THE EFFECT ON CONVERGENCE DIAGNOSTIC TESTS AND MODEL PARAMETERS OF THINNING RATE

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The Effect on Convergence Diagnostic Tests and Model Parameters of Thinning Rate

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Abstract
The basic subjects for the most users of Bayesian approach can determine prior distributions, the number of samples, start point of sample, number of burn-in and thinning rates by running Markov chain. Prior distributions represent expert opinion before data collection and the sample size is prespecified due to limitation of resources. The other subjects are associated with the speed of convergence of the Markov chains and they are not really problems due to the advancement in computing power. In this paper, after establishing appropriate model and determining the appropriate prior distributions, we have researched whether different thinning rates are an effect on convergence diagnostic tests by keeping the number of samples and the number of burn in a constant. Consequently, the thinning rate has been found to have no effect on the output of the convergence diagnostics and on the parameters. It is important for autocorrelation and memory.

Keywords: Bayesian Logistic Random Effect Models, Markov Chain Monte Carlo (MCMC), Thinning rate, Convergence diagnostic tests.

I. Introduction

It should be sure of achieving convergence to achieve true value of the parameter in Bayesian approach. Therefore, whether or not the convergence of Markov chain should firstly be examined. There is no definitive way to hold convergence. Many formal and graphical methods have been developed to evaluate the convergence of the Markov chain. Geweke (1992), Raftery and Lewis (1996), Heidelberger and Welch' (1981) are a few of the formal statistical tests to evaluate of convergence 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 assess 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. Cengiz et al.(2012) investigated convergence diagnostic techniques for MCMC algorithms with two real data application to logistic regression. Ozturk and Cengiz (2016) considers comparisons of Markov Chain Monte Carlo convergence diagnostic tests for Bayesian logistic random effect models. Most important points for convergence diagnostics are the “burn-in” period of the chain, which is discarding initial part of the chain, and the thinning rate is referred to as the “burn-in” period of the chain and the remaining part is called the stationary part or the part where the chain has “converged in distribution”. Sahlin (2011) constructed a diagnostic for estimating the burn-in

of the chain. Link and Eaton (2012) gave details about the background and prevalence of thinning.

The last two decades have seen that generalized linear mixed models (GLMMs) became popular when the non-normal data with random effect is analyzed. Within a frame of GLMM, the logistic random effects models are a standard tool to analyze multilevel data for a binary outcome. Logistic random effects models examine the relationship between the binary output independent observations and the explanatory variables that are a special case of GLMM. The likelihood function in the logistic random effects models likelihood function cannot be in closed form. In order to overcome the analytical intractability of Bayesian approach, which is used to make inferences with the posterior distribution of the parameters, can be employed. In the last two decades, there are some related studies.

In Bayesian approach, after determining the prior distributions and establishing the models in applications, it is determined the number of samples, start point of sample, number of burn-in and thinning rates of the MCMC methods and when to stop sampling. In this article, firstly, Bayesian logistic random effect models, some convergence diagnostics (Geweke, Heidelberger and Welch', Raftery and Lewis, autocorrelation, effective sample size, Monte Carlo standard errors diagnostic methods and trace plots) are explained. The performance of the different convergence diagnostics are also studied on a real medicine data set. How impact on convergence diagnostic tests and estimates of the different thinning rates is also investigated and compared.

II. Bayesian Approach to Logistic Random Effects Models

Bayesian logistic random effect models investigate the relationship between independent variables and a binary outcome The likelihood function is given as follow

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

where Y_{ij}: binary dependent variable of the $i-\text{th}$ observation in the $j-\text{th}$ group, $N:$ a total number of groups, n_j: a total number of subjects in the $j-th$ group, $\beta=(\beta_0,\beta_1,\beta_2,...,\beta_p)$: parameter vector of fixed effects, G variance-covariance matrix , $\gamma_1,\gamma_2,...,\gamma_N$: random effects, $\gamma_j\sim N(0,\sigma_{\gamma_j}^2)$, $\sigma_{\gamma_j}^2$ variance component and X_{ij} element of X matrix corresponding to constant effects, Z_{ij} element of Z matrix corresponding to random effects,

$P(Y_{ij}=1\,|\,\gamma_j)=\dfrac{e^{X_{ij}\beta+Z_{ij}\gamma_j}}{1+e^{X_{ij}\beta+Z_{ij}\gamma_j}}$, $j=1,2,...,N \quad i=1,2,...,n_j$.

