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Development of a fuzzy logic based model for HIV risk analysis and prediction

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ABSTRACT

Human Immunodeficiency Virus (HIV) risk analysis and prediction is crucial to effective decision making in sensitizing and providing appropriate support to the population of people in an area. Previous works on applicability of fuzzy logic to HIV analysis and prediction built their models on diagnostic and clinical data of few people who voluntarily submitted themselves for HIV screening test. Besides, most risk factors emanating from socio-cultural, attitudinal, behavioural, and demographic data were not considered in the previous studies. These made the models to have poor analysis and prediction capabilities. This study therefore, aimed at designing a specific HIV risk analysis and prediction model with better prediction capability. The proposed model was designed considering socio-cultural, clinical, behavioural, attitudinal and demographic risk factors relating to HIV risk and the knowledge obtained from experts of Virology Department of Obafemi Awolowo University Teaching Hospital (OAUTHC). Research data were collected majorly on HIV from experts and through a google questionnaire sent to individuals and various groups. Fuzzy logic toolbox in MATLAB 2018b and triangular membership function were used to model the proposed system. The results from the study showed that the model developed is reliable in analyzing and predicting HIV risk level of individuals and population of people in an area for effective decision making. In conclusion, the model developed in the study produced a viable tool for HIV analysis and prediction with a linguistic interpretation feature, reliable analysis and prediction capabilities.

Keywords: Fuzzy logic, HIV risk prediction analysis, Epidemiology - mathematical models

Introduction

The Human Immunodeficiency Virus (HIV) and Acquired Immunodeficiency Syndrome (AIDS) have continued to be a major health priority issue. There is currently no cure for the disease as it is transmitted through various means including sharing infected needles, contaminated blood transfusion and practicing of unsafe sex (W.H.O, 2013). Determining HIV status of individual is crucial to healthy living and longevity. However, most people do not want to know their HIV status, because of fear of stigma and death sentence people ignorantly associate with HIV infection. This attitude has rendered ineffective, several efforts put in place for curtailing the spread and total eradication of the virus.

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Therefore, the virus keeps spreading and ravaging humanity, causing health deterioration, economic hardship and eventual death of thousands of people. One of the ways to address this challenge is to devise a means of analysing risk factors responsible for HIV virus spread in a population. Based on the analysis of the risk factor, make predictions on likelihood of its spread for informed and effective decision to curtail its spread. Risk factors in this context may be attitudinal, behavioral, social, demographic and clinical data which could aid analysis and prediction of risk of HIV. This will enable susceptibility of individuals and population to be determined. As a result, concerned stakeholders and the government can use the analysed data to make informed decisions on appropriate action to be taken in getting people tested, or deploying aids to curb the spread among the people.

Several approaches and models, especially data mining techniques (Tang et al., 2018; Blaizot et al., 2015) have been used in predicting risks of HIV and associated diseases in various instances. Though Fuzzy logic has been less specifically applied to HIV risk prediction, the technique has been applied severally in disease prediction, risk analysis and diagnosis (Oluwagbemi et al., 2020; Balogun et al., 2020; Sharma and Saxena, 2017; Vaanathi, 2018; Oad et al., 2014). Fuzzy logic has shown to achieve a high accuracy in classification and prediction of risk levels for diseases. Based on the foregoing, HIV risk prediction could also be achieved by the application of fuzzy logic theory (Zadeh, 1965). Fuzzy logic provides a simple way to arrive at a definite conclusion based upon vague, ambiguous, imprecise, noisy, or missing input information. The concept of fuzzy logic is based near human thinking and natural activities. The fuzzy logic works on the level of possibilities of input to achieve the definite output.

However, available models in this regard have poor analysis and prediction capabilities. This is because of risk factors considered, inclusiveness and coverage of data used in the studies. To address these challenges, a specialised and more inclusive model in terms of risk factors and data is desirable.

This study therefore seeks to develop a viable model based on fuzzy logic technique to analyse the risk of individual and population of people to HIV infection by considering most risk factors emanating from socio-cultural, attitudinal, behavioural, and demographic data which predispose people to HIV infection, and are not commonly considered in the previous studies.

Literature Review

There are quite a good number of works regarding the state- of- the- art, fuzzy logic theory application in HIV and other diseases prediction in related studies. In some of these works, various data mining algorithms have been used on data sets from various sources to establish relationships and discover new knowledge regarding HIV/AIDS dynamics.

