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An Econometric Model for the Explanation of Clinic Attendance Due to Malaria

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Abstract

The work is on the application of Poisson Regression to data on vital signs of persons treated of malaria collected on 153 patients from Federal University of Technology, Owerri, Nigeria, Medical Centre for 46 weeks in 2014. The purpose is to know the significant vital signs measurement that best explained clinic attendance due to malaria. which was not quite clear from the Principal Component Analysis (PCA) of similar data by earlier researchers. Our findings showed that the only significant variable that explained clinic attendance due to malaria was 'temperature'. It was significant even at 1% level of significance. It was further found that a 1% change in temperature would lead to a 1% change in the number of clinic visits due to malaria. The study therefore recommended the use of 'temperature' as the only vital sign in diagnosing malaria, among others.

Keywords: Malaria, principal component analysis, poisson regression, temperature

1.0. Introduction

Malaria has a high level of mortality and is the world's most prevalent parasitic disease. It is caused by infection with single-celled parasites of the genus *Plasmodium*, which is transmitted by the bite of *Anopheles* mosquitoes. Apart from the endemic tropical and sub-tropical regions, malaria was once widespread in North America and other temperate countries. Today the disease occurs mostly in sub-Saharan Africa and Southeast Asia (Onyiri, 2015). Malaria is the second leading cause of death from infectious diseases in Africa after HIV/AIDS, with Nigeria and the Democratic Republic of Congo (DRC) accounting for 40% of the global malaria deaths (WHO, 2014). Almost 20% of all deaths of children under-five in Africa are

due to malaria (WHO, 2014). In Nigeria, statistics shows that malaria accounts for 25% of the under-five mortality, 30% of childhood mortality and 11% of maternal mortality (Okonko *et al*., 2009). All Nigerians are at risk of malaria and the problem is compounded by the increasing resistance of malaria to hitherto cost-effective drugs (Okonko *et al*., 2009).

Several statistical researches have been conducted about malarial infections. The studies ranged from exploration of determinants of malaria (Sekou *et.al,*2014), trend analysis of malaria (Abebe Alemu *et al.*, 2012; Evans and Adenomon, 2014; Leey *et al.*, 2015), relationship between meteorological variables and malaria incidence (Fang *et al*., 2011), to relationship between age and environmental covariates and malaria (Onyiri, 2015); among others. None of these studies looked at the diagnosis of malaria using vital signs. It is this vacuum that this study intends to fill. The work of Iwu and Nwachukwu (2014) discussed in the next paragraph motivated this work.

In their analysis of vital signs measurement of persons treated of malaria, Iwu and Nwachukwu (2014) collected data on six vital signs of malaria from 200 patients at Federal University of Technology (FUTO) medical centre in 2014 and applied the statistical tool of principal component analysis (PCA) in the analysis. They discovered that 'about 80% of the total variations in vital signs measurements of persons treated of malaria were explained by the first four (4) principal components (temperature, pulse, systolic blood pressure and diastolic blood pressure)'. They therefore recommended that in the diagnosis of malaria on the basis of vital signs, that these four measurements are sufficient. However, the process through which these four components were chosen were not clear as only two components contributing to 48.3% of the total variability in the set of data were at least 1.00. Other components were below 1, and such components are usually dropped in analysis (Hamilton, 2006). Again, it was observed that the first component consisted of X_3, X_4 and X_6 (systolic, diastolic and body weight) measurements, the second component consisted of X_2 and X_5 (pulse and respiration) measurements while the fourth component consisted of X_1 (Temperature) measurement. The process through which only four measurements of 'temperature, pulse, systolic blood pressure and diastolic blood pressure' were chosen was unclear. Due to this lack of clarity, it became imperative for additional studies to be conducted in order to identify

the significant vital signs variables for diagnosing malaria. In this study, we propose the use of Poisson Regression. A Poisson regression is a count regression which involves the relationship between the number of events of interest in a fixed time interval and a set of covariates. The interest focuses on how the mean number of events changes due to changes in one or more of the regressors. A statistical study of malaria using the Poisson Regression approach is not new. For instance, Evans and Adenomon (2014) already cited above, studied the trend of malaria prevalence in Minna, Niger State of Nigeria using monthly malaria outpatient data collected from the General Hospital, Minna using the Poisson regression and the Negative Binomial regression models. The results from the Poisson regression and the Negative Binomial regression models revealed that the prevalence of Malaria in Minna, Niger State increased by approximately 6% every month.

