimation techniques, Bayesian models for small areas, ranked set sampling, fuzzy supply chain, probabilistic supply chain models, dynamic Gaussian process models, grey relational analysis, multi-item inventory models, etc., are well presented. The possible use of the other models including generalized Lindley shared frailty models, Benktander Gibrat risk model, decision-consistent randomization method for SMART designs and different reliability models is also discussed. This book includes many detailed practical and worked examples that illustrate the real-life applications of recently developed statistical methods. The titles included in this volume are designed to appeal to applied statisticians, students, research project leaders and practitioners of various marginal disciplines and interdisciplinary research. The relative scarcity of reference material covering statistical applications as compared with the readily available books also enhances the utility of this book. We are sure that the book will benefit researchers and students of different disciplines for improving research through the methodological and practical knowledge of applied statistics.

Chapter "Bayesian Order-Restricted Inference of Multinomial Counts from Small Areas" provides the use of Bayesian paradigm to adaptively pool the data on body mass index cell probabilities over small areas. To estimate the finite population proportion of healthy individuals in each household, a hierarchical Bayesian sub-area beta-binomial models presented in Chapter "A Hierarchical Bayesian Beta-Binomial Model for Sub-areas". Chapter "Hierarchical Bayes Inference from Survey-Weighted Small Domain Proportions" also focuses on the hierarchical Bayes approach of small area estimation for survey-weighted proportions of district level employment. Chapter "Efficiency of Ranked Set Sampling Design in Goodness of Fit Tests for Cauchy Distribution" discusses the use of ranked-set sampling in goodness of fit tests by considering the particular Cauchy distribution. The fuzzy supply chain single period (newsboy) inventory model has been used to obtain optimal order quantity, retailers profit, manufacturers profit and total supply chain profit under decentralized supply chain in Chapter "Fuzzy Supply Chain Newsboy Problem Under Lognormal Distributed Demand for Bakery Products". Chapter "Probabilistic Supply Chain Models with Partial Backlogging for Deteriorating Items" deals with the newly developed inventory models by assuming various probability distributions for demand and deterioration rate under shortages of items. In Chapter "The Evolution of Dynamic Gaussian Process Model with Applications to Malaria Vaccine Coverage Prediction", several popular test function-based computer simulators to illustrate the evolution of dynamic Gaussian process models have been used along with its application to predict the coverage of malaria vaccine worldwide.

Chapter "Grey Relational Analysis for the Selection of Potential Isolates of *Alternaria Alternata of Poplar*" narrates the use of gray relational analysis method for obtaining the best fungal isolates of *Alternaria Alternata* of poplar *(Populus deltoides)* tree. Chapter "Decision Making for Multi-Items Inventory Models" proposes the multi-item inventory models under declining demand with the Weibull distributed deterioration rate for credit period and quantity discount. The Bayesian estimation of generalized Lindley-shared frailty models based on reversed hazard rate for Australian twin data is proposed in Chapter "Modeling Australian Twin Data Using Generalized Lindley Shared Frailty Models". Chapter "Ultimate Ruin Probability for Benktander Gibrat Risk Model" obtains the ultimate ruin probability for Benktander–Gibrat risk model using the Laplace transform, generalized exponential integrals, Meijer G-function and Bromwich integral. Chapter "Test of Homogeneity of Scale Parameters Based on Function of Sample Quasi Ranges" presents a multi-sample test for homogeneity of scale parameters against simple ordered alternative based on function of sample quasi-ranges given censored data, as well as for data contaminated with outliers. To combine the advantages of Q-learning-decision-consistent strategies and response-adaptive designs while controlling for covariate balance, a Bayesian response-adaptive, covariate-balanced and Q-learning-decision-consistent randomization method for SMART designs is proposed in Chapter "A Bayesian Response-Adaptive, Covariate-Balanced and Q-Learning-Decision-Consistent Randomization Method for SMART Designs". The Bayesian inference for finite population characteristics is presented in Chapter "An Introduction to Bayesian Inference for Finite Population Characteristics". Important reliability applications through repairable systems with arrival time of server and stress-strength reliability estimation for multi-component system are given in Chapters "Reliability Measures of Repairable Systems with Arrival Time of Server" and "Stress-strength Reliability Estimation for Multi-component System Based on Upper Record Values Under New Weibull-Pareto Distribution". Chapter "Record Values and Associated Inference on Muth Distribution" describes the record values and associated inference on Muth distribution. The book ends with the statistical linear calibration in data with measurement errors and given in Chapter "Statistical Linear Calibration in Data with Measurement Errors".

Pune, India	David D. Hanagal
Pune, India	Raosaheb V. Latpate
Dehradun, India	Girish Chandra

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David D. Hanagal
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Obituary

Dr. Hukum Chandra

(7 November 1972 to 26 April 2021)

