ISSN 1996-3343

Asian Journal of Applied Sciences

http://knowledgiascientific.com

Knowledgia SCIENTIFIC
A Place to Publish Outstanding Research

Asian Journal of Applied Sciences, 2 (4): 402-413, 2009
ISSN 1996-3343

Population Projection of Kerala using Bayesian Methodology

[1]Rahul, [2]Gyan Prakash Singh and [3]Om Prakash Singh
[1]Department of Statistics, Invertis Institute of Management and Studies, Bareilly 243001, India
[2]Department of Community Medicine, Institute of Medical Sciences, BHU, Varanasi, India
[3]Department of Statistics, UP College Varanasi, 221002, India

Abstract: This study considers use of Bayesian methodology for the population projection of an Indian Province, Kerala using logistic growth model. The study presents probabilistic projections of the population and estimates of the parameters of the model along with their highest posterior density intervals. Getting actual expressions of posterior distributions in Bayesian setup with large number of parameters is a difficult task. To overcome the problem, Markov Chain Monte Carlo (MCMC) technique has been used for getting samples from the posterior distribution. The projections have been compared with those made in earlier studies to check the suitability of the projections. We have also discussed the asymptotic behavior of population projection to know the total population at which Kerala population will be stabilized.

Key words: Logistic model, Markov Chain Monte Carlo, WinBUGS, non-linear regression model, Monte Carlo error, highest posterior density, population projection

INTRODUCTION

The government and corporate sector always require precise idea about the future size of various entities like population, resources, demands, consumptions etc., for their planning purposes. To get this information, the behavior of the related variables is analyzed based on the past data by the statisticians at first and using the inferences drawn from the analysis they make future projections of the variable desired. At present, there exist two major paradigms in statistics namely conventional (frequentist) and Bayesian for the purpose of data analysis. Use of Bayesian methodology in the field of data analysis is comparatively new and has found massive support in last two decades from the people belonging to various disciplines. Probably the main reason behind the increasing support is its flexibility and generality that allows it to deal with the complex situations. The present study is based on the Bayesian approach of data analysis.

A Bayesian approach to a problem starts with the formulation of a probability model that is thought adequate to describe the underlying mechanism based on the past studies and sample collection process. The next step in the process is to devise prior distributions to the parameters, the unobserved quantities of ultimate interest, which is intended to capture the beliefs about the situation before seeing the data on the basis of past experiences. After observing the data, Bayes' rule is applied to obtain a posterior distribution for these parameters, which is conditional probability distribution of the unobserved quantities of ultimate interest, given the observed data. It takes in to account of both, the prior knowledge about the parameter and the observed data. The final step is concerned with the evaluation of the fit of the model to the data and implications of the resulting posterior distributions and sensitivity of the conclusions to the assumptions. This stage enables us to get the answer of the queries like - are the substantive conclusions obtained reasonable? (Gelman *et al*., 2003; Gill, 2002).

Corresponding Author: Om Prakash Singh, Department of Statistics, UP College Varanasi, 221002 and DST-CIMS, BHU, Varanasi, 221005, India

After the analysis of the data, the projections for the future are made on the basis of the chosen model which seems to explain the data suitably. There are a number of methodologies being used for the population projections. One of the most popular methods is cohort component method which is based on the estimates about the future levels of the fertility, mortality, sex composition, migration etc. Apart from it, many time series and mathematical models are also being used for the purpose with varying complexity. Recently, many studies have examined the relative performance of simple mathematical models, extrapolation based on time series and cohort-component models of population forecasting. Most have found that constant growth mathematical models or standard time series models of population growth are at least as accurate as cohort-component models (Pflaumer, 1992; Smith, 1997; Smith and Sincich, 1992).

Present study is not intended to study the relative accuracy of the various projection models. Rather, it only aims to investigate the usefulness of age old logistic growth model in making the population projection in Indian context and verify its suitability by comparing projections made using other methods. The estimation of the parameters of the logistic model with the classical methods carries substantial difficulties. Bayesian analysis provides a neat and transparent way of their estimation. It provides probabilistic point estimates of the parameters as well as of the projections along with highest posterior density interval. The interval is like confidence interval in the classical but with more clear interpretation. A 95% confidence interval of a parameter in the classical sense, with fixed numbers as endpoints cannot be interpreted as it contains the parameter with probability 0.95. A confidence interval is a random interval having different values in repeated samples. It only says that in repeated samples the confidence interval will contain the parameter in 95% cases. While in Bayesian setup, the 95% HPD interval is straightforward interpreted, as the probability that it contains the parameter is 0.95. The present study aims to provide some long time projection of the Indian Province, Kerala. The methodology and approach adopted in the present study is a similar to Rahul *et al*. (2007) where the probabilistic projections were made of the whole population of India and the estimates were found satisfactory. It desires to investigate whether the logistic model can suitably be applied for population projection satisfactorily in a demographically advance state of India also. Among all the Indian states, Kerala is the forerunner in terms of demographic transition. Its total fertility rate is 1.7 much below to the replacement level whereas the rate for the whole country is estimated between 2.5 to 3.1 in 2001. It has lowest rate of population growth among all states in India with decadal growth (9.42% in 2001) less than half the all-India average of 21.34%. Women compose 51.42% of the population. Kerala's human development indicators-elimination of poverty, primary level education and health care-are among the best in India. Kerala has the second highest literacy rate (90.92%) among Indian states after Mizoram and life expectancy (73 years) is among the highest in India. According to the 2001 census, literacy rate among females is 87.86% and among males it is 94.20%. There are several variants of the logistic models for the growth. Here, we are presenting the analysis and forecasts based only on the four parameter logistic model which we found more appropriate. A comparison of its three variants for the purpose of population projection of India and its three provinces has been made by Rahul (2007).

