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An Enhanced Adaptive Medical Diagnostic Model Driven By Genetic–Neuro-Fuzzy Algorithms

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Abstract

This research aims at developing adaptive medical diagnostic system driven by genetic, neural network and fuzzy logic algorithms for effective diagnosis of tuberculosis. Medical diagnosis for tuberculosis disease is a complex decision process that involves a lot of vagueness and uncertainty management, since the disease has multiple symptoms. The use of several algorithms has been explored in clinical diagnosis models for diagnosing and prescribing therapy for tuberculosis, but has challenges in transforming the vagueness and uncertainty of multiple symptoms due to the noisy nature of the disease data and over fitting of the models, this had led to the challenge of accurate classification, training, optimization, diagnosis and prescription of therapy. Object Oriented Analysis and Design (OOAD) and System Structured Analysis and Design (SSAD) methodologies were adopted in the research. The methodology involved obtaining four hundred and thirty (430) clinical data from patients with tuberculosis records at the Tuberculosis and Leprosy Hospital, Eku, Delta State. The obtained data were pre-processed using missing values imputation and numeric data encoding methods. Thereafter, a genetic algorithm was applied to the processed data to select six relevant features from the initial number of 16 features (Cough, Night sweats, Fever, Systolic Blood Pressure, Difficulty in Breathing, Loss of appetite, Sputum, Chills, Loss of pleasure, Immune Suppression, Chest Pain, Lack of concentration, Irritation, Loss of energy, Lymph Node Enlargement, Body Mass Index). The reduced dataset was split into training and test sets. The ANFIS (Adaptive Neuro-Fuzzy Inference System) was applied to perform diagnosis in which it was trained and validated on training and test sets respectively. The ANFIS was driven by Mamdani's inference mechanism with sixty-four (64) generated rules with confidence and support scores of above 10% and 15% respectively. The developed model performance on the test sets gave an accuracy of 90% precision, sensitivity, and specificity of 100%. The results showed that all the attributes of tuberculosis contributed to the degree of the diseases based on their respective weights. Conclusively, the system accurately classified, trained attributes, and predicts the severity of tuberculosis.

Keywords: Neuro-Fuzzy; Algorithm; Medical diagnosis; Tuberculosis, Genetic.

1. Introduction

In the field of medical science diagnosis of disease is a major problem, which involves conducting various tests upon the patient. The task of carrying out an effective and efficient disparity medical diagnosis is a complex one. It involves a state space search of medical knowledge, which could become unwieldy; especially when the variables involved are numerous [1] Medical diagnosis involves a complex decision process that involves a lot of vagueness and uncertainty management, since a disease may have multiple symptoms. The use of several algorithms has been explored in clinical diagnosis models for diagnosing and prescribing therapy for several serious diseases, but have limitations in transforming the vagueness and uncertainty of multiple symptoms due to the noisy nature of the disease data and overfitting of the models, which has led to the challenge of accurate classification, diagnosis and prescription of therapy. Even though several tests were conducted, it is difficult for the medical expert to arrive at the final diagnosis. It is recognized that a very important task in achieving hospital efficiency is to optimize the diagnostic process in terms of the number and duration of the patients' examinations, with accompanying accuracy, sensitivity, and specificity [2]. The task of medical diagnosis like other diagnosis processes is made more complex because a lot of imprecision is involved. Patients cannot describe exactly what has happened to them or how they feel; doctors and nurses cannot tell exactly what they observe; laboratories report results with some degree of errors; medical researchers cannot precisely characterize how disease alters the normal functioning of the body. This reflects the fact that almost all the symptoms are experienced and described differently by each patient. Providing accurate diagnosis and related treatment is arduous especially in cases of multiple differential diagnoses. Therefore, medical problems cannot be generalized or analyzed by using binary logic including “yes” or “no” options. So, an analytical program is needed. The medical diagnosis process can be interpreted as a decision-making process, during which the physician activates the diagnosis of a new and unknown case from an available set of clinical data [2]

Tuberculosis (TB) is a communicable disease that was discovered by German physician Robert Koch in 1882 [3]. In 2015, 1.8 million Tuberculosis related deaths were reported (Centres for Disease Control and Prevention (CDC). Tuberculosis is the second leading cause of death from an infectious disease worldwide, after the human immunodeficiency virus (HIV) [1]. Tuberculosis is caused by a bacterium called Mycobacterium tuberculosis. Basically there are two types of tuberculosis namely Pulmonary TB (PTB) and Extra-pulmonary TB (ETB).

Methods commonly used to diagnose TB include, GeneXpert assay, sputum-smear microscopy and chest radiography. These orthodox methods of diagnosing TB are primarily through physical examination and laboratory tests. The former involves asking patients certain questions for prognosis purposes while tests are carried out to affirm physical examination. Diagnosis can be stopped if medical practitioner is totally convinced after physical examination. However, this is not advised. This orthodox method is currently faced with a number of challenges such as lack of medical facilities in most medical centres and as a result, inhibiting the management of TB in developing countries. Culture method is considered the gold standard for the detection of the causative agent of TB, Mycobacterium tuberculosis (MTB) but it is time-consuming in diagnosis and the chances of contamination are high. Some common issues reported from other diagnostics methods include performance issues, sputum samples from children (paediatric cases); live MTB, highly skilled medical personnel for high throughput tools and high cost [4]. Delay in diagnosis may lead to drug resistance, multidrug resistance (MDR), where an isolate shows resistance to two first line drugs, rifampic and isoniazid, and extensive drug resistance (XDR) which includes MDR and also show resistance to fluoroquinolones and at least one of the injectable drugs [5].

Since the traditional way of determining suspicion of TB is usually carried out by the physicians by looking at the signs and symptoms, it does not consider the above uncertain phenomenon. Thus, the method jeopardizes the accuracy of the detection of TB. However, an expert system which emulates the decision-making process of human being can be considered as an appropriate tool to address the uncertain phenomenon to accurately detect the suspicion of Tuberculosis. This process can be computerized in to present medical diagnostic procedures in a rational, accurate and fast way. Studies showed that diagnosis can considerably reduce the inefficiency, so one of the most important tasks in achieving greater hospital efficiency is to optimize the diagnostic process [6].

Expert Systems (ES) uses human knowledge to solve problems which that normally require human intelligence. Expert system (ES) is complex software designed with the ability to reason and think like human expert in a particular key domain area using rules [7]. ES belongs to a branch of Artificial Intelligence that engages the usage of human knowledge to solve complex issues that require the human expert to naturally probe and diagnose using clinical aids [8]. These rules and data can be called upon when needed to solve problems

2. Motivation for the Research

Some of the notable challenges of the existing intelligent systems and orthodox methods in diagnosing tuberculosis are:

i. Challenge of accurate classification, training, and diagnosis due to lack of adoption of optimal algorithm in their design,
ii. Inaccurate prediction of the severity level of tuberculosis in affected patients,
iii. Lack of features and learning optimization,
iv. Problem of ranking symptoms of tuberculosis based on their influence on the degree of tuberculosis infection, and
v. There is low sensitivity and specificity.

