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Bayesian Analysis of Count Data with R Using Laplace Approximation and Simulation Tools

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Abstract: The Poisson regression model for count data belongs to the family of "generalized linear models", and is available in the R system for statistical computing. In this article, the Bayesian methods are applied to fit the Poisson model using analytic and simulation tools. Laplace Approximation is implemented for approximating posterior densities of the parameters. Moreover, parallel simulation tools are implemented using LaplacesDemon and R2jags packages of R. A data set "DoctorVisits" is used for the purpose of illustrations.

Keywords: Bayesian, Poisson Model, Laplace Approximation, LaplacesDemon, Posterior density, Simulation, JAGS, R.

1 Introduction

The main landmark in the development of count data models for regression was the emergence of the "generalized linear models", of which the Poisson regression is a particular case, first described by Nelder and Wedderburn [1] and detailed in McCullagh and Nelder [2]. Given the nature of discrete non-negative integer value of count data, the Poisson distribution has been verified to be the perfect distribution describing count data. But, the existing econometrics literature on count data models has been disregarded in Bayesian inference. Similarly, in Zellner's [3] dominant book on Bayesian inference in econometrics, the Poisson model is not addressed. The feasible reasons for this overlook are computational complexities that made the Bayesian analysis of count data models unattractive in the past. However, added computer ability now allows for fast appraisal of posterior distributions using simulation methods. The fundamental approaches to Bayesian inference by simulation are addressed in this paper.

In Bayesian econometrics, more concern is given to the posterior distribution $p(\theta|y)$ which is a product of the likelihood function $p(y|\theta)$ and a prior distribution $p(\theta)$. The proper basis of this approach is provided by the Baye's rule, expressed as

$$p\,(\theta|y) \propto p\,(y|\theta)\,p\,(\theta) \tag{1}$$

where, $p\,(\theta)$ is the prior distribution, $p\,(y|\theta)$ is the likelihood, and $p\,(\theta|y)$ is the posterior distribution. In contrast to Frequentist inference, Bayesian approach is an approach of data analysis in which parameters are treated as random variable and data are constant. In this modeling, we use prior information along with the observed data to present our views on the parameter Gelman et al. [4]. Using modern simulation methods, the Bayesian approach can provide comparatively simple solutions in models where frequentists methods fail, or at best, are complicated to implement. Objectives of the present study are defined, as follows:

- To define a Bayesian model, i.e. specification of likelihood and prior distribution.
- To write down the R code for approximating posterior densities with Laplace approximation and simulation tools (R Core Team [5]).
- To illustrate numeric as well as graphic summaries of the posterior densities.

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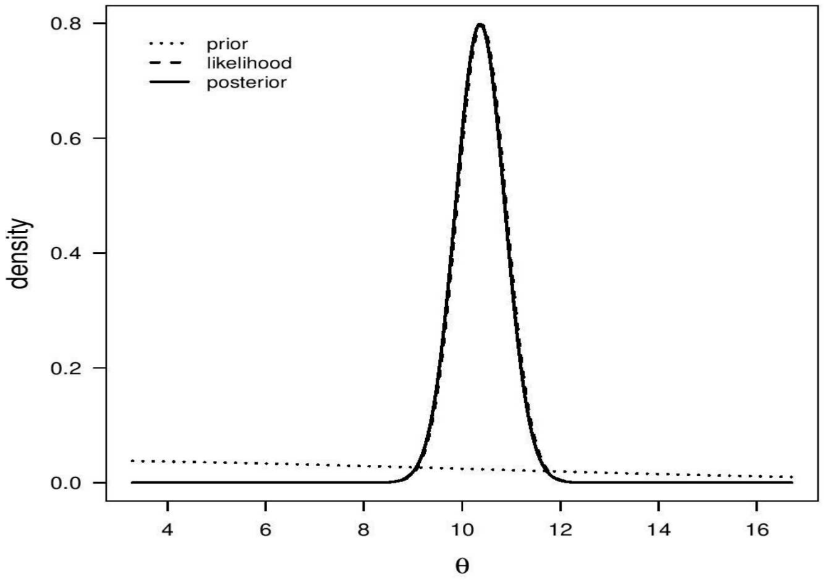


Fig. 1: Prior distribution, likelihood, and posterior distribution of the mean θ.