THE MODEL, METHODOLOGY, MCMC AND DIAGNOSTICS

The Model

Here, we assume Y_i to denote the population size of Kerala in the year t_i ($i = 1, 2,\ldots, 11$) where, i refers to successive census data starting from 1901 for which $i = 1$. The data are given in the Table 1. The four-parameter logistic growth model used for the projection may be described as follows. Assume general regression equation:

$$Y_i = \eta_i + \varepsilon_i$$

Table 1: Population of Kerala from 1901 to 2001 (in millions)

Year (t_i)	1901	1911	1921	1931	1941	1951	1961	1971	1981	1991	2001
Population	6.396	7.148	7.802	9.507	11.032	13.549	16.904	21.347	25.454	29.099	31.839

where, the population size Y_i, in the year t_i has been assumed to follow normal distribution with respective means η_i and common precision (=1/variance) τ. Here, η_i is the deterministic part and ε_i is the disturbance part. Therefore, the disturbances $\varepsilon_i \sim$ iid $N(0, \tau)$. For the implementation of four parameter logistic model with some reparametrization, we assume the deterministic part η_i as:

$$\eta_i = \frac{\theta_1\theta_2}{\theta_1+(\theta_2-\theta_1)e^{\theta_3(t_i-\text{mean}(t[]))/\text{sd}(t[])}} + \theta_4$$

In the above logistic function, the upper asymptote of the curve approaches to $\theta_2+\theta_4$ which is also called the carrying capacity of the population. Again, $-\theta_3$ is called the rate of growth of the population. In the above expression of η_i the time variable t_i has been standardized for suitable execution of the program in the WinBUGS using mean (t[]) and sd (t[]). For the same purpose, we also make some more reparametrization in bugs program as:

$$\theta_1 = e^{\phi_1}, \theta_2 = \phi_2, \theta_3 = \phi_3, \theta_4 = e^{\phi_4}$$

For the Bayesian analysis, we need to provide prior distributions to all the parameters present in the model ϕ_1, ϕ_2, ϕ_3, ϕ_4 and τ. We do not have any previous knowledge about the nature of the probability distribution of the parameters involved in the model for such type of data. Thus we prefer to assign non-informative priors for them. Normal (0, 0.001) (variance = 1/0.001) prior has been assigned to all of the parameters ϕ_1, ϕ_2, ϕ_3, ϕ_4 and Gamma (0.001, 0.001) prior to the parameter τ. The choice of suitable priors is widely discussed area in Bayesian methods. A massive discussion on the choice of priors is also available in the Bugs manual by Spiegelhalter *et al*. (1996).

Bayesian Method

Here, we present some basics of the Bayesian method for the data analysis. We may propose a probability model for describing the underlying mechanism of the data, X and let it be denoted by $p(x, \Theta)$ where, Θ denotes the set of parameters. The next step in the process is to devise some prior distributions to the parameters Θ of the model. Here, Θ is completely general and it may be vector valued entity. The parameters of the model are unobservable quantities of ultimate interest. The prior is intended to capture the beliefs about the situation before seeing the data based on the past experiences. Suppose the prior distribution of Θ be $p(\Theta)$. After observing the data, suppose the likelihood function be $p(x|\Theta)$. The likelihood function provides the distribution of the data, X, given the parameter value Θ. Using Bayes' rule we obtain a posterior distribution for these unobserved parameters, which is conditional probability distribution of the unobserved quantities of ultimate interest, given the observed data. It takes into account of both, the prior knowledge about the parameter and the observed data. Suppose the posterior distribution of the parameters Θ be $p(\Theta|x)$. The Bayes' formula for the posterior distribution of the parameter Θ has following expression.

$$\text{Posterior } p(\theta|x) = \frac{\text{Prior} \times \text{Likelihood}}{\text{Marginal}} = \frac{p(\theta)\times p(x|\theta)}{\int p(\theta)\times p(x|\theta)d\theta}$$
$$\propto p(\theta)\times p(x|\theta)$$