Dr. Hukum Chandra passed away on 26 April 2021 at the age of 48. He contributed to this book as a resource person. He was an eminent scientist who pioneered the inception and popularization of "Small Area Estimation" technique in the official statistics system of India. He was working as National Fellow and Principal Scientist at the ICAR-Indian Agricultural Statistics Research Institute, New Delhi, India. He did his M.Sc. in statistics from the University of Delhi, Ph.D. from the University of Southampton, UK, and Postdoctoral Research from the University of Wollongong, Australia. He worked on diverse areas of methodological and applied problems in statistics, including survey design and estimation methods; small area estimation; bootstrap methods; disaggregate-level estimation and analysis of agricultural, socio-economic and health indicators; spatial models for survey data; statistical methodology for improvement in agricultural and livestock statistics; energy management in production agriculture; evaluation of agriculture census and survey schemes. He has received number of awards and appreciations for his research contributions such as National Award in Statistics from the Ministry of Statistics and Programme Implementation, Government of India; ICAR National Fellow Award; Cochran-Hansen Award from International Association of Survey Statisticians; Young Researcher/Student Award of the American Statistical Association; Lal Bahadur Shastri Outstanding Young Scientist Award of ICAR; Recognition Award of the National Academy of Agricultural Sciences; Prof. P. V. Sukhatme Gold Medal Award; and Dr. D. N. Lal Memorial Award of Indian Society of Agricultural Statistics. He was a recipient of the Commonwealth Scholarship offered by the Commonwealth Scholarship Commission in the UK. He was Elected Member of International Statistical Institute, The Netherlands; Fellow of National Academy of Agricultural Sciences, India; and Fellow of Indian Society of Agricultural Statistics. He has worked as Council Member of the International Association of Survey Statisticians. As International Consultant of Food and Agricultural Organization of the United Nations, he has worked in Sri Lanka, Ethiopia and Myanmar to strengthen the Agricultural Statistics System. He has published more than 125 research papers in reputed journals of high impact factor. He has published four books, several technical bulletins, project reports, chapters, working papers and training and teaching reference manuals. He has delivered a number of invited talks in many national and international platforms of repute worldwide. He has supervised four Ph.D. and four M.Sc. students. Our heartfelt tribute to Dr. Hukum Chandra.

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Editors and Contributors

About the Editors

David D. Hanagal is Honorary Professor at the Symbiosis Statistical Institute, Symbiosis International University, Pune, India. He was previously a professor at the Department of Statistics, Savitribai Phule Pune University, India. He is an elected fellow of the Royal Statistical Society, UK and also an elected fellow of the Indian Society for Probability and Statistics. He is an editor and on the editorial board of several respected international journals. He has authored five books, six book-chapters and published over 135 research publications in leading journals. He guided 9 Ph.D. students in different areas of Statistics namely, Reliability, Survival analysis, Frailty models, Repair and replacement models, Software reliability, and Quality loss index. He has delivered more than 100 invited talks in many national and international platforms of repute worldwide. He has supervised nine Ph.D. students. He also has worked as a visiting professor at several universities in the USA, Germany, and Mexico, and delivered a number of talks at conferences around the globe. His research interests include statistical inference, selection problems, reliability, survival analysis, frailty models, Bayesian inference, stress–strength models, Monte Carlo methods, MCMC algorithms, bootstrapping, censoring schemes, distribution theory, multivariate models, characterizations, repair and replacement models, software reliability, quality loss index, and nonparametric inference. With more than 40 years of teaching experience and more than 35 years of research experience, he is an expert on writing programs using SAS, R, MATLAB, MINITAB, SPSS, and SPLUS statistical packages.

Raosaheb V. Latpate graduated from the Department of Statistics, Dr. Babasaheb Ambedkar Marathwada University, Aurangabad, in 2005. He had completed his Ph.D. degree from Dr. Babasaheb Ambedkar Marathwada University, Aurangabad. He is working as Assistant Professor in Department of Statistics and Center for Advanced Studies, Savitribai Phule Pune University, Pune, India. He has organized three International conferences and three national conference/workshop/Faculty

Development Programme on statistical methods and applications. Dr. Raosaheb Latpate is a member of number of professional societies and institutions, namely, the International Statistical Institute, International Indian Statistical Association, Society for Statistics and Computer Applications, and the Indian Society for Probability and Statistics. He has published project reports, book chapters. His research interests include genetic algorithm, fuzzy set theory, supply chain management, logistics and transportation problem, simulation and modeling and Sample Survey.

Girish Chandra is presently working as Scientist in the Division of Forestry Statistics, Indian Council of Forestry Research and Education (ICFRE), Dehradun (an autonomous body under the Ministry of Environment, Forest and Climate Change, Govertment of India). Before joining ICFRE (HQ) in 2013, he worked at the Tropical Forest Research Institute, Jabalpur and at Central Agricultural University, Sikkim for about 7 years. Dr. Girish is a recipient of Cochran–Hansen Prize 2017 of International Association of Survey Statisticians, the Netherlands. He is also honoured with ICFRE Outstanding Research Award 2018 besides Young Scientist Award in Mathematical Sciences from the Government of Uttarakhand, India. He has published over 45 research papers in various respected journals and have three books. He has organised two national conferences on Forestry and Environmental Statistics. Dr. Girish is a member of various scientific institutions, including the International Statistical Institute, International Indian Statistical Association, Computational and Methodological Statistics.

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Bayesian Order-Restricted Inference of Multinomial Counts from Small Areas

Xinyu Chen and Balgobin Nandram

Abstract Body mass index (BMI) can be a useful indicator of health status, and people can fall in different cells. Estimating BMI cell probabilities for small areas can be difficult, due to a lack of available data from national surveys. We have data from a number of counties in the USA, and it is sensible to assume that BMI may be similar across the counties for each cell. Overall, the cell probabilities for each county follow a unimodal order restriction, and so, it is sensible to assume the same for the individual counties (small areas). Moreover, we assume that the counties are similar with some variations. In this setting, it is convenient to use the Bayesian paradigm to adaptively pool the data over areas. Therefore, we use a hierarchical multinomial Dirichlet model with order restrictions, to model the cell counts and the cell probabilities, thereby permitting a borrowing of strength across areas. We provide efficient Gibbs samplers to make inference about the cell probabilities for multinomial Dirichlet models with and without order restrictions (a model with the same pooling structure). To make inference, we compute the posterior distributions of the cell probabilities for both models. In general for most counties, as expected, the posterior distributions of cell probabilities of the model with order restrictions have significantly less variation, as measured by posterior standard deviations and coefficients of variation, than those of the model without order restrictions.