Balogun *et al.*, 2020 presented a model for monitoring the risk of sexually transmitted diseases (STDs) among females using non-invasive risk factor information. The model was simulated using fuzzy logic toolbox in MATLAB and the results showed that nine non-invasive risk factors were associated with the risk of STDs among female patients. The study concluded that the fuzzy logic approach was adequate for predicting the risk of STDs based on knowledge of risk factors. Predicting the risk of a particular disease such as HIV will streamline inputs and corresponding output which will give more accurate results.

Ekpenyong *et al.*, 2019 proposed a framework for the prediction of patients' response to antiretroviral therapy. The authors experimented with publicly available HIV datasets and locally sourced datasets. A hybridized classification system (Fuzzy Logic and Deep Neural Network) was used to model patients' response and achieved improved drug pattern prediction.

Oye and Isah, 2019, presented a fuzzy model for the management of HIV/AIDS providing a decision support platform to HIV/AIDS researchers and healthcare practitioners. The fuzzy expert system was designed based on clinical observations, medical diagnosis and expert knowledge with 30 patients selected and achieved an accuracy of 87.1% .

Oluwagbemi *et al.*, 2020 presented a system named Multilingual HIV indigenous fuzzy logic based diagnostic system (MAVSCOT) implementing fuzzy logic and speech technology in order to efficiently diagnose HIV. MAVSCOT was reported to perform better because of its implementation of fuzzy logic. This further shows that fuzzy logic is powerful because of its ability to model linguistic terms.

Dennis, 2018, predicted HIV status among female sex workers in Ghana using data mining techniques. The study, which used random tree, J48, naïve bayes, logistic regression and neural network algorithms made it possible to determinine if a female sex worker has ever tested for HIV. The study also adapted the CRISP–DM methodology and concluded that the best performance was achieved by the Random Tree classifier with an accuracy of 98.9%.

John and Ji, 2018, predicted HIV-1 and HIV-2 proteins using Chou's pseudo amino acid compositions and different classifiers. Results of classification concluded that the support vector machine (SVM) has the highest prediction accuracy of 0.9909 when predictng HIV-1 and HIV-2 proteins.

Idowu *et al.*, 2016, worked on the prediction of pediatric HIV/AIDS patient survival. The authors demonstrated how a data mining algorithm using naïve bayes classification could be used to classify the survival of pediatric HIV/AIDS patients with an accuracy of 60% to 100% based on selected dependent variables. The research concluded that the naïve bayes' classifier was able to predict the survival of YES more accurately than the survival of NO and about 68% of the survival of NO was correctly classified.

Sean et al., 2017, worked on how machine learning approaches could be used to assist a domain expert who manually searches social data for HIV related content. The authors used an existing social media dataset associated with HIV. Four commonly used machine learning methods were selected and given trial to know whether they could learn the patterns associated with HIV risk behavior. Tenfold cross validation was used to examine the speed and accuracy of the models in applying that knowledge to detect HIV content in social media data. The study concluded that logistic regression and random forest resulted in the highest accuracy in detecting HIV related social data (85.3%) while the regression classifier resulted in the lowest accuracy.

Lakshmi and Isakki (2017) worked on the prediction of HIV patients in comparative study of data mining classification techniques using HIV/AIDS and STD data. The study which used Decision Tree, Support Vector Machine (SVM), and Naïve Bayes' Classification algorithms made it possible in determining if an individual would test positive for HIV. The result showed that out of the three methods, the decision tree had the highest accuracy of 90.0741%.

Preety and Deepti (2015) worked on medical diagnosis using fuzzy logic and also concluded that the technique of fuzzy logic can contribute a reliable result in order to notify the disease. Other related works which demonstrated applicability of fuzzy logic techniques in diagnosis, analysis and prediction of related diseases are reported in Fazad (2015) , Alaa and Asem (2017) Girdhar et al. (2019).

Existing works reviewed above contributed immensely to applicability of fuzzy logic and other machine learning approaches to prediction of HIV and other related diseases. Previous works on applicability of fuzzy logic to HIV analysis and prediction built their models on diagnostic and clinical data of people who voluntarily submitted themselves for HIV screening test. However, in reality, people do not normally want to submit themselves for screening. Besides, most risk factors emanating from socio-cultural, attitudinal, behavioural, and demographic data were not considered in the previous studies. These are indications that models based on previous study may have poor analysis and prediction capabilities. Therefore, in this study, a robust model which considered predisposing HIV factors, such as attitudinal, behavioural, demographic and socio-cultural data was proposed

