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On the Performance of Dirichlet Prior Mixture of Generalized Linear Mixed Models for Zero Truncated Count Data

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Abstract: In this study, the performance of Dirichlet Process Mixture of Generalized Linear Mixed Models (DPMGLMMs) was examined against some competing models for fitting zero-truncated count data. The Bayesian models such as Monte Carlo Markov Chain GLMMs, Bayesian Discrete Weibull and the frequentists models such as Zero truncated Poisson, Zero truncated Binomial and Zero truncated Geometric models were compared with the proposed DPMGLMMs model. Simulation and life count data from health domain was used to compare the performance of DPMGLMM with the Bayesian and frequentist models considered in this study. The results showed that the DPMGLMM outperformed other models considered for fitting count data that is truncated at zero.

Keywords: Count data, Dirichlet Mixture, Bayesian model, Zero-truncated, dispersion, health

1 INTRODUCTION

Count data can exhibit equi-dispersion, over-dispersion, or under-dispersion. One popular model for fitting count data is the Poisson model, but it is only suitable for equi-dispersed data due to the equal mean and variance associated with Poisson distribution [1]. Relative to Poisson regression, negative binomial regression is suitable for over-dispersed data because it has a parameter that takes care of over-dispersion in count data. There are models suitable to fit different types of count data based on dispersion type, presence or absence of zeros, and other forms. Some techniques which are an improvement on the Poisson regression model can be found in the works of [2-6]. If a count response variable contains zero counts, a zero-inflated and hurdle model can be suitably applied such as [7, 8] who applied a zero-inflated model to fit time series COVID-19 count data. In the same vein, zero truncated models are suitable for count data that is truncated at zero. Models different from zero truncated models may be used such as Negative binomial or discrete Weibull, but might give misleading results [4]. Modelling of count data has been applied in disciplines such as biological sciences [9, 10], in insurance [6, 11], in Education [12], in medicine [13-19].

Studies such as [20] showed the strength of Monte Carlo Markov Chain of Generalized Mixed Models (MCMCGLMMs) in fitting zero truncated count data count data. Haselimashhadi [17] showed the strength of Bayesian discrete Weibull to fit count data that is either under- or over-dispersed. In this study, Dirichlet Prior Mixture of (DPMGLMMs) was proposed to fit a special case of count data with no zero and compare it with competing models.

In the study by [20, 21], the zero-truncated were found to sufficiently fit zero-truncated data relative to other models for fitting zero-truncated data. This study aims to identify the strength of zero truncated models dedicated to fitting count data compared to Bayesian models. The DPMGLMMs, as [22] found to be robust for fitting over-or-under-dispersed count data. Some zero truncated models considered in this study are zero truncated Poisson, zero truncated Negative Binomial, and zero truncated Geometric; the zero truncated models are frequentist based. Another frequentist-based model is the Generalized mixed models Template model builder. We aim to compare these models with one another to determine which is best suited for the data.

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Studies such as [23-27] gave compelling advantages of Bayesian estimation techniques over frequentist models. Therefore, we also considered modelling and comparing the frequentist zero truncated models with Bayesian models such as Bayesian Discrete Weibull, Monte Carlo Markov Chain of Generalized Mixed Models, and Dirichlet Prior Mixture of Monte Carlo Markov Chain of Generalized Mixed Models.

2 METHODOLOGY

2.1 Generalized Linear Model (GLM)

The frameworks of GLM and its extension have been useful for modelling count data. GLM operates with a link function that links the response variable to the predictors.

If $y_i = 1,2,...n$ is a response variable of a given set of data and it is a function of the covariates $x_{i1}, x_{i2}...x_{ik}$, then a classical linear regression can be expressed as

$$y_i = \beta_0 + \beta_1 x_{i1} + ...\beta_k x_{ik} + \varepsilon_i, \qquad i = 1,2,...n \tag{1}$$

where β_0 and β_k are parameters to be estimated, and ε is the error term.