The research is therefore motivated by the need to overcome these limitations through the hybridization of genetic, neural network and fuzzy logic algorithms to design and develop an enhanced adaptive Medical Diagnostic System to diagnose and predict the degree of tuberculosis with the following objectives:

i. To determine and select relevant features or symptoms of tuberculosis for accurate and easy prediction using genetic algorithm;
ii. To design an ANFIS (Adaptive Neuro-Fuzzy Inference System) and implement the diagnosis model using selected features or symptoms in (I); and
iii. To evaluate the performance of the developed model based on standard performance metrics.

3. Review of Related Works

3.1. Concept Definition

3.1.1. Overview of Genetic Algorithm (GA)

Genetic algorithm (GA) was introduced by Holland in 2013. It illustrates the biological evolutionary mechanism and has been widely recognized in abroad variety of domains, like functional value optimization, Pattern recognition, and control [8]. GA employs a search technique based on the concept of evolution, in particular with the concept of the survival of the fittest [9]. The technique is conceptually based on evolution mechanism which works on population of solutions in contrast to other search techniques that work on a single solution [10]. The workability of GA is based on Darwinian's theory of survival of the fittest. GA usually contains a chromosome, a gene, a set of population, fitness function, breeding, mutation and selection. GA technique begins with a set of solutions represented by chromosomes, called population. Solutions from one population are taken and used to form a new population, which is motivated by the possibility that the new population will be better than the old one. Further, solutions are selected according to their fitness score to form new solution known as offspring. The above procedure is repeated until certain conditions are satisfied [11]. Its basic implementation involves the following processes: initial population generation; fitness evaluation; and the application of genetic operations of selection, crossover, and mutation and it usually provide acceptable solution within a reasonable time frame when solving optimization problems [12]. In summary, GA has the capability of evolving the best set of connection weights for optimal training of NN. Therefore, there is need to apply GA technique in order to automatically generate a set of connection weight that would be used to train the NN module. According to Shir [13], the advantages of the GAs can be summarized as follows:

i. It can solve every optimization problem, which can be described with the chromosome encoding,
ii. It creates multiple solutions,
iii. It can solve multi-dimensional, non-differential, non-continuous, and even non-parametrical problems,
iv. Structural GA enables the possibility to solve the solution structure and solution parameter Problems at the same time,
v. The method is very easy to understand, and it practically does not demand the knowledge of mathematics,
vi. GAs is easily transferred to existing simulations and models.
vii. GAs works on population of solutions.

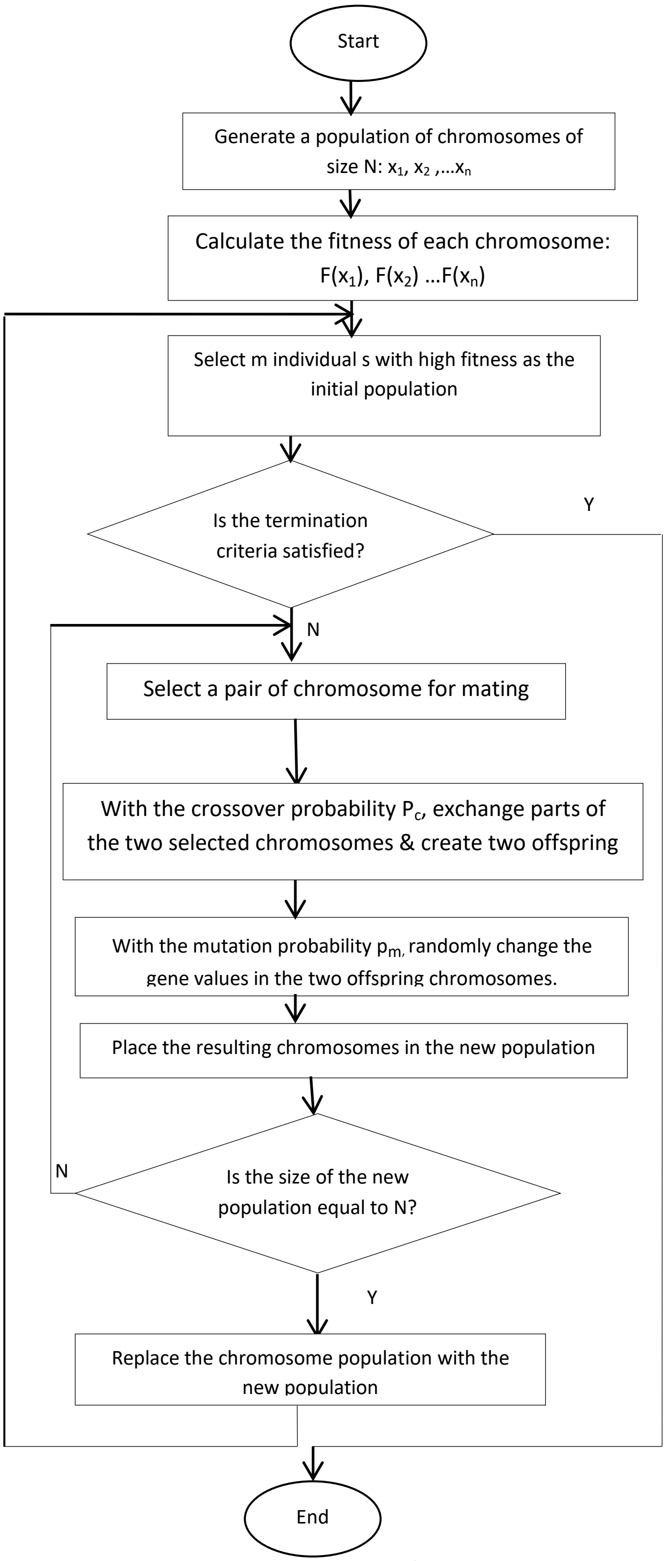


Figure-1. Genetic algorithm flow chart [13].

3.1.2. Overview of Fuzzy Logic

Fuzzy Logic (FL) which was introduced by Lofti Zadeh, a professor at the University California, in his paper “Fuzzy Sets’’ in 1965, is a problem-solving control system methodology and one of the strongest tools to scheme the independent intelligent systems [14]. It is very useful for solving the problems that are not easy to model mathematically. FL can be operated on problem that is based on vague, imprecise and incomplete data, and this is its very positive point. In a Fuzzy Logic process, a crisp set of input data congregates and transforms to a fuzzy set with a reliable set of inference rules during fuzzification step, and then during the defuzzification process the generated outputs get converted into a crisp set using a membership function [15].

3.1.2.1. Structure of fuzzy Systems

Fuzzy systems use the linguistic variables to make decisions based on fuzzy rules and this is the reason why these systems get a better response compared to systems using crisp values. A basic structure of a fuzzy system can be seen in Figure 2.

