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COMPARISONS OF MARKOV CHAIN MONTE CARLO CONVERGENCE DIAGNOSTIC TESTS FOR BAYESIAN LOGISTIC RANDOM EFFECT MODELS

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ABSTRACT

In mixed models, posterior densities are too difficult to work with directly. With the Markov chain Monte Carlo (MCMC) methods, to do statistical inference requires the convergence of the MCMC chain to its stationary distribution. To assess convergence of Markov chain has not a specific way. Assessing convergence of Markov chain has been developed many techniques. Although increasingly popularity MCMC methods, use of MCMC convergence diagnostics is not still common. Usually, the most MCMC users address the convergence problem by applying a diagnostic means by running their samplers. That's why in this article we discuss the problem of assessing the performance of MCMC algorithms. We compare convergence diagnostic tests to achieve target distribution. Bayesian logistic random effects models are intended to be interpreted with emphasis on mathematical expansions under these techniques. We have used a real data that wants to know what patient and physician factors are most related to whether a patient's lung cancer goes into remission after treatment outcomes and quality of life in patients with lung cancer. Our results show that convergence needs to enough time and experience.

Keywords: MCMC; Bayesian logistic random effect models; Convergence diagnostic tests

1. INTRODUCTION

In recent years, generalized linear mixed models (GLMMs) have become ever popular for the analysis of non-normal data with random effects generally encountered in many disciplines. Logistic random effects models are used to analyze multilevel data with a binary or ordinal outcome. Multilevel data are analyzed often in medical literature.Logistic random effects models examine the relationship between the binary output of dependent observations and the explanatory variables that are a special case of GLMM. Logistic random effect models, firstly in an unpublished report of Oregon State University by Pierce and Sands (1975) are discussed in the biostatistics literature. They univariate random constant term has proposed a Gaussian distribution. Stiratelli et al. (1984) developed a random effect logit models. Larsen et al. (2000) have discussed fixed effect models, as well as the interpretation of the random effect parameters, were studied in detail in logistic random effects models.

Unlike frequentist analysis where are convergence to a single point, MCMC output is convergence to a distribution. Thus, specialized diagnostic tools are needed in the Bayesian framework. In Bayesian inference, interest lies in estimating posterior distributions of model parameters rather than individual parameter values and asymptotic standard errors. An analytical solution of the posterior probability distribution is to use Markov chain Monte Carlo (MCMC) methods to simulate from the posterior distribution. Metropolis-Hastings sampling and Gibbs sampling are MCMC methods that can be utilized to generate draws, in turn, from full conditional distributions of model parameters (Hastings, 1970).

The GLMM likelihood function is expressed as an integral with respect to the random effects and does not have a closed form. An alternative to likelihood-based, there is a Bayesian approach in which MCMC methods are used to make inferences based on the posterior distribution of the parameters. Zeger and Karim (1991) investigated the use of Gibbs sampling to fit GLMMs. Other implementations that involved Monte Carlo methods were adopted by

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Gamerman (1997), Booth and Hobert (1999), and Natarajan and Kass (2000).

In Bayesian approach, it should be sure of achieving convergence to achieve true value of the parameter. Therefore, whether or not the convergence of Markov chain should firstly be examined. There is no certain way to assessment convergence; it is only possible to ascertain when convergence definitely has not been achieved (Toft et al., 2007). Assessing convergence of Markov chain has been developed many techniques. Some of these convergence diagnostics are simple graphical ways of summarizing the data. Others are formal statistical tests. Geweke (1992), Raftery and Lewis (1996), Heidelberger and Welch' (1981) developed methods for formal statistical tests for convergence diagnostics. It is improved autocorrelations that are calculated within each chain for each monitored variable at lags of 1, 5, 10, and 50, effective sample size and Monte Carlo standard errors to assess convergence.

Brooks and Roberts (1997) motivate the use of convergence diagnostic techniques for MCMC algorithms and review methods proposed. Brooks and Roberts (1998) review some convergence methods. Sinharay (2003) submitted knowledge about the diagnostics tools to asses convergence of the MCMC algorithms. Toft, N. et al (2007) considers a pragmatic approach towards assessing the convergence of MCMC methods illustrated by a Bayesian analysis of the Hui–Walter model for evaluating diagnostic tests. Sahlin (2011) construct a diagnostic for estimating the burn-in of the chain.