Equation 1 in matrix form is

$$Y_{n\times 1} = X_{n\times p}\beta_{p\times 1} + \varepsilon_{p\times 1} \tag{2}$$

A random variable has a distribution in the exponential family, if the probability mass function (pmf) of observation is of the form,

The distribution the exponential of family of random variable y is of the form:

$$f(y|\theta) = c(y,\phi)exp(y\theta - \alpha(\theta))/\phi, g(\mu_i) = x^{'}\beta \tag{3}$$

Eq.3 is as provided by [28] where θ is the location parameter ,φ is the dispersion parameter, and c(y,φ) is the normalizing factor.

The two basic components of GLM are the link function and the canonical link. The link function is expressed as

$$\eta = \sum_{j=1}^{p} x_j\beta_j = x^{'}\beta \tag{4}$$

To identify a model that can suitably fit zero truncated count data obtained, the following models were considered in this study:

Zero truncated models, Bayesian estimation techniques such as Discrete Weibull of type III [29], Generalized Linear Mixed Models (MCMCglmms), and Bayesian Dirichlet Process Mixture Prior of GLMMs (DPMglmm).

Zero Truncated Models

Let f(x; θ) be the original Poisson distribution. Then the probability density function (pdf) of zero-truncated form of f(x; θ) is given as follows

$$f(x;\theta) = P(X = x|X > 0) = \frac{f(x;\theta)}{1 - P_0(0;\theta)} = \frac{\theta^x e^{-\theta}}{x!(1 - e^{-\theta})} = \frac{\theta^x}{x!(e^{\theta} - 1)} \tag{5}$$

The mean is

$$E(X) = \frac{\theta e^{\theta}}{e^{\theta} - 1} \tag{6}$$

and the variance is

$$var(X) = E(X)[1 + \theta - E(X)] \tag{7}$$

The pdf for zero-truncated binomial and zero truncated Poisson can be found in [20, 30]. The study by [30] outlined the parameter estimation for zero-tuncated models such as zero-tuncated Poisson, zero-tuncated Binomial, and zero-tuncated geometric.

Bayesian Discrete Weibull

The cumulative distribution function of the discrete Weibull of type III is given as

$$G(y;q,\beta)=\begin{cases}1-q^{y^{\beta}}, & \text{y=0,1,2...}\\ 0, & \text{otherwise}\end{cases} \tag{8}$$

The probability mass function is given as:

$$G(y;q,\beta)=\begin{cases}q^{y^{\beta}}-q^{(1+y)^{\beta}}, & \text{y=0,1,2...}\\ 0, & \text{otherwise}\end{cases} \tag{9}$$

$$0<q<1 \text{ and } \beta>0$$

Let y be a count response variable, and $x_1,x_2 \ldots x_p$ be p covariates, the logit link follows that

$$log(q/1-q)=\theta_0+\theta_1x_1+\ldots+\theta_px_p \tag{10}$$

$$q=e^{x_i\theta}/1+e^{x_i\theta}$$

$$\ell(\theta,\beta|x,y)=\prod_{i=1}^{n}log\left(\left(\frac{e^{x_i\theta}}{1+e^{x_i\theta}}\right)^{y\beta}-\left(\frac{e^{x_i\theta}}{1+e^{x_i\theta}}\right)^{(1+y)^{\beta}}\right) \tag{11}$$

The Bayesian technique is widely applied in fitting data, following the specification of the prior distribution, hyper prior, and hyper-parameters, respectively. Among other specifications necessary in Bayesian is the thinning interval, and burn-in interval for the chain to stabilize. For Bayesian Discrete Weibull, 20,000 iterations were implemented using logit link; Laplace prior was used to allow for shrinkage with Gamma hyper-parameter. Twenty percent burn-in was allowed at both ends of the distribution to stabilize the chain.

2.2 Generalized Linear Mixed Models (GLMMs)

The GLMMs is formed when a random effect is added to the fixed effect model in generalized linear model. GLMMs are robust in fitting both data sets that are normally distributed and ones that are not normally distributed. The model in a matrix form is given as

$$y=X\beta+Z\gamma+\varepsilon \tag{12}$$

The dimensions of Equation (12) are expressed as:

$$y_{N\times 1}=X_{N\times 1}\beta_{p\times 1}+Z_{N\times q}\gamma_{q\times 1}+\varepsilon_{N\times 1} \tag{13}$$

where X and Z are the fixed and random predictors, and the corresponding parameter vectors β and γ, and E is the residuals.