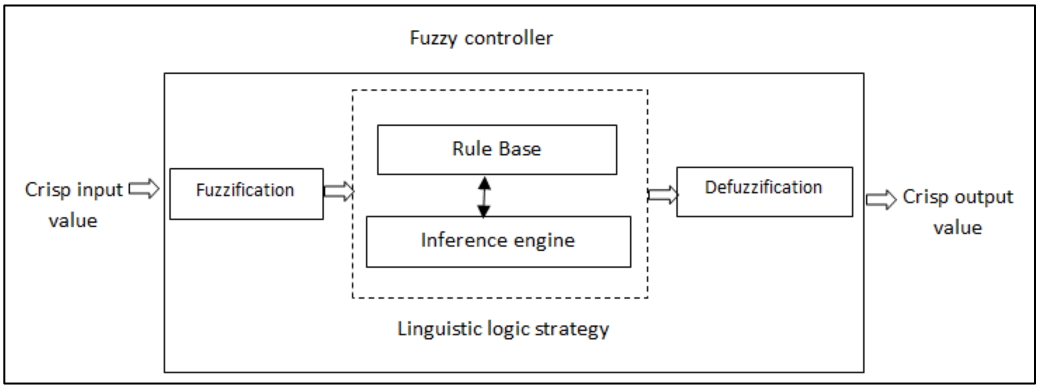


Figure-2. Fuzzy Logic Controller [16]

3.1.3. Overview of Artificial Neural Network (ANN)

ANNs are nonlinear mapping structures resembling the human brain. A combination of predictors is handled by a sequence of neurons and will ultimately lead to the response variable. As a consequence, ANNs are considered to be a “black-box” approach that uses predictors to predict the response variable without reporting intermediate predictor combinations and transformations. ANNs have been applied in ecology to describe, for instance, the probability of occurrence, species distribution, and abundance [17]. Important advantages are related to the high tolerance for noise and measurement errors and the ability to recognize relations between predictors and response variables without ecological knowledge and regardless of the system's nonlinearity and the problem's dimensionality.

Figure 3 show the illustration of a single neuron in a single hidden layer ANN receiving input values from n predictors (x), associated with a specific weight (w_j) and an overall bias term (z_j). A new variable (a_j) is calculated and transformed by a transfer function (f), resulting in the j^{th} output (y_j).

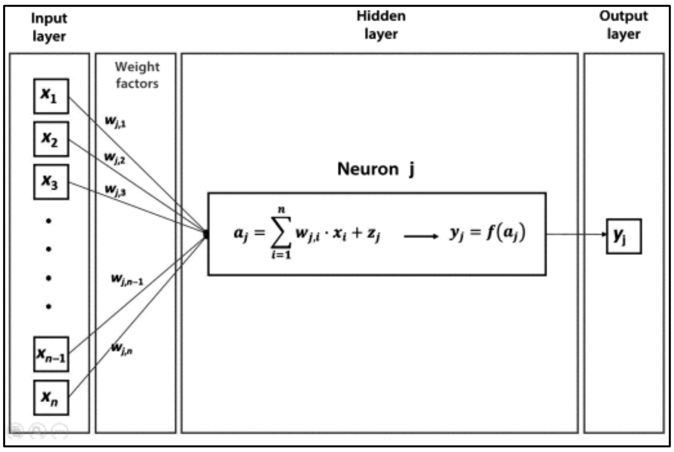


Figure-3.A Single Neuron in a Single Hidden Layer ANN with Inputs from *N* Predictors (*x*) [17].

Neural Network has the capability of capturing domain knowledge from available symptoms and can readily handle both continuous and discrete data. NN is used to train and test the designed fuzzy system to optimize the performance of the overall system. Each diagnosis variable weights $W_{j,}$ which shows its contribution in the diagnosis process.

3.2. Research Work in Tuberculosis Diagnosis

A lot of research work has been conducted and published in the field of medicine with regards to tuberculosis diagnosis, analysis and prescriptions.

Francesca [18], Carried reviews on present and future of pediatric tuberculosis diagnostics. The researchers analyze the peculiarities and challenges of diagnosing pediatric tuberculosis. The difficulties of diagnosing tuberculosis in children were spotted and highlighted. Diagnostics tools for microbiological diagnosis (microscopy, culture and rapid molecular test) were also review with short coming highlighted. The researchers spotted that data from 21 national TB programs have not only shown improvement in the uptake of Xpert MTB/RIF but have also revealed that the technology (Xpert) has been under-utilized for TB detection. The review highlighted the diagnostic advantages of Xpert over smear microscope, despite that Xpert as a standalone test has not proven able to overcome the intrinsic challenges of pediatric TB detection. Conclusively, the researchers proposed computer Aid TB detection for both pediatric and adult whose specificity and precision will improve.

Mohammad, *et al.* [19], developed a model to detect tuberculosis disease using image processing technique. To carry out the classification, features were extracted using deep learning and the RESNET50 neural network. Cross-validation and the formation of training and test sets were the two classification scenarios used. The scenario with the best results was the one in which the training and test sets were formed with an accuracy greater than 85%. The classification method that shows the best performance in the two scenarios implemented in this work is SVM. Computer tomography (CT) of the abdomen, CT of the head, magnetic resonance imaging (MRI) of the brain, and MRI of the spine were all used in this investigation. CNN architecture was used to categorize the 4 sets of medical photos by image modality and anatomic location after converting them to JPEG format. In both the validation and test sets, they achieved overall classification accuracy of greater than 99.5%. The collected results showed the viability of the methods adopted. It also showed the best classification scenario and machine learning method to carry out the classification of radiographs with and without tuberculosis.

Mohamed, *et al.* [20], Developed Artificial Neural Networks for Prediction of Tuberculosis Disease. The data was collected from the TB suspects, guardians or care takers along with samples, referred by TB units and health centres. All the samples were processed and cultured. Data was trained on 12,636 records of TB patients, collected during the years 2016 and 2017 from the provincial TB reference laboratory in Khyber Pakhtunkhwa and Pakistan. The training and test set of the suspect data were kept as 70% and 30% respectively, followed by validation and normalization. Artificial neural network approach was used to analyze the data. Back-propagation algorithm based on gradient descent search algorithms was used in training the dataset. The model includes 70% training and 30% test set of the entire data set (12636 records) where the validation score was achieved with an accuracy of 94%. The accuracies of test and validation to predict TB based on patient data were found at 93.90% and 93.71% respectively. The approach was written in MATLAB script where prediction accuracy was achieved as >94% based on ANN. Based on TB patient data, ANN accurately predicted the Mycobacterium tuberculosis (MTB) positive or negative with an overall accuracy of >94%. Further, the accuracy of the test and validation were found to be >93%. This increased accuracy of ANN in the detection of TB suspected patients might be useful for early management of disease to adopt some control measures in further transmission and reduce the drug resistance burden. Alone algorithm was used and the system is not easily accessible. Data attributes were manual entered.