Keywords Bayesian computation · Body mass index · Multinomial distribution · Monte Carlo methods · Unimodal order restrictions

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1 Introduction

In many surveys, questionnaires have items that are categorized into several cells. These items may be filled in by people from different areas or groups, which may be small. Estimates of cell probabilities for individual areas may not be reliable, and a statistician might need to pool data from different small areas (Rao and Molina, 2015). Furthermore, there may be important information over the cells from each area and this information can be incorporated into a model to provide additional improvement. So, our problem is to obtain a methodology to pool information across areas and to incorporate information across the cells in each area. The Bayesian paradigm is attractive for this problem, and we start with the hierarchical Bayesian multinomial Dirichlet model; then, we incorporate the order restrictions over the cell probabilities into this model. We have a specific application on body mass index (BMI), a lifestyle variable in the USA, where BMI can be categorized into five cells, where the order restriction might hold.

Body mass index (BMI) is a person's weight in kilograms divided by the square of height in meters. BMI provides a simple numeric measure of a person's fatness. A person with a higher BMI may have higher chance to get certain diseases (e.g., diabetes). BMI can be used to categorize people's weight that may lead to health problems, but it cannot provide medical diagnostics of the health of an individual. Knowing BMI status well among different areas can help politicians to make better health plans and improve medical care. We use data from the third National Health and Nutrition Examination Health Survey (NHANES III) to provide improved inference for each of 35 largest counties with a population of at least 500,000. But the sample size of small areas such as counties may be too small to generate reliable and accurate estimates. Borrowing strength across small areas to find more accurate estimates is necessary and possible. The hierarchical Bayesian model is straightforward and easy to understand, and Markov chain Monte Carlo method can overcome computational difficulties. Here, it is natural to use the hierarchical Bayesian multinomial Dirichlet model to understand the BMI data. It is important to note that when all counties are combined into a large sample, the order restriction that we use in our model holds, but because of the sparseness of the data within counties the order restrictions might fail.

BMI data are usually categorized into different cells such as underweight (cell 1), normal (cell 2), overweight (cell 3), obese1 (cell 4) and obese2 (cell 5). We assume that there are ℓ areas and the cell counts are denoted by n_{ij}, $i = 1, \ldots, I$, $j = 1, \ldots, K$, where $K = 5$ and $I = 35$ in our application on BMI. We assume that $(n_{i1}, \ldots, n_{i5})$ are multinomial counts with probabilities $(\theta_{i1}, \ldots, \theta_{i5})$ and in a Bayesian model $(\theta_{i1}, \ldots, \theta_{i5})$ follow a Dirichlet distribution with common hyperparameters, which have noninformative priors. This is the hierarchical Bayesian multinomial Dirichlet model; see Nandram (1998). Our new model puts the same order restriction over the θ_{ij} for the i^{th} area. So in the second stage, a Dirichlet distribution with parameters $\boldsymbol{\mu}$ and τ will be an appropriate choice. It can be considered as a baseline, and parameters $\boldsymbol{\mu}$ and τ increase the model flexibility. Without any specification or prior knowledge, a vague and flat prior should be used for parameters $\boldsymbol{\mu}$ and τ.

Wu et al. (2016) combined domain estimation and the pooled adjacent violator algorithm to construct new design-weighted constrained estimators of wage for U.S. National Compensation Survey. They assumed constrained estimators satisfying the monotonicity. Malinovsky and Rinott (2010) presented predictors with an appropriate amount of shrinkage for the particular problem of ordered parameters in the context of small area estimation. Their performance is close to that of the optimal predictors. Heck and Davis-Stober (2019) provided a comprehensive discussion about linear inequality constraints, such as the set of monotonic order constraints for binary choice probabilities on the parameters of multinomial distributions for psychological theories. They also described a general Gibbs sampler for drawing posterior samples. A suitable order restriction assumption can increase model precision. Li (2008) made a great overview about statistical inference under order restrictions. He also considered the inference of ordered binomial probabilities in frequentist statistics. From Wu, Meyer and Opsomer's research about order restriction to Li's review, they proved that the order constraints should be considered in order to improve efficiency and minimize bias, which can be done in different aspects.

Dunson and Neelon (2003) proposed a general and easy to implement approach for order-restricted inferences on regression parameters in generalized linear models. Their approach is interesting because instead of choosing a prior distribution with the support on the constrained space, which is expected to result in major computational difficulties, they proposed to map draws from an unconstrained posterior density using an isotonic regression transformation. In particular, Gelfand et al. (1992) suggested first choosing a prior density without considering the constraint and then discarding draws inconsistent with the constraint. However, they were not working within the context of small area estimation and their problem is not about order cell probabilities in several multinomial distributions. Therefore, our approach of incorporating order restriction into the prior distributions is natural in our study on BMI.

In the small area context, most of these papers cover order restriction across areas (e.g., Wu et al., 2016). However, in this paper, we are not interested in order restriction across areas, but rather we are interested in order restriction across the cell probabilities within each area. Nandram (1997) provided a good discussion about a hierarchical Bayesian approach for taste-testing experiment and appropriate methods for the model. To select the best population, he studied three criteria based on the distribution of random variables representing values on a hedonic scale using the simple tree order (see also Nandram, 1998).

Nandram, Sedransk and Smith (1997) improved estimation of the age composition of a population of fish with the help of order restrictions. They proposed different order restrictions for different fish length strata. With the help of the Gibbs sampler, they showed that order restrictions provided large gains in precision for estimating the proportion of fish in each age class. The research of Nandram, Sedransk and

Smith (1997) was motivated by Gelfand et al. (1992) and earlier Sedransk et al. (1985).