To model the Bayesian MCMCGLMM, the Iterated Weighted Least Square prior was used and Gamma hyper prior. The parameters of Wishart distribution were used as hyper-parameters for the scale matrix.

2.3 Dirichlet Process Mixture Models

If a sample space is represented by Ω, the Dirichlet process is made up of partitions of the sample space Ω. If a distribution of G is drawn from the Dirichlet process, then Ω will have partition $(B_1,B_2,\ldots B_k)$, [12]. The α_i and ρ_i are the parameters of Dirichlet distribution, where α_i the concentration parameter.

$\sigma=\sum_{i=1}^{k}\alpha_i$ and $E(\rho)=\dfrac{\alpha_i}{\sigma}=\alpha_i^{'}$

Then the base measure, $G_o=(\alpha_1^{'},\ldots,\alpha_k^{'})$ the association can be expressed as

$$(G(B_1),\ldots,G(B_k))\sim(\alpha G_O(B_1),\ldots,\alpha G(B_k)) \tag{14}$$

Let $y_1, \ldots, y_i$ be taken from unidentified distribution, and y_i is multivariate real-valued [31], and modelling y_i takes the distribution of the form $F(\theta)$, with the mixing distribution over θ taken as G. The Diritchlet mixing process is of the form.

$$G \sim DP(|G_o, \alpha)$$

$$\theta_i | G \sim G$$

$$y_i | \theta_i \sim F(\theta) \tag{15}$$

From Eq. 15, αG_0 is the mean of the dirichlet process. The Iterated weighed Least Square (IWLS) proposal discussed by [32] was used to sample from the posterior distribution.

If the prior for β is represented by $N(a, R)$, then following Eq. 3, the posterior distribution for the fixed effect model is of the form:

$$\pi(\beta | y_i) \propto exp \left\{ -\frac{1}{2}(\beta - \mathbf{a})' \mathbf{R}^{-1} (\beta - \mathbf{a}) + \sum_{\mathbf{i=1}}^{\mathbf{n}} \frac{\mathbf{y_i} \theta_\mathbf{i} - \mathbf{b}(\theta_\mathbf{i})}{\phi_\mathbf{i}} \right\} \tag{16}$$

Wishart distribution prior was used, if $\mathbf{R}^{-1} \rightarrow \mathbf{0}$, but a non-informative prior would be used.

3 RESULTS

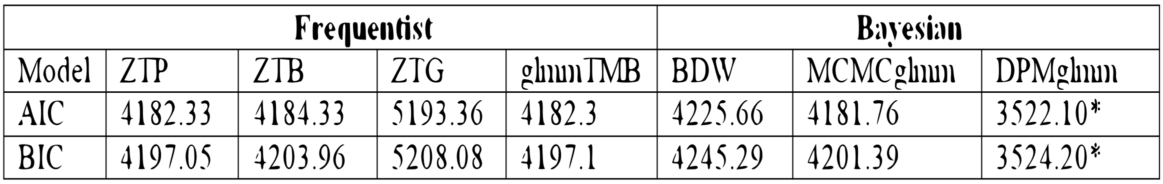
3.1 Simulation Study

One thousand samples of over- and under-dispersed zero-truncated count data response variable from Poisson distribution were randomly generated. The parameters of over-dispersed count response is θ=20, lower truncation =1 and upper truncation =60, and two predictors from the uniform distribution in the interval (0,1), and (1,1.5) respectively. For under-dispersed, two predictors were simulated from the uniform distribution in the interval (0,1), and (1,1.5) respectively, the parameters of the count response variable is $\theta = 20$, lower truncation =2, and upper truncation =10. Function in the package “extraDistr” by [33] was used to carry out the zero-truncated models. In the estimation stage of DPMglmm, response variable was controlled for in the random part of the model. The mean of the simulated over-dispersed count response 19.976, and variance is 21.020, while the mean of the simulated under-dispersed count response is 9.212, and variance is 1.076