When we have found the posterior distribution of the parameter θ, we may easily obtain an estimate of $f(\Theta)$, a function of θ, under the chosen loss function depending on the nature of decision

making. For example under squared error loss $E(f(\theta|x))$ is found to be Bayes estimator for $f(\theta)$. Clearly:

$$E(f(\theta|x)) = \int f(\theta)p(\theta|x)d\theta$$

When we do not have a closed form for the Bayes estimate $E(f(\theta|x))$ then we may easily estimate it by obtaining a sufficiently large random sample $\theta_1, \theta_2, ..., \theta_n$ of size n from the posterior distribution of the parameter θ and utilizing following approximation:

$$E(f(\theta|x)) \approx \frac{1}{n}\sum_{i=1}^{n} f(\theta_i)$$

Markov Chain Monte Carlo and WinBUGS

Bayesian approach faces serious computational difficulties due to likely involvement of complicated mathematical expressions in the posterior distributions. Many of these have been suitably addressed with greater ease using Markov Chain Monte Carlo methods. More than 50 years ago, Metropolis *et al*. (1953) introduced the Metropolis algorithm that appeared in the physics literature. However, there was little interest from statisticians in such Markov Chain Monte Carlo (MCMC) methods, perhaps because they did not have easy access to fast computers. MCMC has brought a radical change in the job of data analysis. It is now routine to fit extremely complex formulations in the Bayesian paradigm that still seem out of reach of frequentist methods. Beginning of MCMC in Bayesian setup can roughly attributed to Geman and Geman (1984) providing introduction of the Gibbs sampler as a method for obtaining difficult posterior distribution in the process of image attributes.

The Markov Chain Monte Carlo (MCMC) method is an iterative tool. The term Monte Carlo method refers to simulation of processes, using random numbers. This method is commonly used to evaluate, iteratively, approximate value of some of the complex integrals involving expectation of a function of a random variable. The evaluation is made by generating large independent simulated samples from the (complex) distribution of the random variable and taking the average of the function values obtained on these sample points. The main difference between standard Monte Carlo method and MCMC method is the dependence structure between successive simulated values obtained from the distribution. Standard Monte Carlo method produces a set of independent simulated values whereas MCMC method produces a chain of simulated values in which each of the simulated value is dependent on the preceding value. The basic principle based on the ergodic theorem of Markov chain is that once the chain has run sufficiently large and has converged then it will approximate the desired integral. Since, complex expressions with difficult to solve integrals are often involved in Bayesian analysis, therefore this method has become much more attractive in these analyses. More details with examples of the MCMC implementation in Bayesian inference can be found from Gilks *et al*. (1996) and Congdon (2001).

WinBUGS (Bayesian inference Using Gibbs Sampling for Windows) Version 1.4.1 is a computer software which is freely available for the realization of Bayesian inference using MCMC tool from http://www.mrc-bsu.cam.ac.uk/bugs/welcome.shtml along with comprehensive manual. Imperial College School of Medicine, UK has its copyright. The software has become much popular and it can be run stand alone or from many other statistical packages like R, SAS, MS-EXCEL, Matlab, STATA etc. using the appropriate add-ons. There are several add-ons available on the web site developed to help different users' requirements. Although, the program basically uses Gibbs sampling however, it uses other methods also like Metropolis, Slice sampling etc. The exact sampling method used by WinBUGS varies for different types of models. The inbuilt intelligent program decides about choice of sampling method itself depending on the nature of the model. In the simplest case, when a conjugate

prior distribution is used with a standard likelihood to yield a posterior distribution from which parameters may be directly sampled. In more complicated cases, the form of the posterior distribution does not allow for direct sampling. Instead, some form of Gibbs sampling or Metropolis-Hastings sampling is used to sample from the posterior distribution. These techniques generally work by first sampling from a known distribution that is similar in shape to the posterior distribution and then accepting the sample with some probability. To learn more about these sampling schemes, see the MCMC methods section (and the cited references) in the first chapter Introduction of the WinBUGS user manual that comes (electronically) with the WinBUGS program. The manual describes the uses of WinBUGS for Bayesian analysis and the simple BUGS language (available also with graphical method named DoodleBUGS) in detail. WinBUGS is quite user friendly software. It hides complexities of the MCMC algorithms from the users. The users need only to expertise in the Bayesian methods and BUGS language.

Diagnostics

MCMC tool has been used in the WinBUGS to obtain the posterior distribution of the unknown parameters in the model. In the process we need to run a number of chains for each parameter for a long time. When the chains have run sufficiently large number of iterations and have reached to the stationary distribution then the samples obtained by further running of the chains are supposed to be drawn randomly from the posterior distribution of the parameter. Although, at any point of time it is very difficult to say conclusively that a running chain has converged. Using various diagnostic tools, developed for assessing the convergence of chains, we can only diagnose that chains have not yet converged. However, it is generally easy to diagnose the non-convergence of the chains and one can be happy with the convergence at any moment of time if some of the diagnostics do not detect any non-convergence of chains. WinBUGS provides a number of inbuilt diagnostics to assess the convergence of chains. In practice, one should use multiple diagnostics on a single chain. A few of the diagnostics available with the WinBUGS and used in this study are briefly described blow.