1.1 Poisson regression model

In statistics, the distribution of random variable Y belongs to an exponential family if its probability density function (or probability mass function for the case of a discrete distribution) can be written in the form

$$f(y|\theta,\phi) = \exp\left\{\frac{y\theta - b(\theta)}{a(\phi)} + c(y,\phi)\right\} \tag{2}$$

where, $\theta = g(\mu)$ is the canonical parameter and its function of the expectation $\mu = E(Y)$ of Y, and the canonical link function $g(.)$ do not depend on ϕ . The parameter $\phi>0$, i.e. the dispersion parameter, denotes the scale of the distribution. The functions $a(.), b(.), c(.)$ are known functions that vary from one distribution to another.

The distribution used for modeling count data is the Poisson distribution. Its probability mass function is $f(y|\mu) = \exp(-\mu)\mu^y/y!$, which can be rewritten as follows:

$$f(y|\theta,\phi) = \exp(y\theta - \exp(\theta) - \log y!).$$

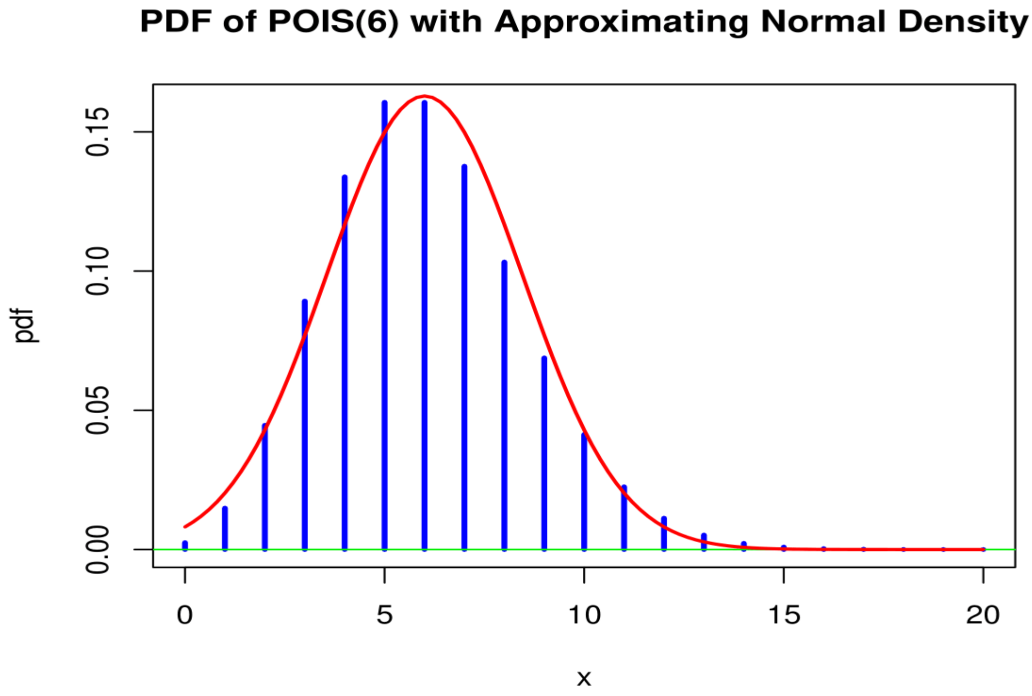
Here $\theta = \log(\mu)$, $\phi = 1$, $a(\phi) = 1$, $b(\theta) = \exp(\theta)$ and $c(y,\phi) = -\log y!$.

The basic GLM for count data is the Poisson regression. In this technique, a count response variable, which follows a Poisson distribution consisting of zero and positive integers, is modeled. Early references in econometrics include Hausman et al. [6] as well as Cameron and Trivedi [7]. The Poisson model is easy and robust. It can be used for any constant elasticity mean function, whether the response variable is a count or continuous. In addition, there are good reasons why it should be preferred to the more common log transformation of the response variable. Thus, the distribution used for modeling count data is the Poisson distribution. Its probability mass function is

$$f(y|\mu) = \frac{\exp(-\mu)\mu^y}{y!}, \quad y = 0,1,2,\ldots, \tag{3}$$

The distribution has the canonical parameter $\theta = \log\mu$, the dispersion parameter $\phi = 1$, and its variance function equals μ. The canonical link function; the logarithm link leads to the Poisson regression model,

$$\begin{cases} Y_i \sim \text{Poisson}(\mu_i), \\ \log(\mu_i) = \beta_0 + \beta_1 x_{i1} + \ldots + \beta_p x_i p \end{cases}$$



