Journal of the Nigerian Association of Mathematical Physics
Volume27, (*July, 2014*), pp 129 – 132

Comparison Between Artificial Neural Network Models and Multiple Regression Models In the Tracking of CD4 Cell Counts of HIV Patients. A Case Study of Anambra State

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Abstract

Artificial Neural Network models are relatively new computational tools which their inherent ability to learn and recognize highly non-linear and complex relationships make them ideally suited in solving a wide range of complex real-world problems. In this research, the Artificial Neural Network model is compared with the multiple Regression Model (MRM) in the tracking of CD_4 cell counts of HIV positive patients. Modeling is performed based on 250 datasets of HIV positive patients from a cohort study with follow-up collected from the continuous quality improvement HIV care of Nnamdi Azikiwe University Teaching Hospital (NAUTH) Nnewi. The predictive results of the CD_4 cell counts from the two models from the historical data and their mean absolute error (MAE) were analysed and compared. The results indicated that the Artificial Neural Network model gave the most accurate prediction of the CD_4 cell counts. The artificial neural network model outperformed the multiple regression model.

Keywords: Artificial Neural Network model, CD_4 cell counts, multiple regression model, prediction, HIV.

1.0 Introduction

AIDS is one of the most serious illness. It has killed over 3,000,000 people since 1981. AIDS is caused by the Human Immunodeficiency Virus (HIV) which can destroy the human's immune system and cause the loss of resistant ability or even lives. The cell of CD_4 in the immune system plays a pivotal regulatory role in the immune response to infections and tumours. When the CD_4 cells break down with the inroad of HIV, the number of the CD_4 cells will decrease rapidly and the number of HIV will increase which will cause the outbreak of AIDS.

It has been stressed [1, 2] that the immune suppression resulting from the CD_4 cell decline leads to a high susceptibility of opportunistic infections and possibly unusual tumours, and without appropriate HAART (Highly Active Anti-Retroviral Therapy) is lethal. A number of approaches have been used to quantify the magnitude of HIV.AIDS dynamics [3, 4], and the future predictive trend. In this paper, we shall compare the Artificial Neural Network Model and Multiple Regression Model (MRM) in the tracking of CD_4 cell counts in the HIV patients.

2.0 Data Collection

The data were sourced from the Medical Examination Department of the Nnamdi Azikiwe Teaching Hospital Continuous Quality Improvement HIV/Care (NAUTH) Nnewi – Anambra State, Nigeria.

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3.0 Method

Artificial Neural Network Model

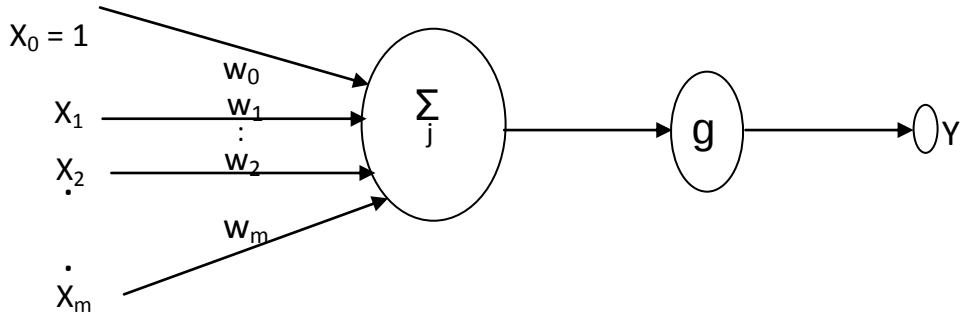

Fig: 1: Sketch of Model

$$V = w_0 + \sum_{j=1}^{m} w_j x_j \qquad (1)$$

Where V = The mode (summation) output of the body weights of patients and viral load copies, X_j = body weights of patients and viral load copies, w_j (j = 1, … m) = the weights of inputs, $g(V_k)$ = sigmoid function (a non linear operator) that gives the output Y_i, Y_i is the CD_4 cell counts of patients and W_0 = biase.

Multiple Layer Perceptron

The multiple layer perceptron is the neural network used in the tracking of the CD_4 cell counts of patients. The multiple layer perceptrons are the most popular network used in application [5, 6, 7]. While it is possible to consider many activation functions in practice it has been found that the logistics (the sigmoid) function works best, and it is given by;

$$g(v) = \left(\frac{e^v}{1+e^v}\right) \qquad (2)$$

The goal of this type of model is to create a model that correctly maps the input to the output using historical data so that the model can then be used to produce output when the desired output is unknown.

Learning Process of the Multiple Layer Perceptron (Gradient Descent)

The multiple layer perceptron learning rule is an algorithm that adjust the network weights W_{mm} to minimize the difference between the actual output y_{ki} and the target output t_{ki}. We can quantify this difference by defining over all output units i and all training pattern m.

$$E(W_{mn}) = \frac{1}{2}\sum_{i=1}^{m}\sum_{k=1}^{n}(t_{ki} - y_{ki})^2 \qquad (3)$$

It is the general aim of the network learning to minimize this error by adjusting W_{mn}. Typically, we make a series of small adjustments to the weights $W_{mn} \longrightarrow W_{mn} + \Delta W_{mn}$ until the $E(W_{mn})$ is small enough. We can determine which direction to change the weights m by looking at the gradient (ie partial derivative) of E with respect to each weight W_{mn}.