The integral in (1) does not have an analytic solution. For Bayesian approach, we treat all unknown quantities as random variables and assign 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(β , G) represent the joint prior distribution for β and G .Then posterior distribution of logistic random effects models given by

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

III. Markov Chain Monte Carlo Method (MCMC)

The Markov chain Monte Carlo (MCMC) method is a simulation method developed for the posterior distributions and for the calculation of the corresponding posterior quantities. 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}. it is possible to generate samples from an arbitrary posterior density $p(\theta \mid y)$ with the MCMC method. Gibbs sampling algorithm is a sampling method in MCMC methods.

Gibbs Sampling

Gibbs sampling requires that the joint posterior distribution for each parameter in the model be sampled from full conditional distributions.Suppose $\theta = (\theta_1, \ldots, \theta_k)'$ is the parameter vector, $p(y|\theta)$ is the likelihood, and $\pi(\theta)$ is the prior distribution. The full posterior conditional distribution of $\pi(\theta_i | \theta_j, i \neq j, y)$ is proportional to the joint posterior density; that is,

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

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

3. Set $t = t+1$. If $t < T$, return to step 2. If not, stop.

IV.Thinning rate

If there exists autocorrelation between outputs, the thinning rate, which is the reduction of the output by systematically using every mth sample (for m≥1) and discarding the others, should be carefully selected. This process needs less computer storage space and reduces the number of values that must be input into further routines. Furthermore, the thinning requires less computational time and declines the autocorrelation. If the thinning parameter is taken as large as possible, it yields two results. First, the output is less dependent. Second, the accuracy of the asymptotic approximations decreases (Brooks and etc., 2003).

V. Assessing Markov Chain Convergence and Convergence diagnostics tests

The Bayesian approach includes many statistical diagnostic tests that can help evaluate the convergence of the Markov chain. But, A detailed description of some of the diagnostic tests will be given.

Geweke Diagnostic

The Geweke test whether the mean estimates have converged by comparing means from the last part of the Markov chain. Details are given in Geweke (1992).

Let the two parts of the markov chain be $\{\theta_1^t : t = 1, \ldots, n_1\}$ and $\{\theta_2^t : t = n_a, \ldots, n\}$ which $1 < n_1 < n_a < n$ and now let be $n_1 = n - n_a + 1$, $\bar{\theta}_1 = \frac{1}{n_1}\sum_{t=1}^{n_1}\theta^t$ and $\bar{\theta}_2 = \frac{1}{n_2}\sum_{t=n_a}^{n}\theta^t$ The form of The Geweke diagnostic test is given as follow:

$$Z_n = \frac{\bar{\theta}_1 - \bar{\theta}_2}{\sqrt{\hat{s}_1(0)/n_1 + \hat{s}_2(0)/n_2}} \rightarrow N(0,1) \qquad (3)$$

where $\hat{s}_i(0)$ is variance estimation. 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.

Heidelberger and Welch Diagnostic

The Heidelberger and Welch stationarity test is a one-way test; when the p-value is greater than $1-\alpha$, the null hypothesis is rejected. It is needed to select an alpha level and a predetermined accuracy value to perform the half-width test. Heidelberger and Welch (1981) and Heidelberger and Welch (1983). Given an MCMC chain, the null hypothesis of convergence is based on Brownian bridge theory and uses the Cramer-Von-Mises test statistic

$$\int_0^1 B_n(s)^2\, ds = CVM(B_n) \qquad (4)$$

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 (SAS, 2016).

