Symposium on BioMathematics 2019 (SYMOMATH 2019)
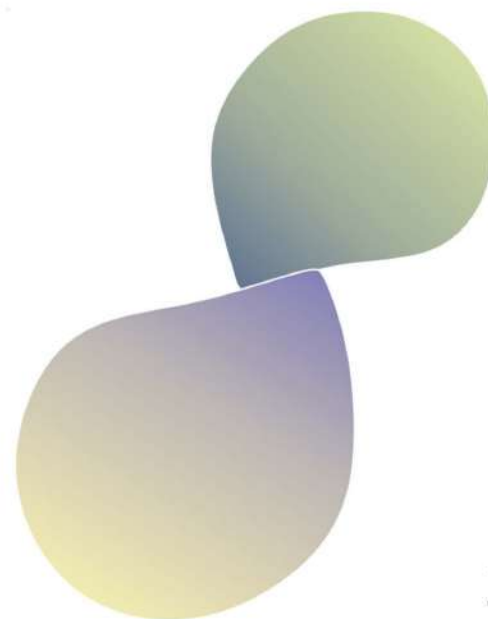
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Preface: Symposium on Biomathematics 2019

This volume consists of the refereed papers presented at Symposium on Biomathematics (Symomath) 2019 held on August 25-28, 2019 in Bali, Indonesia. This conference was sponsored by Institute for Research and Community Services (LPPM-ITB), International Mathematical Union (IMU), Center for Mathematical Modelling and Simulation (P2MS-ITB) and also Indonesian Biomathematical Society (IBMS).

This Symposium is intended as a medium to disseminate and share knowledge in the area of biomathematics. Research in biomathematics is a multidisciplinary activity. As indicated by the name, it is a study of biological phenomena using mathematical methods and tools. This symposium is devoted to facilitate and to enable communication among these scientists. It is expected that through this conference a closer connection will emerge, further multi-disciplinary collaborations will appear, and in turn will give benefits, both in solving biological problems and in the advancement of mathematical sciences.

This Symposium was attended by participants from all over the countries: Germany, UK, USA, Scotland, New Zeeland, Ukraine, Malaysia, Philippines and Indonesia. There were two keynote talks, four plenary talks, eight invited talks and 65 contributed talks. About 32 selected papers from contributed talks (after peer review process) are published in this volume.

We thank all organizing committee members and referees for their excellent works. Our high appreciation also goes to all invited speakers and to all participants for making this conference successful and enjoyable.

Bandung, February 2020

Sponsors

Financial support for this conference is mainly provided by the Center of Mathematical Modelling and Simulation (PPMS) Institut Teknologi Bandung, Institute for Research and Community Services (LPPM) ITB, International Mathematical Union, and Indonesian Biomathematical Societies.

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Estimating Model of The Number of HIV and AIDS Cases in East Java Using Bi-response Negative Binomial Regression Based on Local Linear Estimator

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Abstract. The number of HIV and AIDS cases is a count data correlated with each other. The common model to regress two response variables in the form of count data is bi-response Poisson regression. One infraction of assumptions in the Poisson regression is over dispersion. Negative binomial regression is is to be solution to this over dispersion case. This study aims to estimate bi-response negative binomial nonparametric regression model based on local linear estimators for modeling the number of HIV and AIDS cases in East Java. The results give the deviance value as the goodness of fit criterion of bi-response negative binomial nonparametric regression model by using local linear estimator of 2.263 which is smaller than the deviance value of the parametric regression model of 3.926. It means that the bi-response negative binomial nonparametric regression model by using local linear estimator is better than that by using parametric regression model approach to explain the relationship between HIV and AIDS cases affected by drug users in East Java.

INTRODUCTION

Regression analysis is one of procedurers in statistic that can be used to describe the functional relationship between response variables and predictor variables. While the form of regression function known and the relationship between the response variables and predictor variables are assumed to be certain curves, so parametric approach is appropriate to be used, while the relationship between the response variables and predictor variables is not in accordance to a particular pattern or there is no information about the form of regression, so nonparametric approach is appropriate to be used. The nonparametric regression approach has high usefulness because the regression function is not specified in certain forms, but it is assumed to be smooth. So it is estimated by using smoothing method based on data patterns [1].