Since people have similarity that the majority in each county will be in the same level of BMI, it is reasonable to assume that the cell probabilities share a common effect and have the same order restrictions in each county. Actually, it seems that most people will have a third-level BMI, which is overweight, among those counties. So, it is reasonable to believe that the cell probabilities are unimodal in each county and the third level is the mode. With this information, our estimates for each county can be improved using a multinomial Dirichlet model with order restrictions such as $\theta_{i1} \leqslant \theta_{i2} \leqslant \theta_{i3} \geqslant \theta_{i4} \geqslant \theta_{i5}$ for the i^{th} area. One feature of our approach is that Dirichlet distribution with parameters $\boldsymbol{\mu}$ and τ embodies the common effect and the same order restriction. At the second stage of model, parameter $\boldsymbol{\mu}$ has a similar order restriction as cell probabilities $\boldsymbol{\theta}_i$. It has more flexibility without increasing computation difficulty. The work in this paper is a large step forward from Chen and Nandram (2019), which appeared the Proceedings of the American Statistical Association.

The article is organized as follows. In Sect. 2, we present the hierarchical Bayesian multinomial Dirichlet model with order restrictions. In Sect. 3, we present our algorithms; specifically, we describe how to generate samples from posterior distributions and how to handle difficulties caused by order restrictions. In Sect. 4, we show how to analyze the BMI data in our application. Specifically, we show how to run the Gibbs sampler, assess the convergence of the Gibbs sampler and, more importantly, demonstrate how much improvement there is under the order restrictions. In Sect. 5, we also present a Bayesian diagnostic for the model with order restrictions and we discuss difficulties associated with a standard Bayesian diagnostic measure that may not be appropriate. Section 6 has a summary of our work. Also, there is an appendix with technical details and an important table, which shows the improvement that can occur under the order restrictions.

2 Multinomial Dirichlet Models

In this section, we describe the Bayesian methodology for the cell counts over the small areas. First, we give a review of the hierarchical Bayesian multinomial Dirichlet model without the order restriction. Then, we describe the hierarchical Bayesian multinomial Dirichlet model with the order restriction.

It is convenient to give some standard notations here. The multinomial distribution, $\boldsymbol{n} \sim \text{Multinomial}(n_{.}\,, \boldsymbol{\theta})$, is a discrete distribution over K-dimensional nonnegative integer vectors $\boldsymbol{n}$, where $\sum_{j=1}^{K} n_j = n_{.}$ and $\boldsymbol{\theta} = (\theta_1, \ldots, \theta_K)$. The probability mass function is given as

$$f(\boldsymbol{n}|\boldsymbol{\theta}) = \frac{\Gamma(n_{.}+1)}{\prod_{j=1}^{K}\Gamma(n_j+1)}\prod_{j=1}^{K}\theta_j^{n_j}, \qquad \sum_{j=1}^{K} n_j = n_{.}, \qquad n_i \geqslant 0.$$

This is a generalization of the binomial distribution. The Dirichlet distribution, $\boldsymbol{x} \sim$ Dirichlet$(\boldsymbol{\alpha})$, is parameterized by positive scalar $\alpha_j > 0$ for $j = 1, 2, \ldots, K$, where $K \geqslant 2$. The probability density of $\boldsymbol{x}$ is

$$f(\boldsymbol{X}|\boldsymbol{\alpha}) = \frac{\Gamma(\sum_{j=1}^{K}\alpha_j)}{\prod_{j=1}^{K}\Gamma(\alpha_j)}\prod_{j=1}^{K}x_j^{\alpha_j-1}, \sum_{j=1}^{K}x_j = 1, x_j \geq 0, j = 1, \ldots, K.$$

The Dirichlet distribution is multivariate generalization of the univariate beta distribution. It is convenient that the Dirichlet forms a conjugate prior for the multinomial distribution, thereby leading to relatively simpler computations.

2.1 Model Without Order Restriction (M1)

Nandram et al. (2019) have a useful discussion of hierarchical Bayesian multinomial Dirichlet model without order restriction and the methodology needed to fit it.

We provide the Bayesian hierarchical multinomial Dirichlet model. Letting n_{ij} be the cell counts, θ_{ij} the corresponding cell probabilities, $i = 1, 2, \ldots, I$, $j = 1, 2, \ldots, K$ and $n_{i.} = \sum_{j=1}^{K} n_{ij}$.

The general hierarchical Bayesian model is

$$\boldsymbol{n}_i|\boldsymbol{\theta}_i \overset{ind}{\sim} \text{Multinomial}(\boldsymbol{n}_{i.}, \boldsymbol{\theta}_i),$$

$$n_{ij} \geqslant 0, \qquad \theta_{ij} \geqslant 0, \qquad \sum_{j=1}^{K}\theta_{ij} = 1,$$

$$\boldsymbol{\theta}_i|\boldsymbol{\mu}, \tau \overset{ind}{\sim} \text{Dirichlet}(\boldsymbol{\mu}\tau),$$

$$\pi(\boldsymbol{\mu}, \tau) = \frac{(K-1)!}{(1+\tau)^2},$$

$$\mu_j \geqslant 0, \qquad \sum_{j=1}^{K}\mu_j = 1, \qquad \tau > 0,$$

where, without any prior information, we take $\boldsymbol{\mu}$ and τ to be independent. Also, $E(\theta_{ij}) = \mu_j$, $\sum_{j=1}^{K}\mu_j = 1$ and $\boldsymbol{\mu}$ are cell means and τ is a prior sample size. Nandram, Sedransk and Smith (1997) had a similar model for stratified random sampling, not small areas, and they set the hyperparameters to be fixed. Therefore, our computations for order- restricted inference are much more difficult.

2.2 Model with Order Restrictions (M2)

We incorporate the order restriction into the hierarchical Bayesian Dirichlet multinomial model. We use a grid method in Gibbs sampler. This is more efficient than the method by Nandram (1998). Letting n_{ij} be the cell counts, θ_{ij} the corresponding cell probabilities, $i = 1, 2, \ldots, I$, $j = 1, 2, \ldots, K$,$\boldsymbol{n}_{i.} = \sum_{j=1}^{K} n_{ij}$ and we believe the mode of $\boldsymbol{\theta}_i s$ is θ_{im}, $1 \leqslant m \leqslant K$.