Wishart distribution prior, suitable for DPMglmm, was used based on hyper-parameters. Twenty-thousand (20000) iterations were initiated, with 100 thinning intervals and 200 burn-in. The software package by [34] was used to implement the analysis. R package such as “MuMIn” by [35], “glmmTMB” by [36], “MCMCglmm” [37], “DPpackage” by [38, 39], “BDWreg” by [40], “AER” by [41], and “countreg” by [42].

Models such as zero truncated Poisson (ZTP), zero truncated Binomial (ZTB), zero truncated Geometric (ZTG), Template model Builder of GLMMs (glmmTMB), Bayesian discrete Weibull (BDW), Dirichlet process mixture of GLMMs (DPMglmm), Monte Carlo Markov Chain of GLMMs (MCMCglmm) were used to model the data, both for simulation and real-life data. Model selection criteria such as AIC and BIC were used to select the best model(s). Simulation of under-dispersed zero-truncated data for both Frequentist and Bayesian estimation techniques is presented in **Table 1** and Table 2 respectively following the procedure parameter and the truncation condition outlined in first paragraph of this section. While the results for frequentist and Bayesian models for real-life application is presented in Table 3. Considering both frequentist and Bayesian is justified by the last two paragraphs in the introductory part of this paper. The result for the Bayesian regression model is presented in Table 4, Table 5 and Table 6.

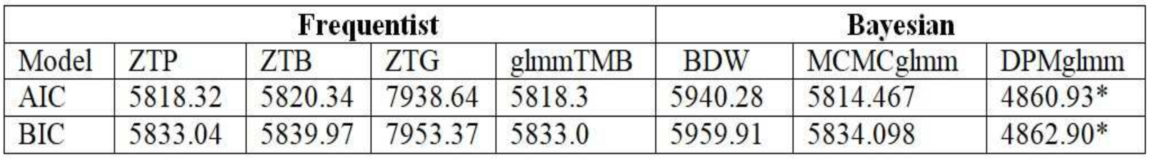
Table 1: Simulated Under-dispersed Zero-truncated data



Frequentist					Bayesian		
Model	ZTP	ZTB	ZTG	glmmTMB	BDW	MCMCglmm	DPMglmm
AIC	4182.33	4184.33	5193.36	4182.3	4225.66	4181.76	3522.10*
BIC	4197.05	4203.96	5208.08	4197.1	4245.29	4201.39	3524.20*

From **Table 1**, the results of simulated under-dispersed zero-truncated data using AIC and BIC, showed that DPMglmm outperformed BDW, MCMCglmm, ZTP, ZTB, ZTG, glmmTMB. Also, ZTP and glmmTMB outperformed ZTB and ZTG among the frequentist models.

Table 2: Simulated Over-dispersed Zero-truncated data



	Frequentist				Bayesian		
Model	ZTP	ZTB	ZTG	glmmTMB	BDW	MCMCglmm	DPMglmm
AIC	5818.32	5820.34	7938.64	5818.3	5940.28	5814.467	4860.93*
BIC	5833.04	5839.97	7953.37	5833.0	5959.91	5834.098	4862.90*

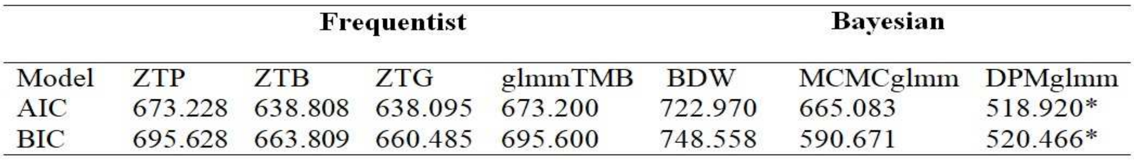
From **Table 2**, the results of simulated over-dispersed zero-truncated data are similar to that of over-dispersed. The AIC and BIC showed that DPMglmm outperformed BDW, MCMCglmm, ZTP, ZTB, ZTG, glmmTMB, while ZTP and glmmTMB outperformed ZTB and ZTG among the frequentist models.