Based on the type of response variable, there are various types of regression models. One of the regression models with discrete response variables is Poisson regression model. The response variable (Y) in the Poisson regression model must meet the assumption $\text{var}(Y) = E(Y)$ that called equidispersion. To avoid the problem of over-dispersion in the Poisson regression model, in the parametric regression model has a rapidly developed regression model that does not assumed a Poisson distribution on the response variable. Some of the research include: [2] have used generalized Poisson to be applied to accident data; [3] and [4] have developed a negative binomial regression. In the case of bi-response, [5] has discussed the bivariate generalized Poisson model with moment estimates and maximum likelihood; [6] and [7] have discussed the bivariate negative binomial regression model.

Nonparametric approaches with continuous responses in bi-response and multi-response cases have also been developed by several researchers, including by [8], [9], [10], [11], [12], [13], [14], [15], [16], [17], [18], and [19]. Nonparametric regression models with discrete type response variables have not been developed by researchers yet.

[20] has used kernel estimators on Poisson regression; [21] has used a spline estimator in Poisson regression to model the relationship between socioeconomic status with mortality; [22] has discussed Poisson regression with a local linear estimator; and [23] has discussed Poisson regression with kernel estimator for machine order claims; [24] used kernel; [25] has used local linear estimator; [26] has used local polynomial estimators in generalized Poisson regression to model infant mortality based on age.

There is no development estimation theory used for negative binomial regression by using local linear estimator approach so far. The local linear approach is good for use at the parsimony principle model, so it is easily interpreted. In this study, bi-response negative binomial regression with local linear estimator approach will be implemented in the data the number of HIV and AIDS cases in East Java with predictors the number of drug users. In Indonesia, reports of new HIV cases have continued to increase every year since it was first reported (1987), in 2017 report data shows that the five provinces with the highest number of infections are East Java, Jakarta, West Java, Central Java and Papua [27]. The Number of HIV case and AIDS case in East Java is a count data that correlate with each other, so bi-response negative binomial regression is an appropriate model to use.

MATERIAL AND METHODS

In this study, the data used are secondary data obtained from the Health Department of East Java consists of 17 regencies. Steps used to estimate the model in modeling the number of HIV cases and AIDS cases in East Java with the number of drug users as predictor variable is as follows, The first step starts with conducting a correlation test between response variables, and then estimates bi-response negative binomial regression model with local linear estimator approach. Two response variables $(y_1 \text{ and } y_2)$ are known to be correlated. Suppose given (x_i, y_{1i}, y_{2i}) which is paired data, with $i = 1, 2, ..., n$ and n is the amount of observation data. Regression models for the response variable y_{1i} and y_{2i} which are discrete random variable type and it is assumed that both response variables have a bivariate negative binomial distribution as follows [28]:

$$f(y_{1i}, y_{2i} \mid x_i) = \frac{\Gamma\left(\frac{1}{\alpha} + y_{1i} + y_{2i}\right)}{\Gamma\left(\frac{1}{\alpha}\right)\Gamma(y_{1i}+1)\Gamma(y_{2i}+1)}[\mu_1(x_i)]^{y_{1i}}[\mu_2(x_i)]^{y_{2i}} \times \alpha^{-\frac{1}{\alpha}}\left(\frac{1}{\alpha} + \mu_1(x_i) + \mu_2(x_i)\right)^{-\left(\frac{1}{\alpha} + y_{1i} + y_{2i}\right)} \tag{1}$$

where $\mu_1(x_i) = \exp\left(x_i^T \underset{\sim}{\beta_1}\right)$ (2)

$\mu_2(x_i) = \exp\left(x_i^T \underset{\sim}{\beta_2}\right).$ (3)

We estimate the parameters $\underset{\sim}{\beta_1}$ and $\underset{\sim}{\beta_2}$ in (2) and (3) by using locally weighted maximum likelihood the method. This method is done through the following steps:

1) Taking random samples size n :

$(y_{1i}, y_{2i}, x_i) \quad i = 1, 2, \cdots, n$

2) Determining the likelihood function as follows:

$$\ell\left(\underset{\sim}{\beta_1}, \underset{\sim}{\beta_2}, \alpha, x_0\right) = \prod_{i=1}^{n}\left[\left\{\frac{\Gamma\left(\frac{1}{\alpha} + y_{1i} + y_{2i}\right)}{\Gamma\left(\frac{1}{\alpha}\right)\Gamma(y_{1i}+1)\Gamma(y_{2i}+1)}[\mu_1(\underset{\sim}{x_i})]^{y_{1i}}[\mu_2(\underset{\sim}{x_i})]^{y_{2i}} \times \alpha^{-\frac{1}{\alpha}}\left(\frac{1}{\alpha} + \mu_1(\underset{\sim}{x_i}) + \mu_2(\underset{\sim}{x_i})\right)^{-\left(\frac{1}{\alpha} + y_{1i} + y_{2i}\right)}\right\}^{K_h(x_i - x_0)}\right] \tag{4}$$

3) Determining the log-likelihood function as follows :

$$L\left(\underset{\sim}{\beta_1}, \underset{\sim}{\beta_2}, \alpha, x_0\right) = \sum_{i=1}^{n} K_h(x_i - x_0)\left\{\ln\Gamma\left(\frac{1}{\alpha} + y_{1i} + y_{2i}\right) - \ln\Gamma\left(\frac{1}{\alpha}\right) - \ln\Gamma(y_{1i}+1) - \ln\Gamma(y_{2i}+1) + y_{1i}\ln\left(\mu_1(\underset{\sim}{x_i})\right) + y_{2i}\ln\left(\mu_2(\underset{\sim}{x_i})\right)\right.$$
$$\left. - \frac{1}{\alpha}\ln\alpha - \left(\frac{1}{\alpha} + y_{1i} + y_{2i}\right)\ln\left(\frac{1}{\alpha} + \mu_1(\underset{\sim}{x_i}) + \mu_2(\underset{\sim}{x_i})\right)\right\} \tag{5}$$

4) Maximizing the log-likelihood function in (5):

the first derivative $L\left(\underset{\sim}{\beta_1}, \underset{\sim}{\beta_2}, \alpha\right)$ to $\underset{\sim}{\beta_1}$ is:

$$\frac{dL(\underset{\sim}{\beta_1},\underset{\sim}{\beta_2},\alpha,x_0)}{d\underset{\sim}{\beta_1}} = \sum_{i=1}^{n} K_h(x_i - x_0) \left\{ \left(\frac{y_{1i}}{\mu_1(\underset{\sim}{x_i})} - \frac{\left(\alpha^{-1} + y_{1i} + y_{2i}\right)}{\left(\alpha^{-1} + \mu_1(\underset{\sim}{x_i}) + \mu_2(\underset{\sim}{x_i})\right)} \right) \underset{\sim}{x_i}\mu_1(\underset{\sim}{x_i}) \right\} \quad (6)$$

the first derivative $L(\underset{\sim}{\beta_1},\underset{\sim}{\beta_2},\alpha)$ to $\underset{\sim}{\beta_2}$ is:

$$\frac{dL(\underset{\sim}{\beta_1},\underset{\sim}{\beta_2},\alpha,x_0)}{d\underset{\sim}{\beta_2}} = \sum_{i=1}^{n} K_h(x_i - x_0) \left\{ \left(\frac{y_{2i}}{\mu_2(\underset{\sim}{x_i})} - \frac{\left(\alpha^{-1} + y_{1i} + y_{2i}\right)}{\left(\alpha^{-1} + \mu_1(\underset{\sim}{x_i}) + \mu_2(\underset{\sim}{x_i})\right)} \right) \mu_2(\underset{\sim}{x_i})\underset{\sim}{x_i} \right\} \quad (7)$$