Specifically, we take

$$\boldsymbol{n}_i|\boldsymbol{\theta}_i \overset{ind}{\sim} \text{Multinomial}(\boldsymbol{n}_i., \boldsymbol{\theta}_i), \qquad \boldsymbol{\theta}_i \in C \quad i = 1, \ldots, I,$$

where $C = \{\boldsymbol{\theta}_i : \theta_{i1} \leqslant \ldots \leqslant \theta_{im} \geqslant \ldots \geqslant \theta_{iK}, i = 1, \ldots, I\}$, and assume C is known. As mentioned above, in our BMI study, $C = \{\boldsymbol{\theta}_i : \theta_{i1} \leqslant \theta_{i2} \leqslant \theta_{i3} \geqslant \theta_{i4} \geqslant \theta_{i5}, i = 1, 2, \ldots, 35\}$.

At the second stage, we take

$$\boldsymbol{\theta}_i|\boldsymbol{\mu}, \tau \overset{ind}{\sim} \text{Dirichlet}(\boldsymbol{\mu}\tau), i = 1, \ldots, I,$$

$$\pi(\boldsymbol{\mu}, \tau) = \frac{K(m-1)!(K-m)!}{(1+\tau)^2}, \qquad \mu_j > 0, \quad \sum_{j=1}^{K} \mu_j = 1, \quad \boldsymbol{\mu} \in C_{\mu}.$$

Since $E(\theta_{ij}) = \mu_j$, $\boldsymbol{\mu}$ should have the same order restriction as $\boldsymbol{\theta}_i$, which is $\boldsymbol{\mu} \in C_{\mu}$,

$$C_{\mu} = \{\boldsymbol{\mu} : \mu_1 \leqslant \ldots \leqslant \mu_m \geqslant \ldots \geqslant \mu_K\}.$$

Using Bayes' theorem, the joint posterior distribution of all variables is

$$\begin{aligned}\pi(\boldsymbol{\theta}, \boldsymbol{\mu}, \boldsymbol{\tau}|\boldsymbol{n}) &\propto \prod_{i=1}^{I}\{\prod_{j=1}^{K} \theta_{ij}^{n_{ij}} \frac{\prod_{j=1}^{K} \theta_{ij}^{\mu_j\tau-1} I_C I_{C_\mu}}{D(\boldsymbol{\mu}\tau)C(\boldsymbol{\mu}\tau)}\}\frac{1}{(1+\tau)^2} \\ &\propto \prod_{i=1}^{I}\{\frac{\prod_{j=1}^{K} \theta_{ij}^{n_{ij}+\mu_j\tau-1} I_C I_{C_\mu}}{D(\boldsymbol{\mu}\tau)C(\boldsymbol{\mu}\tau)}\}\frac{1}{(1+\tau)^2},\end{aligned}$$

where I_C and I_{C_μ} are the indicator functions under those order restrictions, and

$$C(\boldsymbol{\mu}\tau) \overset{denote}{=} \int_{\boldsymbol{\theta}_i \in C} \frac{\Gamma(\sum_{j=1}^{K} \mu_j\tau)}{\prod_{j=1}^{K} \Gamma(\mu_j\tau)} \prod_{j=1}^{K} \theta_{ij}^{\mu_j\tau-1} d\boldsymbol{\theta}_i,$$

$$D(\boldsymbol{\mu}\tau) = \frac{\prod_{j=1}^{K} \Gamma(\mu_j \tau)}{\Gamma[\sum_{j=1}^{K} \mu_j \tau]}.$$

A posteriori $\boldsymbol{\theta}_i | \boldsymbol{\mu}, \tau, \boldsymbol{n}_i \overset{ind}{\sim} \text{Dirichlet}(\boldsymbol{n}_i + \boldsymbol{\mu}\tau), \qquad \boldsymbol{\theta}_i \in C_i, i = 1, \ldots, I,$ where

$$f_{\boldsymbol{\theta}_i|\boldsymbol{\mu},\tau,\boldsymbol{n}} = \frac{\frac{\Gamma[\sum_{j=1}^{K}(n_{ij}+\mu_j\tau)]}{\prod_{j=1}^{K}\Gamma(n_{ij}+\mu_j\tau)} \prod_{j=1}^{K} \theta_{ij}^{n_{ij}+\mu_j\tau-1}}{\int_{\boldsymbol{\theta}_i \in C_i} \frac{\Gamma[\sum_{j=1}^{K}(n_{ij}+\mu_j\tau)]}{\prod_{j=1}^{K}\Gamma(n_{ij}+\mu_j\tau)} \prod_{j=1}^{K} \theta_{ij}^{n_{ij}+\mu_j\tau-1} d\boldsymbol{\theta}_i}$$

$$= \frac{\frac{\Gamma[\sum_{j=1}^{K}(n_{ij}+\mu_j\tau)]}{\prod_{j=1}^{K}\Gamma(n_{ij}+\mu_j\tau)} \prod_{j=1}^{K} \theta_{ij}^{n_{ij}+\mu_j\tau-1}}{C(\boldsymbol{n}_i + \boldsymbol{\mu}\tau)}.$$

3 Computations

It is straightforward to generate samples from M1; see Nandram (1998). In fact, using the Griddy Gibbs sampler, it can be done easier than the method in Nandram (1998). We present a new method for the order restrictions of $\boldsymbol{\mu}$ and $\boldsymbol{\theta}$ into two parts for model M2.

3.1 *Sampling $\boldsymbol{\theta}$ in M2*

In the first part of new method, the posterior of $\boldsymbol{\theta}$ has a recognizable distribution, which is the Dirichlet distribution with the order restriction. Sedransk et al. (1985) provided an efficient algorithm to generate random vectors from the constrained density. However, instead of drawing samples directly from the Dirichlet distribution with the order restriction, we present a direct sampling from truncated gamma distributions as from truncated Dirichlet distribution. Nadarajah and Kotz (2006) offered a method for truncated gamma distributions.