WinBUGS allows multiple chains for each parameter to run simultaneously. Running multiple chains is also a way to check the convergence of MCMC simulations. WinBUGS provides a running trace plot of the chains of updates for the parameters. When the different chains do not provide sufficient mixing of chains even after a long run then it will be an evidence of lack of convergence of the chains.

Another diagnostic available with WinBUGS is Brooks-Gelman-Rubin (bgr). It calculates the Gelman-Rubin convergence statistic, as modified by Brooks and Gelman (1998). It provides a plot of the statistic in which the width of the central 80% intervals of the pooled runs is green, the average width of the 80% intervals within the individual runs is blue and their ratio R (= pooled / within) is red. For plotting purposes the pooled and within interval widths are normalized to have an overall maximum of one. Brooks and Gelman (1998) emphasized that one should be concerned both with convergence of R to 1 and with convergence of both the pooled and within interval widths to stability.

WinBUGS also provides smoothed density plots of the chains. When the chains approach to stationarity, then the density plot shall take a normal shape. A lack of normality or multimodality is also an indication of the absence of convergence of the chain. Auto correlation is another diagnostic available. If the chains converge to the stationary distribution then the auto correlation shall decrease with the increase in lags. It also provides us a basis to assess the convergence of the chain. A detailed discussion on the diagnostics can be found by Gill (2002).

Once we are convinced that chains have been converged through the diagnostics, we will need to run the simulation for a further number of iterations to obtain samples that can be used for posterior inference. The more samples we save, the more accurate will be our posterior estimates. Once we have run enough updates and are satisfied with the history of chains, we discard the earlier samples. We obtain the summary statistics only from the samples generated afterwards.

THE ANALYSIS

Table 1 provides the census figures of Kerala at the interval of 10 years from 1901 to 2001, which have been used to fit the model and to make the future projections.

Using this census data and the logistic growth model described above, a WinBUGS program was developed to make a Bayesian analysis of the data and to provide projections of the population of Kerala. WinBUGS codes for the model are given in the appendix. During the implementation of the program, we have taken three chains to run for each parameter.

We have obtained summary statistics for the estimates of the parameters of the model after discarding 20,000 initial updates. During these updates none of the diagnostics indicated any symptom of non-convergence of the chains. The number of iterations required to run after the convergence of the chains is assessed on the basis of Monte Carlo error (MC error) for each parameter. Simulation shall be continued until MC error for each parameter comes below 5% of the sample standard deviation as suggested in the WinBUGS manual. Therefore, 20,000 updates were run after the initial burn-in and from Table 3 we see that MC error for each parameter were less than about 5% of the sample standard deviation.

While running present model with the WinBUGS, we monitored five nodes ϕ_1, ϕ_2, ϕ_3, ϕ_4 and ($\sigma = 1/\sqrt{\tau}$). Here, we present the various diagnostics and estimates based on later 20,000 iterations (after discarding 20,000 initial iterations).

The history plots of the sample values of five nodes ϕ_1, ϕ_2, ϕ_3, ϕ_4 and σ against iterations for the three chains of the Model have been shown in the Fig. 1a-e. The mixing of the three chains (in different colors) for all the five nodes in this model looks quite good giving us a confidence of the convergence of chains. The values of R, the bgr diagnostic for the all these nodes are also close to one as shown in the Table 2. Their graphical traces against iterations are also shown in the Fig. 2a-e. The traces of blue and green lines are stable and the red one has converged to one for all the five parameters monitored. Figure 3a-e shows smoothed curves of the posterior densities of the nodes monitored. The appearance of all the curves is bell shaped indicating asymptotically normal. Figure 4a-e presents autocorrelations for different lags for all the five nodes which shows declining trend with increase in lags. The summary statistics for the selected nodes for the model have been shown in the Table 3. The Markov chain errors for all the nodes are below the 5% of their sample standard deviation. Ninety five percent confidence limits of the nodes called HPD (highest posterior density) region along with sample mean, median and standard deviation values are also shown in the Table 4. The fitted values and the projections for the future using the logistic model are given in the Table 4. If we look the proximity between observed and estimated (sample mean) values from 1901 to 2001 in the Table 4 we find that

Table 2: R (bgr ratio) for different nodes of the model

ϕ_1	ϕ_2	ϕ_3	ϕ_4	σ
0.9998	0.9999	1.000	0.9995	1.003

Table 3: Summary statistics for the model

Node	Mean	SD	MC error
phi[1]	2.8600	0.01710	0.004580
phi[2]	31.9800	1.39700	0.043890
phi[3]	-2.5030	0.14320	0.004426
phi[4]	1.7650	0.05411	0.001678
sigma C	0.2474	0.08065	0.001150
theta[1]	17.4600	0.29880	0.008009
theta[2]	31.9800	1.39700	0.043890
theta[3]	-2.5030	0.14320	0.004426
theta[4]	5.8520	0.31100	0.009597

