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Inference on parameter β of the Generalized Negative Binomial Distribution

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In this paper, we propose a generalized likelihood ratio test to discern whether a set of data fits a Negative Binomial as a particular case of the Generalized Negative Binomial Distribution(GNBD). The test attempts to differentiate the GNBD from Negative Binomial (NBD) distribution when fitting discrete data. A Monte Carlo simulation study was performed to investigate the power and the size of the proposed test, and results shows good performance in power and size under moderate sample sizes of the LRT test for testing hypotheses on parameter β of the Generalized Negative Binomial Distribution. A Parametric Bootstrap for investigating the distribution of parameter β of the GNBD and a Bayesian approach for obtaining the posterior distribution of the GNBD parameters were also implemented. In order to illustrate the proposed methodology, we included two cases: a dataset of an entomological study on mosquitoes of malaria and another study on species of Malaysian butterflies.

keywords: Bootstrap, discrete distributions, count data, hypothesis testing, simulation.

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1 Introduction

Count data occur in many fields, including biology, agronomy, environmental sciences, medicine and epidemiology. Some examples are the number of deaths, number of accidents, number of insects, number of inundations, etc. (Cameron and Trivedi, 1998). Discrete probability distributions are fitted to observed counts to find a pattern which may lead an investigator to see if some generating models can be set up for the process under study (Consul and Famoye, 2006). Jain and Consul (1971) introduced the Generalized Negative Binomial Distribution (GNBD), a model that includes as particular cases Negative Binomial and Binomial distributions. The GNBD defined by Jain and Consul (1971) generalizes the Negative Binomial distribution by including another parameter which takes into account variations in the mean and variance. The GNBD is also a member of the Lagrangian distributions studied by Consul and Shenton (1972) and it is also a member of the Modified Power Series distributions studied by Gupta (1974).

Parameter estimation in the case of GNBD has been addressed by several researchers. Jain and Consul (1971) used the method of moments to estimate parameters of GNBD, Famoye (1998a) obtained estimates by the maximum likelihood method, Gupta (1977) and Jani (1977) studied the minimum variance unbiased estimation, Hassan et al. (2004) suggested a simple method for estimating the parameters of this distribution and Islam and Consul (1986) introduced a Bayesian estimation approach for estimating parameter β given the other as known in GNBD. However, Consul and Famoye (1995) found that when estimating parameter β, most of the times, the resulting parameter lies in the $(0, 1)$ interval. Something similar was observed by Famoye (1998b) and Hassan et al. (2004). Famoye (1998a) studied the performance of goodness of fit tests based on the empirical distribution function for the GNBD by using Bootstrap.

Kumar et al. (2014) proposed an alternative estimator of GNBD parameters, but no further properties of the estimators are given. Arefi et al. (2016) studied some confidence intervals (Wald's score, skewness-corrected score, likelihood ratio, and mid-P intervals) for the mean of the generalized Poisson and generalized negative binomial distributions, by means of a simulation study.

The purpose of this paper is to study a Generalized Likelihood Ratio Test (LRT) for testing if a GNBD can be reduced to a NBD. Bayes estimates by using Markov Chain Monte Carlo (MCMC) methods with their posterior density and credible intervals of the parameters of the GNBD are also obtained. Additionally the Bootstrap method was implemented for obtaining a confidence interval for parameter β of the GNDB.

2 The Generalized Negative Binomial distribution

If X is a random variable whose probability mass function is given by:

$$f_X(x;\theta,\beta,m) = \begin{cases} \frac{m}{m+\beta x}\binom{m+\beta x}{x}\theta^x(1-\theta)^{m+\beta x-x} & x = 0, 1, \ldots, \\ 0 & \text{otherwise} \end{cases} \tag{1}$$

then X is said to have a GNBD distribution for $x = 0, 1, 2, 3, ...$ and zero otherwise, where $0 < \theta < 1$, $m > 0$, $\beta = 0$ or $1 \leq \beta \leq \theta^{-1}$. Also, when $\beta = 0$, the parameter m is a positive integer.