3.2 Life Data

The life data used is on one hundred and eighty-one (181) patients with high and low Blood Pressure diagnosis. The data consists of visits to the doctor between the periods of July 2020 to July 2021. The variables include visit to doctor (Count Response); while the predictor variables are: Age, Sex coded as (male=1, female=0), Hypertensive Follow-up (HFollowp, F=1, N/F=0), Hypertensive Heart Disease (HHeartD, HHD=1, N/HHD=0), Poor Blood pressure control (Poor.BPC, PBPC=1, N/PBPC=0) and Hypotension (Hypo=1, Hyper=0). For the period observed, a patient must have been diagnosed with either high blood pressure or low blood pressure. If a patient's condition is not suffering from hypotension (Low BP), then it is a case of hypertension (High BP). Hypertensive Heart Disease, Poor BPC, HFollowup were captured as cases associated with patients diagnosed for blood pressure.

The mean is 2.801, and the variance is 4.616, by implication, the data is over-dispersed. The model performance of Frequentist and Bayesian Models for the Blood pressure data are presented in Table 3. The AIC and BIC were used as model selection criteria in this study. The results in Table 3 are for the Zero-truncated Poisson (ZTP), Zero-truncated Binomial(ZTB), Zero-truncated Geometric (ZTG), and GLMMs Template model Builder (glmmTMB).

Table 3: Model performance of Frequentist and Bayesian Models for life data

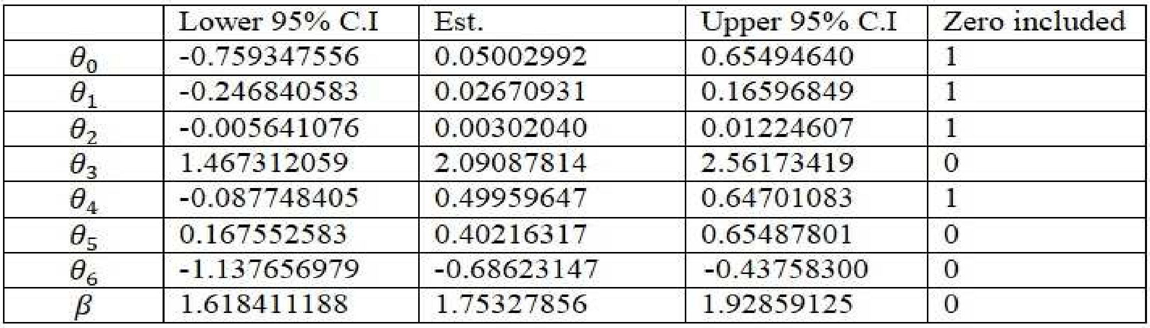


	Frequentist				Bayesian		
Model	ZTP	ZTB	ZTG	glmmTMB	BDW	MCMCglmm	DPMglmm
AIC	673.228	638.808	638.095	673.200	722.970	665.083	518.920*
BIC	695.628	663.809	660.485	695.600	748.558	590.671	520.466*

The results in **Table 3** showed that DPMglmm outperformed all the Bayesian and Frequentist models, while Truncated Geometric distribution outperformed ZTP, ZTB, ZTG, and glmmTMB on BIC value. **Table 4** contains the results of Bayesian Discrete Weibull regression. Laplace prior was used, with 0.25 percent of the 30,000 iteratins was allowed in the burn-in stage to allow stability in the chain.

From **Table 4**, θ_0 is the intercept, θ_1 is sex, θ_2 is Age, θ_3 is HFollowup, θ_4 is HHearthD, θ_5 is Poor.BPC, and θ_6 is Hypotension. The results show that θ_0, θ_1, θ_2, and θ_4 are zero included. While θ_3, θ_5, θ_6, and β are not zero included, so, θ_3 (Hypertensive Heart disease), θ_5 (Poor BP control), and θ_6 (Hypotension), and β significantly impact on the number of visits of Blood pressure cases to the health facility. The results in **Table 4** are demonstrated in Fig 1. Significant parameters are in red.