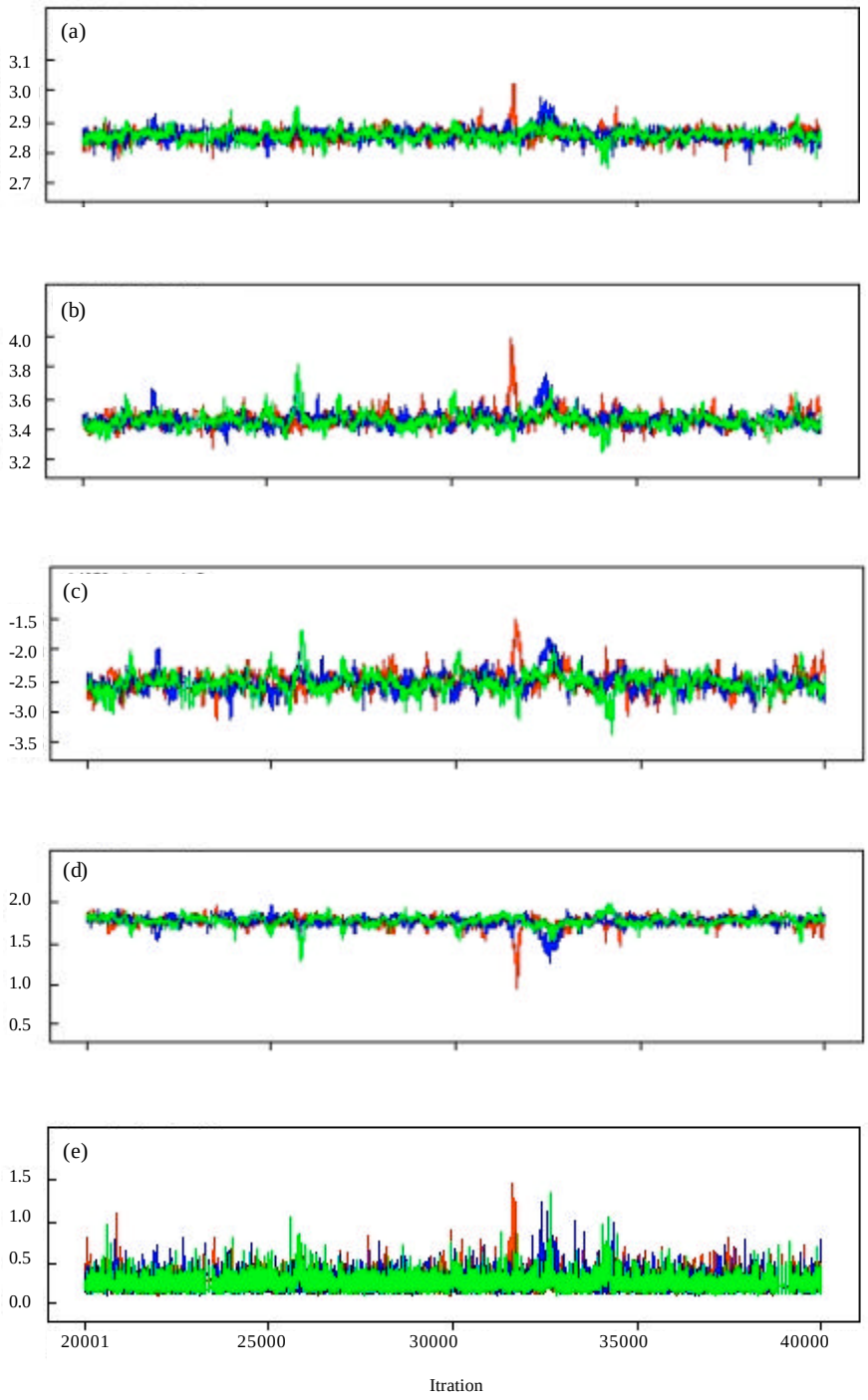

Fig. 1: History of the sample values of the nodes against, (a) phi[1], (b) phi[2], (c) phi[3], (d) phi[4] and (e) sigma C chains 1:3

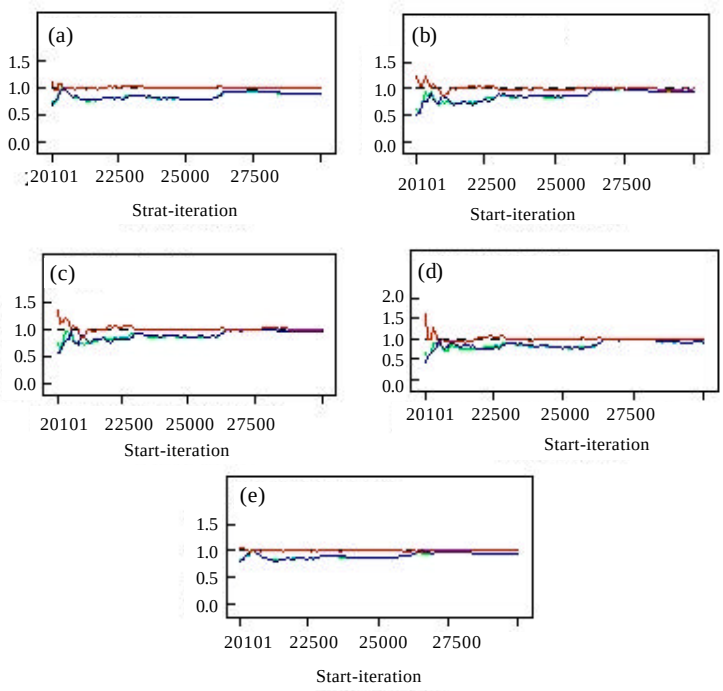

Fig. 2: The graphical traces of bgr diagnostic R against iteration for the model, (a) phi[1], (b) phi[2], (c) phi[3], (d) phi[4] and (e) sigma C chains 1:3