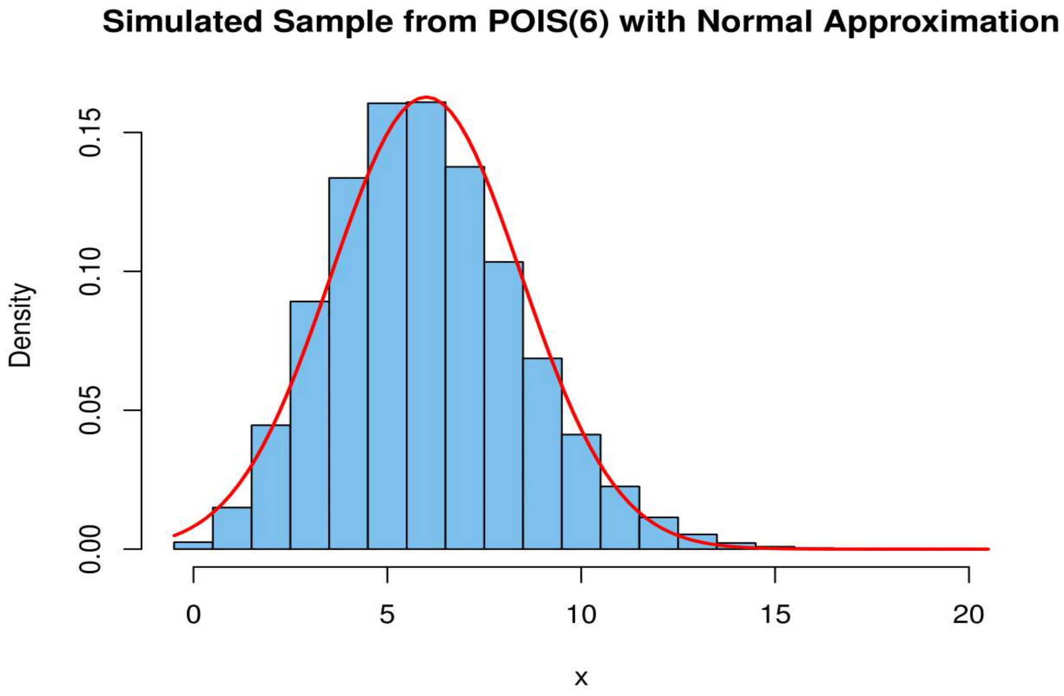


Fig. 2: Probability density functions of Poisson model with $\lambda = 6$, approximating normal density.

2 Data Set: DoctorVisits

The data set "DoctorVisits" is available in `AER` package in R software. For illustration, we use the data set previously analyzed by Cameron et al. [8] in the brightness of an economic model of the joint determination of health service utilization and health insurance choice. It is the cross-section data on the number of doctor visits in the past two weeks for a single-adult sample of size 5190 from the Australian Health Survey 1977-78. To load the library AER which intended for DoctorVisits analysis with R, we use the function library as follows:

library(AER)
To load the data DoctorVisits, use the function data
data("DoctorVisits",package="AER")
To print the names of the variables, use the function names
names(DoctorVisits)
visits, gender, age, income, illness, reduced, health, private, freepoor, freerepat, nchronic, lchronic

The data frame DoctorVisits has 5190 rows and 12 columns, but we can display only the few rows using the function head
head(DoctorVisits)

	visits	gender	age	income	illness	reduced	health	private	freepoor	freerepat	nchronic	lchronic
1	1	female	0.19	0.55	1	4	1	yes	no	no	no	no
2	1	female	0.19	0.45	1	2	1	yes	no	no	no	no
3	1	male	0.19	0.90	3	0	0	no	no	no	no	no
4	1	male	0.19	0.15	2	5	1	no	no	no	no	no
5	1	male	0.19	0.45	2	5	1	no	no	no	yes	no
6	1	female	0.19	0.35	5	1	9	no	no	no	yes	no

R provides a very flexible implementation of the generalized linear model (GLM) using the glm() function (see Chambers and Hastie [9]) in the `stats` package. We begin with the benchmark model for count data, a Poisson regression. As noted above, this is a "generalized linear model". Using the canonical link for the Poisson family (the log link), the model is

$$E\left(y_i|x_i\right) = \mu_i = \exp\left(x_i'\beta\right)$$

Fitting is as simple as

```
M1<-glm(visits˜.+I(ageˆ2),data=DoctorVisits,family=poisson)
```