Table 4: Estimation Based on Bayesian Discrete Weibull



	Lower 95% C.I	Est.	Upper 95% C.I	Zero included
θ_0	-0.759347556	0.05002992	0.65494640	1
θ_1	-0.246840583	0.02670931	0.16596849	1
θ_2	-0.005641076	0.00302040	0.01224607	1
θ_3	1.467312059	2.09087814	2.56173419	0
θ_4	-0.087748405	0.49959647	0.64701083	1
θ_5	0.167552583	0.40216317	0.65487801	0
θ_6	-1.137656979	-0.68623147	-0.43758300	0
β	1.618411188	1.75327856	1.92859125	0

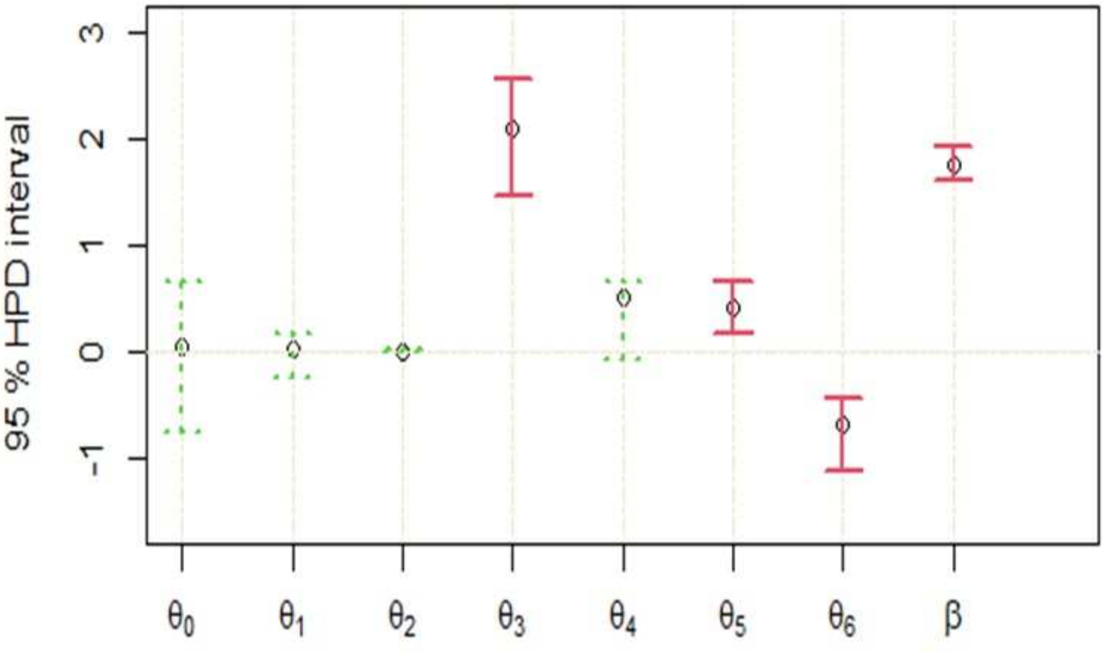


Fig. 1: Plots showing the significance of the parameters.

Table 5 represents the results of the MCMCGLMMs. 3000 iterations was conducted and 10%, that is, 300 iterations were allowed in the burn-in stage to allow stability in the chain.

Table 5 shows that HFolloup (hypertensive follow-up) and Poor.BPC account for number of visits of hypertensive patients to the doctor at the health facility. Figure **??** shows the iterations (left) and the density (right).