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Method1 : To draw $\boldsymbol{\theta} = (\theta_1, \ldots, \theta_K) \sim \text{Dirichlet}(\alpha_1, \ldots, \alpha_K), \boldsymbol{\theta} \in C$,
                                        denote $\boldsymbol{\beta} = (\beta_1, \ldots, \beta_K)$,
    If $0 \leqslant \theta_1 \leqslant \theta_2 \leqslant \ldots \leqslant \theta_m \geqslant \ldots \geqslant \theta_K$, the mode is $\theta_m$,
        $0 \leqslant \beta_1 \leqslant \beta_2 \leqslant \ldots \leqslant \beta_m \geqslant \ldots \geqslant \beta_K$, the mode is $\beta_m$,
    1. Draw $\beta_m \sim \text{Gamma}(\alpha_m, 1)$, where $0 \leqslant \beta_m < \infty$,
    2. Draw $\beta_{m-1} \sim \text{Truncated Gamma}(\alpha_{m-1}, 1)$, where $0 \leqslant \beta_{m-1} \leqslant \beta_m$,
        $\ldots \beta_1 \sim \text{Truncated Gamma}(\alpha_1, 1)$, where $0 \leqslant \beta_1 \leqslant \beta_2$,
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3. Draw $\beta_{m+1} \sim$ Truncated Gamma$(\alpha_{m+1}, 1)$, where $0 \leqslant \beta_{m+1} \leqslant \beta_m$, $\ldots \beta_K \sim$ Truncated Gamma$(\alpha_K, 1)$, where $0 \leqslant \beta_K \leqslant \beta_{K-1}$.

Then,

$$\theta_1 = \frac{\beta_1}{\beta_1 + \beta_2 + \ldots + \beta_K}, \ldots, \theta_{K-1} = \frac{\beta_{K-1}}{\beta_1 + \beta_2 + \ldots + \beta_K}, \theta_K = 1 - \sum_{i=1}^{K-1} \theta_i.$$

3.2 Gibbs Sampling for $\boldsymbol{\mu}$ and $\boldsymbol{\tau}$

In the second part of new method, we present Gibbs sampling, a Markov chain Monte Carlo (MCMC) algorithm, for $\boldsymbol{\mu}$ with an order restriction. We present the modified Gibbs sampler for $\boldsymbol{\mu} \in C_\mu$ and τ. The joint posterior density is

$$\pi(\boldsymbol{\theta}, \boldsymbol{\mu}, \tau | \boldsymbol{n}) \propto \prod_{i=1}^{I} \{ \frac{\prod_{j=1}^{K} \theta_{ij}^{n_{ij}+\mu_j\tau-1} I_C I_{C_\mu}}{D(\boldsymbol{\mu}\tau) C(\boldsymbol{\mu}\tau)} \} \frac{1}{(1+\tau)^2},$$

where

$$C(\boldsymbol{\mu}\tau) = \int_{\boldsymbol{\theta}_i \in C} \frac{\Gamma(\sum_{j=1}^{K} \mu_j \tau)}{\prod_{j=1}^{K} \Gamma(\mu_j \tau)} \prod_{j=1}^{K} \theta_{ij}^{\mu_j \tau - 1} d\boldsymbol{\theta}_i.$$

There is no recognizable conditional distribution of $\boldsymbol{\mu}$ and τ to generate samples. We use a griddy Gibbs sampling (See Nandram 1998) to draw $\boldsymbol{\mu}$ and τ from $\pi(\boldsymbol{\mu}, \tau | \boldsymbol{n})$ after integrating with respect to $\boldsymbol{\theta}$, we get

$$\pi(\boldsymbol{\mu}, \tau | \boldsymbol{n}) \propto \prod_{i=1}^{I} \{ \frac{D(\boldsymbol{\mu}\tau + \boldsymbol{n}_i) C(\boldsymbol{\mu}\tau + \boldsymbol{n}_i)}{D(\boldsymbol{\mu}\tau) C(\boldsymbol{\mu}\tau)} \} \frac{I_{C_\mu}}{(1+\tau)^2}$$
$$\propto \prod_{i=1}^{I} \{ \frac{\int_{\boldsymbol{\theta}_i \in C} \prod_{j=1}^{K} \theta_{ij}^{\mu_j\tau+n_{ij}-1} d\boldsymbol{\theta}_i}{\int_{\boldsymbol{\theta}_i \in C} \prod_{j=1}^{K} \theta_{ij}^{\mu_j\tau-1} d\boldsymbol{\theta}_i} \} \frac{I_{C_\mu}}{(1+\tau)^2}.$$

Chen and Shao (1997) mentioned that the importance sampling could be used to estimate the ratio, $\frac{\int_{\boldsymbol{\theta}_i \in C} \prod_{j=1}^{K} \theta_{ij}^{\mu_j\tau+n_{ij}-1} d\boldsymbol{\theta}_i}{\int_{\boldsymbol{\theta}_i \in C} \prod_{j=1}^{K} \theta_{ij}^{\mu_j\tau-1} d\boldsymbol{\theta}_i}$. We consider Dirichlet $(r\bar{n_j})$, where r is an adjustable ratio and $\bar{n_j} = \frac{\sum_{i=1}^{I} n_{ij}}{I}$. More details can be found in appendix.