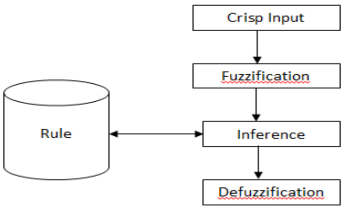
Methodology

The methodology of this research includes various methods proposed to achieve the goal of the paper. The methods consist of: data collection and description, model formulation, simulation and evaluation of the proposed model performance. Figure 1 is a typical fuzzy logic model adopted in this study. It has four main parts including: fuzzification module, which transforms the system inputs, which are crisp numbers, into fuzzy sets; knowledge base, which stores IF-THEN rules provided by experts; inference engine, this simulates the human reasoning process by making fuzzy inference on the inputs and IF-THEN rules; defuzzification module, this transforms the fuzzy set obtained by the inference engine into a crisp value. Fuzzy logic toolbox in MATLAB 2018b and triangular membership function were used to model the system.

Description of Dataset

In this research, socio-cultural, behavioural, attitudinal, clinical and demographic data relating to HIV risk infection outbreak in a population of people were collected through google form questionnaires sent to individual and various groups. The google form questionnaire was designed to capture information relating to HIV risk as elicited from experts in the virology department of Obafemi Awolowo University Teaching Hospital (OAUTHC). The information collected are as contained in the description column of Table 1. Expert knowledge was used in designing the membership function of the various risk factors considered and the resulting output in the study.

Figure 1: Fuzzy logic Model



Model Formulation

Model formulation was done following four phases of fuzzy logic technique as described in Figure 1:

Phase 1: Crisp Input

This consists of responders' responses to the information requested in the google form questionnaire as contained in Table 1.

Given the universal set U

Let $x_1, x_2, x_3, x_4, x_5, \ldots\ldots\ldots\ldots x_i \in X$, and $i = 20$ (1)

Where,

x_1 = 'Frequent headache

x_2 = 'Chronic cough'

x_3 = 'Diarrhea'

x_4 = 'Swollen gland'

x_5 = 'Loss of appetite'

.

x_i = 'usage of sharp object and genital mutilation'

x_{i+1} = 'level of education'

x_{i+2} = 'Practice of safe sex

Phase 2: Fuzzification

The process of fuzzification involves fuzzy inference, membership functions, fuzzy logic operators, and if-then rules design

Given the universal set U, a fuzzy set A is defined as the ordered pair $A = \{x, M_{A(X)}\}$

Where,

$x \in X$ and $0 <= M_{A(X)} <= 1$ (2)

The membership function $M_{A(X)}$ describes the degree to which the object x belongs to the set A. There are different forms of membership function, such as triangle, trapezoid, Gaussian, etc.

The triangular membership function was adopted in this research work.

it assumes the following values:

$$M_{A(xi)} = \{1\,; if\ x\ \in A\ 0 < M_{A(xi)} \leq 1\,; if\ x\ partially\ belongs\ to\ A\ \ 0\,; if\ x\ \ni A \qquad (3)$$

Phase 3: Inference

There are usually two types of fuzzy inference systems differing in the defuzzification part, namely Mamdani-type and Sugeno-type. Mamdani-type inference was adopted in this study. It expects the output membership functions to be fuzzy sets. After the aggregation process, there is a fuzzy set for each output variable that needs defuzzification. The fuzzy rules R^n created in this model has the general form:

$$R^n : \text{if } X^1 = A^{1n} \text{ and } \ldots\ldots\ldots X^m = A^{mn} \text{ then } Y = B^n \qquad (4)$$

Details of all the rules created are contained and shown in Figures 2 and Table 1

Phase 4: Defuzzification

The fuzzy output of a rule depends on the degree of activation of its antecedent. Mamdani inference scheme aggregates these outputs into a single fuzzy set for the variable Y. Lastly, defuzzification is applied to transform the output fuzzy set into a crisp control variable, usually by calculating its centroid. It is calculated as follows