3 Fitting of Poisson Model Using Laplace Approximation

The special technique of asymptotic approximation is the Laplace Approximation which accurately approximates the unimodal posterior moments and marginal posterior densities in various cases. The Laplace Approximation is a family of asymptotic techniques used to approximate integrals, and the objective of Laplace Approximation is to find out the posterior mode and variance of each parameter. LaplaceApproximation and LaplacesDemon are the two main functions of `LaplacesDemon` package. The function LaplaceApproximation is available in `LaplacesDemon` package (Statisticat LLC [10]), and it is an implementation of Laplace Approximation of Tierney and Kadane [11]. The function LaplaceApproximation deterministically maximizes the logarithm of the unnormalized joint posterior density with MCMC and provides samples of the marginal posterior distributions, deviance, and other monitored variables. Moreover, it has the implementation of sampling importance resampling (SIR) algorithm to simulate observation from posterior. By default, there is a TR method, the Trust Region algorithm of Nocedal and Wright [12], but Laplace Approximation can deal with some other methods. Methods, including AGA, BFGS, HAR, LBFGS, LM, NM are available in Laplace Approximation. It is effective with any Bayesian model for which the likelihood is specified. LaplacesDemon is the execution of Markov chain Monte Carlo (MCMC) tools. It is a very extensive function which implements around 35 MCMC algorithms. The most effective is the Independent Metropolis algorithm (IM) which was proposed by Hastings [13] and popularized by Tierney [14]. The IM algorithm (the independence sampler) is an algorithm in which the proposal distribution does not depend on the previous state or iteration. To use these two functions, the user must specify a model, a prior for parameters and a data object which is required for fitting. The fitting details which involve code for creation of data, definition of model and its fitting with Laplace Approximation are reported as

```
##creation of a data
library(LaplacesDemon)
library(AER)
data("DoctorVisits",package="AER")
M1<-glm(visits~.+I(age^2),data=DoctorVisits,family=poisson)
X<-model.matrix(M1)
N<-nrow(X)
J<-ncol(X)
y<-DoctorVisits$visits
mon.names<-"LP"
parm.names<-as.parm.names(list(beta=rep(0,J)))
MyData<-list(J=J,X=X,mon.names=mon.names,parm.names=parm.names,y=y)
## Specifying a model
Model<-function(parm,Data)
{
## parameters
beta<-parm[1:Data$J]
## Log(prior Densities)
beta.prior<-dnormv(beta,0,10000,log=T)
mu<-tcrossprod(Data$X,t(beta))
## Log-Likelihood
lambda<-exp(mu)
LL<-sum(dpois(Data$y,lambda,log=T))
##Log-posterior
LP<-LL+sum(beta.prior)
Modelout<-list(LP=LP,Dev=-2*LL,Monitor=LP,
yhat=rnorm(length(mu),mu),parm=parm)
return(Modelout)
}
## Initial values
Initial.Values<-c(rep(0,J))
```

Now, we fit the model using the LaplacesApproximation() function, and display the results numerically and graphically:

```
M2<-LaplaceApproximation(Model,Initial.Values,Data = MyData,sir=TRUE,
Iterations=5000,Method="TR")
print(M2)
caterpillar.plot(M2,Parms="beta")
```

Table 1: Summary of the asymptotic approximation using the function LaplaceApproximation

Parameters	Mode	SD	LB	UB
beta[1]	-2.22	0.19	-2.60	-1.85
beta[2]	0.16	0.06	0.04	0.27
beta[3]	1.06	0.99	-0.93	3.04
beta[4]	-0.21	0.09	-0.38	-0.03
beta[5]	0.19	0.02	0.15	0.22
beta[6]	0.13	0.01	0.12	0.14
beta[7]	0.03	0.01	0.01	0.05
beta[8]	0.12	0.07	-0.02	0.27
beta[9]	-0.44	0.18	-0.80	-0.08
beta[10]	0.08	0.09	-0.10	0.26
beta[11]	0.11	0.07	-0.02	0.25
beta[12]	0.14	0.08	-0.03	0.31
beta[13]	-0.85	1.07	-2.99	1.29

Table 2: Summary of the simulated results due to sampling importance resampling algorithm using the function LaplaceApproximation

Parameters	Mode	SD	MCSE	ESS	LB	Median	UB
beta[1]	-2.22	0.20	0.01	1000.00	-2.62	-2.22	-1.85
beta[2]	0.15	0.06	0.00	1000.00	0.05	0.15	0.26
beta[3]	1.06	1.02	0.03	1000.00	-1.06	1.05	3.07
beta[4]	-0.21	0.09	0.00	1000.00	-0.38	-0.21	-0.04
beta[5]	0.19	0.02	0.00	1000.00	0.15	0.19	0.22
beta[6]	0.13	0.01	0.00	1000.00	0.12	0.13	0.14
beta[7]	0.03	0.01	0.00	1000.00	0.01	0.03	0.05
beta[8]	0.13	0.07	0.00	1000.00	-0.01	0.13	0.26
beta[9]	-0.44	0.18	0.01	1000.00	-0.87	-0.43	-0.12
beta[10]	0.08	0.09	0.00	1000.00	-0.08	0.09	0.26
beta[11]	0.11	0.06	0.00	1000.00	-0.02	0.11	0.24
beta[12]	0.14	0.09	0.00	1000.00	-0.04	0.13	0.31
beta[13]	-0.87	1.08	0.03	1000.00	-2.98	-0.85	1.29
Deviance	6724.22	5.06	0.16	1000.00	6716.04	6723.61	6736.58
LP	-3433.92	2.53	0.08	1000.00	-3440.10	-3433.62	-3429.83