while the first derivative $L(\underset{\sim}{\beta_1},\underset{\sim}{\beta_2},\alpha)$ to α is:

$$\frac{dL(\underset{\sim}{\beta_1},\underset{\sim}{\beta_2},\alpha,x_0)}{d\alpha} = \sum_{i=1}^{n} K_h(x_i - x_0) \left\{ \psi\left(\frac{1}{\alpha} + y_{1i} + y_{2i}\right) - \psi\left(\frac{1}{\alpha}\right) + \frac{\ln\left(\frac{1}{\alpha} + \mu_1(\underset{\sim}{x_i}) + \mu_2(\underset{\sim}{x_i})\right)}{\alpha^2} - \frac{\frac{1}{\alpha^2}\left[-\frac{1}{\alpha}\ln\alpha - \left(\frac{1}{\alpha} + y_{1i} + y_{2i}\right)\right]}{\left(\frac{1}{\alpha} + \mu_1(\underset{\sim}{x_i}) + \mu_2(\underset{\sim}{x_i})\right)} \right\} \quad (8)$$

Because of equations (6), (7) and (8) do not provide explicit equations, we use the Newton-Raphson method to obtain the solutions to these equations as a numerical approach. Newton-Raphson iteration is an algorithm that utilizes first-order derivative vectors and second-order derivative matrices of maximized likelihood functions.

RESULTS AND DISCUSSION

Based on Pearson correlation test result, we get p-value of 0.001 that is less than $\alpha = 0.05$. It means that there is a significant correlation between the number of HIV and AIDS cases. Therefore, we can model the number of HIV cases and AIDS cases simultaneously by using bi-response negative binomial regression.

The following figure is plots of number of HIV (1st response) and AIDS (2nd response) cases versus drug users.
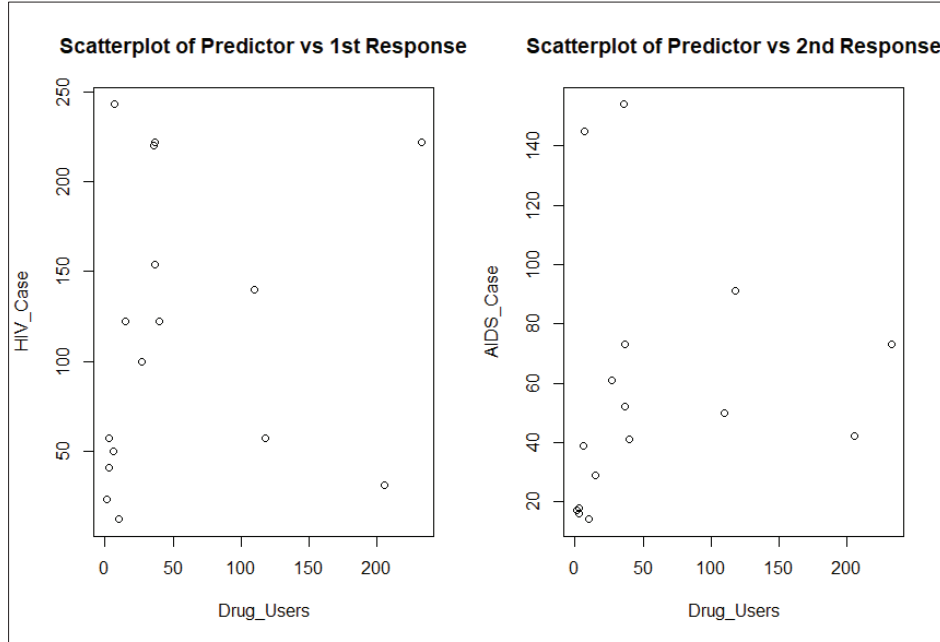

FIGURE. 1. Plots of number of HIV (1st response) and AIDS (2nd response) cases versus drug users.

Figure 1 shows that patterns of the number of HIV and AIDS cases over the drug users spread and they do not follow a specific pattern. So, bi-response negative binomial nonparametric regression is appropriate for modelling them.