Syeda, *et al.* [21], Carried reviews on Artificial Intelligence in Diagnosing Tuberculosis. The researchers applied comparison of various AI algorithms used for diagnosing tuberculosis (TB) to differentiate their strength and weakness in designing intelligent system. The comparison was done based on the size of dataset used, the no features/parameters, methodology, the technique used to train the data and the accuracy in (%) of each of these techniques. In their review the Multilayer Neural Network (MLNNs) with the Leven Berg-Marquardt (LM) training algorithm obtained better results compared to the BP algorithm. As BP algorithm suffers from slow convergence rate, yielding suboptimal results. However, the LM algorithm overcomes this and converges faster and gives better estimation results. The researchers conclude that as technology had advanced and broadened the horizons of AI, the focus has dramatically shifted from predictive algorithms to CADx systems and deep learning (CNN). This is due to the ease they present in recognition of the images. Nonetheless, there has been little outstanding research in the medical field using CNN. However, the work is just paper review.

Ibrahim, *et al.* [22], Present adaptive Neuro-Fuzzy approach in designing and implementing intelligent system to diagnose tuberculosis. The data used were collected in June 2018 from general hospital Mubi and discussion with the medical experts to know the symptoms and the linguistic variables of every symptom of TB. The data are used for training and testing the system. Trapezoidal Membership function was used in the fuzzification, while back propagation algorithm was used for training and testing the data. The error obtained is 0.41777 at epoch 2 which shows that the training performance is exactly 99.58223 and testing performance of the system are 99.58197 at epoch 2. Sugeno methodology was used to build the interface of this system in which eleven inputs were used and one output was produced that is TB or Not TB. The size of database is 270 with attribute of 11. ANFIS training was completed at epoch 2 using back propagation algorithm and the error obtain is 0.41777 and check is 0.431356 which shows that the training performance is exactly 99.58223 at epoch 2. The system has classification accuracy of 99.6%

Beaulah and Bala [23], Developed Genetic-Neuro-Fuzzy Inferential Model for Tuberculosis Detection. The medical records of 100 TB patients aged 15 to 75 were used to evaluate the performance of the multi-technique decision support system. 70% of the dataset was used for training the data, 15% was used for validation while the remaining 15% was used to observe the performance of the proposed system. In the study, genetic optimization is performed to choose optimal values from a group of diagnostic parameters which serve as input. There are 23 diagnostic parameters in the NN, but the task is to decide which parameters are taken as input in order to minimize complexity. The sensitivity and accuracy of the proposed model are 72% and 82%. The research work was only simulated. Validation was not done. Also, few datasets were implored during the training. The sensitivity and the accuracy were probably due to the size of the dataset. Also, the system is not easily accessible.

Jerome, *et al.* [3], Used Neuro-Fuzzy Approach for diagnosing and Control of Tuberculosis. The symptoms of Tuberculosis were analyzed based on the information gathered from Experts. The linguistic variables are evaluated using Gaussian membership function with a database size of 270, while the data were trained using back propagation algorithm. The system is structured with eleven (11) inputs and one output of which one hundred and twenty (120) rules were generated. Sugeno inference engine is adopted for this research work and centre of gravity method is used for the defuzzification. The classification accuracy of the system is 99.6%. The system was not tested with clinical data. It was only stimulated using MATLAB.

4. Materials and Methodology

In this work the research methodology is in multi-level processes. These levels are:

a. The first level of the process is an extensive review of relevant literature on intelligent systems and diagnosis of tuberculosis with a view to acquire in depth knowledge of the current technology and tools for tuberculosis system development. Thereafter, detailed review on knowledge discovery, machine learning algorithms, data training methods and application of the internet in medical domain was done.

b. In the second level, consultations with experts and patients of tuberculosis were carried out to ascertain best practice.

c. In the third level of the process involves feature selection using genetic algorithm.

d. In the fourth level of the process, the fuzzy logic component was designed in the following stages; fuzzification (fuzzifier), fuzzy inference engine and defuzzification (defuzzifier). The fuzzifier converts crisp input values to their corresponding fuzzy values.

e. In the fifth level, a two layered feed forward neural network was designed. Suppose, the input layer has *m* neurons, input vectors $x \epsilon R_{m,}$ $X = (x_1, x_2, \ldots x_m)$, an input layer neurons *i* is a component of the input vector $x_{i.}$ Let the number of nodes in the hidden layer be represented by *q*, $y \epsilon R_{q,}$ $y = (y_1, y_2, \ldots y_q)$. We represent the link weight between the i^{th} input layer neuron and the j^{th} hidden layer neuron as ω_{ij} and value of j^{th} hidden neuron as θ_j, the output of the hidden layer neuron is

$$y_j = f(\mathrm{net}_{ij}) = f\left(\sum_{i=1}^{m} \omega_{ij}\ x_i - \theta_j\right) \quad (1)$$

Where i =1, 2, 3, 4, …, m, j = 1,2,3,….q. *f* is the sigmoid function for neuron activation. Thus the output of the j^{th} hidden layer neuron is as follows

$$Z_k = [\,1 + \exp\left(-\sum_{j=1}^{q} \omega_{ij} y_j - \theta_k\right)]^{-1} \quad (2)$$

The neural network is trained with genetic algorithm (GA). The GA begin by creating an initial population of weights, thereafter, the input variables were first encoded in binary and then converted to real value weights using the functions in equations (11) and (12).

$$g_i = \begin{cases} 1 \ if \ \ b_i = 1 \\ -1 \ if \ \ b_i = 0 \end{cases} \quad (3)$$

$$R_i = \frac{g_i}{10} \ \sum_{i=2}^{m} (b_k \ x \ 2^{m-k} \quad (4)$$

Where g_i is the sign bit of $\mathrm{gene}_{i,\ R_i}$ is the real value encoding for the *ith* gene, m represents the length of the gene, i = 2, 3, … m. b_k is the *kth* bit in the gene. GA operators were applied to adjust the weights of the neural network and the outcome of each adjustment was evaluated by the GA fitness function until 2n generations was reached and an optimal combination of weights chosen. The normalized fitness function is given as:

$$T_i = \frac{f_i}{\frac{1}{n}\sum_{j=1}^{n} f_i} \quad (5)$$

Where T_i is the normalized fitness of the *ith* chromosome, n is the total number of nodes in the neural network; f_i is the fitness of the *ith* chromosome; j = 1, 2, …n.

f. In the sixth level, a six layered neuro-fuzzy inference engine was developed. The first, second and fifth layers consist of adaptive nodes while the third, fourth and sixth layers are fixed nodes. The architecture implements the Mamdani’s inference mechanism and can handle rules of the form:

IF (x is A) AND (y is B) AND (Z is C) THEN (S is O)

Where X, Y, Z are inputs variables, A, B, C are fuzzy sets of the input variables, S is the output and O is fuzzy set of the output variable within the fuzzy region specified by the rule. Based on the architecture, an expert system driven by Fuzzy logic, Neural Network and Genetic Algorithm was developed using matrix laboratory (Mat Lab) and Python programming languages with Microsoft excel. Data on tuberculosis were collected from Tuberculosis and leprosy hospital Eku, delta state and used as the case study. To determine the efficiency and effectiveness of the system, the results obtained were analyzed using precision, accuracy, sensitivity and receivers operating characteristics curve as measures.

4.1. System Design

System design is the process of defining the architecture, components, modules, interfaces and data for a system to satisfy specified requirements. The principle goal of system design is to establish a design approach that provides the functions described in the system specification and requirement documentations.