The gradient descent update equation (with positive learning rate n) is given by

$$\Delta W_{ki} = \underline{\eta \partial E(W_{mn})} \qquad (4)$$
$$\partial W_{ki}$$

which can be applied iteratively to minimize the error. For the present research, the output is the forecast/tracking of the CD_4 cell counts of the patients while the independent variables are the body weights and viral load copies of patients.

Testing and Validation of Artificial Neural Network.

The entire experimental data set is divided into training set and testing set. The error on the testing set is monitored during the training process. The testing error will normally decrease during the initial phase of training as does the training set of error. However, when the network begins to over fit the data, the error on the testing set will typically begin to rise. When the testing error starts increasing for a specified number of iteration, the training is stopped, and the weights at the minimum value of the testing error are returned. Out of the 250 data set of the HIV patients, 185 were used as a training set and 65 for testing data points.

4.0 Results and Discussion

All data analysis methods used 185 training and 65 testing data points. Different combinations of the data set are used during the process, so all the data points have eventually been tested. Two inputs parameters were set up as network inputs into the input layer. These parameters were the body weights and the viral load copies of these patients are considered as inputs which have influence in the tracking of the CD_4 cells and the CD_4 cell counts are considered as output parameters (see Appendix A for predicted values). The artificial neural network model, predicted the CD_4 cell counts of these patients with a mean absolute error of 0.04992, and means square error of 0.00092 respectively.

5.0. Multiple Regression Model

The same approach used in the artificial neural network model (ANN) was used in the multiple regression model (MRM). 185 sets of data were selected for simulating the regression model, and 65 data were used to test the performance of the model, where inputs are referred to as independent variables which are inputs are the same input (body weights of patients and viral load copies) used in the artificial neural network (ANN) with the fitted equation from multiple repression equation (MRM)

$$Y = 148.063 + 5.439X_1 + 0.00011276X_2 \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \quad (5)$$

The multiple regression model equation forecasted the CD_4 counts with a correlation coefficient of 0.141 and 0.101 respectively (see Appendix A). The mean square error (MSE) and the mean absolute error (MAE) were 0.06551 and 0.00432 respectively. Results show that the average error for the multiple regression models was considerably higher than that of the artificial neural network (ANN) [8]. The regression coefficient obtained from equation (5) showed that the variable and their interactions had an effect on the tracking of the CD_4 cell counts.

6.0 Comparison of Models (By Errors)

Table I: Shows the comparison of the two models using the mean absolute error (MAE) and mean square error (MSE).

	Number of Observation	Mean Absolute Error (MAE)	Mean Square Error (MSE)
Regression	250	0.06551	0.00432
ANN	250	0.04992	0.00092

7.0 Conclusion

The predicted CD_4 cell counts from the artificial neural network model (ANN) were conceptually better than the predicated CD_4 cell counts from the multiple regression model (MRM) (See Appendix A) the results obtained from the mean absolute error, (MAE) and mean square error (MSE) showed that the artificial neural network is a better model considering the small values of these errors compared to the multiple regression model (MRM). Unlike the multiple regression model (MRM), the artificial neural network model (ANN) is not limited to linear functions [9], it can deal with observations that lie far from the best line of fit. The multiple regression models fail whenever the predictions exceed the confidence interval and also when the data set have outliers. A more homogenous dataset with no outliers however would show the regression method a better advantage. Though the artificial neural network will perform better on such dataset. Although the artificial neural network has demonstrated significant advantages in certain circumstances, as in the tracking of CD_4 cell counts, it does not replace regression, rather should be regarded as a powerful tool to be used in complex situation in prediction.

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APPENDIX A

PREDICTED VALUES OF CD_4 CELL COUNTS FROM ANN AND REGRESSION MODEL

	Y HISTORICAL DATA	X BODY WEIGHTS OF DATEIRNS (KG)	X2 (CM^3) VIRAL LOAD COPIES OF PALENT	PREDICTED CD_4 CELL COUNTS FROM ANN	PREDICATED CD_4 CELL COUNTS FROM REGRESSION MODEL
1	544	66	251223	568.41	539.09
2	497	68	91287	540.65	529.56
3	234	70	4150	520.78	529.32
4	765	70	144058	520.45	547.17
5	202	70	4235	520.78	529.33
6	654	70	731600	519.12	622.15
7	633	60	4421	429.22	474.97
8	532	61	1092	484.67	479.98
9	234	61	4250	484.85	480.38
10	230	61	4812	484.88	480.46
11	605	63	4211	594.34	491.26
12	357	63	30196	594.83	494.57
13	290	70	42576	520.69	534.23
14	385	74	156918	500.60	570.57
. . .	. . .	. . .	. . .	. . .	. . .
240	575	61	124998	491.74	495.79
241	525	62	105621	561.45	498.76
242	285	60	84961	431.69	485.24
243	315	60	215621	435.98	501.92
244	285	60	94521	431.99	486.46
245	565	61	251894	499.12	511.98
246	580	62	284611	569.42	511.60
247	585	61	228491	497.75	509.00
248	612	63	254628	598.60	523.21
249	610	62	214284	566.37	512.62
250	510	61	109485	490.85	493.81