Method 2:

1. Draw τ from $\pi(\tau|\boldsymbol{\mu}, \boldsymbol{n})$.

2. For j from m-1 to 1, draw μ_j from $\pi(\mu_j|\boldsymbol{\mu}^{(-j)}, \tau, \boldsymbol{n})$,

$$\text{where } 0 < \mu_j < \min\{\mu_{j+1}, \tfrac{1-\sum_{t=1,t\neq m,t\neq j}^{K}\mu_t}{2}\}.$$

3. For j from m+1 to K, draw μ_j from $\pi(\mu_j|\boldsymbol{\mu}^{(-j)}, \tau, \boldsymbol{n})$,

$$\text{where } 0 < \mu_j < \min\{\mu_{j-1}, \tfrac{1-\sum_{t=1,t\neq m,t\neq j}^{K}\mu_t}{2}\}.$$

4. Get $\mu_m = 1 - \sum_{j=1,j\neq m}^{K}\mu_j$; repeat Step 1 to Step 4 to get converged MCMC samples,

$$\mu^{(-j)} = (\mu_1, \ldots, \mu_{j-1}, \mu_{j+1}, \ldots, \mu_K).$$

4 Application to BMI

4.1 Body Mass Index

In our application, we use a selected subset of the female BMI data from NHANES III, where we use only the female BMI data from the 35 largest counties with a population at least 500,000. Our goal is to estimate the proportions of the BMI levels. Table 1 gives an illustration of the female BMI data of a few counties, where it can be seen that the cell probability is largest for the normal range and other probabilities roughly tail off on both sides to form the unimodal order restriction. Indeed, there are violations in some counties in the earliest and latest cells.

For large population counties, we consider that people randomly fall into five BMI categorical levels, which are underweight, normal, overweight, obese1 and obese2. Thus, for each county, the BMI counts can be assumed to follow a multinomial distribution because each individual person can be assumed to exist independently. Figure 1 shows a histogram of all BMI values for females aggregated into a single large sample. It can be clearly seen that the unimodal order restriction holds. Because the data in the individual counties are generally sparse, it is difficult to tell whether the unimodal order restrictions holds, a way to improve posterior inference. However, it is sensible to assume that the same unimodal restriction holds within all the counties. Therefore, we can use multinomial distributions to model the female BMI counts.

4.2 MCMC Convergence

We run 20,000 MCMC iterations, take 10,000 as a ‘burn-in’ and use every 10th to obtain 1,000 converged posterior samples. Table 2 gives the effective sample size of the parameters $\boldsymbol{\mu}, \tau$ for the model with the order restriction and the general model. The effective sample sizes are almost 1,000. Table 3 gives the p-values of the Geweke test for the parameters (Cowles and Carlin, 1996). The p-values are all large, so

Table 1 US female BMI data

State ID	County ID	BMI_lvl1	BMI_lvl2	BMI_lvl3	BMI_lvl4	BMI_lvl5
4	13	3	40	37	13	4
6	1	1	36	38	15	1
6	19	3	20	49	13	5
6	37	2	145	174	77	14
6	59	1	29	31	16	3
…	…	…	…	…	…	…

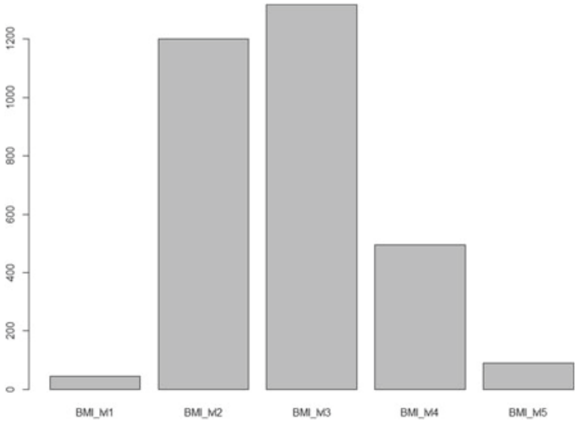

Fig. 1 Total counts for 35 counties

Table 2 Effective sizes

Models	μ_1	μ_2	μ_3	μ_4	μ_5	τ
W. order	974	1000	1000	1000	1000	1000
W/O order	859	1000	1000	971	1000	1032

Table 3 Geweke diagnostics

Models	μ_1	μ_2	μ_3	μ_4	μ_5	τ
W. order	0.4275	0.3221	0.2376	0.0895	0.3784	0.1393
W/O order	0.8352	0.785	0.6931	0.4425	0.3692	0.8983

we cannot reject that null hypothesis that the MCMC is stationary. Then, posterior samples can be used for the further inference (Table 4).

In Fig. 2, posterior densities of μ show a nice pattern and μ_3 is centered at the largest value. It means that our samples from μ posterior densities have an order restriction. It matches our model assumptions. But we notice that there is an overlap

Table 4 $\log(CPOi)$ for each county by model

County	Size	M1	M2	County	Size	M1	M2
1	97	−10.33	−9.73	18	61	−7.88	−7.78
2	91	−8.71	−7.87	19	52	−7.72	−7.72
3	90	−12.50	−13.40	20	64	−8.21	−8.17
4	412	−14.38	−13.36	21	49	−11.64	−13.40
5	80	−9.13	−8.26	22	77	−8.83	−8.62
6	66	−9.32	−9.64	23	50	−7.04	−6.42
7	62	−7.87	−7.37	24	70	−8.41	−7.91
8	53	−7.70	−7.16	25	64	−8.90	−9.98
9	73	−8.37	−7.69	26	60	−8.65	−7.91
10	81	−8.35	−8.54	27	48	−9.75	−9.78
11	98	−10.94	−10.42	28	52	−7.59	−7.11
12	84	−8.87	−9.13	29	75	−7.72	−7.21
13	217	−12.35	−12.56	30	82	−9.51	−9.29
14	72	−8.93	−8.81	31	75	−9.02	−8.31
15	87	−10.22	−9.54	32	102	−9.98	−10.20
16	101	−9.03	−8.12	33	129	−10.02	−8.84
17	99	−10.79	−10.48	34	84	−8.79	−7.85
				35	92	−9.31	−9.81

[1] *Note* Shaded Area: The model without order restrictions (M1)
Unshaded Area: The model with any order restrictions (M2)