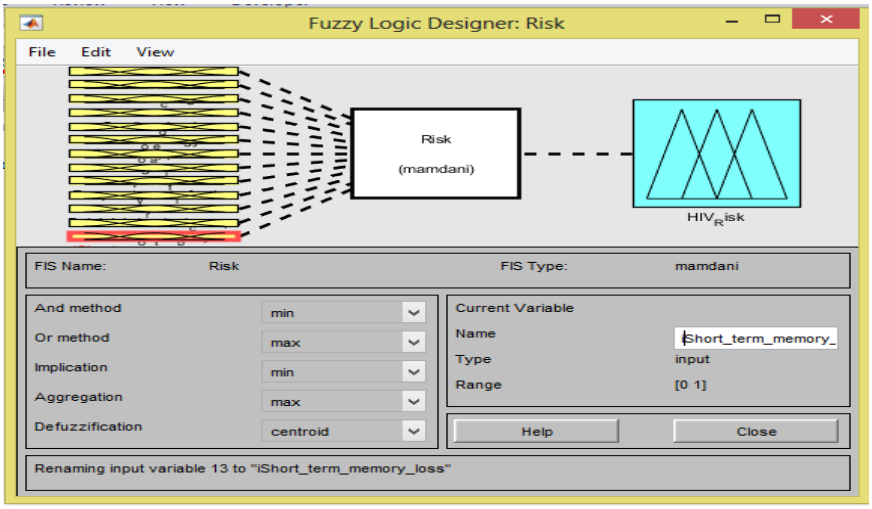
$$x_{def} = \frac{\int \mu_A(x) x \, dx}{\int \mu_A(x) \, dx} \tag{5}$$

Where X_{def} is the defuzzified output and μA (x) is the output fuzzy set after aggregation of individual implication results.

A. Fuzzy Inference System Design

Fuzzy Inference System (FIS) Toolbox in MATLAB is a very powerful Graphical User Interface (GUI). The FIS editor displays information about a fuzzy inference system.

The FIS of the proposed model is as shown in Figure 2. The FIS editor shows a diagram of the fuzzy inference system with the label of each input variable on the left, and the output variable on the right. Table 1 contains all the inputs, output and their membership function designed for the FIS of the proposed model.



FIS Name: Risk

FIS Type: mamdani

And method: min

Or method: max

Implication: min

Aggregation: max

Defuzzification: centroid

Current Variable

Name: iShort_term_memory_

Type: input

Range: [0 1]

Renaming input variable 13 to "iShort_term_memory_loss"

Figure 2: Fuzzy Inference System Editor

Table 1: Dataset Description and Membership function design

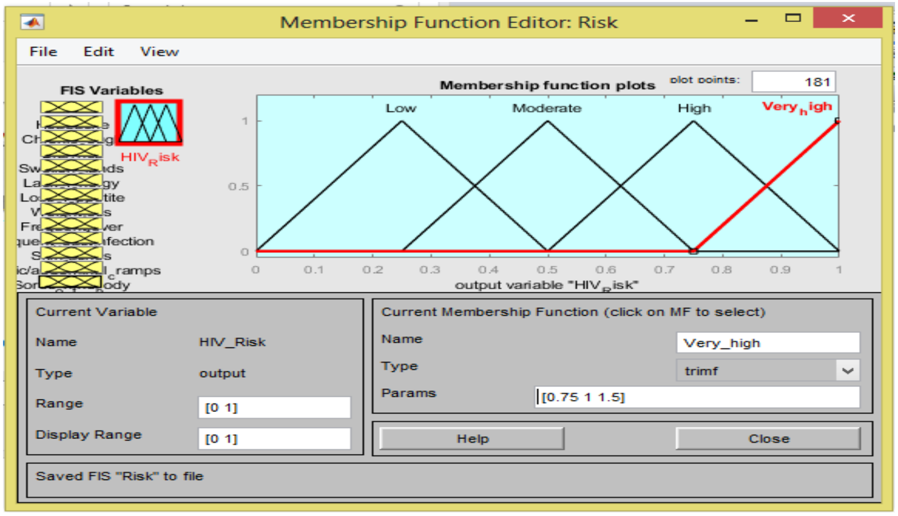
Input	Description	Membership function
x_1	Headache	MF1 - Low.'trimf', [0 0.25 0.5] MF2 - Moderate. 'trimf', [0.25 0.5 0.75] MF3 - High. 'trimf', [0.5 0.75 0.85] MF4 - Very high. 'trimf', [0.75 0.85 1.0]
x_2	Chronic cough	MF1 - Low.'trimf', [0 0.25 0.5] MF2 - Moderate. 'trimf', [0.25 0.5 0.75] MF3 - High. 'trimf', [0.5 0.75 0.85] MF4 - Very high. 'trimf', [0.75 0.85 1.0]
x_3	Diarrhea	MF1 - Low.'trimf', [0 0.25 0.5] MF2 - Moderate. 'trimf', [0.25 0.5 0.75] MF3 - High. 'trimf', [0.5 0.75 0.85] MF4 - Very high. 'trimf', [0.75 0.85 1.0]
x_4	Swollen glands	MF1 - Low.'trimf', [0 0.25 0.5] MF2 - Moderate. 'trimf', [0.25 0.5 0.75] MF3 - High. 'trimf', [0.5 0.75 0.85]