Raftery and Lewis Diagnostics

Suppose some posterior quantile of interest q should be measured. If an acceptable tolerance r is defined for q and the probability of being within this tolerance is defined, the Raftery and Lewis diagnostic will calculate the number of iterations N and the number of burn-in necessary to satisfy the specified conditions. Run a "pilot" sampler to generate a Markov chain of minimum length given by rounding up $n_{min} = \left[\phi^{-1}\left(\frac{s+1}{2}\right)\frac{\sqrt{q(1-q)}}{r}\right]^2$ where $\phi^{-1}(.)$ is the inverse of the normal cumulative distribution function

Autocorrelation

Autocorrelations measure dependency among Markov chain samples. Large autocorrelations within chains indicate slow mixing and slow convergence. In order to overcome the difficulty, reparameterizations can help. It can be useful to increase the thinning rate to achieve a less highly correlated sample.

The Effective Sample Size (ESS)

The effective sample size (ESS) can be used to view the mixing of a Markov chain. ESS is shown as:

$$ESS = \frac{n}{\tau} = \frac{n}{1 + 2\sum_{k=1}^{\infty} \rho_k(\theta)} \qquad (5)$$

where τ is the autocorrelation time, n is the sample size and $\rho_k(\theta)$ is the autocorrelation of lag k for θ (Kass et al. (1998)).

Monte Carlo Standard Errors (MCSE)

Monte Carlo (MC) error, which is an estimate of the difference between the mean of the sampled values, can be used to assess convergence.

VI. Results

Our dataset is a part of a larger study of treatment outcomes and quality of life in patients with lung cancer. We are interested in what patient and physician factors most related to whether a patient's lung cancer goes into remission after treatment are. A variety of outcomes were colle cted on patients, who are in turn nested within hospitals. 9 doctors were selected from among 457 doctors in this study.

Doctors (q=9) that indexed by the j subscript each sees n_j patients. So our grouping variable is the doctor. Each doctor treats the same number of patients, 40 patients. The total number of pa tients is the sum of the patients treated by each doctor; 360.

We constructed 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 categ orical predictor (I, II, III, or IV), and a random intercept by DID, doctor ID. Age: continuous i n years but recorded at a higher degree of accuracy. Family Hx: binary (yes/no), does the patie nt have a family history (Hx) of cancer? Cancer stage: categorical with four levels, stages 1-4. IL6: continuous, interleukin 6, a pro-inflammatory cytokine commonly examined as an indicat or of inflammation, cannot be lower than zero. CRP: continuous, C-reactive protein, a protein in the blood also used as an indicator of inflammation. It is also impacted by BMI. Lung capac ity: It is lung capacity of all patients.

Remission is dependent variable and IL6, CRP, lung capacity, age, cancer stage and Family Hx are fixed effects variables. Patients who are nested within doctors are random and are taken as doctors are random effects variables. X matrix is 360x7 dimensional fixed effect design matrix, Z matrix 360x9 random effect design matrix, β_{7x1} is the parameter vector of fixed effects and γ_{9x1} is the parameter vector of random effects. The dependent variable y_{ij} is a data of binary outcomes; therefore, it has Bernoulli distribution that one of exponential distribution family. Logistic random effects model is

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

$$\eta_{ij} = lojit(\mu_{ij}) = \log\left(\frac{\mu_{ij}}{1-\mu_{ij}}\right) \qquad (6)$$

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

The shape of the correlation matrix that shows the relationship between random effects and errors (units) or shape of the correlation matrix that showing the relationship between random variables and fixed effect variables is as follows.

Figure I Here

From Figure 1, There is a low positive correlation between random variables and errors and the high positive correlation between random variables and fixed effect variables.

In Bayesian Analysis, all unknown parameters are treated as random variables. So, we used “non-informative” priors for all the regression coefficients, i.e. a normal distribution with zero mean and a large variance (10^4) and 0 centered and 2.5 scales Cauchy distribution that suggested by Gelman (2006) for variance components. Alpha significance level of 0.05 for all statistical analyzes and confidence intervals are taken as 0,95. The total number of iterations for logistic random effects models was 2500000 with Metropolis Algorithm and burn-in of 15000. Thinning number is taken as 5, 10, 15, 20, 25, 50, 75, 100, 125. We have used MCMC proc in SAS. The SAS procedure MCMC have offered many convergence diagnostic tests, we used the Geweke, MCSE, Raftery-Lewis, Heidelberger Welch and ESS, trace plot, auto-correlations.

