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Prevalence of Tuberculosis in Nigeria

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Abstract:
Studies on the prevalence and risk of tuberculosis (TB) among diagnosed human immunodeficiency virus (HIV)-infected patients in sub-Saharan Africa are alarming especially Nigeria ranking second in Africa and seventh in the world. In other to ascertain the relationship between new smear positive cure and new smear died, new smear complete, failed and defaulted, and variation also to establish if it's a good fit. In other to get our coefficient of determination at 5% level of significance, on the regression line is 0.963 explaining a 96.3% variation in the patients who died and 0.741 explaining 74.1% variation in patients that where cured. This shows that the models have an unexplained error as 3.7% and 25.9% respectively. There's no first order linear auto-correlation in the multiple linear regression data for Durbin Watson for patient that died. In regressions, this implies an under estimated level of statistical significance for patients cured.

Keywords: *Tuberculosis, multiple regressions, ANOVA, Durbin Watson test*

1. Introduction

Tuberculosis (TB) is a public health matter in developing countries which leads to the high cause of deaths above HIV (human immunodeficiency virus) and AIDS (acquired immune deficiency syndrome) (WHO, 2017). The World Health Organization's (WHO) Global mid report of 2017 accounted for 3 million new cases amid HIV-negative persons in 2016 (WHO, 2017), equated to 6.1 million in 2015 (WHO, 2016). Global Burden of Diseases, Injuries and Risk Factors (GBD) research of 2016 calculated a 9.0 million TB-HIV-negative persons (new and regressive cases) likened to 8.8 million in 2015 (GBD, 2015). These reports highlight a considerable impact of Tuberculosis worldwide. For instance, World Health Organization African region presented a 25% of the incident cases with non-HIV and HIV patients who have tuberculosis worldwide, Nigeria accounting for 407 cases per hundred thousand population i.e.8% in 2016, (WHO 2017), 322 per hundred thousand in 2015 (WHO 2016) these may be lower than the actual estimates in Nigeria because 15% were noted in 2015 (WHO, 2016).

In more than two decades, WHO listed Nigeria as a country with high burden of tuberculosis disease to encourage interventions and influence finance and policies to make better control on TB programmes (WHO, 2015). Theses assessment brought about a concentrated and practical control of tuberculosis worldwide. In a recent treatment regimen made available by the Nigerian TB control programme and its donors, scaled up available and accessible methods to improve TB diagnosis. As these efforts been made in Nigeria are limited, prompt actions to take care of these risk factors evolving in the population such as diabetes (Dooley & Chaisson, 2009, Patra*et.al*, 2014), alcohol consumption(Patra*et.al,* 2014, Rehm*et.al* 2009, Nelson, 2008, Volkmann *et.al*, 2015) and tobacco smoking (Patra*et.al*, 2014, Leung *et.al*, 2015),has to be controlled. Specific epidemiological studies investigating the trend in the burden of TB and its risk factors can be useful for experts in public health and policy matters to improve preventive and control measures in the country.
Research has proved that tuberculosis deaths amongst non HIV persons declined in many developing countries, these include Nigeria but the incident rate remains the same in many communities (WHO, 2017 and GBD, 2015).

In other that reduction in TB burden be realized in Nigeria, it's important to note not only the burden but the event to which the risks adds to the burden so as to inform targeted and prioritized TB programmes. It's usually impractical to have a detailed exposition of the level of TB disease in Nigeria from GBD findings due to its large size and scope that leads to the characterization of finding for other health areas and locations that are focused on (GBD 2015, Akinyemiju*et.al*, 2017,Melaku et.al, 2018,Charara et.al 2015, Fitzmaurice et.al 2017].

Tuberculosis as an air borne infection is caused by a bacterium called mycobacterium tuberculosis which affects the lungs, bone, stomach, etc, though curable and preventable, it has killed many people due to lack of prompt treatment. The disease spreads from person to person through an unventilated environment. It takes just a droplet of the

bacteria in the air for another person to get infected. This disease in most cases affects young adults in their most productive years; however, all age groups are at risk.

People with tuberculosis have a lifetime risk of falling ill by 10%. However, people having compromised immune systems, such as those living with (HIV) Human Immunodeficiency Virus, malnutrition, diabetes, or people who use tobacco are more at risk of falling sick with tuberculosis disease.