After giving a brief overview of the introduction, structure of logistic random effect models and Bayesian logistic random effect models have formed. We provide an expository review of 7 convergence diagnostic tests, describing the theoretical basis. We then compare their performance for logistic random effect models. It has obtained results with Proc MCMC in SAS programme. Bayesian GLMM methods have been applied.Methods

1.1. Logistic random effects models

Logistic random effects models are widely used and flexible models for all applied sciences. Each term in a statistical model represents either a fixed effect or a random effect. Logistic regression with random effects is used to study the relationship between explanatory variables and a binary outcome in cases with nonindependent outcomes. A dichotomous or binary logistic random effects models have a binary outcome (Y = 0 or 1) and regresses the log odds of the outcome probability on various predictors to estimate the probability that Y = 1 happens, given the random effects (Li et al., 2011). The simplest binary model is given by

$$\pi(x_{ij}) = E(Y_{ij} \mid \gamma_j) = P(Y_{ij} = 1 \mid \gamma_j) = \frac{e^{X_{ij}\beta + Z_{ij}\gamma_j}}{1 + e^{X_{ij}\beta + Z_{ij}\gamma_j}}$$

,

$j = 1, 2, ..., N \quad i = 1, 2, ..., nj$

$$\gamma_j \sim N(0, \sigma^2_{\gamma_j})$$

with Y_{ij} : binary dependent variable of the i – th observation in the $j-\text{th}$ group, N : total number of groups, n_j total number of subjects in the j-th group $\beta = (\beta_0, \beta_1, \beta_2, ..., \beta_p)$: parameter vector of fixed effects and $g_1, g_2, ,..., g_N$:random effects (Diggle et al., 1998).

As following assumptions of random effects logistic regression:

- the conditional distribution of Y_{ij} given γ_j , follows Bernoulli distribution that a distribution from the exponential family with density $f(y_{ij} \mid \gamma_j, \beta)$
- given γ_j , the repeated measurements, $Y_{i1}, Y_{i2}, ..., Y_{inj}$ are independent;

the γ_j , are independent and identically distributed with density function $f(\gamma_j)$ (Diggle et al., 1998).

1.2. Bayesian approach of Logistic random effects models

The likelihood function for the parameters β and G . has the form

$$L(\beta, G \mid y) \propto \prod_{j=1}^{N} \int \prod_{i=1}^{n_j} P(Y_{ij} = 1 \mid \gamma_j, \beta) |G|^{-1/2} \exp(-\frac{1}{2}\gamma_j' G^{-1} \gamma_j) d\gamma_j$$

Except in the linear model with Gaussian errors, the integral above does not have an analytic solution. Hence, likelihood inference requires numerical evaluation. The integral's dimension is equal to the number of random

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effects. A Bayesian approach treats all unknown quantities as random variables and assigns prior probability distributions ($\pi(\beta)$ and $\pi(G)$) for the unknown parameters β and G . It is used usually non-informative priors in random effects models. It is assumed that priors are independent. by the Gibbs sampler require full-conditional calculations, therefore leads to an improper joint posterior distribution for β and G . Let $p(\beta,G)$ represent the joint prior distribution for β and G .Then posterior distribution of logistic random effects models given by

$$p(\beta,\sigma^2\mid y)=\frac{\prod_{j=1}^{N}\int_{-\infty}^{\infty}\prod_{i=1}^{n_j}P(Y_{ij}=1\mid\gamma_j,\beta)\,f(\gamma_j\mid G)\,p(\beta,G)d\gamma_j}{\int\prod_{j=1}^{N}\int_{-\infty}^{\infty}P(Y_{ij}=1\mid\gamma_j,\beta)\,f(\gamma_j)\gamma_j\,p(\beta,G)d\beta d\gamma}$$

Note that the denominator is a normalizing constant independent of β and G . so those estimators, such as the posterior mode, can be derived from the numerator alone. Also, note that if $p(\beta,G)$ is constant, the numerator is just the likelihood function.

$$p(\beta,\sigma^2\mid y)\propto\prod_{j=1}^{N}\int_{-\infty}^{\infty}\prod_{i=1}^{n_j}P(Y_{ij}=1\mid\gamma_j,\beta)\,f(\gamma_j\mid G)\,p(\beta,G)d\gamma_j$$

1.3. Markov ChainMonte Carlo Method (MCMC)

The Markov chain Monte Carlo (MCMC) method is a general simulation method for sampling from posterior distributions and computing posterior quantities of interest. A Markov chain is a sequence of random variables, $\theta^1,\theta^2,\ldots,\theta^t$, for which the random variable θ^t depends on all previous only through its immediate predecessor θ^{t-1}. With the MCMC method, it is possible to generate samples from an arbitrary posterior density $p(\theta\mid y)$ and to use these samples to approximate expectations of quantities of interest. Gibbs sampling and Metropolis and Metropolis-Hastings algorithms are sampling methods in MCMC methods.