From following Tables and Figures, we see that whether how the changing of effects of the thinning rate on convergence diagnostic tests and posterior estimates in logistic random effects models for real cancer data.

Table I Here

From Table, when thinning rates have increased, posterior estimations don’t change much. Besides, the significance of parameters remains the same.

Table II Here

From Table 2, when thinning rates have increased, it is seen that Monte Carlo Standard errors increase and is not the desired situation.

Table III Here

From Table 3 when thinning rates are increased, it is seen that increases efficiency that is ratio of the effective sample size to the total sample size after thinning. For every thinning rate, ESS of MCMC chain and the total sample size is given in Table 4.

Table IV Here

ESS measure has the large different between the effective sample size and the simulation sample size for variance parameter in all simulations.

Figure II Here

From Figure 2, when thinning rates really have increased, autocorrelation has decreased is to thin the sample, using only every n^{th} step.

Table V,
Table VI, Here

From Table 5, Geweke' s convergence diagnostic produces hence significantly high p values for all the parameters in all the chains, indicating a significant difference between the first part and the last part of the chains for with thinning rates all simulations. That is, we cannot reject the hypothesis of convergence according to Geweke test for all simulations.

From Table 6, Heidelberger and Welch diagnostic tests for the last part of a chain the null hypothesis that the generated Markov chain has stabilized (stationarity test) in all simulations.

Table VII Here

From Table 7, The Raftery and Lewis measure, when run with quantile = 0.025, accuracy = 0.005, and probability = 0.95, doesn't give values of required number of iterations of some parameters for thin=50, 75, 100, 125 simulations. Because, Markov chain hasn't adequated sample.

Figure IIIa Here
Figure IIIb Here
Figure IIIc Here

We produce a number of graphs which also aid convergence diagnostic checks. As an example, Figure 3a, Figure 3b and Figure 3c shows diagnostic plots for fixed effects parameter beta 1 (**Lungcap)** that thin is 5, 20 and 125. From the trace plots, we can say that the mean of the Markov chain has stabilized and appears constant over the graphs. The plots show that the chains appear to have reached convergence. The posterior autocorrelations are quite small and the posterior density appears bell-shaped.

VII. Discussion

A critical issue for users of Markov Chain Monte Carlo (MCMC) methods in applications is how to determine necessary the thinning rate and one should want to answer example "how much should the thinning rate be effective on convergence diagnostic tests?" Link and Eaton (2012) are said that thinning is often unnecessary and always inefficient, reducing the precision with which features of the Markov chain are summarized.

In this paper, the effects of the thinning rate on convergence diagnostic tests wanted to be shown. But, the thinning rate was found ineffective on convergence diagnostic tests. Different thinning rates were decreased autocorrelation, ESS and total sample sizes but also is increased MCSE. That is, memory is affected. But, none of the diagnostic tests were affected from different thinning rates up to convergence has been achieved. So, the thinning rate is unimportant and unnecessary to reach convergence of MCMC chain. It is important only for autocorrelation and memory.

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Figures with caption (s)

Figure I. Correlation matrix between random effect and fixed effect variables

Figure II. The relationship between thin numbers and autocorrelation time of variance component

Figure IIIa. Trace plot of beta 1 parameter when thinning rate is 5.

Figure IIIb. Trace plot of beta 1 parameter when thinning rate is 20.

Figure IIIc. Trace plots of beta 1 parameter when thinning rate is 125.