In the estimation of nonparametric regression models based on local linear estimators, optimal bandwidth values are needed. The determination of the optimal bandwidth is based on the maximum value of the maximum likelihood cross-validation (MLCV) criteria. Table 1 gives the bandwidth and MLCV values.

TABLE 1. Values of bandwidth and MLCV

Bandwidth	MLCV
10.4	82.13287
10.5	82.26105
10.6	**82.37577**
10.7	81.35707
10.8	81. 44846

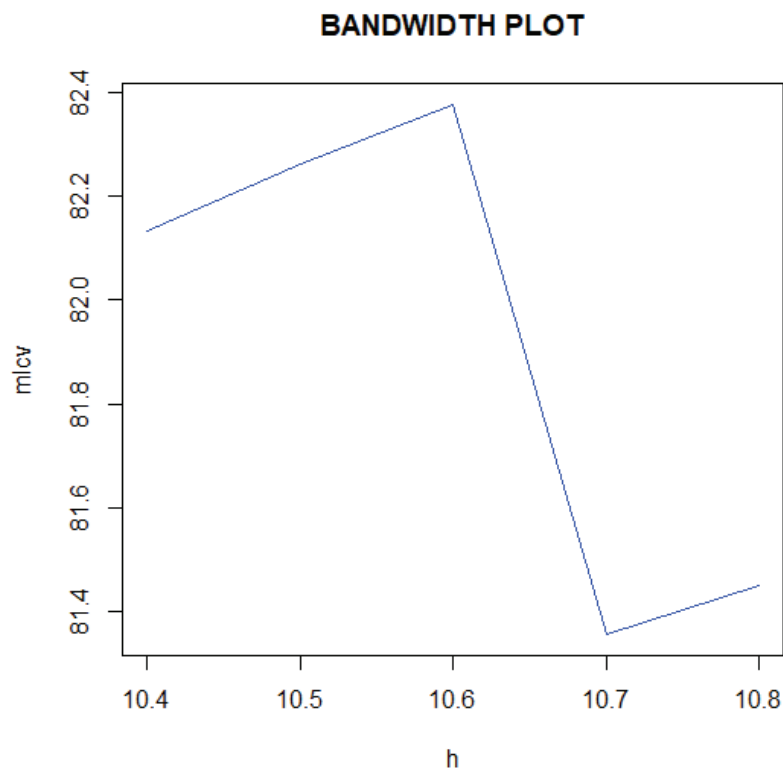The plot of MLCV versus bandwidth is shown in Fig. 2.

FIGURE. 2. Plot of MLCV versus Bandwidth

Based on Fig. 2, the optimal bandwidth is 10.6, with a maximum MLCV of 82.37577. After obtaining the optimal bandwidth value, we estimate the bi-response negative binomial nonparametric regression model by using local linear estimator. The estimated model has different coefficients depending on the location. One of the estimation results of the model obtained in Pasuruan Regency, which has the highest number of HIV sufferers as follows:

$$\hat{\mu}_1 = \exp\left(5.064 + 0.00046(x-7)\right), 0 < x < 17.6 \tag{9}$$

$$\hat{\mu}_2 = \exp\left(4.377 + 0.00041(x-7)\right), 0 < x < 17.6 \tag{10}$$

Based on equation (9) we can interpret, for every addition of ten drug users will give a change in the number of HIV cases by 1.0046 times compared with the previous case. Based on equation (10) we can interpret, for every addition of ten drug users will provide a change in the number of AIDS cases by 1.0041 times compared with the previous case.

Goodness of fit test on bi-response negative binomial nonparametric regression model by using local linear estimator for the number of HIV and AIDS cases in East Java over the number of drug users gives deviance value of 2.623 which is smaller than $\chi^2_{(\alpha, 2*n-(p+1))} = 40.113$. It means that the model is appropriate. Next, we also estimate the number of HIV case and AIDS cases in East Java by using parametric regression model approach. Thus, we get the estimated model as follows:

$$\hat{\mu}_1 = \exp(4.316 + 0.00179x) \text{ and } \hat{\mu}_2 = \exp(3.614 + 0.0032x) \tag{11}$$

based on the estimated model, we obtain deviance value of 3.926.