1.3.1. Gibbs Sampling

Gibbs sampling requires you to complicate the joint posterior distribution into full conditional distributions for each parameter in the model and then sample from them. The sampler can be efficient when the parameters are not highly dependent on each other and the full conditional distributions are easy to sample from. Suppose $\theta=(\theta_1,\ldots,\theta_k)'$ is the parameter vector, $p(y\mid\theta)$ is the likelihood, and $\pi(\theta)$ is the prior distribution. The full posterior conditional distribution of $\pi(\theta_i\mid\theta_j\ ,i\neq j,y)$ is proportional to the joint posterior density; that is,

$$\pi(\theta_i\mid\theta_j,i\neq j,y)\propto p(y\mid\theta)\pi(\theta)$$

The Gibbs sampler works as follows:

1. Set $t=0$, and choose an arbitrary initial value of $\theta^{(0)}=\{\theta_1^{(0)},\ldots,\theta_k^{(0)}\}$

2. Generate each component of θ as follows:

- draw $\theta_1^{(t+1)}$ from $\pi(\theta_1\mid\theta_2^{(t)},\ldots,\theta_k^{(t)}\ ,\ y)$
- draw $\theta_2^{(t+1)}$ from $\pi(\theta_2\mid\theta_1^{(t+1)},\theta_3^{(t)},\ldots,\theta_k^{(t)}\ ,\ y)$
- …
- draw $\theta_k^{(t+1)}$ from $\pi(\theta_k\mid\theta_1^{(t+1)},\ldots,\theta_{k-1}^{(t+1)}\ ,\ y)$

2. Set $t=t+1$. If $t<T$, the number of desired samples, return to step 2. Otherwise, stop.

2.4. Burn-in and Thinning

Burn-in refers to the practice of discarding an initial portion of a Markov chain sample so that the effect of initial values on the posterior inference is minimized. Discarding initial part of the chain is referred to as the burn-in period of the chain and the remaining part is called the stationary part.
If there is significant autocorrelation between the observed output terms, then we can reduce the output by systematically using every mth sample (for m≥1) and discarding the others. This is known as thinning.

2.5. Assessing Markov Chain Convergence and Convergence Diagnostics Tests

In practical applications of Markov chain Monte Carlo (MCMC) methods several questions remain unsolved (Adlouni et al. 2006):

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1. From which observation has the generated chain reached stationarity?
2. Is the chain long enough to cover the whole support of the distribution of interest?
3. Do the generated observations allow to estimate adequately the parameters with a given precision?

The Bayesian methods include several statistical diagnostic tests that can help you assess Markov chain convergence. We will explain a detailed description of each of the some diagnostic tests.

2.5.1. Geweke Diagnostic

The Geweke test compares the sample mean in the early segment of the Markov chain to the mean in the latter segment of the chain in order to detect failure of convergence (Geweke, 1992). This is a two-sided test, and large absolute *z*-scores indicate convergence problems. The statistic upon which this diagnostic has the following general form

$$Z_n = \frac{\bar{x}_1 - \bar{x}_2}{\sqrt{\hat{s}_1(0)/n_1 + \hat{s}_2(0)/n_2}} \rightarrow N(0,1)$$

where the variance estimate $\hat{s}_i(0)$ is calculated as the spectral density at frequency zero to account for serial correlation in the sampler output. We can use this result to test the null hypothesis of equal location, which, if it is rejected (i.e.; $|Z_n|$ is large), indicates that the chain has not converged.