Tables with caption (s)

Table I. Mean values of parameter estimates and corresponding standard errors from different simulations of thinning rate

Table II MCSE of parameters from different simulations of thinning rate

Table III Efficiency of parameters from different simulations of thinning rate

Table IV ESS from different simulations of thinning rate

Table V Geweke Diagnostics Pr > |z| from different simulations of thinning rate

Table VI Heidelberger-Welch Diagnostics Test Outcome from different simulations of thinning rate

Table VII Raftery-Lewis Diagnostics Dependence factor from different simulations of thinning rate

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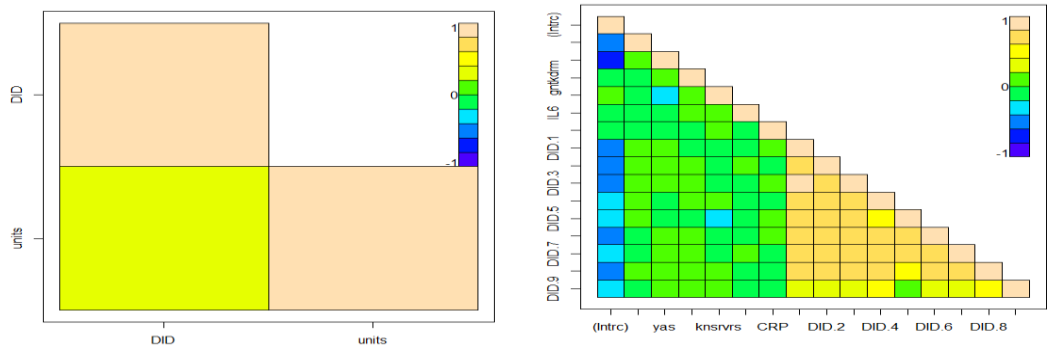

Figure I. Correlation matrix between random effect and fixed effect variables

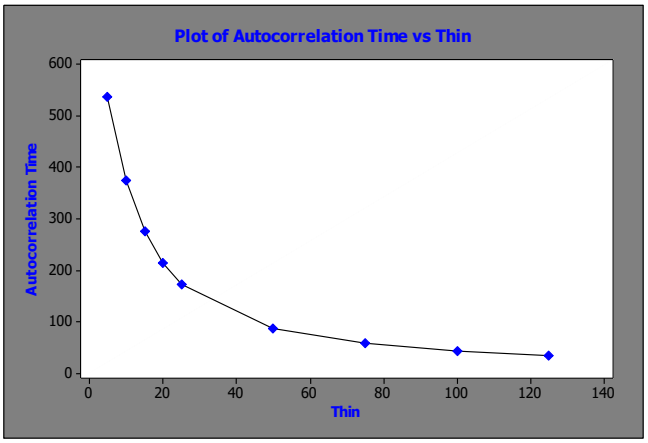

Figure II. The relationship between thin numbers and autocorrelation time of variance component

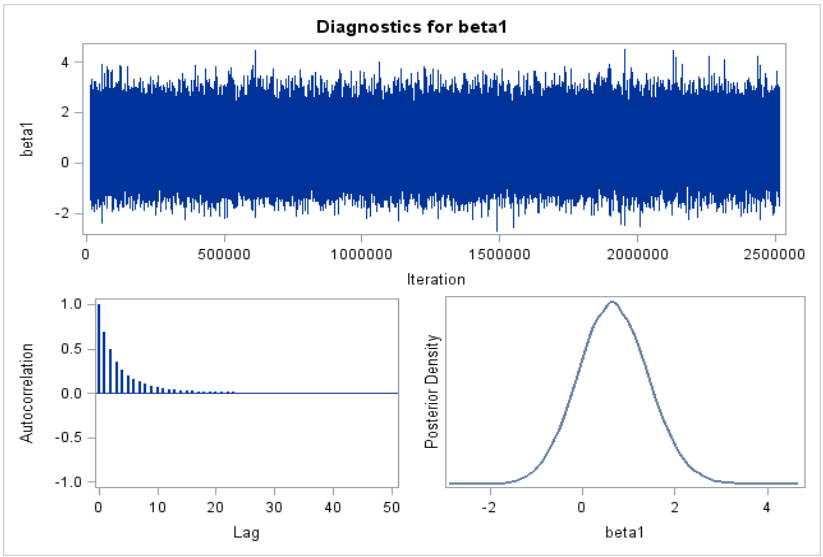

Figure IIIa. Trace plot of beta 1 parameter when thinning rate is 5.