4.1.1. Architecture of the Propose Model

The architecture of the tuberculosis diagnostic system is presented in Figure 4.

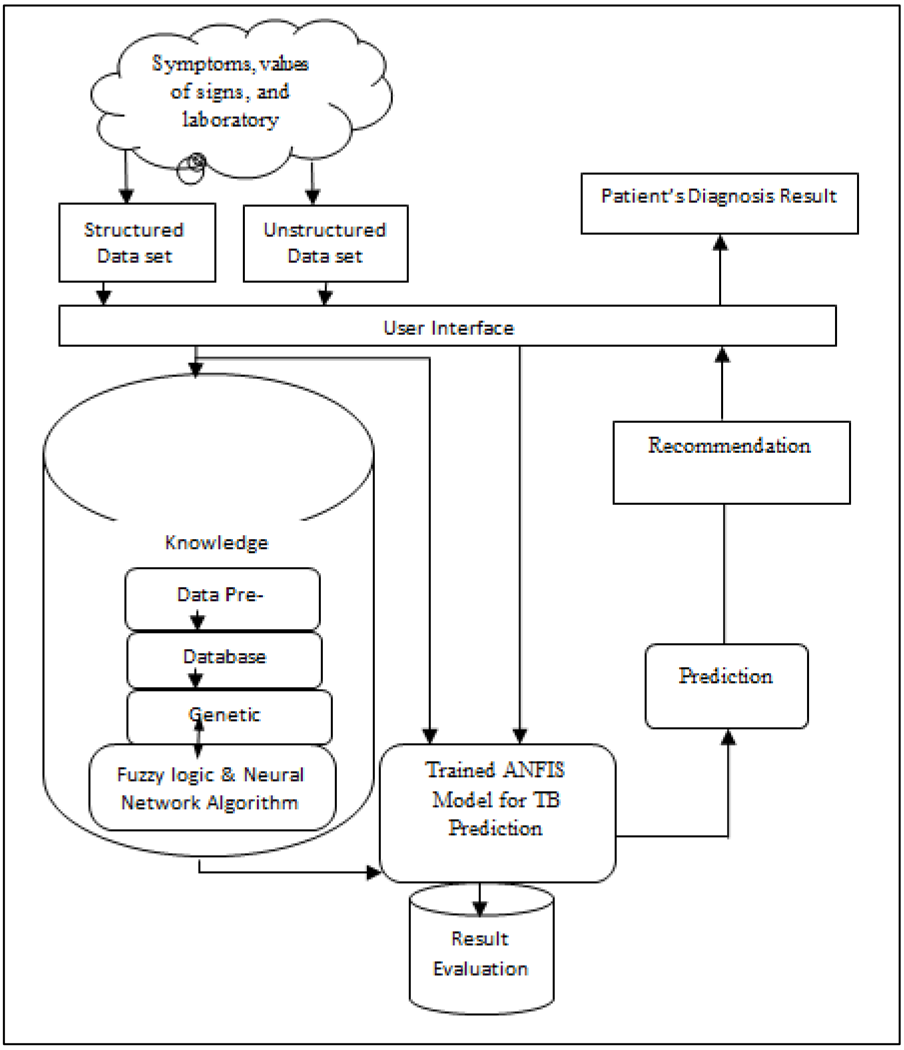


Figure-4. Architecture of Tuberculosis Diagnosis

4.1.2. Components of the Architecture

The proposed TB diagnosis model is composed of mainly five components namely; User interface, Knowledge warehouse, ANFIS model, Prediction and, Recommendation model. The detailed description of each component, including their functions is presented in the following subsections

- **User interface (UI)**

The user interface is the point at which human users (medical practitioners and system designer) interact with the developed application. The goal of the UI is to make the user's experience easy and intuitive, requiring minimum effort on the user's part to receive the maximum desired outcome. This component specifically accepting patients input (structured and unstructured data).

- **Knowledge warehouse**

The knowledge warehouse (KW) is the component where knowledge is developed, stored, organized, processed and disseminated. It is a network of semantically related static and dynamic entities, each of which is modeled in a relational form Akinyokun and Angaye [1]. The KW in this design is a collection of knowledge marts. Each knowledge mart design follows the hierarchical approach and is viewed as an integrated collection of the following components:

i. Pre-processing
ii. Database
iii. Genetic Algorithm and
iv. Adaptive neuro-fuzzy inference system (ANFIS).

- **Pre-processing component**

Data pre-processing is an essential stage that is applied to dataset to transform input dataset into a machine format for soft computing techniques. The common pretreatment methods include flipping, gray scale transformation, standardization, cropping [24] and so on. The standardization method is adopted in this work. The need for data pre-processing ensued from the fact that medical data as well as tuberculosis data obtained for this study contain redundant, irrelevant, and un-scaled features, and if passed directly to the ANFIS could either cause the malfunction or affect classification performance. In this research, the pre-processing component handles missing values challenges and high variation values using mean-value imputation and min-max methods respectively. Data encoding involves converting non-numeric feature values to numeric feature values to ensure smooth mathematical operations during model processing. In this study, the feature value for all the feature categories are in non-numeric form and requires encoding. Table 1 shows the attributes of tuberculosis and their code definition, while Table 2 shows the non-numeric features of the obtained tuberculosis dataset with their list of values; also information in Table 3 provides the encoded features in the sample dataset.

Table-1. Tuberculosis Attributes

S/N	**Category**	**TB Symptoms/Attributes**	**Code Definition (CD)**
1		Cough	CO
2		Night sweats	NS
3	Physical symptoms (PS)	Difficulty in Breathing	DB
4		Fever	FV
5		Chest Pain	CP
6	Laboratory Investigation (LI)	Sputum	SP
7		Loss of pleasure	LP
8	Emotional symptoms (ES)	Chills	CH
9		Lack of concentration	LC
10		Irritation	IR
11		Loss of appetite	LA
12	Motivational symptoms (MS)	Loss of energy	LE
13	Physiological symptoms (PHS)	Lymph Node Enlargement	LN
14		Systolic Blood Pressure	SB
15		Body Mass Index	BMI
16		Immune Suppression	IS