2.5.2. Heidelberger and Welch Diagnostic

The stationarity test is one-sided; rejection occurs when the *p*-value is greater than 1-alpha. To perform the half-width test, we need to select an alpha level and a predetermined accuracy value. If the calculated relative half-width of the confidence interval is greater than the accuracy value, we conclude that there are not enough data to accurately estimate the mean with 1-alpha confidence under that specific accuracy value (Heidelberger and Welch, 1981 and 1983). Given an MCMC chain, the null hypothesis of convergence is based on Brownian bridge theory and uses the Cramer-von-Mises test statistic

$$\int_0^1 B_n(s)^2 \, ds = CVM(B_n)$$

where

$$B_n(s) = \frac{\left(S_{[ns]} - [ns]\bar{\theta}\right)}{\left(n\hat{p}(0)\right)^{1/2}}$$

where $[\ ]$ is the rounding operator, and $\hat{p}(0)$ is an estimate of the spectral density at zero frequency that uses the second half of the sequence.

2.5.3. Raftery and Lewis diagnostics

The methods of Raftery and Lewis are designed to estimate the number of MCMC samples needed when quantiles are the posterior summaries of interest Raftery and Lewis (1996). Their diagnostic is applicable for the univariate analysis of a single parameter and chain.

i. Nmin is the minimum number of iterations required to estimate the quantile of interest with the prespecified accuracy under the assumption of independence (i.e., with zero autocorrelation).

ii. N is the total number of iterations that the chain must run.

iii. M is the number of burn-in iterations.

iv. I is the dependence factor given by $I = N / Nmin$, which indicates the relative increase of the total sample due to autocorrelations. If I is equal to one, then the generated values are independent. On the other hand, values greater than 5 often indicate a problematic behavior; for details, see Best et al., (1996).

2.5.4. Autocorrelation

Autocorrelations are calculated within each chain for each monitored variable at lags of 1, 5, 10, and 50. High autocorrelations within chains indicate slow mixing and slow convergence. Reparametrizations might help. It might be necessary to increase the thinning interval. The sample autocorrelation of lag h is defined in terms of the sample autocovariance function

$$\hat{\rho}_h = \frac{\hat{\gamma}(h)}{\hat{\gamma}(0)}, \quad |h| < n$$

2.5.5. The Effective Sample Size (ESS)

You can use autocorrelation and trace plots to examine the mixing of a Markov chain. A closely related measure of mixing is the

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effective sample size (Kass et al., 1998). ESS is defined as follows:

$$ESS = \frac{n}{\tau} = \frac{n}{1 + 2\sum_{k=1}^{\infty} \rho_k(\theta)}$$

where n is the total sample size and $\rho_k(\theta)$ is the autocorrelation of lag k for θ The quantity τ is referred to as the autocorrelation time.

2.5.6. Visual Analysis via Trace Plots

Trace plots of samples versus the simulation index can be very useful in assessing convergence. The trace tells you if the chain has not yet converged to its stationary distribution—that is, if it needs a longer burn-in period.

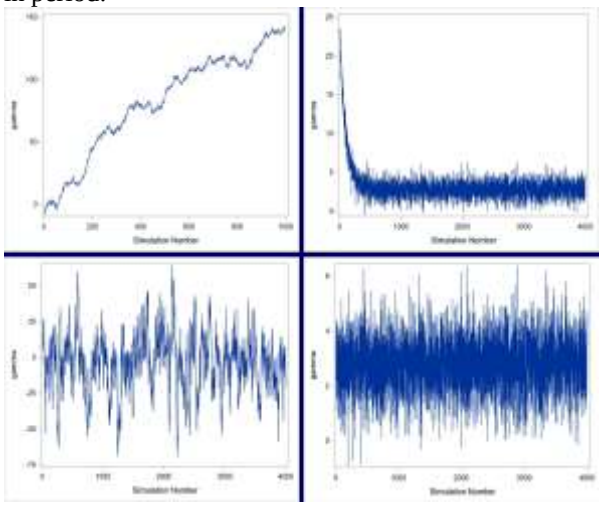

Figure 1 Some typical features that can be seen in the trace graph

From Figure 1, (a) trace graph shows a chain with serious problems. It is mixing very slowly, and it offers no evidence of convergence, (b) displays very well mixed of the chain when the first few hundred observations are discarded, (c) shows the marginal mixing. The chain needs to run for much longer. (d) indicates that the chain could have reached the right distribution.