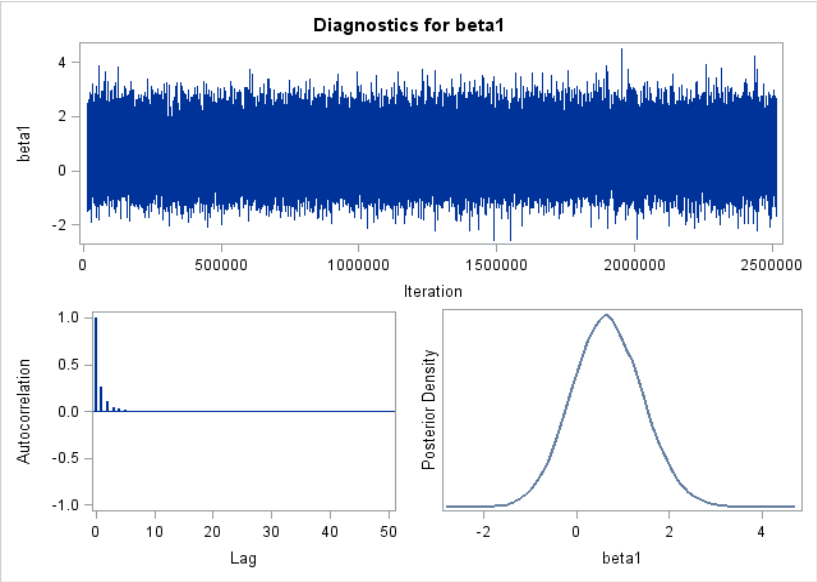

Figure IIIb. Trace plot of beta 1 parameter when thinning rate is 20.

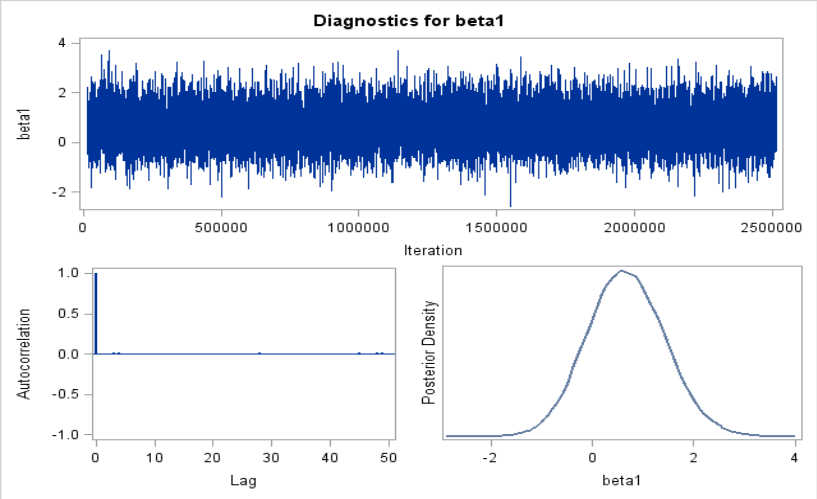

Figure IIIc. Trace plots of beta 1 parameter when thinning rate is 125.

Table I Mean values of parameter estimates and corresponding standard errors from different simulations of thinning rate