Source: Field Survey, 2022

Table-2. Encoding Parameters for Non-Numeric Feature Values

S/N	**Feature**	**Feature Values**	**Feature Encoding**
1	Cough	'Severe', 'mild', 'moderate'	'mild' = 0, 'moderate' =1, 'severe' = 2
2	Night_sweat	'Severe', 'mild', 'moderate'	'mild' = 0, 'moderate' =1, 'severe' = 2
3	Breathing_difficulty	'Severe', 'mild', 'moderate'	'mild' = 0, 'moderate' =1, 'severe' = 2
4	Fever	'Severe', 'mild', 'moderate'	'mild' = 0, 'moderate' =1, 'severe' = 2
5	Chest_pain	'Severe', 'mild', 'moderate'	'mild' = 0, 'moderate' =1, 'severe' = 2
6	Sputum	'bloody', 'colorless', 'green'	'bloody' = 0, 'colorless' = 1, 'green' = 2
7	Immune_suppression	'Severe', 'mild', 'moderate'	'mild' = 0, 'moderate' =1, 'severe' = 2
8	Loss_of_pleasure	'Severe', 'mild', 'moderate'	'mild' = 0, 'moderate' =1, 'severe' = 2
9	Chill	'Severe', 'mild', 'moderate'	'mild' = 0, 'moderate' =1, 'severe' = 2
10	lack_of_concentration	'Severe', 'mild', 'moderate'	'mild' = 0, 'moderate' =1, 'severe' = 2
11	Irritation	'Severe', 'mild', 'moderate'	'mild' = 0, 'moderate' =1, 'severe' = 2
12	Loss_of_appetite	'Severe', 'mild', 'moderate'	'mild' = 0, 'moderate' =1, 'severe' = 2
13	Loss_of_energy	'Severe', 'mild', 'moderate'	'mild' = 0, 'moderate' =1, 'severe' = 2
14	Lymph_node_enlargement	'Severe', 'mild', 'moderate'	'mild' = 0, 'moderate' =1, 'severe' = 2
15	Systolic_blood_pressure	'Severe', 'mild', 'moderate'	'mild' = 0, 'moderate' =1, 'severe' = 2
16	BMI	'Severe', 'mild', 'moderate'	'mild' = 0, 'moderate' =1, 'severe' = 2

Source: Field Survey, 2022

Table-3. Sample of Encoded Dataset

CO	**NS**	**BD**	**FV**	**CP**	**SP**	**IS**	**LP**	**CH**	**LC**	**IR**	**LA**	**LE**	**LNE**	**SBP**	**BMI**
0	2	2	1	2	0	1	1	1	2	2	1	1	1	0	0
0	0	2	0	1	1	0	1	0	2	2	0	0	0	2	1
1	1	2	0	2	0	1	2	2	2	0	1	0	2	2	0
0	0	1	2	0	0	1	0	0	1	1	0	1	1	1	0
1	2	1	1	0	2	2	1	0	1	2	0	2	0	1	1
1	2	0	2	1	2	0	1	1	0	1	0	2	0	0	2
1	1	1	1	1	0	0	2	1	0	0	0	0	1	2	0
1	2	2	2	1	1	1	1	1	2	1	2	0	1	0	1
1	1	1	0	2	1	2	0	1	2	2	2	1	0	2	1
0	2	1	1	2	2	0	2	1	1	2	2	1	1	2	0
0	2	1	2	0	2	1	2	2	2	0	1	1	2	2	1
2	1	2	0	2	1	0	2	1	1	2	2	2	1	1	2
2	2	1	0	0	0	2	0	0	2	2	1	0	1	0	0
0	1	0	2	1	1	1	1	0	0	1	1	2	0	1	0
1	1	1	2	1	2	0	2	0	0	2	0	2	1	0	1
2	0	0	0	2	2	0	2	1	0	2	0	1	0	1	2
1	2	1	1	2	1	0	1	2	1	1	1	2	1	1	1
0	1	2	0	2	1	0	2	1	1	2	2	0	1	2	2
0	1	1	2	1	0	0	0	0	2	1	1	2	2	0	2

0	0	2	0	1	1	0	0	1	2	0	2	1	2	2	0
2	1	0	0	0	2	1	2	0	0	2	0	1	2	0	0

Source: Field Survey, 2022

4.2. Genetic-neuro-fuzzy hybrid platform

The design algorithm of hybrid platforms described in Shanthi, *et al.* [25], are studied and modified to suit the design of the knowledge warehouse. Figure 5 shows the hybridization block diagram of the genetic -neuro –fuzzy.

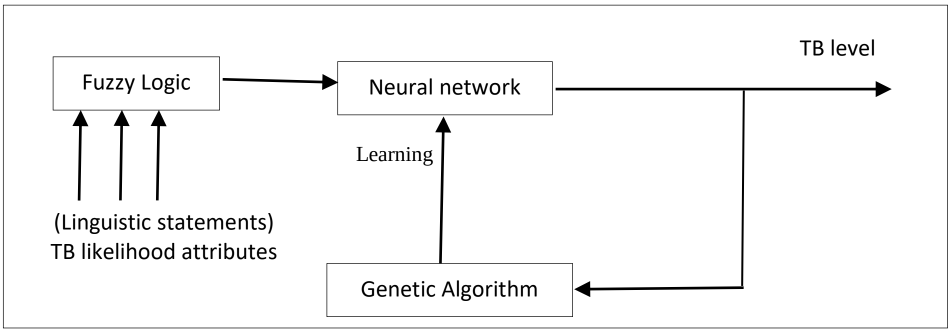
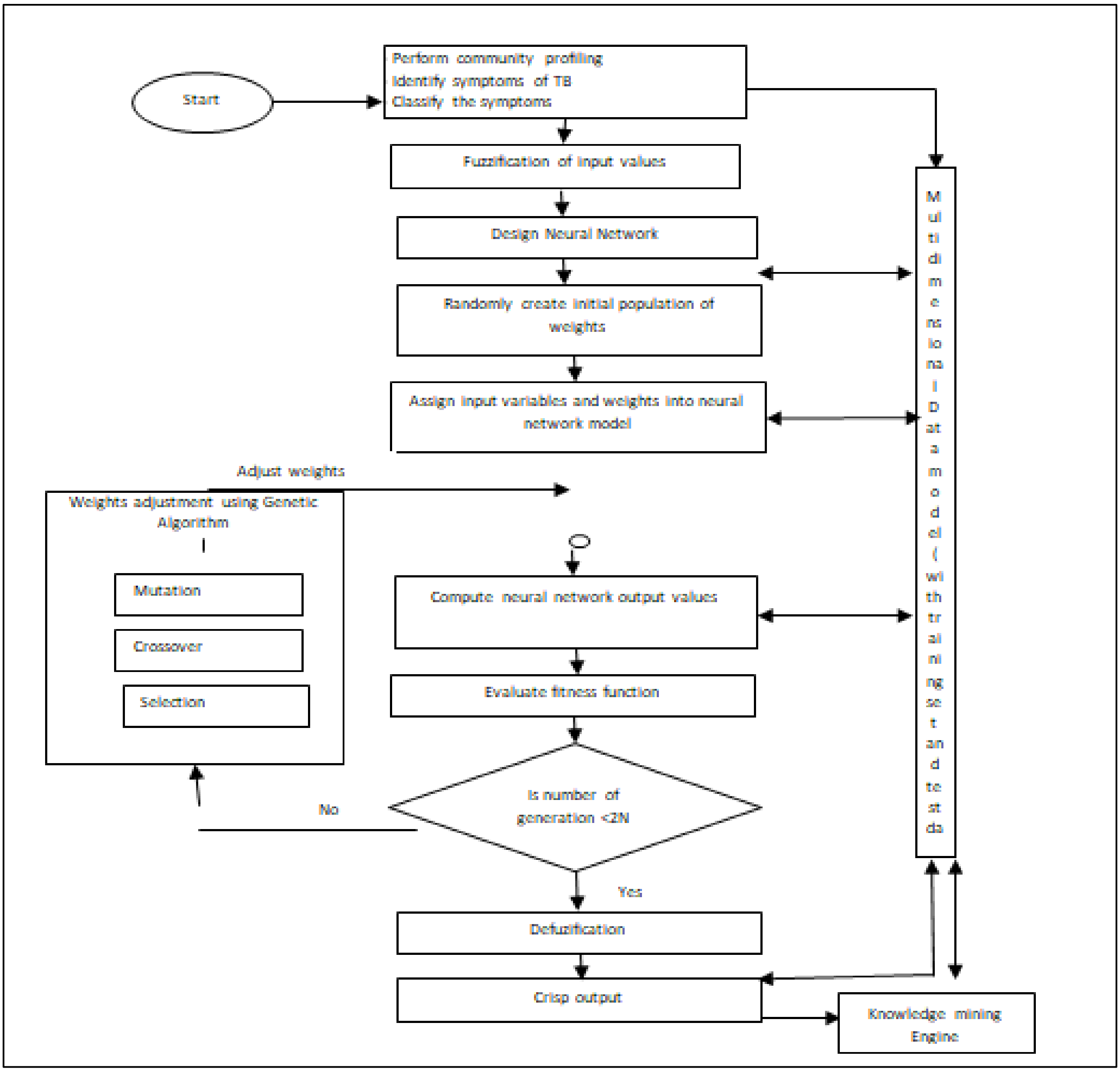