2. Materials and Methods

The word regression was introduced by Sir. Francis GoIton in 1877 in his study of hereditary, where he discovered that the heights of descendants (children) of tall parents tends to (go backward) towards the average height of the population. The mathematical line he developed was called the 'regression line'. Today, regression is understood as a scientific study that attempts to determine the strength and character of the relationship between two or more variables usually Yi as dependent variable and Xi as independent...

A regression line and its equation represent a numerical linear relationship between the variables concerned. The word 'regression' has maintained its name till today. In order to determine the mathematical equation that best fits the data of relationship and use it to predict variables, a powerful statistical tool is required. This tool is called regression analysis.

A regression assesses the predictor variables to account for variability in a dependent variable. Regression analysis is applied to many fields such as economics, health, social sciences, education, natural sciences, and business just to mention a few.

2.1. The Population Model

A simple linear regression model is a single response measurement Y relating to a single predictor (covariate, regressor) X for every observation. This assumption in the model is that the conditional mean function is linear with:

$$E(Y\,|X) \;=\; \alpha \;+\; \beta_k X_k.$$

In almost every case, more than one predictor variable is always available. Leading to a 'multiple regression' mean function:

$$E(Y/X) \;=\; \alpha \;+\; \beta_1 X_1 + \cdots + \beta_p X_p$$

Where$\alpha$is called the intercept and β_k are called slopes or coefficients and$k = 1,2, \ldots, p$.

Going further, we can say the responses vary around their mean values.Leading to a model

$$Y_i \;=\; \alpha \;+\; \beta_1 X_{i,1} + \cdots + \beta_p X_{i,p} \;+\; \varepsilon_i\,.$$

which is the same as writing $Y_i = E(Y\,|Xi) + \varepsilon_i$. Writing$X_{i,k}$ for the k^{th} predictor variable measuringfor the i^{th} observation,the main assumption for the errors ε_i is that $E\varepsilon_i = 0$ and $var(\varepsilon_i) = \sigma^2$ for all variances equal. Also the errors (ε_i) should be independent of each other. For small sample sizes, it's also important to note that the ε_i approximately have a normal distribution.

3. Interpretation of Result

In multiple regressions, the model takes the form of an equation that contains the coefficient β for each predictor. The first part, of the table gives us an estimate for the values β and these values indicates the contribution each predictor has on the model.

The β values tell us about the relationship between new smear positive cure or died and each predictor. If the value is positive, we can tell there is a positive relationship between the predictor and the outcome whereas a negative coefficient represents a negative relationship. For these data, all but new smear positive defaulted have a negative relationship for dependent variable new smear positive cure. So, as defaulters' increase by 10.634, the number of patients cured will decrease. Similarly, as the number of patients who completed treatment decrease by -0.948, the number of patients cured increase. Same applies to the number of failed patients decreasing by -2.746, patients cured will increase.

Model		Unstandardized Coefficients		Standardized Coefficients	T	Sig.	Correlations			Collinearity Statistics	
		B	Std. Error	Beta			Zero-order	Partial	Part	Tolerance	VIF
1	(Constant)	-5707.867	4016.953		-1.421	.177					
	new_smearpositive_complete	-.948	1.541	-.160	-.615	.548	.679	-.162	-.084	.272	3.678
	new_smearpositive_failed	-2.746	3.485	-.139	-.788	.444	.456	-.206	-.107	.594	1.684
	new_smearpositive_defaulted	10.634	2.772	1.075	3.836	.002	.850	.716	.521	.235	4.253

Table 1: Showing Table of Coefficients for New Smear Positive Cure
Dependent Variable: New_Smearpositive_Cure

For this table of coefficients (Table 1), there are two types of coefficients that are typically displayed in the table: unstandardized coefficients, and standardized coefficients. Un-standardized coefficients indicate how much the dependent variable differs from an independent variable when all other independent variables were held constant. For the un-standardized regression coefficient: every metric unit change in the independent variable new smear positive for patients who completed their medication, those whose bodies failed to respond to medication and those who defaulted (did not complete medication), the dependent variable new smear positive cure changes. This set of variables forms the estimated regression line as:

$$\hat{y} = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3$$
$$\hat{y}(\text{cure}) = -5707.867 - 0.948(\text{complete}) - 2.746(\text{failed}) + 10.634(\text{defaulted}) \ldots . (4.1.1)$$