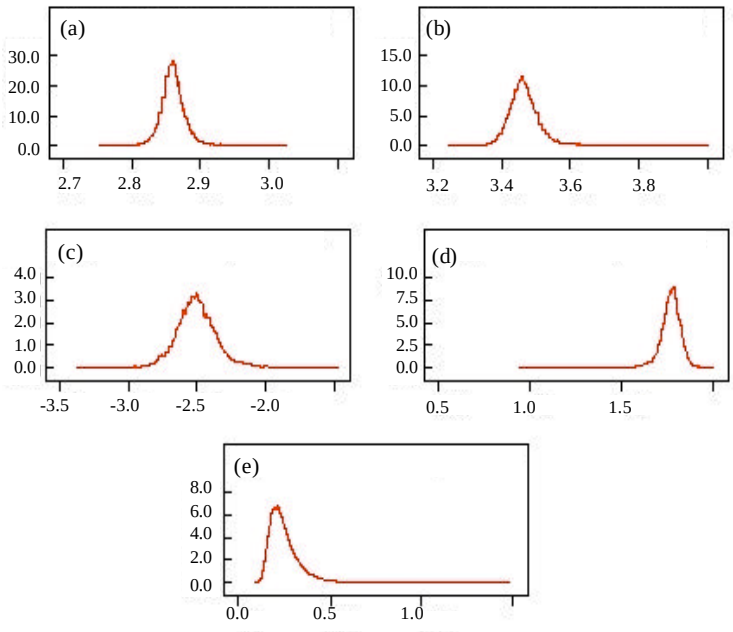

Fig. 3: Smoothed density estimates of the parameters, (a) phi[1], (b) phi[2], (c) phi[3], (d) phi[4] and (e) sigma C chains 1:3 sample: 60000

Table 4: Population estimates and projections of Kerala (1901-2051)

		Estimates and projections			
		Population estimate		HPD Region (%)	
Year	Census (in millions)	Mean	Median	2.5	97.5
1901	6.396	6.578	6.584	6.172	6.952
1911	7.148	7.074	7.077	6.767	7.372
1921	7.802	7.873	7.873	7.631	8.117
1931	9.507	9.127	9.124	8.883	9.392
1941	11.032	11.02	11.01	10.73	11.33
1951	13.549	13.69	13.69	13.39	14.01
1961	16.904	17.17	17.17	16.89	17.45
1971	21.347	21.21	21.22	20.89	21.52
1981	25.454	25.33	25.34	24.97	25.66
1991	29.099	29.02	29.02	28.71	29.32
2001	31.839	31.96	31.95	31.49	32.46
2006	NA	33.12	33.10	32.49	33.83
2011	NA	34.09	34.06	33.28	35.04
2016	NA	34.88	34.85	33.89	36.08
2021	NA	35.53	35.48	34.37	36.97
2026	NA	36.05	35.99	34.73	37.72
2031	NA	36.47	36.40	35.01	38.34
2041	NA	37.06	36.97	35.39	39.26
2051	NA	37.42	37.31	35.60	39.89

NA: Not applicable

Table 5: Population projections (millions) of Kerala (2006-2051)

	Present study			Dyson T.				
Year	2.5	Estimate	97.5	Low	Standard	High	Technical group	PFI and PRB
2006	32.49	33.12	33.83		33.668		33.265	
2011	33.28	34.09	35.04	-----	35.302	-----	34.563	34.705
2016	33.89	34.88	36.08		36.652		35.577	
2021	34.37	35.53	36.97	-----	37.674	-----	36.569	36.920
2026	34.73	36.05	37.72		38.451		37.254	
2031	35.01	36.47	38.34					38.184
2041	35.39	37.06	39.26					38.570
2051	35.60	37.42	39.89	33.6	39.000	45.0	-----	37.912

Source: Dyson (2004), Registrar General of India (2006), Population Foundation of India (PFI) and Population Reference Bureau (PRB) (2007)

differences were less than 1% except in the years 1901, 1931 and 1961 where they were 2.9, 4.0 and 1.6%, respectively. Figure 5 provides graphical presentation of the fitting of the model. It looks from the graph that the Model provides a close fit (the closeness of the smoothed line representing the estimated values and the dots showing the observed values) to the census data. Dotted blue lines provide 95% HPD (highest posterior density) region. Looking at the future projections, we see that the trace approaches to upper asymptote near 2050 at around 38 millions. The value of the carrying capacity or the upper asymptote can be estimated as $\theta_2+\theta_4 = 31.98+5.82 = 37.832$ millions.