This work is organized into five sections. Following this introduction therefore, are: Literature Review, Methodology, Results and Conclusion, in this order.

2.0. Literature Review

The Poisson regression is the common starting point for count data analysis, and is well motivated by assuming a Poisson process (Cameron and Trivedi, 2009). The Poisson regression model assumes that y_i given X_i is Poisson distributed with density:

$$f(y/x) = \frac{\mu^y e^{-\mu}}{y!}; \qquad y = 0,1,2,... \tag{1}$$

The Poisson distribution is unimodal and skewed to the right over the possible values 0, 1, 2, …It has a single parameter $\mu > 0$, which is both its mean and its variance (Agresti, 2007). Haight (1967) cited in Frome *et al*, (2012) described the historical development of the Poisson and related distributions from 1781 to 1920 and noted that although Poisson discovered the mathematical expression, Bortkiewicz discovered its use as a probability distribution for discrete data. He further claimed that the Poisson distribution is second in importance to the normal from both a theoretical and applied perspective.

Poisson regression model expresses the natural logarithm of the event or outcome of interest as a linear function of a set of predictors. The dependent variable is a count of the occurrences of interest e.g. the number of cases of a disease that occur over a period of follow-up. Typically, one can estimate a rate ratio associated with a given predictor or exposure. For a single explanatory variable, the Poisson loglinear model has the form:

$$\log(\mu) = \alpha + \beta X \tag{2}$$

The mean satisfies the exponential relationship:

$$\mu = \exp(\alpha + \beta X) = e^{\alpha}(e^{\beta})^{X} \tag{3}$$

A one-unit increase in $X = x$ has a multiplicative impact of e^{β} on μ: the mean at $X = x+1$ equals the mean of Y at x multiplied by e^{β}. If $\beta = 0$, then $e^{\beta} = e^{0} = 1$ and the multiplicative factor is 1. This means that the mean of Y does not change as X changes. If $\beta > 0$, then $e^{\beta} > 1$, and the mean of Y increases as X increases. If $\beta < 0$, then $e^{\beta} < 1$, the mean of Y decreases as X increases (Agresti, 2007).

Data frequently exhibit important “non-Poisson” features which include:

(a) Overdispersion: the conditional variance exceeds the conditional mean, whereas the Poisson distribution imposes equality of the two.

(b) Excess zeros: a higher frequency of zeros (or some other integer count) than that predicted by the Poisson distribution with a given mean.

(c) Truncation from the left: small counts (particularly zeros) are excluded.

(d) Censoring from the right: counts larger than some specified integer are grouped (Cameron & Trivedi, 2009).

The use of Poisson regression in the presence of any of these features leads to a loss of efficiency (and sometimes consistency), incorrect reported standard errors and a poor fit. These considerations motivate the use of distributions other than the Poisson.

Generalized Poisson (GP) and Negative Binomial (NB) regression models have been suggested to deal with over-dispersion. Zero-inflated count regression models such as the Zero-Inflated Poisson (ZIP), Zero-Inflated Negative Binomial (ZINB) and

Zero-Inflated Generalized Poisson (ZIGP) regression models have been used to handle count data with many zeros (Ilknur and Famoye, 2007).

The NB regression model with mean, $E(Y \mid x_i) = \mu_i$ and $V(Y \mid x_i) = \mu_i(1+\alpha\mu_i)$ as given by Lawless (1987) and quoted in Ilknur and Famoye (2007) is:

$$p(u_i, \alpha_i, y_i) = \frac{\Gamma(y_i + \alpha^{-1})}{y_i!\Gamma\alpha^{-1})}\left(\frac{\alpha\mu_i}{1+\alpha\mu_i}\right)^{y_i}\left(\frac{1}{1+\alpha\mu_i}\right)^{\alpha-1}; y_i = 0,1,2,... \quad (4)$$

where $\Gamma(.)$ denotes the gamma function and the dispersion parameter, α is unknown. In the limit as $\alpha \to 0$, (4) yields the Poisson regression model. When $\alpha > 0$, there is over-dispersion.