The distribution given in model (1) is denoted as $X \sim$ GNBD (θ, β, m). The mean and the variance of the GNBD are $\mu = m\theta(1 - \theta\beta)^{-1}$ and $\sigma^2 = m\theta(1 - \theta)(1 - \theta\beta)^{-3}$, respectively. The mean and the variance exist for $1 \leq \beta < \theta^{-1}$. If $\beta\theta = 1$ then the mean and variance of GNBD do not exist. In Consul and Famoye (2006) a complete study of GNBD probability distribution and some of their properties and applications is given.

3 Maximum likelihood estimators of GNBD parameters

Suppose we have a random sample from the GNBD with probability function given in (1), and let n_0 is the observed frequencies for 0, n_1 is the observed frequencies for 1,...,n_k is the observed frequencies for k, with k is the maximum observed value in the sample, $n = \sum n_x$ and $\bar{x}$ the sample mean. The log-likelihood function is (Famoye, 1997):

$$\begin{aligned} l(\theta, \beta, m|data) &= \log\left\{\prod_{x=0}^{k}[f_X(x; \theta, \beta, m)]^{n_x}\right\} \\ &= (n - n_0)\log(m) + n\bar{x}\log(\theta) + n[m + (\beta - 1)\bar{x}]\log(1 - \theta) \\ &\quad + \sum_{x=2}^{k} n_x\left[\sum_{i=1}^{x-1}\log(m + \beta x - i) - \log(x!)\right]. \end{aligned} \tag{2}$$

The partial derivatives of the log-likelihood with respect to each parameter are as follows:

$$\frac{\partial l(\theta, \beta, m|data)}{\delta\theta} = \frac{n[\bar{x} - \theta(m + \beta\bar{x})]}{\theta(1 - \theta)} = 0, \tag{3}$$

$$\frac{\partial l(\theta, \beta, m|data)}{\delta\beta} = n\bar{x}\log(1 - \theta) + \sum_{x=2}^{k}\sum_{i=1}^{x-1}\frac{x n_x}{m + \beta x - i} = 0, \tag{4}$$

$$\frac{\partial l(\theta, \beta, m|data)}{\delta m} = \frac{n - n_0}{m} + n\log(1 - \theta) + \sum_{x=2}^{k}\sum_{i=1}^{x-1}\frac{n_x}{m + \beta x - i} = 0. \tag{5}$$

The maximum likelihood estimates θ, β and m are obtained by solving (3), (4) and (5) iteratively, taking as initial values the moment estimators (Consul and Famoye, 1995).

3.1 The moment estimators for the GNBD

The moment estimators for the GNBD were obtained by Jain and Consul (1971). Suppose that a random sample of size n is taken from the GNBD model and let the observed values be $x_1, x_2, ..., x_n$ and define $\bar{x} = \sum_{i=1}^{n} x_i/n$, $s_2 = \sum_{i=1}^{n}(x_i - \bar{x})^2/(n-1)$, $s_3 = \sum_{i=1}^{n}(x_i - \bar{x})^3/(n-1)$. The moment estimators are:

$$\begin{aligned}
\tilde{\theta} &= 1 - \frac{1}{2}\left[-2 + \frac{(\bar{x}s_3 - 3s_2^2)^2}{\bar{x}s_2^3}\right] + \left\{\left[-2 + \frac{(\bar{x}s_3 - 3s_2^2)^2}{\bar{x}s_2^3}\right]^2 /4 - 1\right\}, \qquad (6)\\
\tilde{\beta} &= \frac{1}{\tilde{\theta}}\left\{1 - \left(\frac{\bar{x}(1-\tilde{\theta})}{s_2}\right)^{1/2}\right\}, \qquad (7)\\
\tilde{m} &= \frac{\overline{x}(1 - \tilde{\theta}\tilde{\beta})}{\tilde{\theta}}. \qquad (8)
\end{aligned}$$

The moment estimators exist for $1 \leq \beta < \theta^{-1}$ (Jain and Consul, 1971).

4 A LRT test on parameter β of the GNBD

The binomial and negative binomial distributions are members of generalized negative binomial class of distributions for β=0 and β=1, respectively. The problem of interest is to test if a random sample that follows a GNBD distribution can be reduced to the Binomial or Negative Binomial Distributions.