Thinning rates	Parameters Mean (Standard deviation)							
	İntercept	**Lungcap**	**Age**	**Genetichx**	**Cancerstage**	**IL6**	**CRP**	**S2**
5	-1.1421 (1.2035)	0.6765 (0.7615)	0.0218 (0.0229)	-0.2654 (0.3602)	-0.7631 (0.1748)	-0.0552 (0.0500	0.0234 (0.0395)	-0.7064 (11.3693
10	-1.1419 (1.2044)	0.6767 (0.7619)	0.0218 (0.0229)	-0.2654 (0.3603)	-0.7631 (0.1747)	-0.0552 (0.0499	0.0233 (0.0395)	-0.7064 (11.3665)
15	-1.1431 (1.2043)	0.6765 (0.7617)	0.0218 (0.0229)	-0.2659 (0.3597)	-0.7630 (0.1749)	-0.0552 (0.0500	0.0234 (0.0396)	-0.7077 (11.3701
20	-1.1407 (1.2039)	0.6759 (0.7605)	0.0218 (0.0229)	-0.2650 (0.3602)	-0.7630 (0.1748)	-0.0553 (0.0499	0.0233 (0.0395)	0.7077 (11.3688
25	-1.1437 (1.2042)	0.6764 (0.7619)	0.0219 (0.0229)	-0.2665 (0.3593)	-0.7633 (0.1746)	-0.0554 (0.0500	0.0234 (0.0395)	-0.7120 (11.3620)
50	-1.1382 (1.2041)	0.6758 (0.7623)	0.0218 (0.0228)	-0.2655 (0.3590)	-0.7628 (0.1742)	-0.0553 (0.0500	-0.0233 0.0395)	-0.7145 (11.3571)
75	-1.1455 (1.2097)	0.6769 (0.7620)	0.0218 (0.0229)	-0.2653 (0.3602)	-0.7618 (0.1741)	-0.0552 (0.0501	0.0232 (0.0395)	-0.6970 (11.3639)
100	-1.1317 (1.2019)	0.6777 (0.7595)	0.0216 (0.0228)	-0.2664 (0.3604)	-0.7622 (0.1738)	-0.0552 (0.0500	0.0233 (0.0396)	-0.7043 (11.3821)
125	-1.1358 (1.1955)	0.6729 (0.7621)	0.0218 (0.0227)	-0.2711 (0.3595)	-0.7628 (0.1736)	-0.0552 (0.0500	0.0235 (0.0397)	-0.7241 (11.3554)

Table II MCSE of parameters from different simulations of thinning rate

	Thinning rates								
Parameters	**5**	**10**	**15**	**20**	**25**	**50**	**75**	**100**	**125**
Intercept	0.00464	0.00472	0.00479	0.00493	0.00508	0.00604	0.00683	0.00793	0.00857
Lungcap	0.00279	0.00283	0.00288	0.00297	0.00308	0.00365	0.00429	0.00489	0.00539
Age	0.00008	0.000085	0.000087	0.000090	0.000092	0.000110	0.000128	0.000144	0.000161
genetichx	0.00118	0.00121	0.00124	0.00129	0.00133	0.00166	0.00197	0.00228	0.00248
CancerStage	0.00052	0.000538	0.000561	0.000585	0.000614	0.000779	0.000964	0.00110	0.00123
IL6	0.00016	0.000167	0.000171	0.000178	0.000186	0.000233	0.000282	0.000316	0.000354
CRP	0.00013	0.000133	0.000136	0.000141	0.000147	0.000183	0.000217	0.000250	0.000281
S2	0.3725	0.4401	0.4618	0.4705	0.4721	0.4721	0.4726	0.4729	0.4727

Table III Efficiency of parameters from different simulations of thinning rate

	Thinning rates								
Parameters	**5**	**10**	**15**	**20**	**25**	**50**	**75**	**100**	**125**
Intercept	0.1344	0.2606	0.3791	0.4767	0.5618	0.7953	0.9407	0.9199	0.9721
Lungcap	0.1490	0.2893	0.4183	0.5247	0.6106	0.8701	0.9446	0.9635	1.0000
Age	0.1470	0.2861	0.4166	0.5182	0.6145	0.8646	0.9564	1.0000	1.0000
genetichx	0.1853	0.3564	0.5031	0.6255	0.7283	0.9371	0.9999	1.0000	1.0502
CancerStage	0.2216	0.4213	0.5821	0.7156	0.8093	1.0000	0.9782	1.0000	1.0000
IL6	0.1870	0.3596	0.5114	0.6311	0.7192	0.9177	0.9490	1.0025	1.0000
CRP	0.1843	0.3552	0.5093	0.6258	0.7279	0.9318	1.0000	1.0000	1.0000
S2	0.0019	0.0027	0.0036	0.0047	0.0058	0.0116	0.0173	0.0232	0.0289