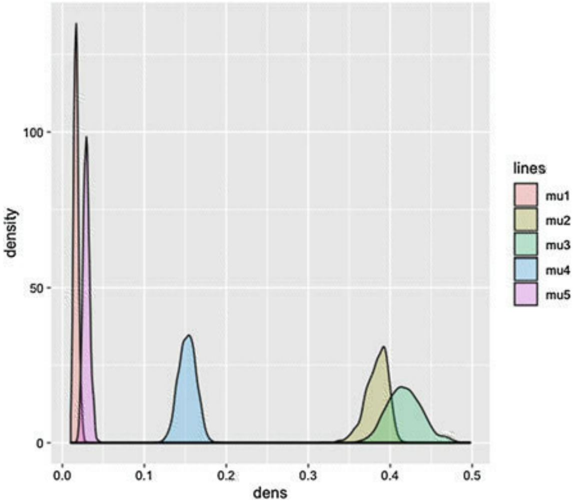

Fig. 2 Posterior density of μ

between μ_2 and μ_3. It is apparent that $\mu_2 \leqslant \mu_3$ may not be appropriate for BMI counts. The order restriction assumption may be too strong in this case.

4.3 Model Comparison

We compute the estimated cell probabilities for each county and their variances, which are the posterior sample means and posterior standard deviations of parameter $\boldsymbol{\theta}$. In Table 5 (appendix), we show their posterior means, standard deviations and coefficients of variation. We notice that the posterior means from the model with order restrictions (M2) have lower variances compared with the general model (M1). Generally, we have higher accuracy for the estimation of the cell probabilities $\boldsymbol{\theta}$. But for parameters θ_1 and θ_5 in some counties, such as the second county in Table 4, the model with order restriction does not gain precision on them. This is expected because the extreme cells are generally sparse. In general, many of the coefficients of variation are small enough to declare that the posterior means are reliable.

In Fig. 3, the top panel is the model with order restrictions and the bottom panel is the model without any order restriction for the same county, county 1. It can be seen from the plots of the posterior densities of the θ's that $\boldsymbol{\theta}$ in this county has an order restriction. Our unimodal assumption for this county holds. However in the first density (top panel) and the second density (bottom panel), there are overlaps between θ_2 and θ_3. It means that the order restriction may not hold for this county. The overlap between θ_1 and θ_5 is acceptable, since there is no direct comparison between them. Specially in the bottom panel, the densities from the model without order restriction show that θ_2 is even larger than θ_3. Our unimodal assumption may not be proper in this county.

n Fig. 4, the top panel is the model with order restrictions and the bottom panel is the model without any order restriction for another county, county 3. Plots of the posterior densities of the θ's without any order restriction show that $\boldsymbol{\theta}$s in each county may have an order restriction. It can be seen from the second density (bottom) that θ_3 is the mode for the cell probabilities even without order restriction assumption. It means that our unimodal assumption in this county is valid. Like in Fig. 3, the overlap between θ_1 and θ_5 is acceptable, since there is no direct comparison between them.

In Fig. 5, we use posterior standard deviation (PSD) to generate regression lines. Those regression lines show the overall PSD comparison between the model with order restrictions (M2) and the model without order restriction (M1). If the slope of regression line is larger than the black reference line whose slope is one, it means that M2 has smaller PSDs than M1. For each cell probability θ shown in different colors, the slope is larger than the reference lines. Therefore, we gain higher precision on estimation of cell probabilities among 35 counties.

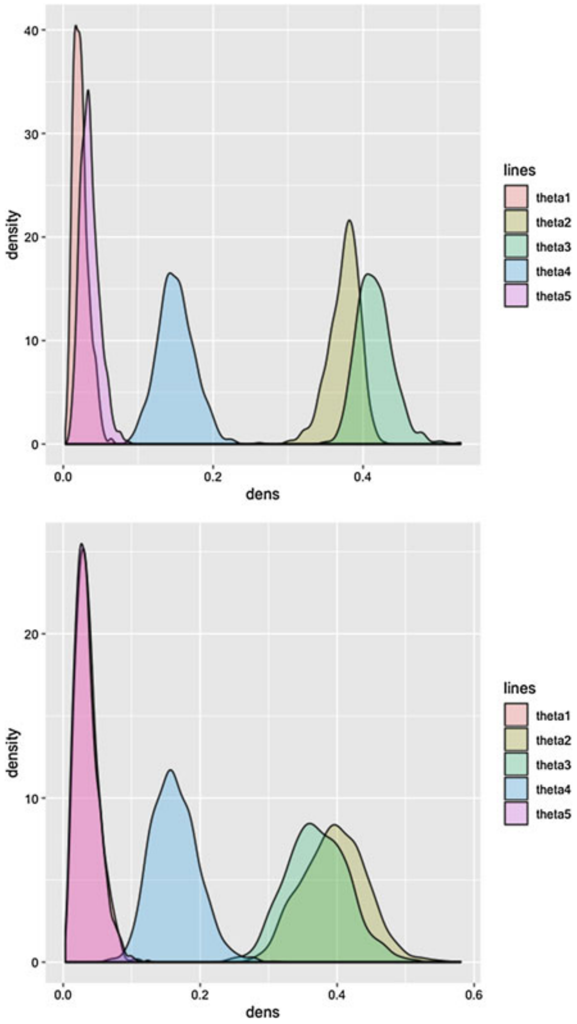

Fig. 3 Posterior densities of $\boldsymbol{\theta}$ for county 1

5 Bayesian Diagnostics

In the Bayesian framework, the logarithm of the pseudo-marginal likelihood (LPML) is a well-known Bayesian criterion for comparing models. A ratio of LPMLs is a surrogate for the Bayes factor. The best model among competing models has the largest LPML,

$$LPML = \sum_{i=1}^{I} \log(CPO_i),$$