For the purpose of comparison with other studies, we have produced projections made by Dyson (2004), Population Foundation of India and Population Reference Bureau (2007) and Technical Group of Registrar General of India (2006) in Table 5. A comparison of projections provided by present logistic model and those presented from other studies in the table are not much different. The differences in the projections from Dyson (2004) were below 6.7%, from Population Foundation of India and Population Reference Bureau (2007) were below 4.7% and from Technical Group of Registrar General of India (2006) were below 3.3%. Present HPD region and the ranges from low to high provided by Dyson (2004) (Table 5) also agree to some extent, although the HPD region provides a 95% confidence interval while the interval between high and low does not provide a probabilistic interval.

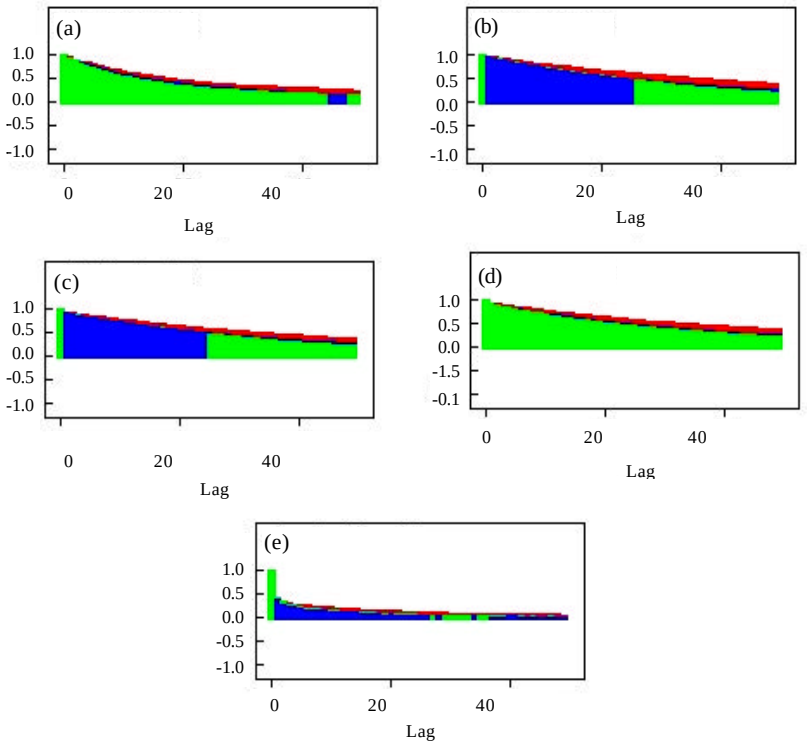

Fig. 4: Autocorrelation plots against lag of the parameters, (a) phi[1], (b) phi[2], (c) phi[3], (d) phi[4] and (e) sigma C chains 1:3

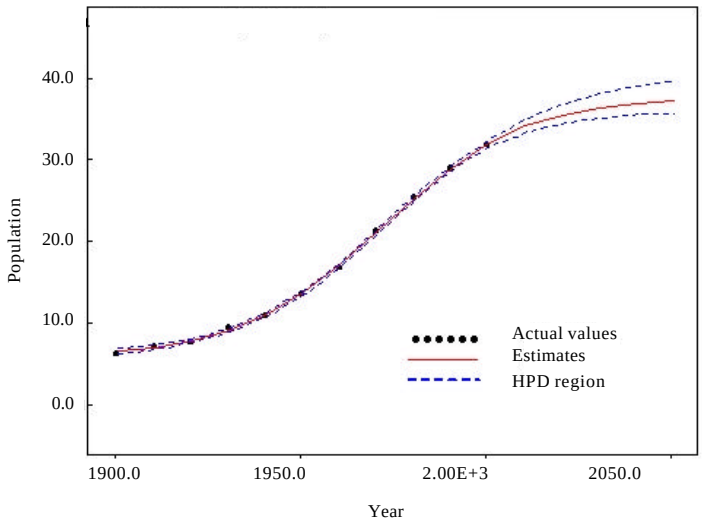

Fig. 5: Fitting, projection and HPD region of the estimates under proposed model. Model fit: Kerela (1901-2051)