Let $X_1, X_2, ..., X_n$ be an observed random sample of size n from a GNBD(θ, β, m). We want to test:

$$H_0 : \beta = 1 \ \text{ vs } \ H_1 : \beta > 1 \text{ (Negative Binomial vs GNBD).} \qquad (9)$$

In these cases the parameters θ, β and m are unknown and are estimated by from the sample data by the maximum likelihood method.

4.1 Generalized likelihood ratio test

Suppose that a given random sample $X_1, \ldots, X_n$ with probability distribution $f_X(x;\theta)$ and Ω be the parametric space. We are interested to test the following hypothesis set: $H_0 : \theta \in \Omega_0$ vs $H_1 : \theta \in \Omega - \Omega_0$. The likelihood ratio statistic to test $H_0 : \theta \in \Omega_0$ vs $H_1 : \theta \in \Omega - \Omega_0$ is given by:

$$\lambda(\boldsymbol{x}) = \frac{\sup\limits_{\theta \in \Omega_0} L(\theta; \boldsymbol{x})}{\sup\limits_{\theta \in \Omega} L(\theta; \boldsymbol{x})}.$$

where $L(\theta; \boldsymbol{x}) = \prod_{i=1}^{n} f_{X_i}(x_i; \theta)$.

Note that under certain regularity conditions (Casella and Berger, 2002), (under the null hypothesis) when $n \to \infty$,

$$-2\log\lambda(\boldsymbol{X}) \xrightarrow{d} \chi^2_\nu$$

where χ^2_ν is χ^2 random variable with ν degrees of freedom. We reject H_0 at level α if, and only if, $-2\log\lambda(X) \geq \chi^2_{\nu,1-\alpha}$ where $\chi^2_{\nu,1-\alpha}$ is the quantile $1-\alpha$ of a χ^2 distribution with ν degrees of freedom. Then to test the hypotheses in (9) we proceed as follows. Suppose that we have a random sample of size n with probability function $f_X(x;\theta)$ and let n_x be the observed frequencies for the classes $x = 0, 1, 2, ..., k$ where k is the largest observed value. Considering the set of hypotheses to test in (9), we calculate the maximum likelihood estimators under the null ($\hat{\theta_0}$, $\beta = 1$ and $\hat{m_0}$) and alternative hypotheses ($\hat{\theta_1}$, $\hat{\beta_1}$ and $\hat{m_1}$) and we have the following statistic:

$$-2\log\lambda(\boldsymbol{X}) = \quad -2\log\left(\frac{sup_{\theta\in\Omega_1}\prod_{x=0}^{k}\frac{(\hat{m_1}+x-1)!}{(\hat{m_1}-1)!\,x!}\hat{\theta_1}^{x}(1-\hat{\theta_1})^{\hat{m_1}}}{sup_{\theta\in\Omega_1}\prod_{x=0}^{k}\frac{\hat{m_1}}{\hat{m_1}+\hat{\beta_1}x}\binom{\hat{m_1}+\hat{\beta_1}x}{x}\hat{\theta_1}^{x}(1-\hat{\theta_1})^{\hat{m_1}+\hat{\beta_1}x-x}}\right)$$

If $-2\log\lambda(\boldsymbol{X}) \geq \chi^2_{1,1-\alpha}$, then we reject H_0 at level $\alpha = 0.05$. We apply the same procedure to the other case in equation (9) to test NBD against GNBD.

4.2 Monte Carlo simulation of the power of the proposed test

4.2.1 Power and size of the test

Power

Monte Carlo simulation experiment was conducted to study the power and size of the proposed test under different values of parameter β and different sample size situations. To generate samples from the GNBD we wrote an R script by using the inversion method (Famoye, 1998b). The MLE estimators were obtained by using the `optim` function in R (R Core Team, 2017).We used the following algorithm for evaluating the power of the test for testing hypotheses in (9):

1. Select the values of n, θ, β and m.
2. Set $Sum = 0$.
3. Generate a random sample $X_1, X_2, ..., X_n$ from the GNBD(θ, β, m).
4. Calculate the maximum likelihood estimates for the parameters under the null and the alternative hypothesis.
5. Calculate the likelihood ratio statistic $-2\log\lambda(\boldsymbol{X})$.
6. If $-2\log\lambda(\boldsymbol{X}) \geq \chi^2_{\nu,1-\alpha}$ then set $Sum = Sum + 1$.
7. Repeat steps 3 to 6 M times.
8. Calculate Sum/M to obtain the estimated power.