The GP model with mean, $E(Y \mid x_i) = \mu_i$ and $V(Y \mid x_i) = \mu_i(1+\alpha\mu_i)^2$ can be written as:

$$p(u_i, \alpha_i, y_i) = \left(\frac{\mu_i}{1+\alpha\mu_i}\right)^{y_i}\left(\frac{1+\alpha\mu_i}{y_i!}\right)^{y_i-1}\exp\left(\frac{-\mu_i(1+\alpha y_i)}{1+\alpha\mu_i}\right); \quad y_i = 0,1,2,... \quad (5)$$

In model (5), α is called dispersion parameter. When $\alpha = 0$, the GP regression model (5) reduces to the Poisson regression model (1) and this is a case of equi-dispersion. When $\alpha > 0$ (or when $\alpha < 0$), the GP regression model represents count data with over-dispersion (or under-dispersion).

A measure of the goodness of fit of the Poisson regression model is obtained by using the deviance statistic of a base-line model against a fuller model. Also, after reviewing the results from fitting a Poisson regression model, some type of model checking may be indicated. There are a number of model-checking techniques that can be considered if there is some indication that the Poisson model is inadequate. These techniques can be both formal and informal and usually involve the analysis of residuals, regression diagnostics, and the fitting of more complex models. Model checking methods are described in detail for count data by Cameron & Trivedi (1998), and for GLMs by McCullagh & Nelder (1989).

The Poisson Regression model is estimated using the Maximum Likelihood (ML) estimation method since the model is non-linear.

As noted earlier, Poisson Regression may analyze Count data (eg. number of surgical site infections). It can also analyze: Binary data (eg. received vaccine (yes/no) as alternative to logistic regression; and Time-to-event data (eg. time-to-stroke with time dependent covariate) as alternative to survival analysis (Kaltenback, 2008).

The first application of Poisson regression as reviewed in Frome *et al* (2012) was given by Cochran (1940) with wireworm counts from an agriculture experiment as the response variable and the regression function $E(Y_i) = \mu_i = (\mathrm{x}_i\,\beta)^2$, where x_i is the ith row of the model matrix for a Latin square design. This model is a GLM with a Poisson response and a "square root" link function — see Frome (1984) for additional details. Jorgenson (1961) proposed Poisson regression with a linear rate function for use in consumer demand analyses and reliability. Nelder and Wedderburn (1972) described GLM for response variables in the regular exponential family. Frome *et al.* (1973) described Poisson regression methods for general models with an emphasis on intrinsically nonlinear models. Frome (1983) described the analysis of event rates for Poisson data and Frome and Checkoway (1985) considered applications of these methods in epidemiologic follow-up studies. Breslow and Day (1987) described the use of Poisson regression in occupational cohort studies and Koch *et al.* (1986) gave a more complete review of Poisson regression methods and areas of applications. Cameron and Trivedi (1986) discussed Poisson regression in econometric applications. Richardson and Loomis (2004) reviewed the use of Poisson regression in occupational and environmental cohort studies and considered problems that may occur when person-time and events are tabulated by levels of an exposure variable that was originally measured on a continuous scale and has been categorized for analysis. Wing et al. (1991) and Frome et al. (1997) have applied these methods to mortality studies of nuclear industry employees. Poisson regression has also been used extensively in mortality studies of atomic bomb survivors. Preston et al. (1993) have developed special purpose software that supports the use of Poisson regression in the atomic bomb survivors' studies and other situations that require Poisson regression with excess relative risk models. Poisson regression has been used extensively in the analysis of motor vehicle accidents Erlander *et al.* (1972), Frome & Walton (1975), Gustavsson & Svensson (1976), Michener & Tighe (1992), Fridstrom *et al.,* (1995), Li *et al.,* (2001), Lord *et al.,* (2005). Other recent studies have also been cited in Section 1.

3.0. Methodology

3.1 Data

The data is a secondary data consisting of daily attendance record of people suffering from malaria in the Federal University of Technology, Owerri (FUTO) Clinic in 2014 (Ugwuanyim & Amachukwu, 2014). The data was aggregated for 46 weeks.

3.2. Model

$$\log(\mu_i) = \beta_o + \beta_1 X_{1i} + \beta_2 X_{2i} + \beta_3 X_{3i} + \beta_4 X_{4i} + \beta_5 X_{5i};\ i = 1, 2, ..., 46 \quad (6)$$

where:

μ_i = $E(Y_i \mid X_i)$

$\beta_j,\ j = 0,1,2,3,4,5$ = slope coefficients

X_{1i} = Temperature

X_{2i} = Pulse

X_{3i} = Systolic Blood Pressure

X_{4i} = Diastolic Blood Pressure

X_{5i} = Respiration.