Table 5: Estimation Based on MCMCGLMMs

	post.mean	l-95% CI	u-95% CI	eff.samp	pMCMC
(Intercept)	0.86328	-1.33389	3.18522	270.0	0.430
Sex	0.05110	-0.55864	0.63536	410.9	0.933
Age	-0.01695	-0.05286	0.01983	270.0	0.370
HFollowup	2.56122	1.26253	3.88199	270.0	<0.004 **
HHearthD	0.48288	-1.74972	2.28932	270.0	0.593
Poor.BPC	1.28210	0.50173	2.08830	270.0	<0.004 **
Hypotension	-0.04898	-3.14676	2.19763	270.0	0.933

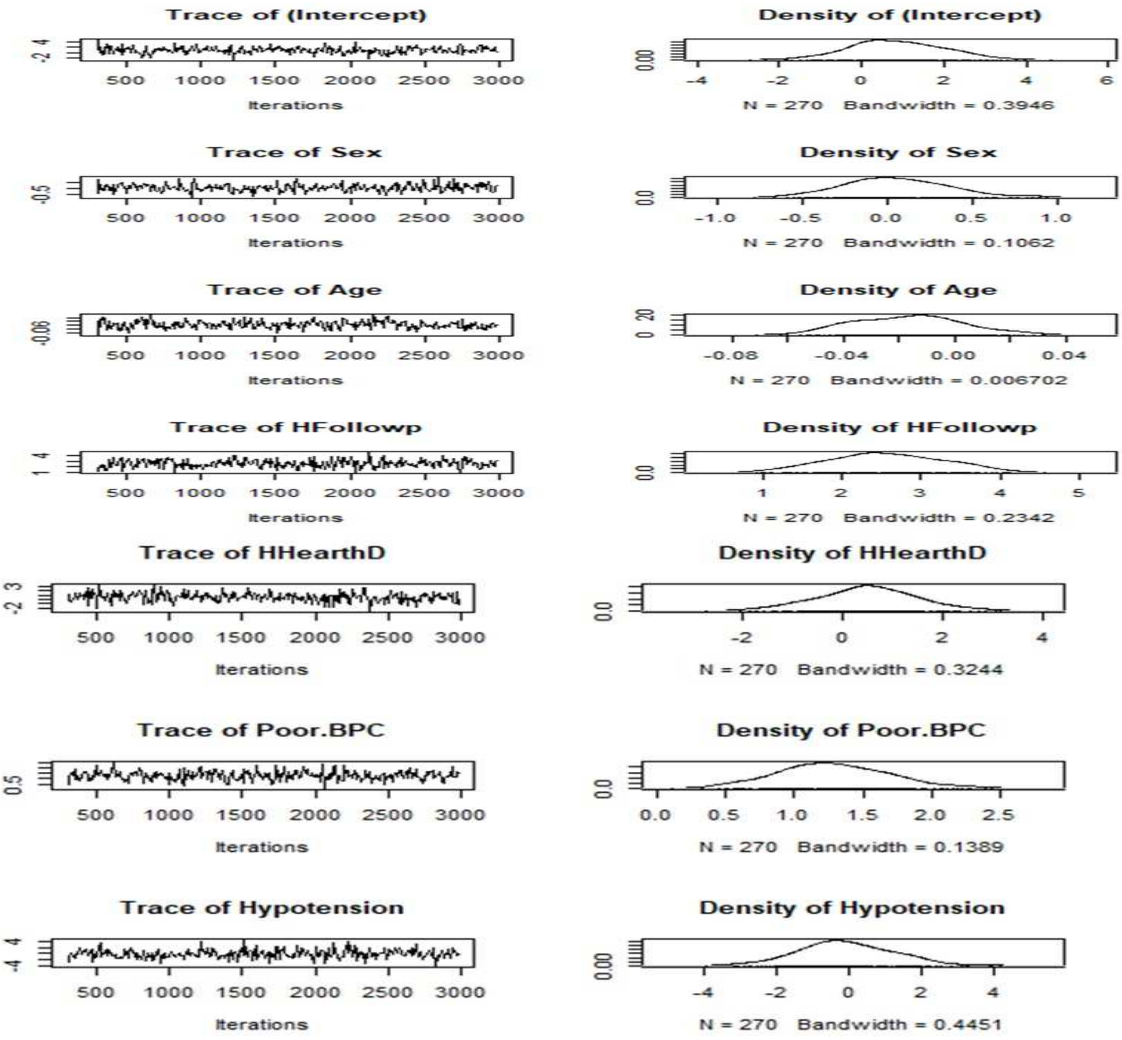
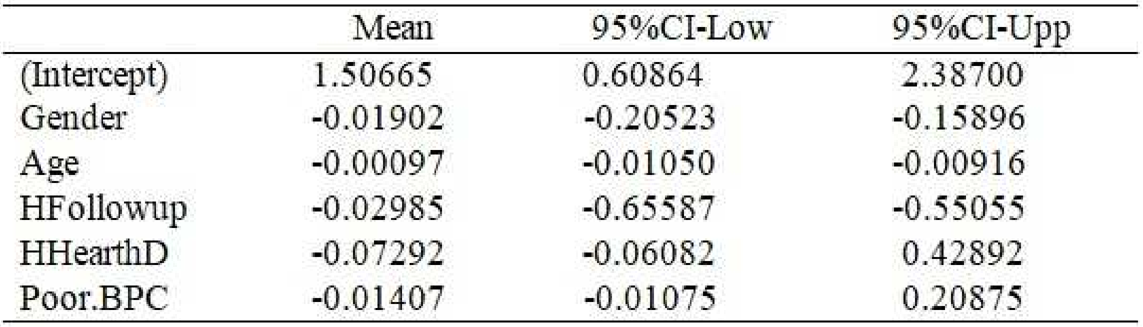