With a critical value for 95% confidence interval or $\alpha = 0.05$ or 5% error rate, and a degree of freedom$N - 4 = 18 - 4 =$ 1418-4=14Same degree of freedom is applied for new smear positive died. The estimated regression line for patients that died is shown below;

$$\hat{y}(\text{died}) = -180.269 + 0.359(\text{complete}) - 0.989(\text{failed}) + 0.391(\text{defaulted}) \ldots . (4.1.2)$$

The β values tell us about the relationship between new smear positive died and each predictor. For this data in table of coefficients, new smear positive complete and defaulted have a positive relationship. So, as patients who failed even when treated decrease by -0.989, the number of patients died will increase. Similarly, as the number of patients who completed treatment increase by 0.359, the number of patients died decrease. Same applies to the number of defaulted patients, as they increase by 0.391, patients died will decrease.

Note: from the table of t-statistics, we take the value from the standard table at$\alpha = 0.05, df = 14$, gives us the value 2.145. When this is multiplied by the standard error, it results to our confidence interval which is $\pm\beta\ value$. This then tells us either to reject or accept our null hypothesis which is shown in the p-value represented in Table 4. From the table of coefficients, we do not accept all but one (patients who defaulted) which show a significance of 0.002 p-value (<0.05) for patients cured. But for the table of coefficients for new smear positive died, our p-values are all significant (p<0.05) for all predictors. This tells us that we accept the null hypothesis.

Our t-score is calculated by dividing our β by standard error. For beta, the data is standardized first by dividing each value of new smear positive cure, complete, failed, and default by their standard deviation i.e. SD cure, SD complete, SD failed, SD default.

The Zero-order column under Correlations, lists the Pearson r values of the dependent variable (new smear positive cure in this case) with each of the predictors indicating nothing influenced the outcome. These values are the same as those shown in the table of correlation (matrix). A partial correlation is the correlation between an independent variable and a dependent variable after controlling for the influence of other variables on both the independent and dependent variable. Partial correlation coefficient is a measure of the strength of the linear relationship between Y and X_k after adjusting for the remaining (p-1) variables. On the Partial column, are lists of partial correlations for each predictor as it was evaluated for its weighting in the model (the correlation between the predictor and the dependent variable when the other predictors are treated as covariates). The Part column under Correlations lists the semi-partial correlations for each predictor once the model is finalized; squaring these values informs us of the percentage of variance each predictor uniquely explains. However, for the part correlation, only the influence of the control variables on the independent variable is taken into account. In other words, the part correlation does not control for the influence of the confounding variables on the dependent variable. The primary reason for conducting the part correlation would be to see how much unique variance the independent variable explains in relation to the total variance in the dependent variable, rather than just the variance unaccounted for by the control variables.

If we force all variables into the multiple linear regression, we find that only new smear positive defaulted is a significant predictor for new smear positive cure dependent variable while all predictors for new smear positive died dependent variable are significant. We can also see that for new smear positive cure, defaulted patients have a high impact by the standardized coefficients (beta = 1.075) and for new smear positive died, complete, and defaulted have high impact by the standardized coefficients (beta =0.773, beta = 0.504 respectively).

The interpretation of the variance inflation factor mirrors the interpretation of the coefficient of multiple determination. If $VIF_k = 1$, variable *k* is not correlated with any other independent variable. Where $k = 1,2,3, \ldots$. As a rule of thumb, multicollinearity is a potential problem when VIF_k is greater than 4; and, a serious problem when it is greater than 10 (field, 2008). The output below shows a VIF of 3.678, 1.684 and 4.253 respectively, which indicates some multicollinearity in new smear positive complete and failed which is not enough to worry about but enough to worry about for new smear positive defaulted because its greater than 4. On Table 4, VIF is the same as that found in Table 1.