Table 1 shows the results of the power obtained for Negative Binomial model with sample size $n = 300, 500$, 800 and 1000 for different values of β and significance level equal to 0.05. Parameter θ and m where fixed in 0.4 and 2 respectively, the number of simulation replicates was 5000. From Table, 1 we can observe that the GLR performs with moderate power in small samples sizes and it increases as the samples size is greater ($n \geq 500$).

Table 1: Power of the Test. Case Negative Binomial vs Generalized Negative Binomial ($H_0 : \beta = 1$ vs $H_1 : \beta \neq 1$) with $\alpha = 0.05$

β	n			
	300	500	800	1000
1.0	0.0420	0.0576	0.0510	0.0509
1.3	0.0456	0.0357	0.0669	0.0689
1.4	0.0489	0.0557	0.1205	0.1923
1.6	0.1340	0.2876	0.4219	0.5280
1.7	0.2026	0.4316	0.6213	0.6667
1.9	0.5216	0.7726	0.9233	0.9710
2.0	0.6960	0.8934	0.9788	0.9980
2.1	0.8688	0.9687	1.0000	1.0000
2.2	0.9646	0.9990	1.0000	1.0000

Size

In this section, we present the results of estimation for the size of the test obtained by simulation for significance level (α) of 0.01, 0.05 and 0.1 with 5000 replicates. Table 2 show the results when the null hypothesis are true, i.e. when the generated random sample is Negative Binomial. Parameter θ and m where fixed in 0.4 and 2 respectively. From Table 2 we conclude that the estimated sizes of test are close to the nominal significance level when the sample size is greater than 500, i.e. the GLR test preserves the nominal significance level α when the sample size is large enough.

Table 2: Empirical size for Negative Binomial vs Generalized Negative Binomial ($H_0 : \beta = 1$).

n	α		
	0.01	0.05	0.1
100	0.2256	0.2200	0.2308
200	0.0618	0.0791	0.1109
500	0.0109	0.0455	0.1299
1000	0.0100	0.0517	0.0983

5 Parametric bootstrap for $\hat{\beta}$

The Bootstrap it is a general technique for constructing confidence intervals using resampling. A parametric bootstrap it proposed for investigating the distribution of $\hat{\beta}$ from the GNBD.

The steps to obtain bootstrap confidence intervals are:

1. Simulate a random sample of GNBD of size n by using maximum likelihood estimates of θ, β and m in section 3.
2. Estimate the MLE of the parameters of GNBD for simulated sample.
3. Save the estimate of β.
4. Repeat step 1-3 for 10000 times.
5. Sort de vector of estimate β and find the quantiles 5% and 95%.
6. Plot the estimated density of $\hat{\beta}$ by using a kernel smoothing nonparametric estimate.

A 95 percent Bootstrap confidence interval for β that includes the value of 1 supports the NBD hypothesis. A program was written in R (R Core Team, 2017) for obtaining the Bootstrap intervals.

6 Bayesian analysis of a generalized negative binomial distribution

A Bayesian approach using MCMC algorithm by assigning a prior distributions on θ, β and m of the GNBD (1) and then deriving the posterior distribution by means of Bayes' theorem.

The likelihood function for a sample $X_1, ..., X_n$ from de GNBD probability function (1) is given by equation (2). The GNBD distribution does not support a conjugated family of previous distributions, so advanced simulation techniques are required to obtain the posterior distribution. The prior distributions of all unknown parameters (θ,β,m) are considered in Bayesian approach. Since we have no information, non informative prior distributions to the parameters are used.

In particular, we used a prior Beta distribution for θ. For β and m we assigned a gamma distribution to each parameter independently. Therefore, the prior distributions are as follows:

$$\theta \sim B(a_0, b_0), \tag{10}$$

$$\beta \sim \Gamma(a_1, b_1), \tag{11}$$

$$m \sim \Gamma(a_2, b_2), \tag{12}$$

where $a_i > 0$ and $b_i > 0$ for $i = 1, 2, 3$.