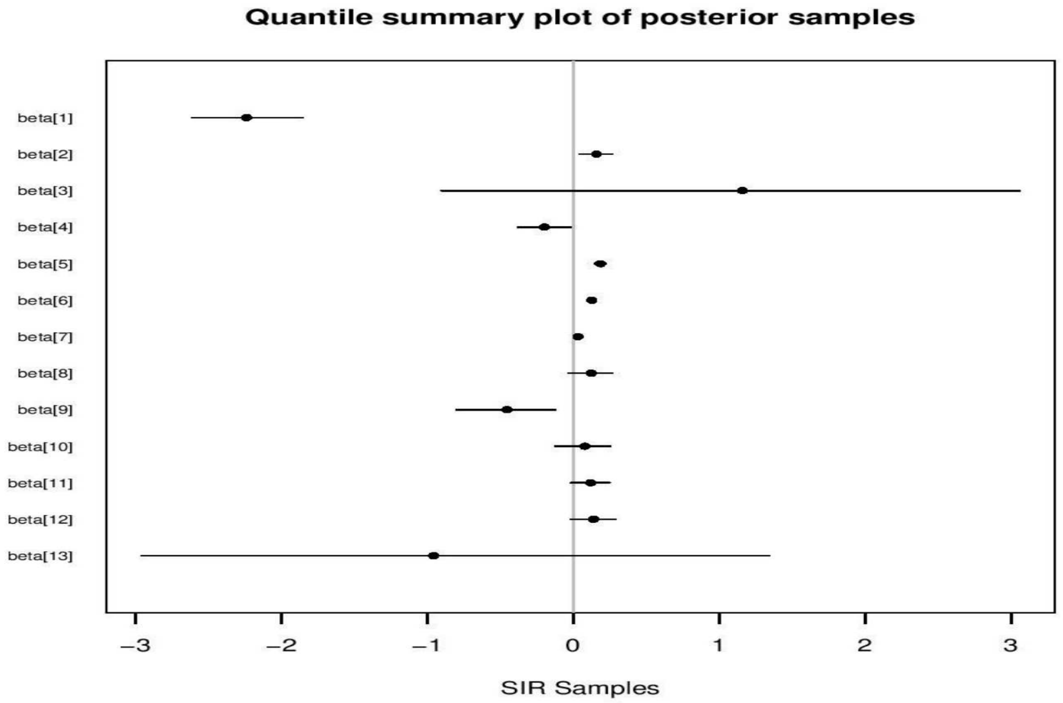


Fig. 3: The graphical view of medians and 95% intervals of all the effects of DoctorVisits data obtained from sampling importance resampling technique.

Output Summary: Table 1 represents the analytic results using Laplace Approximation technique. It is noted that posterior mode of parameters beta[1], beta[2], beta[4], beta[5], beta[6], beta[7] and beta[9] are -2.22 ± 0.19, 0.16 ± 0.06, -0.21 ± 0.09, 0.19 ± 0.02, 0.13 ± 0.01, 0.03 ± 0.01, -0.44 ± 0.18 respectively. According to 95% credible intervals, beta[1], beta[2], beta[4], beta[5], beta[6], beta[7] and beta[9] are statistically significant. Hence, they are suitable variables for modeling count data. Table 2 provides the simulated results using sampling importance resampling (SIR) technique. It also provides posterior mode (Mode), posterior standard deviation (SD), Monte Carlo standard error (MCSC), effective sample size (ESS), lower bound (LB), median, and upper bound (UB) of the parameters. The entire representation of the results obtained in Table 1 can be graphically viewed using a caterpillar plot. Caterpillar plots are popular plots in Bayesian inference for summarizing the quantiles of posterior samples. Figure 3 shows that medians and

95% intervals of all the parameters are obtained using sampling importance resampling technique. The median appears as a black dot and the black line represents the 95% intervals of all the parameters. LB, Median and UB are plotted as a line for each parameter. A vertical, grey line is included at zero. If the horizontal line does not cross the vertical grey line, the parameters are statistically significant. Otherwise, they are insignificant.