Based on equations (9) and (10), we can plot the estimated results for the both response variables and the observations shown in Fig. 3, where the red dot is the observation, the blue line is the parametric estimated results, and the green line is nonparametric estimated results.
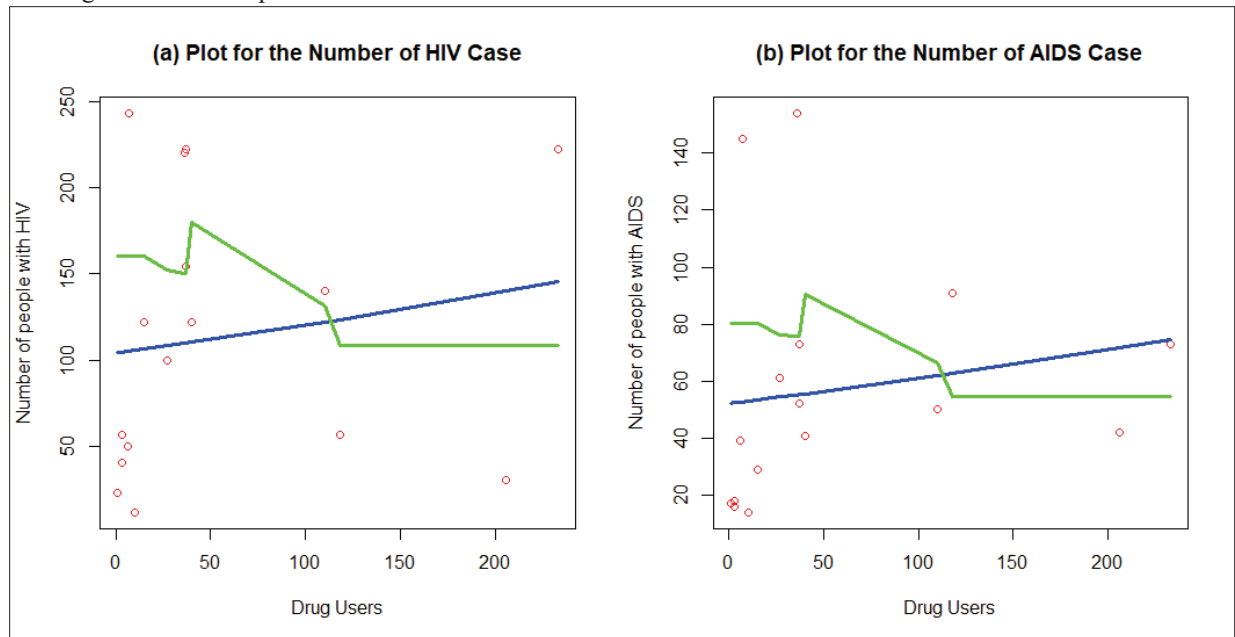

FIGURE. 3. Plots of observations and estimates of (a) HIV cases, and (b) AIDS cases

Based on Fig. 3, the estimated nonparametric regression model by using local linear estimator (green line) is closer to the observations data (red dot) than estimated parametric regression model (blue line). Likewise, based on goodness of fit criterion, i.e., deviance value of the estimated nonparametric regression by using local linear estimator is 2.623, which is less than the deviance value for the estimated parametric regression model of 3.926. It means that bi-response negative binomial nonparametric regression model by using local linear estimator is more appropriate than the estimation results by using the parametric regression model approach.

CONCLUSION

The estimated model we have obtained shows that estimation of the number of HIV and AIDS cases in East Java by using bi-response negative binomial nonparametric regression model based on local linear estimator has satisfied the deviance value as goodness of fit criterion which is less than chi-square value. Based on the estimated model by using local linear estimator we get local models for 17 regencies where they give different effects on the number of HIV and the number of AIDS cases affected by drug users.

ACKNOWLEDGMENT

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