Each parameter is supposed to be independently distributed, and the joint prior distribution of all unknown parameters can be written as:

$$\pi(\theta, \beta, m|a_0, b_0, a_1, b_1, a_2, b_2) = \pi(\theta|a_0, b_0)\pi(\beta|a_1, b_1)\pi(m|a_2, b_2) \tag{13}$$

The setting of hyperparameter values $a_i > 0$ and $b_i > 0$ was done by tunning values around a mean of the prior distribution.

6.1 Posterior inference

Combining equations (2) to (13), the joint posterior distribution of the parameters is given by:

$$\pi(\theta, \beta, m|\boldsymbol{x}) \propto \prod_{i=1}^{n} f_{X_i}(x_i|\theta, \beta, m)\pi(\theta|a_0, b_0)\pi(\beta|a_1, b_1)\pi(m|a_2, b_2). \tag{14}$$

The joint posterior distribution (14) is analytically intractable so inference can be made using simulation with Markov Chain Monte Carlo techniques (MCMC). To obtain the posterior marginal distribution. To draw posterior samples, numerical integration it is required. In this case, we used the random walk Metropolis algorithm (Liu, 2001). We used the proc MCMC of the SAS software (SAS Institute Inc., 2012) to find the posterior marginal distribution of the parameters θ, β, m.

7 Study cases

7.1 Example 1: Number of sporozoite-positive malaria mosquitoes

Drakeley et al. (2003) conducted an entomological study on mosquitoes of malaria and their relative contribution to *Plasmodium falciparum* transmission in the semi-urban area of Ifakara, south-eastern Tanzania. Table 3 shows observed numbers of sporozoite-positive mosquitoes in light trap catches (LTC). Drakeley et al. (2003) found that the negative binomial distribution fitted better than Poisson for data in Table 3.

Table 3: Number of sporozoite-positive malaria mosquitoes (Drakeley et al., 2003).

No. of sporozoite-positive mosquitoies in LTC	No. of times observed
0	761
1	21
2	5
3	0
4	2
5	0
n	789

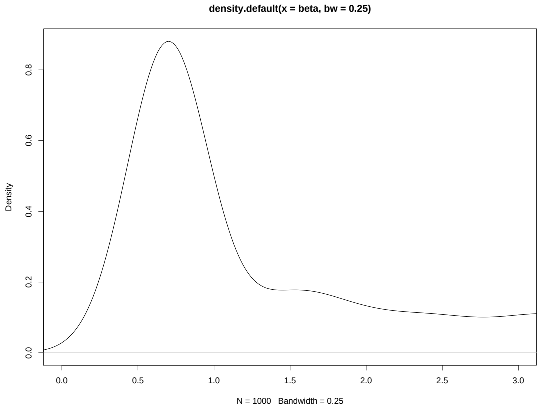

Figure 1: Estimated density of $\hat{\beta}$ parameter of fitted distribution on numbers of mosquitoes by Bootstrap.

7.1.1 testing $H_0 : \beta = 1$ by using a LRT

Now we are interested testing if data comes from a NBD or a GNBD (as in equation 9).

$$H_0 : \beta = 1 \text{ (NBD) vs } H_1 : \beta \neq 1 \text{ (GNBD)}.$$

Steps:

1. The MLE are obtained for NBD and GNBD, see Table 4.
2. Using the statistic from subsection 4.1, for this data the GLR statistic is $-2\log\lambda(\boldsymbol{x}) = 0.031$ and the percentile $\chi^2_{1,0.95} = 3.84$, hence we do not reject $H_0 : \beta = 1$ (NBD), i.e., the number of sporozoite-positive malaria mosquitoes caught by a light trap is distributed according to a Negative Binomial distribution.

Table 4: ML parameters under null and alternative hypotheses for malaria Mosquitoes.

Parameter	H_0	H_1
$\hat{\theta}$	0.549982	0.2532310
$\hat{\beta}$	1 (known)	1.4459204
$\hat{m}$	0.06042140	0.1237229
log likelihood	-143.95	-143.9345

7.1.2 Bootstrap confidence interval for $\hat{\beta}$

A 95 percent Bootstrap confidence interval for β is $(0.53, 5.02)$, note that 1 is included in the interval witch supports the NBD hypothesis. Figure 1 shows the estimated density for $\hat{\beta}$.