3.1 Fitting with laplacesDemon

In this section, the simulation method is applied to analyze the same data with the function LaplacesDemon. Like LaplaceApproximation, LaplacesDemon function also passes two arguments to Model: parm and Data. Both arguments are already defined for Laplace Approximation. It has the high acceptance rate, but requires posterior mode and modal variance which are obtained from Laplace Approximation. Now, we fit the model with the LaplacesDemon() function, and its results are assigned to the object M3. Its summary of results are printed with the print() function.

```
## Fitting with LaplacesDemon
Initial.Values<-as.initial.values(M2)
M3 <-LaplacesDemon(Model, Data=MyData, Initial.Values,
Covar=M3$Covar,Iterations=10000,Algorithm="IM",
Specs=list(mu=M2$Summary1[1:length(Initial.Values),1]))
print(M3)
```

Table 3: Posterior summaries of simulation due to all samples using the function LaplacesDemon

Parameters	Mean	SD	MCSE	ESS	LB	Median	UB
beta[1]	-2.22	0.00	0.00	0.00	-2.22	-2.22	-2.22
beta[2]	0.16	0.00	0.00	0.00	0.16	0.16	0.16
beta[3]	1.06	0.00	0.00	0.00	1.06	1.06	1.06
beta[4]	-0.21	0.00	0.00	0.00	-0.21	-0.21	-0.21
beta[5]	0.19	0.00	0.00	0.00	0.19	0.19	0.19
beta[6]	0.13	0.00	0.00	0.00	0.13	0.13	0.13
beta[7]	0.03	0.00	0.00	0.00	0.03	0.03	0.03
beta[8]	0.12	0.00	0.00	0.00	0.12	0.12	0.12
beta[9]	-0.44	0.00	0.00	0.00	-0.44	-0.44	-0.44
beta[10]	0.08	0.00	0.00	0.00	0.08	0.08	0.08
beta[11]	0.11	0.00	0.00	0.00	0.11	0.11	0.11
beta[12]	0.14	0.00	0.00	0.00	0.14	0.14	0.14
beta[13]	-0.85	0.00	0.00	0.00	-0.85	-0.85	-0.85
Deviance	6711.08	0.00	0.00	0.00	6711.08	6711.08	6711.08
LP	-3427.36	0.00	0.00	0.00	-3427.36	-3427.36	-3427.36

Output Summary: The LaplacesDemon function simulates the data from the posterior density with Independent Metropolis algorithm and approximates the results shown in Table 3. It shows the simulated results in a matrix form that summarizes the marginal posterior densities of the parameters over all samples which contain mean, standard deviation, Monte Carlo Standard Error (MCSE), Effective Sample Size (ESS) and credible intervals LB (2.5%), Median (50%) and UB (97.5%).

4 Fitting of Poisson Model with JAGS

JAGS is “Just Another Gibbs Sampler”, and it was designed by Plummer [15]. It is used for inference on Bayesian models using MCMC simulation. The input to running JAGS from within R is to install and load a library called R2jags. `R2jags` is an R package used to call JAGS from R. Moreover, `R2jags` package is used for the simulation from posterior density. Running a model refers to generating samples from the posterior distribution of the model parameters. The jags function takes data and starting values as input. It automatically writes a jags script, calls the model and saves the simulations for easy access in R. The purpose of R2jags is to allow fitting JAGS models from R and to analyze convergence and perform other diagnostics right within R. Now, the JAGS code for the Poisson model is as follows:

```
## Creation of data
library(R2jags)
library(AER)
data("DoctorVisits",package="AER")
M1<-glm(visits˜.+I(ageˆ2),data=DoctorVisits,family=poisson)
X <-model.matrix(M1)
J<-ncol(X)
N<-length(y)
y<-DoctorVisits$visits
datpjags<-list(J=J,N=N,X=X,y=y)
```

Here *X* is a model matrix which can be extracted by the function model.matrix() from an glm() fitted object. The response variable *y* is a vector of length *N* and *J* represents the number of columns of model matrix. The model definition consists of a series of relations inside a block delimited by curly brackets and preceded by the keyword model. The code for the model defined above is as follows:

```
## Model specification
cat("model{
for(i in 1:N){
y[i]˜dpois(lambda[i])
log(lambda[i])<-inprod(X[i,],beta[])
}
for(j in 1:J){
beta[j]˜dnorm(0,1.0E-06)
}
}",file="poissonmodeljags.txt")
```

In the code below, we express those data elements that are reference in the JAGS model and initial values for the parameters.

```
inits<-function(){list(beta=rnorm(J))}
param<-c("beta")
```