CONCLUSIONS

The present study was an attempt to show the application and suitability of the MCMC tool in Bayesian Data analysis for fitting population data and making projection of the future population using the Logistic growth model. The estimates shown in the Table 4 are the values of fits on the past census data and projections for the future period based on the proposed logistic growth model. This table provides us two estimates for population sizes, sample mean and sample median. Here, the sample mean is the Bayes estimator under quadratic loss function and the sample median is the Bayes estimator under absolute value loss function. Both the estimates are quite close to each other. The table also provides 95% HPD interval for all the population sizes and projections in different years that offers interval estimates for them. The model suggests that the population of Kerala will reach to its maximum of 37.8 millions when it will be stabilized near after 2051. A comparison of the our projections with the other results shown in the Table 5 reveals that their projections are close to those obtained in this study. Here, we will like to mention that the aim was not to make a comparative study of different projection methods. We were, essentially, interested in presenting the basics of the implementation of the Bayesian data analysis with an illustration of the population projection. However, present effort seems to provide reasonable projections for the Kerala, a demographically advance province of India. We want to make further the remark that the logistic growth model can still be used to fit the past census data and to project the future populations. We have not performed the sensitivity analysis taking different prior distributions mainly due to the selected priors were non-informative. These priors did not provide substantial information to the posterior distribution however, they were necessary for the implementation of the Bayesian data analysis.

APPENDIX

```
# Bugs code for the model
model
        {
for( i in 1 : N ) {
Y[i] ~ dnorm(eta[i], tauC)
# four parameter logistic function assigned to the mean of the normal distribution eta[i]
eta[i] <- theta[1]* theta[2] / ( theta[1]+( theta[2]-theta[1])* exp(theta[3] * (t[i]-
mean(t[]))/sd(t[]))+theta[4]
                        }
#reparametrization of the parameters
                        theta[1]<- exp(phi[1])
                        theta[2]<- phi[2]
                        theta[3]<- phi[3]
                        theta[4]<- exp(phi[4])
#non–informative normal priors assigned to the parameters
                        for( i in 1 : 4 ) {
                        phi[i] ~ dnorm(0,.0001)
                                        }
# non–informative gamma priors assigned to the parameters
                        tauC ~ dgamma(.001, .001)
                        sigmaC <- 1 / sqrt(tauC)
        }
Data
```

list(t = c(1901, 1911, 1921, 1931, 1941, 1951, 1961, 1971, 1981, 1991, 2001, 2006, 2011, 2016, 2021, 2026, 2031, 2041, 2051),
Y = c(6.396262, 7.147673, 7.802127, 9.50705, 11.03154, 13.54912, 16.90372, 21.34738, 25.45368, 29.09852, 31.83862, NA, NA, NA, NA, NA, NA, NA, NA), N = 19)

REFERENCES

Brooks, S.P. and A. Gelman, 1998. General methods for monitoring convergence of iterative simulations. J. Comput. Graphical Stat., 7: 434-455.

Congdon, P., 2001. Bayesian Statistical Modeling. 1st Edn., John Wiley and Sons, Chichester, UK.

Dyson, T., 2004. India's Population the Future. In: Twenty-First Century India: Population, Economy, Human Development and The Environment, Dyson, T., R. Cassen and L. Visaria (Eds.). Oxford University Press, Oxford, UK.

Gelman, A., J.B. Carlin, H.S. Stern and D.B. Rubin, 2003. Bayesian Data Analysis. 1st Edn., Chapman and Hall, CRC., USA.

Geman, S. and D. Geman, 1984. Stochastic relaxation, Gibbs distributions and the Bayesian restoration of images. Inst. Electrical Elect. Eng. Trans. Pattern Analysis Machine Intell., 6: 721-741.

Gilks, W.R., S. Richardson and D.J. Spiegelhalter, 1996. Markov Chain Monte Carlo in Practice. Chapman and Hall, London, UK.

Gill, J., 2002. Bayesian Methods: A Social and Behavioral Sciences Approach. 1st Edn., Chapman and Hall, CRC., USA.

Metropolis, N., A.W. Rosenbluth, M.N. Rosenbluth, A.H. Teller and E. Teller, 1953. Equations of state calculations by fast computing machines. J. Chem. Physics, 21: 1087-1092.

Pflaumer, P., 1992. Forecasting US population totals with the Box-Jenkins approach. Int. J. Forecast., 8: 329-338.

Population Foundation of India and Population Reference Bureau, 2007. The Future Population of India: A Long-range Demographic View. Population Foundation of India, New Delhi and Population Reference Bureau, Washington.

Rahul, 2007. Population Projection of India (2011-2051) Using MCMC Technique in Bayesian Inference. Ph.D. Thesis, University of Allahabad, India.

Rahul, P.G.S. and O.P. Singh, 2007. Population projection of India using MCMC technique: A WinBUGS implementation. Demography India, 36: 145-154.

Registrar General of India, 2006. Population Projections for India and States 2001-2026. Office of the Registrar General and Census Commissioner, New Delhi, India.

Smith, S.K. and T. Sincich, 1992. Evaluating the forecast accuracy and bias of alternative population projections for states. Int. J. Forecast., 8: 495-508.

Smith, S.K., 1997. Further thoughts on simplicity and complexity in population projection models. Int. J. Forecast., 13: 557-565.

Spiegelhalter, D.J., A. Thomas, N.G. Best and W.R. Gilks, 1996. BUGS: Bayesian Inference Using Gibbs Sampling. Version 0.5, MRC Biostatistics Unit, Cambridge, UK.