2.5.7. Monte Carlo Standard Errors (MCSE)

One way to assess convergence is by calculating the Monte Carlo (MC) error, which is an estimate of the difference between the mean of the sampled values (i.e. our estimate of the posterior mean) and the true posterior mean. Thus, the MC error can be interpreted somewhat similar to the frequentist concept of a standard error. As a rule of thumb, it is often suggested that the MC error should be less than 5% of the sample standard deviation.

3. RESULTS

3.1. Data and Modelling

We want to know what patient and physician factors are related to whether a patient with lu ng cancer goes into remission after treatment (http://www.karlin.mff.cuni.cz/~pesta/predna sky/NMFM404/Data/hdp.csv). A variety of o utcomes were collected on patients. 9 doctors are selected random between 407 doctors in t his study. Doctors (q=9) indexed by the j sub script each sees nj patients. So our grouping v ariable is the doctor. Every doctor sees the sa me number of patients, 40 patients. The total number of patients is the sum of the patients s een by each doctor; 360.

We use to estimate a logistic random effects model with IL6, CRP, lung capacity and age as patient level continuous predictors, cancer stage and a family history as a patient level ca tegorical predictor (I, II, III, or IV), and a ran dom intercept by did, doctor ID. Age: continu ous in years but recorded at a higher degree o f accuracy. Family Hx: binary (yes/no), does t he patient have a family history (Hx) of cance r? Cancer stage: categorical with four levels, stages 1-4. IL6: continuous, interleukin 6, a p roinflammatory cytokine commonly examine d as an indicator of inflammation, cannot be l ower than zeroCRP: continuous, C-reactive p rotein, a protein in the blood also used as an i ndicator of inflammation. It is also impacted by BMI. Lung capacity: It is lung capacity of all patients. Remission is dependent variable and IL6, CRP, lung capacity, age, cancer stag e and Family Hx are fixed effects variables. P atients who are nested within doctors are rand om and are taken as doctors are random effec ts variables. X matrix is 360x7 dimensional fixed effect design matrix, Z matrix 360x9 r andom effect design matrix, β_{7x1} is the para meter vector of fixed effects and γ_{9x1} is the parameter vector of random effects. The depe ndent variable y_{ij} is a data of binary outcom es. Therefore, it has Bernoulli distribution tha t one of exponential distribution family. Logi stic random effects model is

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$$y_{ij} \mid \gamma_j \sim Bernoulli(\mu_{ij})$$

$$\eta_{ij} = lojit(\mu_{ij}) = \log\left(\frac{\mu_{ij}}{1-\mu_{ij}}\right)$$

$$\gamma_j \sim N(0, G), \qquad j = 1,...,9; \qquad i = 1,...,40$$

The alpha significance level of 0.05 for all statistical analyzes and confidence intervals are taken as 0.95. Statistical analysis was conducted in SAS software. The SAS 9.3 procedure MCMC is a general purpose Markov Chain Monte Carlo simulation procedure that is designed to fit many Bayesian models using the Metropolis-Hastings approach (Li et al., 2011).

We used non-informative priors for all the regression coefficients, i.e. a normal distribution with zero mean and large variance (10^4) and inverse Gamma distribution for variance component that the most widely used.

$$\gamma \sim N(0,\ sd = 10000)$$

$$\beta \propto N(0, sd = 10000)$$

$$\sigma_\gamma^2 \sim \text{igamma}(1, 0.01)$$

The total number of iterations for logistic random effects models was 900000 with a burn-in of 10000 and 25th thinning rate. Posterior sample number is 36000.

Table 1 Posterior Summaries for Fixed and Random Effects

	Posterior Mean	Standard Deviance	HPD Interval	
Intercept	-1.1348	1.2136	-3.5366	1.2367
Lungcapacity	0.6608	0.7616	-0.8001	2.1881
Age	0.0218	0.0229	-0.0243	0.0653
Familyhx	-0.2706	0.3562	-0.9871	0.4071
Cancerstage	-0.7591	0.1753	-1.1014	-0.4219
IL6	-0.0554	0.0507	-0.1537	0.0455
CRP	0.0235	0.0396	-0.0553	0.1000
Covariance	0.0556	0.1546	0.000849	0.2190
DID1	-69.9036	10012.0	-19702.2	19410.7
DID2	-81.1613	9943.1	-19398.2	19228.8
DID3	26.7132	10060.9	-19599.1	19604.5
DID4	-38.5863	10083.9	-19799.4	19813.8
DID5	-104.9	9962.3	-19775.8	19274.1
DID6	27.5696	10018.8	-19839.8	19300.3
DID7	43.7678	9990.6	-19203.6	19835.4

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DID8	-35.1935	10022.8	-19898.9	19305.7
DID9	-1.3859	10000.3	-19460.4	19740.2

From Table 1, Posterior means, standard deviation estimates and HPD intervals have been as seen. According to the results, after treatment received by patients with lung cancer, fixed-effect parameters; intercept, lungcapacity, age, familyhx, IL6 and CRP are did not affect remission of patient. Cancer stage said to have a significant effect.