Now, we fit the model by using the jags() function, and display the results numerically and graphically:

```
M4<-jags(data=datpjags,inits=inits,param=param,model.file
="poissonmodeljags.txt",n.chains=3,n.iter=20000)
print(M4)
plot(M4)
denplot(M4,parms=1:13)
```

Table 4: Summary of simulated result from jags function contains posterior estimates, standard deviation, credible interval, Rhat and effective sample size (n.eff)

Parameters	mu.vector	sd.vector	2.5%	50%	97.5%	Rhat	n.eff
beta[1]	-2.225	0.193	-2.595	-2.227	-1.835	1.003	900
beta[2]	0.181	0.054	0.073	0.181	0.287	1.002	2900
beta[3]	1.377	1.009	-0.653	1.389	3.294	1.004	690
beta[4]	-0.209	0.086	-0.379	-0.207	-0.042	1.002	1800
beta[5]	0.184	0.017	0.151	0.185	0.218	1.007	330
beta[6]	0.129	0.005	0.119	0.129	0.138	1.001	5800
beta[7]	0.027	0.010	0.007	0.027	0.046	1.002	1900
beta[8]	0.078	0.067	-0.053	0.078	0.214	1.003	830
beta[9]	-0.432	0.156	-0.757	-0.429	-0.142	1.002	2400
beta[10]	0.030	0.084	-0.138	0.030	0.194	1.002	1400
beta[11]	0.084	0.066	-0.042	0.084	0.214	1.002	1300
beta[12]	0.124	0.077	-0.026	0.123	0.276	1.004	680
beta[13]	-1.173	1.088	-3.267	-1.177	1.008	1.003	860
deviance	6725.023	5.296	6716.586	6724.361	6736.993	1.005	550