		MF4 = Very high. ‘trimf’, [0.75 0.85 1]
x_5	Lack of energy	MF1 = Low.’trimf’, [0 0.25 0.5] MF2 = Moderate. ‘trimf’, [0.25 0.5 0.75] MF3 = High. ‘trimf’, [0.5 0.75 0.85] MF4 = Very high. ‘trimf’, [0.75 0.85 1]
x_6	Loss of appetite	MF1 = Low.’trimf’, [0 0.25 0.5] MF2 = Moderate. ‘trimf’, [0.25 0.5 0.75] MF3 = High. ‘trimf’, [0.5 0.75 0.85] MF4 = Very high. ‘trimf’, [0.75 0.85t 1]
x_7	Weight loss	MF1 = Low.’trimf’, [0 0.25 0.5] MF2 = Moderate. ‘trimf’, [0.25 0.5 0.75] MF3 = High. ‘trimf’, [0.5 0.75 0.85] MF4 = Very high. ‘trimf’, [0.75 0.85 1]
x_8	Frequent fever	MF1 = Low.’trimf’, [0 0.25 0.5] MF2 = Moderate. ‘trimf’, [0.25 0.5 0.75] MF3 = High. ‘trimf’, [0.5 0.75 0.85] MF4 = Very high. ‘trimf’, [0.75 0.85 1]
x_9	Frequent yeast infection	MF1 = Low.’trimf’, [0 0.25 0.5] MF2 = Moderate. ‘trimf’, [0.25 0.5 0.75] MF3 = High. ‘trimf’, [0.5 0.75 0.85] MF4 = Very high. ‘trimf’, [0.75 0.85 1]
x_{10}	Skin rashes	MF1 = Low.’trimf’, [0 0.25 0.5] MF2 = Moderate. ‘trimf’, [0.25 0.5 0.75] MF3 = High. ‘trimf’, [0.5 0.75 0.85] MF4 = Very high. ‘trimf’, [0.75 1 1.5]
x_{11}	Pelvic/abdominal cramps	MF1 = Low.’trimf’, [0 0.25 0.5] MF2 = Moderate. ‘trimf’, [0.25 0.5 0.75] MF3 = High. ‘trimf’, [0.5 0.75 0.85] MF4 = Very high. ‘trimf’, [0.75 0.85 1]
x_{12}	Sores on certain parts of the body	MF1 = Low.’trimf’, [0 0.25 0.5] MF2 = Moderate. ‘trimf’, [0.25 0.5 0.75] MF3 = High. ‘trimf’, [0.5 0.75 0.85] MF4 = Very high. ‘trimf’, [0.75 0.85 1]
x_{13}	Short term memory loss	MF1 = Low.’trimf’, [0 0.25 0.5] MF2 = Moderate. ‘trimf’, [0.25 0.5 0.75] MF3 = High. ‘trimf’, [0.5 0.75 0.85] MF4 = Very high. ‘trimf’, [0.75 0.85 1]
x_{14}	Sex partner	MF1 = Low.’trimf’, [0 0.25 0.5] MF2 = Moderate. ‘trimf’, [0.25 0.5 0.75] MF3 = High. ‘trimf’, [0.5 0.75 0.85] MF4 = Very high. ‘trimf’, [0.75 0.85 1]
x_{15}	Temperature	MF1 = Low.’trimf’, [0 0.25 0.5] MF2 = Moderate. ‘trimf’, [0.25 0.5 0.75] MF3 = High. ‘trimf’, [0.5 0.75 0.85] MF4 = Very high. ‘trimf’, [0.75 0.85 1]
x_{16}	Usage of sharp object	MF1 = Low.’trimf’, [0 0.25 0.5] MF2 = Moderate. ‘trimf’, [0.25 0.5 0.75] MF3 = High. ‘trimf’, [0.5 0.75 0.85] MF4 = Very high. ‘trimf’, [0.75 0.85 1]
x_{17}	Age range	MF1 = Infant.’trimf’, [0 0.25 0.5] MF2 = Teenage. ‘trimf’, [0.25 0.5 0.75] MF3 = Adolescent. ‘trimf’, [0.5 0.75 0.85] MF4 = Adult. ‘trimf’, [0.75 0.85 1]
x_{18}	Marital status	MF1 = Single.’trimf’, [0 0.25 0.5] MF2 = Married. ‘trimf’, [0.25 0.5 0.75] MF3 = Divorce. ‘trimf’, [0.5 0.75 0.85] MF4 = Widow(er). ‘trimf’, [0.75 0.85 1]
x_{19}	Drug usage	MF1 = Low.’trimf’, [0 0.25 0.5] MF2 = Moderate. ‘trimf’, [0.25 0.5 0.75] MF3 = High. ‘trimf’, [0.5 0.75 0.85] MF4 = Very high. ‘trimf’, [0.75 0.85 1]
x_{20}	Level of Education	MF1 = Primary.’trimf’, [0 0.25 0.5] MF2 = Secondary . ‘trimf’, [0.25 0.5 0.75] MF3 = University . ‘trimf’, [0.5 0.75 0.85] MF4 = Others . ‘trimf’, [0.75 0.85 1]
x_{21}	Practices of safe sex	MF1 = Yes.’trimf’, [0 0.25 0.5] MF2 = No. ‘trimf’, [0.25 0.5 0.75] MF3 = Sometimes . ‘trimf’, [0.5 0.75 1]