Fig. 2: shows the iterations and the density.

From Fig. 2, stability in the chain is observed.

Table 6: Regression coefficients for Bayesian DPMglmm



	Mean	95%CI-Low	95%CI-Upp
(Intercept)	1.50665	0.60864	2.38700
Gender	-0.01902	-0.20523	-0.15896
Age	-0.00097	-0.01050	-0.00916
HFollowup	-0.02985	-0.65587	-0.55055
HHearthD	-0.07292	-0.06082	0.42892
Poor.BPC	-0.01407	-0.01075	0.20875

Table 6 shows the results of fitting the blood pressure count data using Bayesian DPMglmm. The posterior mean for gender was (-0.019), which shows that less males diagnosed for blood pressure cases visit the doctor as compared to their female counterparts. Posterior mean for Age is (-0.00096) which implies that the patients that have more visits to the doctor were not necessarily the older people. The posterior mean for HFollowup was (-0.0298) which implies that blood pressure patients being followed significantly account for the number of visits to the doctor.

The results from zero truncated geometric show that bad blood pressure control is highly significant with a coefficient 0.6337, z-value=2.872 and p-value =0.0041. Indicating that amongst other reasons, ”bad blood pressure control” accounts for visits of patients diagnosed with pressure cases to the doctor. This result agrees with that of the study by [43] that hypertensive patients do not always feel sick; hence do not see reasons why they should pay special attention to their blood pressure.

4 CONCLUSION

In this study, truncated models, glmmTMB, and Bayesian models have been used to fit count data that is truncated at zero. Models that have been proposed for fitting count data in the past were either suitable for fitting under-dispersed count data or for over-dispersed count data. Recent studies have proposed robust models for either under-dispersed or over-dispersed count data. The results in the simulation study show that glmmTMB and zero truncated Poisson outperformed both zero-truncated binomial and zero-truncated Geometric in the under-dispersed and over-dispersed count data. The comparison between Bayesian and frequentist is further to establish the superior strength of Bayesian techniques over the frequents as identified [23-26] which has been demonstrated with the performance of DPMGlmms.

The findings in this study, based on simulated data, show that the Bayesian DPMGlmm is a better model for fitting zero truncated count data for under-or over-dispersed count data; while zero truncated Poisson regression may be used when considering frequentist models for modelling zero truncated data. The result of the life data also shows that Bayesian DPMglmm is superior to all the competing models for both under-dispersed and over-dispersed count data. DPMglmm also outperformed all the frequentist models dedicated to fitting zero-truncated count data.

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