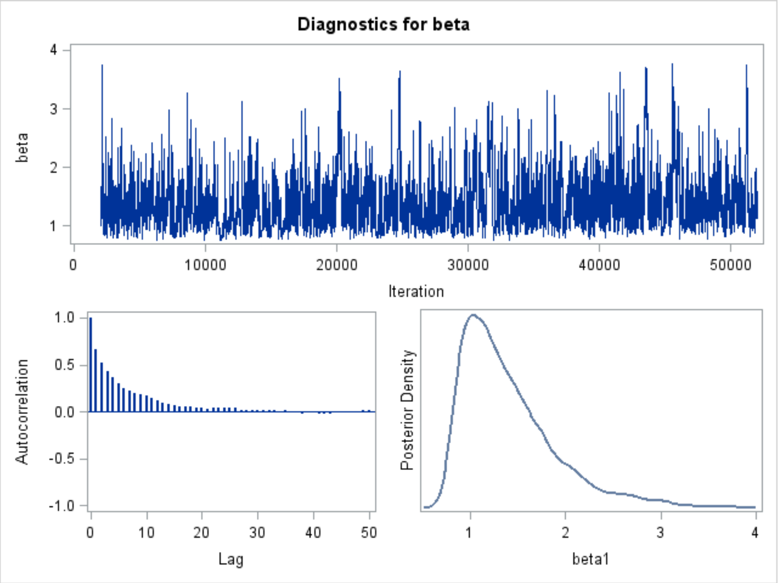

Figure 2: Traceplot, autocorrelation plot and Posterior distribution for parameter β of the GNBD for mosquitoes data.

7.1.3 Posterior distributions using MCMC

A summary of results is given in Table 5, and a posterior density plot of β es given in Figure 2. For the MCMC algorithm we used 100000 iterations, the fist 50000 iterations were considered as burn-in, and we set the thinning rate to 20. In this case the credibility interval for beta includes the 1, then data supports the NBD.

Table 5: Summary of the posterior distribution of the GNBD, using 50000 iterations, (LC,UC) is the credibility interval of 95 %.

Parameter	Mean	Standard Deviation	LC	UC
θ	0.3261	0.1464	0.0854	0.6137
β	1.4083	0.4924	0.7635	2.4243
m	0.1188	0.0764	0.0224	0.2747

7.2 Example 2: Number of species of Malaysian butterflies

A data set on Malaysian butterflies from (Corbet 1942) study is considered. The data contains 9029 individuals belonging to 620 species this data set was used by Izsák (2008) to fit a Poisson lognormal distribution. The data are shown in Table 6.

Table 6: Number of species of Malaysian butterflies, Corbet (1941).

Frequency	N Species	Frequency	N Species	Frequency	N Species	Frequency	N Species
1	118	20	10	39	3	60	2
2	74	21	11	40	1	64	1
3	44	22	5	41	1	66	1
4	24	23	3	42	2	68	1
5	29	24	3	43	1	70	1
6	22	25	5	44	1	71	4
7	20	26	4	45	4	76	1
8	19	27	8	46	2	84	1
9	20	28	3	48	2	89	1
10	15	29	3	49	1	92	1
11	12	30	2	50	3	93	1
12	14	31	5	51	1	100	1
13	6	32	4	52	2	105	1
14	12	33	7	53	1	108	1
15	6	34	4	54	4	119	1
16	9	35	5	55	1	141	1
17	9	36	3	56	5	147	1
18	6	37	3	58	2	194	1
19	10	38	3	59	1		

Table 7: ML parameters under null and alternative hypotheses in spots in southern pine beetle.

Parameter	H_0	H_1
$\hat{\theta}$	0.048988	0.2211
$\hat{\beta}$	1 (known)	3.8195
$\hat{m}$	0.75024	10.2232
log likelihood	-2286.4895	-2247.05

7.2.1 testing $H_0 : \beta = 1$ by using a LRT

for this data the *GLR* statistic is $-2 \log \lambda(\boldsymbol{x}) = 78.879$ and the percentile $\chi^2_{1,0.95} = 3.84$, hence we reject $H_0 : \beta = 1$ (NBD), i.e., the number of species is distributed according to a Generalized Negative Binomial distribution.