Figure-5. Block diagram of the Genetic -Neuro -Fuzzy Hybrid

In Figure 5 the neural network is the front end and the central component of the system as in [26]. It receives inputs from and communicates output to the environment as well. The GA and fuzzy logic components are the backend platform. The GA component is used to optimize the weights of the neural networks by providing optimal set of parameters for training the neural network while the fuzzy logic component acts as a tool for modeling imprecise and vague knowledge and provides evaluation and membership functions for the genetic algorithm and neural networks. Pieces of knowledge are represented by fuzzy production rules. The hybrid platform utilizes the advantages of each tool thereby compensating for the problems of each tool. Fuzzy logic provides an inference mechanism under cognitive uncertainty while the neural network component offers the advantages of adaptation, parallelism, fault tolerance and generalization. Figure 7 shows the interaction of the different components as well as the procedure for the design of the knowledge warehouse. The design of the hybrid platform begins with the multidimensional knowledge model design, which acts as the platform for holding the pieces of knowledge, their relationship and patterns. The community profiling is performed to identify the inputs to the system which are fuzzified to make them suitable for processing by the neural network models. The GA component begins by creating an initial population of weights for the neural network models. The fuzzified inputs variables are first encoded in binary, then converted to real value weights, and assigned to neural network models. GA operators are applied to adjust the weights of the neural network and the outcome of each adjustment is evaluated by the GA fitness function until 2N generations are reached and an optimal combination of weights is chosen. The optimal neural network parameters are subjected to the adaptive neuro-fuzzy inference system (ANFIS).



The crisp input information is first transformed by a fuzzifer into a set of linguistic variables (low, moderate, and severe). Then ANFIS engine evaluates the input variables based on the rules in the fuzzy rule base held in the multidimensional data model, derives a set of conclusions from the rules by means of a defuzzifier, converted into a crisp number (S) which corresponds to the output of the system.

4.3. Model Implementation

After successful design of a system come the implementation activities. The implementation stage is very important stage in software development life cycle. In this phase the design made during the system design phase is coded. The implementation encompasses choice of programming tools, hardware and software requirement.

4.3.1. Environmental setup for ANFIS based TB diagnostic system

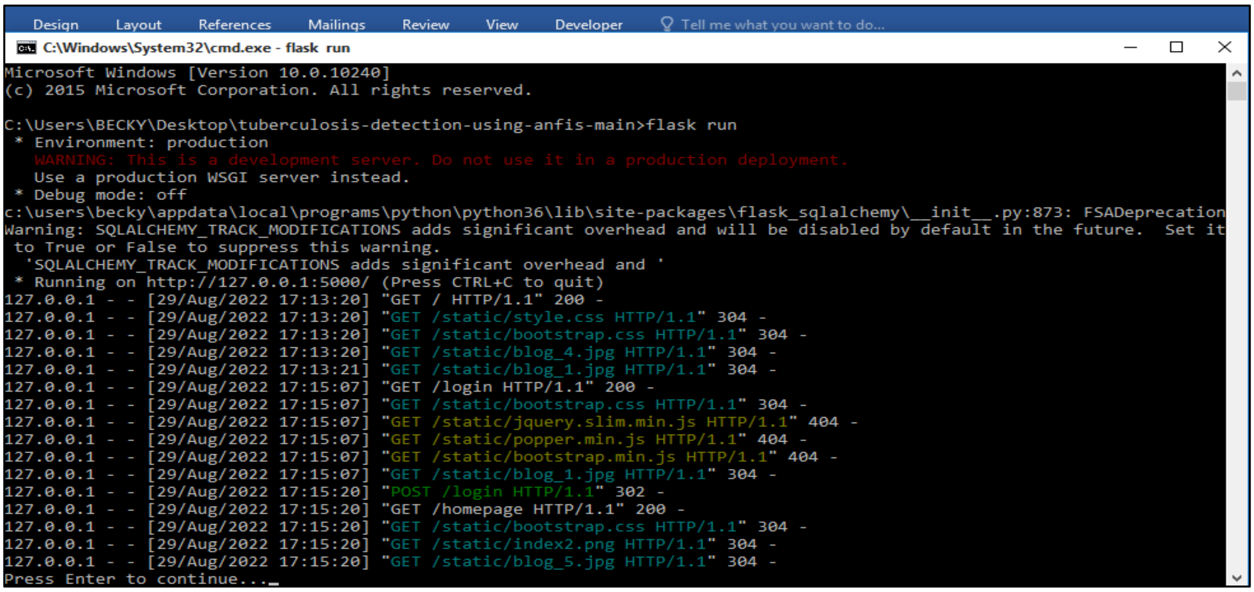
The installation process of the ANFIS based TB diagnostic model requires to install python 3.6.exe setup with other python dependencies for flask kernel, thereafter install and connect matlab.engine, and then run flask kernel. The dependencies are shown in Table 4. Figure 8 shows the windows command prompt where flask run was executed. The execution of flask run automatic invokes the diagnostic system interface on the default browser of the computer system.