Model		Unstandardized Coefficients		Standardized Coefficients	t	Sig.	Correlations			Collinearity Statistics	
		B	Std. Error	Beta			Zero-order	Partial	Part	Tolerance	VIF
1	(Constant)	-180.269	118.643		-1.519	.151					
	new_smear positive_complete	.359	.046	.773	7.878	.000	.847	.903	.403	.272	3.678
	new_smearpositive_failed	-.989	.103	-.638	-9.607	.000	.115	-.932	-.492	.594	1.684
	new_smear positive_defaulted	.391	.082	.504	4.781	.000	.758	.787	.245	.235	4.253

Table 2: Showing the Table of Coefficients for Dependent Variable New Smear Positive Died
A. Dependent Variable: New_Smearpositive_Died

3.1. ANOVA Table

The ANOVA table tests whether the model is significantly better at predicting the outcome than using the mean as a best guess. Specifically, the F-ratio represents the ratio of the improvement in prediction that results from fitting the model (labelled regression) relative to the inaccuracy that still exists in the model (labelled residual). If the improvement due to fitting the regression is much greater than the inaccuracy, within the model, then the value of F will be greater than 1 and in this SPSS calculates the exact probability of obtaining the value of F by chance. For the model with new smear positive cure, the F-ratio is 13.381, which is very unlikely to happen by chance ($p<0.0005$), which is highly significant and for new smear positive died, the F-ratio is 122.656 with a p-value of 0.000. So we can interpret that both models significantly improve our ability to predict the outcome variables.

The *F*-ratio in the ANOVA table tests whether the overall regression model for cure is a good fit for the data. The table below shows that the independent variables statistically significantly predict the dependent variable, $F(3,14) = 13.381,\ p < .05 for\ cure\ and\ F(3,14) = 122.656, p < 0.05\ for\ died$ (i.e., both regression models are a good fit of the data). With the F-test outcome, we can assume that the model explains a significant amount of the variance in new smear positive cure and died (the level at which patients are cured and die of tuberculosis within the study period).

ANOVA[a]						
Model		Sum of Squares	Df	Mean Square	F	Sig.
1	Regression	1692360252.756	3	564120084.252	13.381	.000[b]
	Residual	590200310.855	14	42157165.061		
	Total	2282560563.611	17			

Table 3: Table Showing ANOVA for New Smear Positive Cure
a. Dependent Variable: New_Smearpositive_Cure
b. Predictors: (Constant), New_Smearpositive_Defaulted, New_Smearpositive_ Failed, New_Smearpositive_Complete

ANOVA[a]						
Model		Sum of Squares	Df	Mean Square	F	Sig.
1	Regression	13532377.079	3	4510792.360	122.656	.000[b]
	Residual	514864.921	14	36776.066		
	Total	14047242.000	17			

Table 4: Table Showing ANOVA For New Smear Positive Died
a. Dependent Variable: New_Smearpositive_Died
b. Predictors: (Constant), New_Smearpositive_Defaulted, New_ Smearpositive_Failed, New_Smearpositive_Complete

3.2. Model Summary

The column labelled R on Table 6 and 4.5 are the values of multiple correlation coefficient between the predictors and the outcome.

The next column gives a value R-Square, which is a measure of how much of the variability in the outcome, is accounted for by predictors. The R-square accounts for 0.741 which means 74.1% variability in new smear positive cure and 0.963 which is 96.3% variability in new smear positive died. $R^2 = 0.963\ and\ R^2 = 0.741$ Indicates that 96.3% and 74.1% of the variation in y is explained by R^2 for both independent variables (cure and died respectively). In simple words, the model is 96.3% and 74.1% good.

The adjusted R-square gives us some idea of how well our model generalizes and ideally we would like its value to be the same or very close to the value of R-square. For cure, the difference in the model is fair (0.741-0.686=0.055 or 5.5%) and died the difference in the model is better (0.963-0.955=0.008 or 0.8%) this shrinkage means that if the model was derived from the whole population, it would account for approximately 5.5% less variance in the outcome for cure and 0.8% less variance in the outcome for died.