7.2.2 Bootstrap confidence interval for $\hat{\beta}$

A 95 percent Bootstrap confidence interval for β is $(3.31, 4.12)$, note that 1 is not included in the interval witch supports the GNBD hypothesis, in Figure 3 the estimated density of $\hat{\beta}$ it is shown.

7.2.3 Posterior distributions using MCMC for GNBD in Malayan butterflies data

A summary of results is given in table (8), and a posterior density plot of β es given in figure (4). For the MCMC algorithm, we used 100000 iterations, the fist 50000 iterations

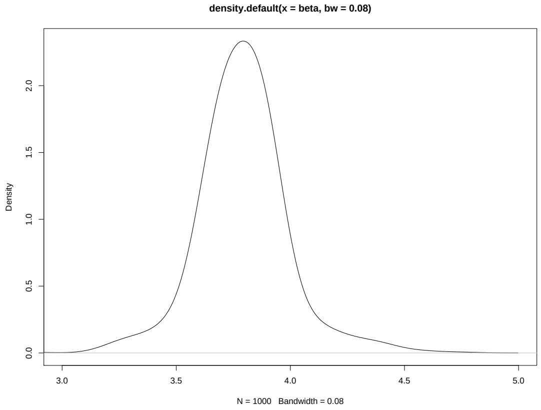

Figure 3: Estimated density of $\hat{\beta}$ parameter of fitted distribution on numbers of Malayan butterflies by Bootstrap.

were considered as burn-in, and we set the thinning rate to 20.

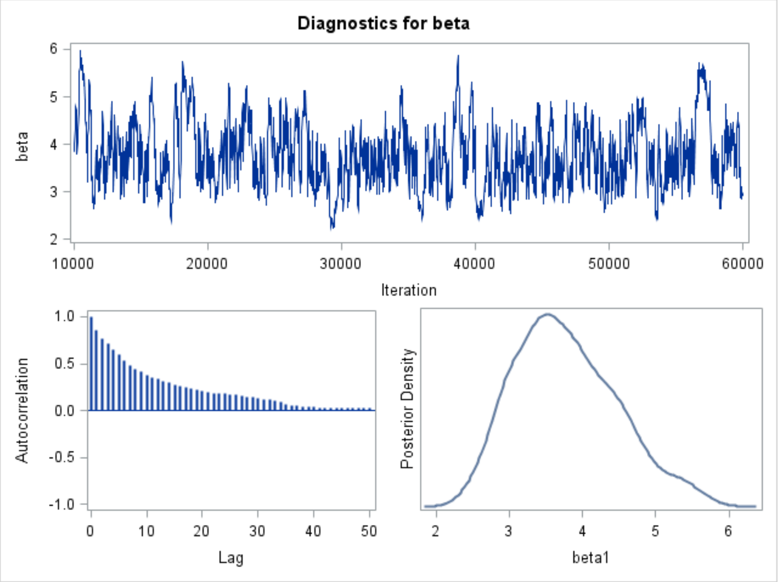

Figure 4: Traceplot, autocorrelation plot and Posterior distribution for parameter β of the GNBD for Malaysian butterflies data.

In this case the credibility interval for beta does no includes the value 1, then data supports the GNBD.

Table 8: Summary of the posterior distribution of the GNBD, using 50000 iterations, (LC,UC) is the credibility interval of 95 %, in Malayan butterflies data.

Parameter	Mean	Standard Deviation	LC	UC
θ	0.2312	0.0438	0.1491	0.3098
β	3.7809	0.6999	2.4804	5.1567
m	10.1811	2.1917	6.428	14.7075

8 Conclusions

We have developed a likelihood ratio test to test if the GNBD or NBD distribution is appropriate for a given data set. We also investigated the performance of this test with respect to its power by simulation. The study shows that the likelihood ratio test has good performance in power and size under moderate sample sizes $n > 200$. The test showed consistency and with sample size $n > 1000$ the test reached the nominal size of the test and the power was acceptable for detecting changes on parameter β. We also proposed a Bayesian analysis and a Bootstrap of testing if β is one. Finally, we present two example where proposed test shows consistency with Bayes and Bootstrap approaches.

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