x_{22}	Practices of blood transfusions	MF1 – Screened .'trimf', [0 0.25 0.5] MF2 – Unscreened. 'trimf', [0.25 0.5 0.75] MF3 – Not sure. 'trimf', [0.5 0.75 1]
x_{23}	Practices of circumcision	MF1 – Yes.'trimf', [0 0.25 0.5] MF2 – No . 'trimf', [0.25 0.5 0.75] MF3 – Maybe . 'trimf', [0.5 0.75 1]
Output	Description	Membership function
Y_i	HIV Risk	MF1 – Low.'trimf', [0 0.25 0.5] MF2 – Moderate. 'trimf', [0.25 0.5 0.75] MF3 – High. 'trimf', [0.5 0.75 0.85] MF4 – Very high. 'trimf', [0.75 0.85 1]

B. Membership Function Design

Figure 3 shows the membership function editor for one of the inputs membership design (headache) for the proposed model. The range is set from 0 to 1, to reflect and capture the degree of responder's experience.



Current Variable
Name HIV_Risk
Type output
Range [0 1]
Display Range [0 1]

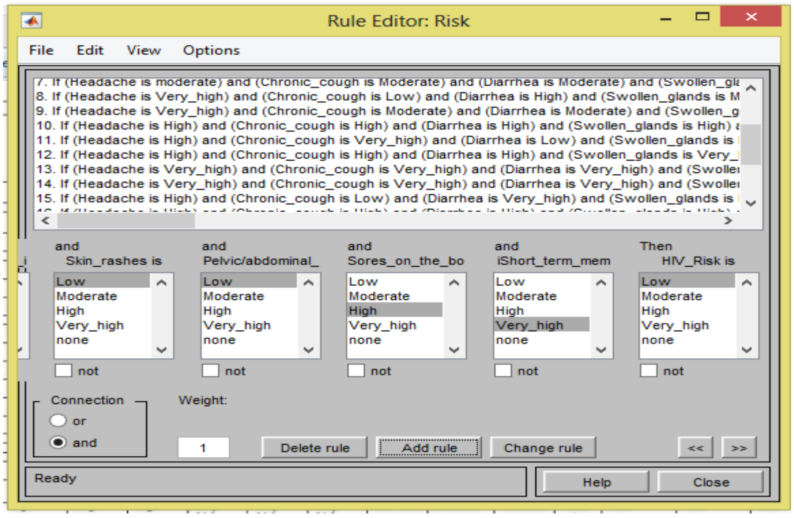
Current Membership Function (click on MF to select)
Name Very_high
Type trimf
Params [0.75 1 1.5]

Saved FIS "Risk" to file

Figure 3: Membership function editor for HIV Risk factors

C. Inference Rule Design

The rule editor in Figure 4 shows the inference rules designed for the proposed model in MATLAB. The rules are constructed on the basis of input- output, and on the knowledge elicited from experts.



```
7. If (Headache is moderate) and (Chronic_cough is Moderate) and (Diarrhea is Moderate) and (Swollen_gla
8. If (Headache is Very_high) and (Chronic_cough is Low) and (Diarrhea is High) and (Swollen_glands is M
9. If (Headache is Very_high) and (Chronic_cough is Moderate) and (Diarrhea is Moderate) and (Swollen_g
10. If (Headache is High) and (Chronic_cough is High) and (Diarrhea is High) and (Swollen_glands is High) a
11. If (Headache is High) and (Chronic_cough is Very_high) and (Diarrhea is Low) and (Swollen_glands is
12. If (Headache is High) and (Chronic_cough is High) and (Diarrhea is High) and (Swollen_glands is Very_
13. If (Headache is Very_high) and (Chronic_cough is Very_high) and (Diarrhea is Very_high) and (Swollei
14. If (Headache is Very_high) and (Chronic_cough is Very_high) and (Diarrhea is Very_high) and (Swollei
15. If (Headache is High) and (Chronic_cough is Low) and (Diarrhea is Very_high) and (Swollen_glands is
```