For Durbin-Watson, the distribution of this test is usually difficult because it involves the X values. Originally, Durbin-Watson (1950, 1951) gave a pair of bounds to be used. However, there is a large range of 'inclusion' found when using these bounds. Instead of using these bounds, we calculate the exact probability using the beta distribution approximation which was suggested by Durbin-Watson (1951). This approximation has been shown to be accurate to three decimal places in most cases which is needed for practical work. Using a Durbin-Watson table by Savin and White (1977), the observed value of the test statistic is less than the tabulated lower bound; this shows that we reject the null hypothesis of non-autocorrelated errors in favor of the hypothesis of positive first-order autocorrelation. Since d calculated 0.508 for cure is less than d tabulated lower bound of 0.933 by Savin and White (Models with an intercept Durbin-Watson Statistic: 5% Significance Points of d-Lower and d-Upper) and 2.381 for died is greater than the upper bound. So we reject the null hypothesis (2) for cure and do not reject for died which states that there is zero autocorrelation in the residuals at$\alpha = 5\%$

According to a rule of thumb says that test statistic values in the range of 1.5 to 2.5 are relatively normal. Values outside of this range could be a cause for concern. Field (2009) suggests that values under 1 or more than 3 are a definite cause for concern. If the test statistic value were greater than d Upper bound, we would not reject the null hypothesis. But in our analysis, Durbin-Watson d = 0.508 for cure, which is less and d = 2.381 is higher in the two critical values of 0.933 < d < 1.696 from $d_{L_{,,0.05}}\ degrees\ of\ freedom\ for\ regression\ k = 3, N = 18$ calls for an alarm for cure because small values of d indicates successive error terms are positively correlated and for died, we can assume that there is no first order linear auto-correlation in our multiple linear regression data.. In regressions, this can imply an under estimated level of statistical significance for cure.

Model Summary[b]					
Model	R	R Square	Adjusted R Square	Std. Error of the Estimate	Durbin-Watson
1	.861[a]	.741	.686	6492.855	.508

Table 5: Showing Table of Model Summary for New Smear Positive Cure
a. Predictors: (Constant), New_Smearpositive_Defaulted, New_Smearpositive_Failed, New_Smearpositive_Complete
b. Dependent Variable: New_Smearpositive_Cure

Model	R	R Square	Adjusted R Square	Std. Error of the Estimate	Durbin-Watson
1	.982[a]	.963	.955	191.771	2.381

Table 6: Showing Table of Model Summary for New Smear Positive Died

a. Predictors: (Constant), New_Smearpositive_Defaulted, New_Smearpositive_Failed, New_Smearpositive_Complete

b. Dependent Variable: New_Smearpositive_Died

4. Summary

This research work was carried out to determine the Prevalence of Tuberculosis disease in Nigeria. To achieve this, multiple regression analysis was done to measure the fitness of the models, check for the presence of autocorrelation in the residuals, to check if there is a significant relationship between the dependent variables and the independent variables and lastly, to test if there are variations in the cured patients and those that died as a result of the disease.

Multicollinearity is a serious problem that may dramatically affect the usefulness of a regression model [Montgomery et.al, 2012]. The existence of high correlations among the independent variables in a regression model is known as multicollinearity [Freund and Wilson, 1998]. Moreover, there are various methods for diagnosing multicollinearity, such as observing the values of Variance Inflation Factors, Variance Proportions, and Principal Components [Freund and Wilson, 1998]. Eigen system analysis [[Montgomery et.al, 2012] and Belsley collinearity diagnostics test are added to the list of diagnostics [Belsley et.al, 2005]. In this study, the variance Inflation Factor test, Variance proportion was employed to determine the degree of multicollinearity in the datasets. The program was run by using SPSS 23.

5. Conclusion

Based on the result of the analysis, we hereby conclude that the data best fit the regression model since the coefficients of the parameters were significant and with a high coefficient of determination, variance inflation factor (VIF) which mirrors the interpretation of multiple determination, indicates that multicollinearity in new smear positive complete, and failed is not enough to worry about but for new smear positive defaulted, its value is greater than 4 for both patients cured and patients that died. F-test explains a significant variance of patients that where cured and those that died within the study period. The coefficient of determination (R^2)indicates a 96.3% and 74.1% variation in both patients that where cured and those that died within the study period. Durbin Watson shows a zero-autocorrelation in the residuals for patients cured and a non-zero autocorrelation for patients that died

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