Table 2 Comparisons of Some Statistical convergence diagnostic tests

	MCSE	**Geweke**	**Raftery Lewis**	**Heidelberger-Welch**		**Effective Sample Sizes**
	MCSE/SD	**Pr>|z|**	**Total No of Samp.**	**p**	**TestOutcome**	**ESS**
Sabit	0.0154	0.3577	12297	0.2104	Geçti	4212.1
Interc	0.0	0.	15	0.	Geçti	48

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ept	144	3049	002	1235		44.2
Lungcapacity	0.01422	0.5681	1214	0.8905	Geçti	4939.1
Age	0.01555	0.38558	1849	0.85595	Geçti	4135.9
Familyhx	0.01400	0.68897	1201	0.95596	Geçti	5127.8
Cancerstage	0.01644	0.50144	1827	0.15000	Geçti	3720.0
IL6	0.01449	0.23117	1472	0.30666	Geçti	4509.5
CRP	0.02922	0.44555	4187	0.37796	Geçti	1170.2
Covariance	0.00604	0.7769	4568	0.4375	Geçti	2740.3
DID1	0.00618	0.1559	4841	0.2524	Geçti	2621.1
DID2	0.012	0.09	1731	0.09	Geçti	6121

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	8	99	4	01		.7
DID3	0.00601	0.84133	4558	0.96776	Geçti	27644.0
DID4	0.00679	0.25955	5424	0.30255	Geçti	21683.3
DID5	0.00573	0.37796	4149	0.72011	Geçti	30501.5
DID6	0.00653	0.45666	5118	0.81311	Geçti	23418.8
DID7	0.00616	0.69200	4644	0.18211	Geçti	26320.2
DID8	0.00600	0.94466	4350	0.81116	Geçti	27820.6
DID9	0.00590	0,81000	5120	0.30544	Geçti	28510.0

From Table 2, to comment convergence of Markov Chain, output of Monte Carlo standard errors, Posterior autocorrelation, Geweke test, Raftery-Lewis test, Heidelberger-Welch test, Effective Sample Sizes have obtained. Convergence has been achieved due to Monte Carlo standard error / standard deviation is smaller than 5%, according to Geweke test statistic p-value large enough and Raftery-Lewis test, a total sample size is larger from the Markov sample (minimum sample number 3746) that has

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been provided convergence. In Heidelberg-Welch test, it was also achieved with large p-values of convergence. Effective sample size and the simulation sample size (36000) indicates that ensure convergence in all parameters except parameter variance.