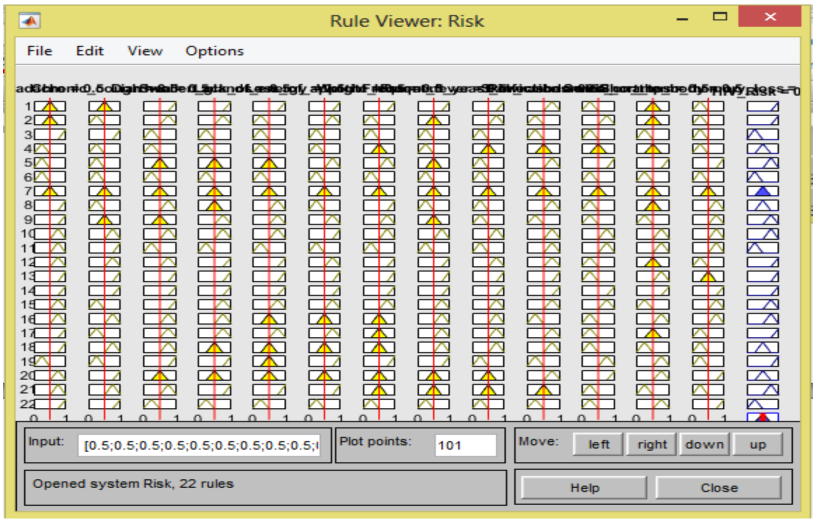
Weight: 1

Ready

Figure 4: Rule Editor for HIV Risk.

D. Rule Viewer Design

The rule viewer in Figure 5 shows a roadmap of the whole fuzzy inference process designed for the proposed model. The characterization of each input variable is specified with respect to the input index line. The rule viewer consists of the inference mechanism and the value of defuzzification.



Input: [0.5;0.5;0.5;0.5;0.5;0.5;0.5;0.5;0.5;

Plot points: 101

Opened system Risk, 22 rules

Figure 5: Rule Viewer for HIV Risk of the Proposed Model

Results and Discussion

The performance of the proposed model was carried out by simulation and the collected data for the study. Varying responses of fifty-six (56) responders and twenty (20) selected clinical record data of confirmed HIV patients obtained from experts in OAUTH were used. Two stages performance evaluation of the model was carried out. First, the data collected through questionnaires were inputted and run on the proposed system. Analysis of the result showed the characteristic of the population in terms of their risk levels to HIV infection in linguistic terms. The proposed model offered added advantage through which the characteristics of the data used were studied. For instance, age, gender and level of education were studied with respect to the HIV risk. Second, the selected 20 confirmed HIV history data were also inputted to the proposed model, the model had accuracy of 95%. Table 2 shows the prediction of the proposed model on the 20 confirmed HIV positive data. Figure 6 shows the bar chart of the gender and the HIV risk of the responders. From Figure 6, while male population shows low risk of having HIV, the female population is at a very high risk of having the virus. This is an impetus for the government to provide support to salvage the predicted situation with the female population. Figure 7 shows the bar chart of the age of the responder against the HIV risk. The sampled population within the age range of 18 – 35 showed very high risk of testing positive to HIV than other age ranges. Figure 8 shows the bar chart of the level of education of the responder with likelihood of testing positive. The analysis in Figure 8 shows that education is a risk factor in contracting the virus. While the population with a low level of education showed a very high level of testing positive, it is very low in the population with a high level of education.

Table 2: Performance of Proposed Model on Sampled Confirmed HIV Records

S/N	Risk Level	Number of Prediction	Percentage Prediction	Accuracy
1	Low	0	0%	5%
2	Modertate	1	5%	
3	High	2	10%	90%
4	Very High	16	80%	
	Total	20	100%	