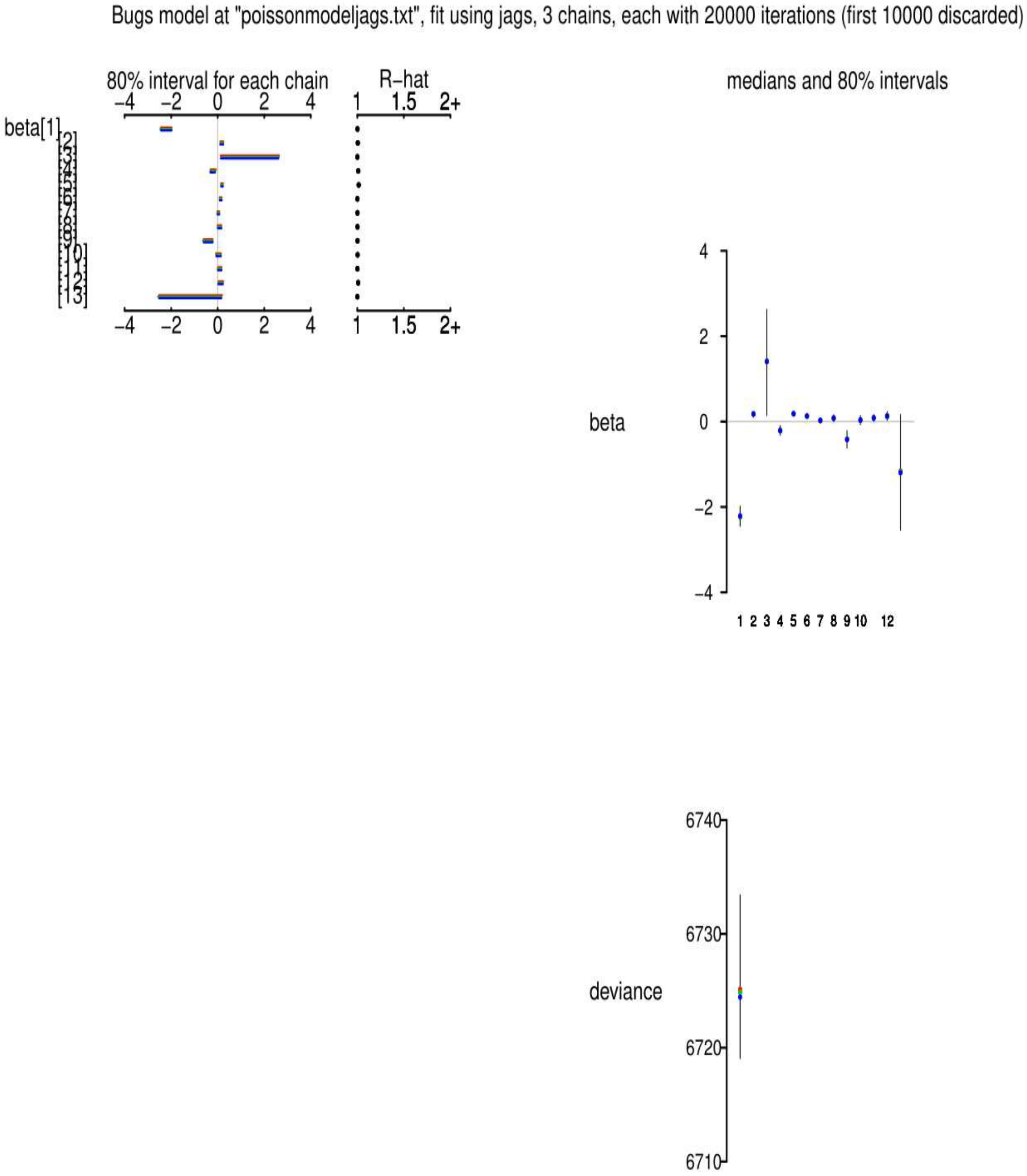


Fig. 4: Graphical representation of posterior summaries of Poisson model. Rhat is near one for all parameters indicating good convergence, and right panel shows the posterior inference for each parameter and the deviance.

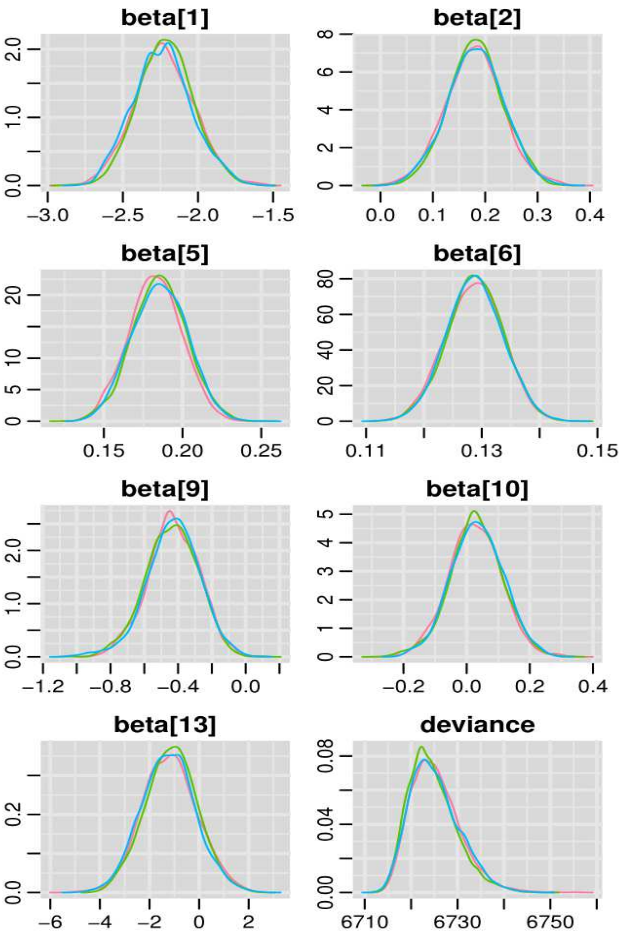


Fig. 5: Posterior density plots of JAGS for the Poisson model, fit to the DoctorVisits data.

Output Summary: The summary of JAGS simulations after being fitted to the Poisson model for the DoctorVisits data. JAGS simulates the data from posterior density using Metropolis-within-Gibbs algorithm and approximate the results, which are reported in Table 4. The column first calls as mu.vect denotes posterior mean of the parameters and column second calls as sd.vect denotes their respective posterior standard deviations. It is also clear that the parameters beta[1], beta[2], beta[4], beta[5], beta[6], beta[7] and beta[9] are statistically significant because zero does not lie in their 95% credible regions. In Figure 4, the upper plot displayed in the right panel shows the significance, medians and 80% intervals of all the parameters. The left panel exhibits the convergence of all the parameters. R-hat is near 1 for all parameters, indicating good convergence. In addition, Figure 5 reveals the entire representation of the results obtained using the denplot() function.

5 Conclusion

In this article, the Bayesian approach is applied to model the count data based on DoctorVisits data. The Poisson distribution is used as a Bayesian model to fit the data and for the analysis. Three essential techniques, i.e. asymptotic approximation, simulation using R2jags and LaplacesDemon have been proposed. Based on their results, it is clear that simulation techniques provide better results regarding standard error compared to those obtained by asymptotic approximation. Thus, it is complicated to analyze these types of data using classical method, whereas it is quite simple in Bayesian paradigm using tools like R.

Acknowledgments

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