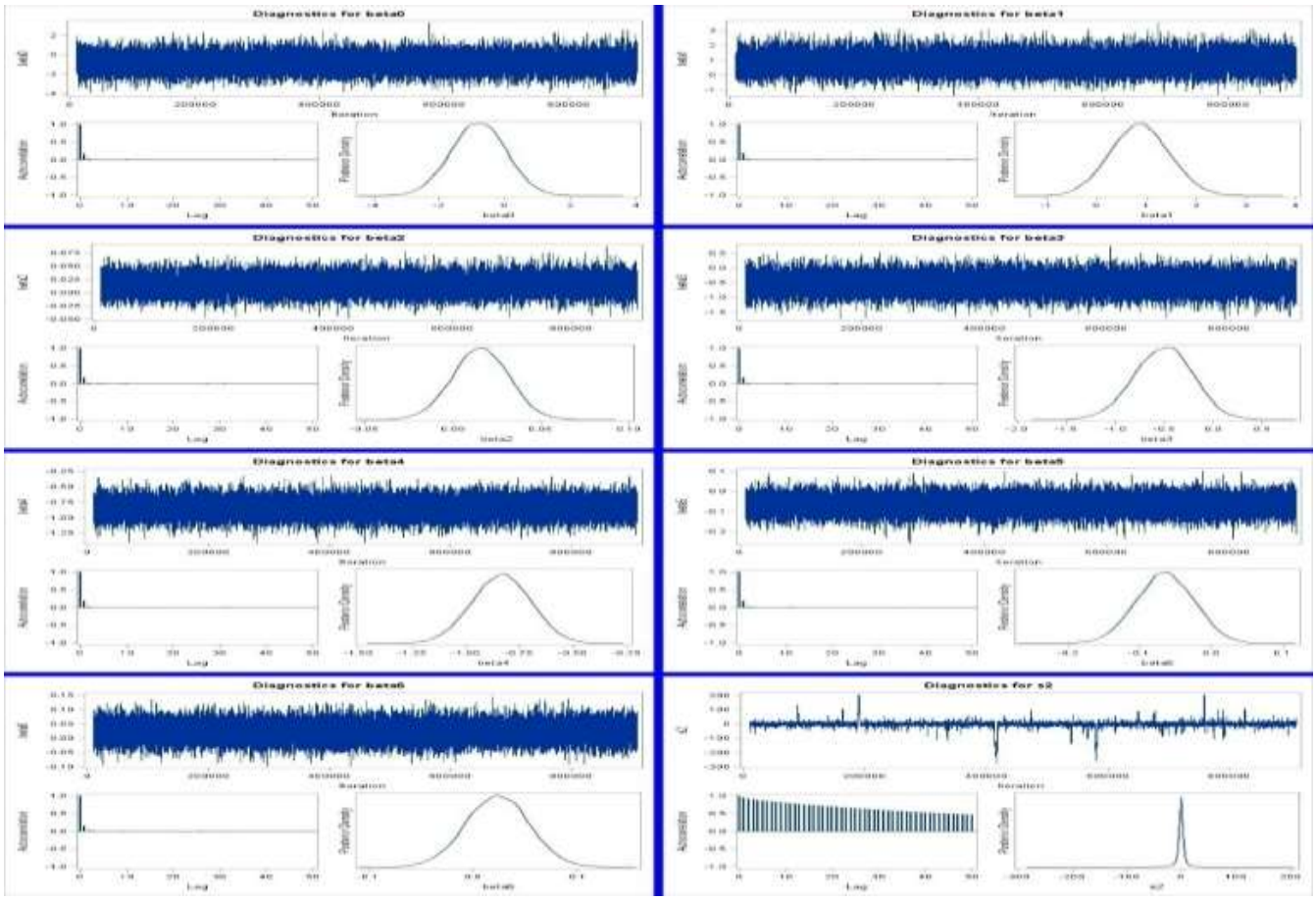

Figure 2 Trace plots of fixed effect parameters and variance components

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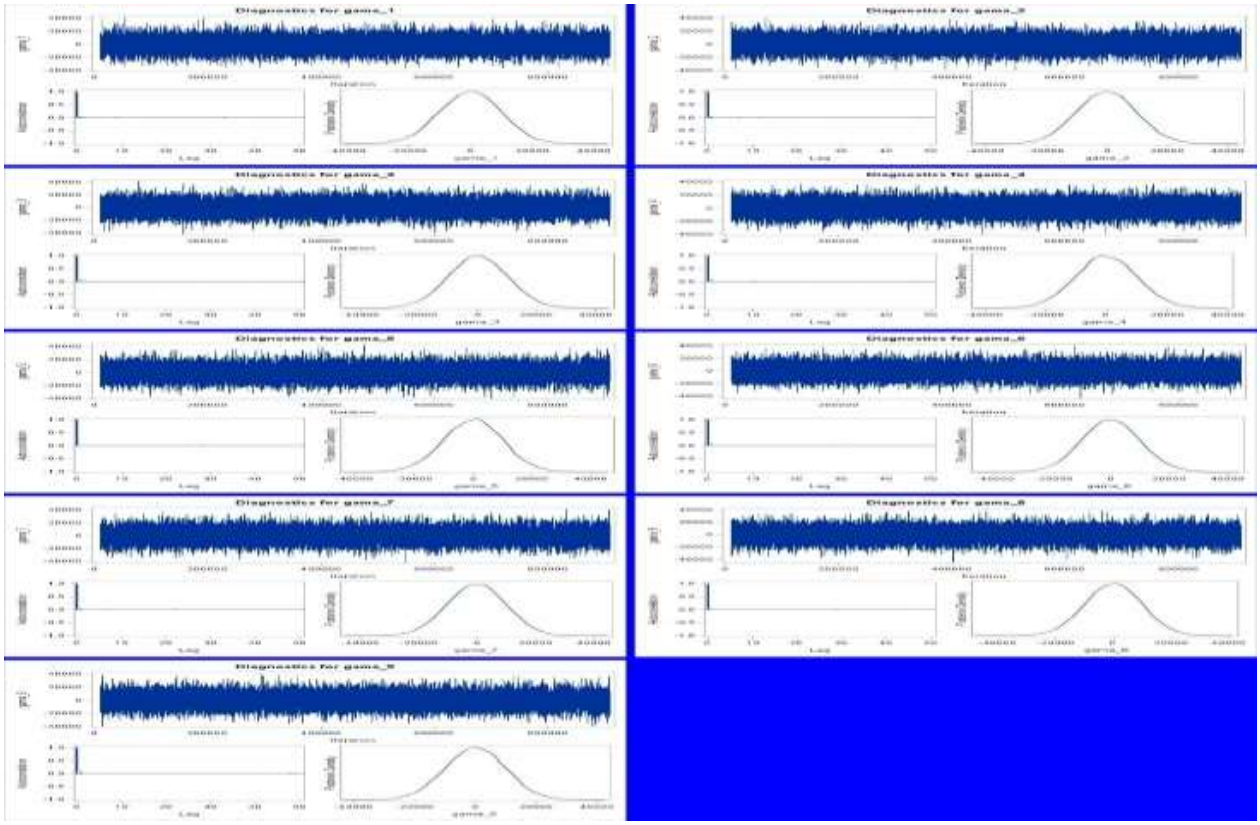

Figure 3 Trace plots of random effect parameters

From Figure 2 and 3, density plots for the model parameters are shown. All indicate satisfactory convergence of the Markov chain.

3. CONCLUSION

A problem for users of Markov chain Monte Carlo (MCMC) methods in applications are how to determine to the convergence of MCMC. Convergence diagnostics are developed to help the user answer these questions. The objective of this paper has been assessed convergence of MCMC chains. As an illustrative model, we have used logistic random effect model. SAS 9.3 macro programming language was used for simulations and SAS procedures MCMC with "diagnostic=all" statement were used for the convergence diagnostic tests of the Bayesian Logistic random effect models.

Some of the convergence diagnostics are density plots (trace graphs) of summarizing the data. Others are formal statistical tests. In general, most investigators examine a convergence diagnostic. In this paper is used both visual analysis and some statistical tests.

The SAS procedure MCMC offers many convergence diagnostic tests, we used the Geweke, MCSE, Raftery-Lewis, Heidelberger Welch and ESS, trace plot, auto-correlations. We are investigated on convergence diagnostic tests and posterior estimates in Bayesian logistic random effects models. Convergence diagnostic tests are compared. Bayesian logistic random effect models are defined. In our study, in the assessment of convergence, the visual analysis performed with trace graph was determined to be a useful method. Geweke test behaved similarly to Heidel-Welch test. They concluded that Markov chain was convergent. Raftery-Lewis test concluded that minimum sample size should be 3746 for convergence. The MCSE/SD ratio was the most sensitive in these tests. Also, iteration number for convergence did not change for each of the convergence diagnostic tests when the sample size changed. Although the high correlation between the covariates increased the necessary number of iterations, there are no definitive tests for convergence. Different convergence criteria were designed to protect you from various potential pitfalls. For this reason, in Bayesian analysis, it is

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advisable to use more than one diagnostic to assess convergence.

Finally, the following must be taken into account for convergence.

- Different convergence diagnostic tests check different aspects of convergence.
- Be cautious when using these diagnostics;
- Use a few diagnostic tools,
- When trace plots look good mixing or any diagnostic tests reach convergence of MCMC, other diagnostic tests can not reach convergence of MCMC.
- So, with experience and carefully, assessing convergence should achieve before to make an inference.

Abbreviations

GLMMs: Generalizesd linear mixed models **SAS**: Statistical Analysis System **MCMC:** Markov Chain Monte Carlo **ESS:** Effective sample size **MCSE:** Monte Carlo Standar Error

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