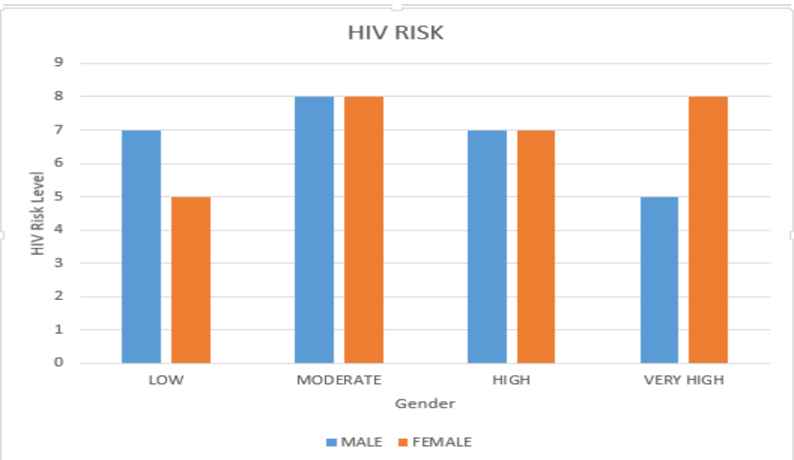


Figure 6: bar chart showing the gender of the tested individual

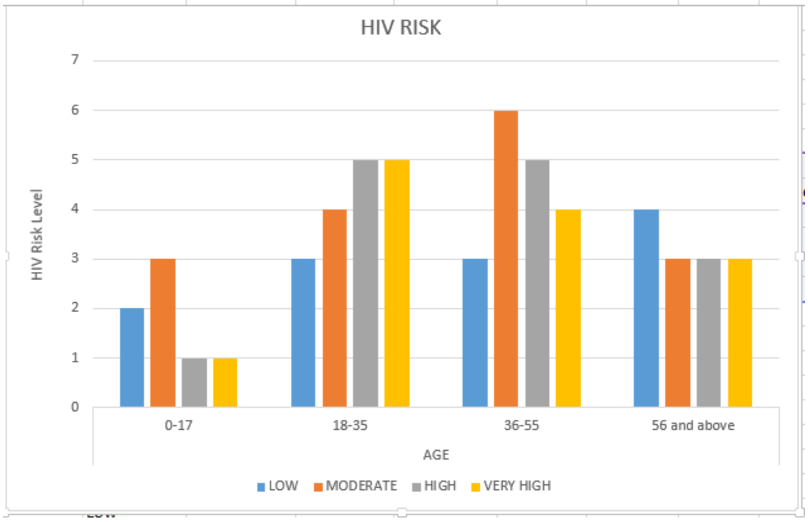


Figure 7: bar chart showing the age of the tested individual

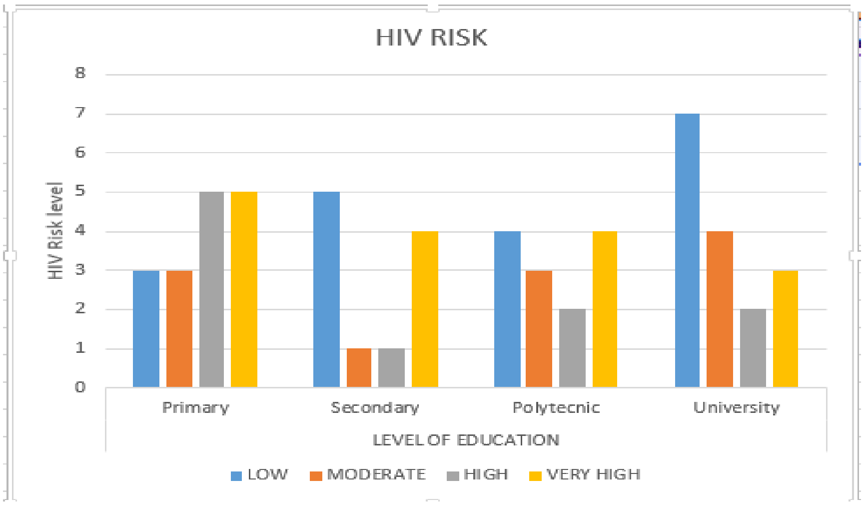


Figure 8: bar chart showing the level of education of the tested individual

Conclusion

In this research work, a model based on fuzzy logic technique was proposed for analysis and prediction of HIV risk in a population. The aim was to design a viable model with flexibility for interpretation of analysed results in linguistic terms without need for expert intervention. The proposed system was designed using fuzzy logic technique. The methods consist of: data collection and description, model formulation, simulation and evaluation of the proposed model performance. Socio-cultural, behavioural, attitudinal, clinical and demographic data relating to HIV risk infection outbreak in a population of people were as well used in the model design, simulation and evaluation. The collected data were categorised on severity level as Low, Moderate, High and Very high based HIV risk factors which served as input to the Fuzzy inference system. The proposed model was accurate and reliable based on experimental results obtained. The model will serve as a useful tool for individuals, government, researchers, and health workers in predicting and analyzing HIV risk of a population in a particular area for effective decision making.

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