Table IV ESS from different simulations of thinning rate

	Thinning rates								
N	500000	250000	166667	125000	100000	50000	33334	25000	20000
Parameters	**5**	**10**	**15**	**20**	**25**	**50**	**75**	**100**	**125**
Intercept	67201.2	65154.4	63184.0	59589.1	56181.0	39767.1	31357.2	22998.5	19441.4
Lungcap	74488.4	72324.9	69722.0	65588.4	61062.5	43503.6	31489.0	24088.6	20000.0
Age	73509.7	71521.5	69439.4	64770.7	61447.8	43229.9	31879.7	25000.0	20000.0
genetichx	92641.3	89094.8	83853.6	78182.4	72829.4	46856.7	33330.2	25000.0	21003.7
CancerStage	110801.4	105324.4	97013.3	89444.0	80928.2	50000.0	32606.3	25000.0	20000.0
IL6	93475.7	89896.4	85239.2	78888.7	71919.5	45886.9	31633.9	25062.2	20000.0
CRP	92168.8	88797.6	84878.0	78225.9	72785.3	46590.5	33334.0	25000.0	20000.0
S2	931.7	667.0	606.3	583.7	579.2	578.8	578.2	579.3	577.1

Table V Geweke Diagnostics Pr > |z| from different simulations of thinning rate

	Thinning rates								
Parameters	**5**	**10**	**15**	**20**	**25**	**50**	**75**	**100**	**125**
Intercept	0.0533	0.0734	0.1016	0.0962	0.0447	0.3116	0.2135	0.5106	0.6817
Lungcap	0.3350	0.3666	0.3255	0.4470	0.2298	0.6690	0.4900	0.5692	0.7860
Age	0.1252	0.1339	0.2162	0.1531	0.1477	0.4070	0.2223	0.5771	0.5986
genetichx	0.9681	0.8671	0.5986	0.9719	0.8237	0.5687	0.1681	0.1486	0.2336
CancerStage	0.6094	0.6899	0.8306	0.7126	0.5408	0.8733	0.5565	0.7858	0.6088
IL6	0.3510	0.4164	0.1180	0.3729	0.1390	0.3826	0.0538	0.1203	0.7542
CRP	0.8155	0.8848	0.9776	0.4193	0.9290	0.7574	0.2584	0.4141	0.5790
S2	0.5147	0.5160	0.5162	0.5124	0.5124	0.4881	0.5293	0.4936	0.5014

Table VI Heidelberger-Welch Diagnostics Test Outcome from different simulations of thinning rate

	Thinning rates								
Parameters	**5**	**10**	**15**	**20**	**25**	**50**	**75**	**100**	**125**
Intercept	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed
Lungcap	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed
Age	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed
genetichx	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed
CancerStage	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed
IL6	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed
CRP	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed
S2	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed	Passed

Table VII Raftery-Lewis Diagnostics Dependence factor from different simulations of thinning rate

	Thinning rates								
Parameters	**5**	**10**	**15**	**20**	**25**	**50**	**75**	**100**	**125**
Intercept	5.6380	3.1791	2.1159	2.1407	1.1260	1.0352	1.0230	1.0117	1.0067
Lungcap	4.7184	2.3588	2.1327	1.1770	1.0977	1.0243	1.0131	1.0251	1.0318
Age	4.7525	2.3823	2.1140	1.1911	1.1204	1.0267	1.0179	1.0318	1.0024
genetichx	4.6943	2.3468	2.1738	1.1749	1.1065	1.0149	.	1.0051	.
CancerStage	4.3964	2.2056	2.1049	1.1153	1.0683	.	1.0179	.	.
IL6	4.5643	2.2923	2.1191	1.1503	1.0806	1.0216	.	.	1.0278
CRP	4.6217	2.3001	2.1356	1.1471	1.0796	1.0283	1.0032	1.0051	.
S2	466.2862	233.1434	155.4290	116.5718	89.9581	44.9792	29.1930	22.8785	18.0985