The data was analyzed using STATA 13.0.

4.0. Results

4.1. Summary Statistics of Data

Table 1 gives a summary statistics of the data described in Subsection 3.1.

Table 1: Descriptive Statistics of Data

Statistics	Y	X_1	X_2	X_3	X_4	X_5
Mean	9.72	371.23	752.72	1090	741.02	187.83
SD	2.67	102.08	209.13	302.32	202.97	54.79
N	46	46	46	46	46	46

The mean number (Y) of times people attended clinic because of malaria within the 46 weeks is 10 times with a standard deviation of 3, i.e. a variance of 9. The average temperature (X_1) is 371.23^{o}C with a standard deviation of 102.08^{o}C. The rest can be interpreted in the same way.

We note here that the mean of Y is almost the same with its variance. There is no over-dispersion and the under-dispersion is minimal. So, the Poisson Regression is appropriate.

4.2. Analyses

The analyses of the collected data shall be presented in Tables 2 and 3 respectively as Poisson Analysis of Data and Elasticities respectively.

Table 2: Poisson Analysis of Data

```
Poisson regression                              Number of obs   =         46
                                                Wald chi2(5)    =     416.44
                                                Prob > chi2     =     0.0000
Log pseudolikelihood = -95.406577               Pseudo R2       =     0.1451
```

y	Coef.	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
temp	.0027169	.0009366	2.90	0.004	.0008812	.0045525
pulse	.0001565	.0002866	0.55	0.585	-.0004052	.0007183
systolic	-.0004482	.0004507	-0.99	0.320	-.0013316	.0004352
diastolic	.000287	.000208	1.38	0.168	-.0001207	.0006948
respiratory	.0007099	.0013483	0.53	0.599	-.0019328	.0033525
_cons	1.260866	.1017662	12.39	0.000	1.061408	1.460324

The Wald Chi-Square statistics is significant even at 1%. This shows that the model is adequate in modeling clinic attendance due to malaria. The body of the table shows that the only significant variable that explains clinic attendance due to malaria is temperature. It is also significant even at 1% level of significance. This can be interpreted as: a one-unit change in temperature is associated with a 0.0027 proportionate rise or a 0.27% increase in clinic visitations due to malaria. This interpretation is due to the fact that if the conditional mean of a regression model is

of the exponential form as the Poisson, then, the coefficient is a semi-elasticity (Cameron & Trivedi, 2009).

Table 3: Elasticities

```
Elasticities after poisson
      y  = Predicted number of events (predict)
         =  9.4384638
```

variable	ey/ex	Std. Err.	z	P>|z|	[95% C.I.]		X
temp	1.008584	.34768	2.90	0.004	.327142	1.69003	371.23
pulse	.1178092	.21574	0.55	0.585	-.30503	.540648	752.717
systolic	-.4885115	.49128	-0.99	0.320	-1.45139	.474371	1090
diasto~c	.21271	.15415	1.38	0.168	-.089422	.514842	741.022
respir~y	.1333357	.25325	0.53	0.599	-.363024	.629696	187.826

What is interesting about this table is that the predicted mean of y, the number of visits to the clinic is 9.43 which is approximately 9 but while using the raw data, and as presented in Table1, the mean is 9.78 which is approximately 10. This again goes to show the adequacy of the model. The elasticity is 1.0086. This means that a 1% increase in temperature, will lead to a 1% increase in the number of clinic visits due to malaria. This again buttresses the adequacy of the model.

5.0. Conclusion

We set out in this work to find out the significant vital signs variable for the diagnosis of malaria given that the work of earlier researchers in this area using principal component analysis was inconclusive. The vital signs considered were: temperature, pulse, systolic blood pressure, diastolic blood pressure and respiration. This study showed that the only variable that significantly explains clinic attendance due to malaria is 'temperature'. It was further discovered that a 1% increase in temperature, will lead to a 1% increase in the number of clinic visits due to malaria. The study therefore concludes by recommending that the only vital sign to be used for the diagnosis of malaria be 'Temperature'. Further studies can be carried out in this area to ascertain if there are gender, blood group and genotype differences in vital signs diagnosis of malaria since patients that visit hospitals differ in age, weight, feeding- pattern, shape, blood group, genotype, etc.

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