Table-4. Python Dependencies for execution of TB Diagnostic System

S/N	Dependencies	S/N	Dependencies
1	attrs==19.3.0	46	packaging==20.3
2	backcall==0.1.0	47	pandas==1.0.3
3	bcrypt==3.2.0	48	pandocfilters==1.4.2
4	bleach==3.1.5	49	parso==0.7.0
5	certifi==2020.4.5.1	50	passlib==1.7.2

S/N	Dependencies	S/N	Dependencies
6	cffi==1.14.4	51	Pillow==7.1.1
7	chardet==3.0.4	52	prometheus-client==0.7.1
8	click==7.1.1	53	prompt-toolkit==3.0.5
9	colorama==0.4.3	54	pycparser==2.20
10	convertdate==2.2.0	55	PyFladesk==1.1
11	cycler==0.10.0	56	Pygments==2.6.1
12	Cython==0.29.17	57	PyMeeus==0.3.7
13	decorator==4.4.2	58	pyparsing==2.4.7
14	defusedxml==0.6.0	59	PyQt5==5.14.2
15	entrypoints==0.3	60	PyQt5-sip==12.8.1
16	Flask==1.0.2	61	PyQtWebEngine==5.15.2
17	Flask-Bcrypt==0.7.1	62	pyrsistent==0.16.0
18	Flask-Login==0.5.0	63	python-dateutil==2.8.1
19	Flask-SQLAlchemy==2.4.4	64	pytorchtools==0.0.2
20	Flask-Validate==0.1.0	65	pytz==2019.3
21	Flask-Validates==0.3.0	66	pywin32==227
22	Flask-WTF==0.14.3	67	pywinpty==0.5.7
23	gunicorn==20.0.4	68	pyzmq==19.0.0
24	idna==2.9	69	requests==2.23.0
25	ipykernel==5.2.1	70	scikit-learn==0.23.1
26	ipython==7.14.0	71	scipy==1.4.1
27	ipython-genutils==0.2.0	72	Send2Trash==1.5.0
28	itsdangerous==1.1.0	73	six==1.14.0
29	jedi==0.17.0	74	sklearn==0.0
30	Jinja2==2.11.2	75	SpeechRecognition==3.8.1
31	joblib==0.15.1	76	SQLAlchemy==1.3.20
32	json5==0.9.4	77	terminado==0.8.3

Source: Field Survey, 2022



```
Microsoft Windows [Version 10.0.10240]
(c) 2015 Microsoft Corporation. All rights reserved.

C:\Users\BECKY\Desktop\tuberculosis-detection-using-anfis-main>flask run
 * Environment: production
   WARNING: This is a development server. Do not use it in a production deployment.
   Use a production WSGI server instead.
 * Debug mode: off
c:\users\becky\appdata\local\programs\python\python36\lib\site-packages\flask_sqlalchemy\__init__.py:873: FSADeprecation
Warning: SQLALCHEMY_TRACK_MODIFICATIONS adds significant overhead and will be disabled by default in the future.  Set it
 to True or False to suppress this warning.
  'SQLALCHEMY_TRACK_MODIFICATIONS adds significant overhead and '
 * Running on http://127.0.0.1:5000/ (Press CTRL+C to quit)
127.0.0.1 - - [29/Aug/2022 17:13:20] "GET / HTTP/1.1" 200 -
127.0.0.1 - - [29/Aug/2022 17:13:20] "GET /static/style.css HTTP/1.1" 304 -
127.0.0.1 - - [29/Aug/2022 17:13:20] "GET /static/bootstrap.css HTTP/1.1" 304 -
127.0.0.1 - - [29/Aug/2022 17:13:20] "GET /static/blog_4.jpg HTTP/1.1" 304 -
127.0.0.1 - - [29/Aug/2022 17:13:21] "GET /static/blog_1.jpg HTTP/1.1" 304 -
127.0.0.1 - - [29/Aug/2022 17:15:07] "GET /login HTTP/1.1" 200 -
127.0.0.1 - - [29/Aug/2022 17:15:07] "GET /static/bootstrap.css HTTP/1.1" 304 -
127.0.0.1 - - [29/Aug/2022 17:15:07] "GET /static/jquery.slim.min.js HTTP/1.1" 404 -
127.0.0.1 - - [29/Aug/2022 17:15:07] "GET /static/popper.min.js HTTP/1.1" 404 -
127.0.0.1 - - [29/Aug/2022 17:15:07] "GET /static/bootstrap.min.js HTTP/1.1" 404 -
127.0.0.1 - - [29/Aug/2022 17:15:07] "GET /static/blog_1.jpg HTTP/1.1" 304 -
127.0.0.1 - - [29/Aug/2022 17:15:20] "POST /login HTTP/1.1" 302 -
127.0.0.1 - - [29/Aug/2022 17:15:20] "GET /homepage HTTP/1.1" 200 -
127.0.0.1 - - [29/Aug/2022 17:15:20] "GET /static/bootstrap.css HTTP/1.1" 304 -
127.0.0.1 - - [29/Aug/2022 17:15:20] "GET /static/index2.png HTTP/1.1" 304 -
127.0.0.1 - - [29/Aug/2022 17:15:20] "GET /static/blog_5.jpg HTTP/1.1" 304 -
Press Enter to continue..._
```

Figure-8. Command prompt for Flask run

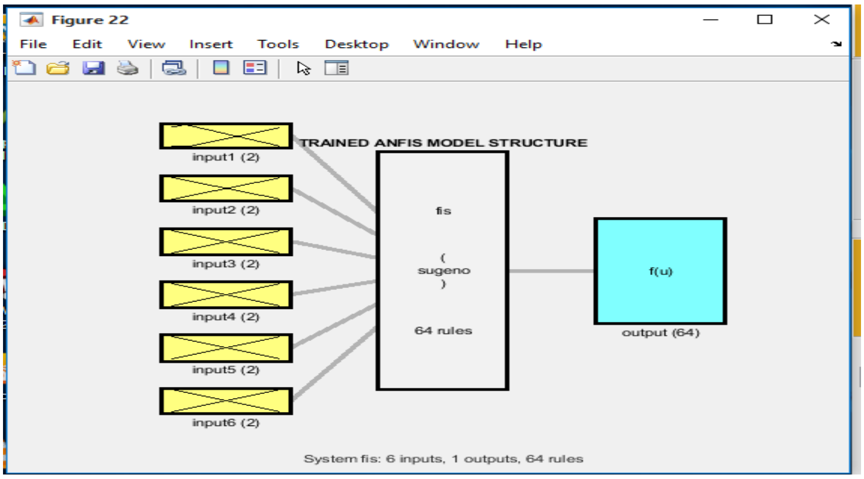


Figure-9. Fuzzy Inference System for TB Diagnosis

In training ANFIS model, the input data and the output data were split using 70:30 per cent ratio. Three Hundred and One (301) data point or instances out of Four Hundred and Thirty (430) instances were used for training; the remaining One Hundred and Twenty-Nine (129) instances represented the test data for the model. For improved accuracy, it was ensured that the test data covered the entire range of the available dataset. Table 5 shows the class distribution for developing the model. The modeling parameters for the developed ANFIS model are listed in Table 6 as follows:

Table-5. TB Dataset Distribution

Target Labels	**Tuberculosis Dataset**			
	Training	**Training (%)**	**Testing**	**Testing (%)**
Mild	106	35.2	42	32.6
Moderate	98	32.6	34	26.3
Severe	97	32.2	53	41.1
Total	**301**	**100**	**129**	**100**

Source: Field Survey, 2022

Table-6. Modelling Parameters for ANFIS Model

S/N	Variable	Value
1	Number of nodes	161
2	Number of linear parameters	448
3	Number of nonlinear parameters	36
4	Total number of parameters	484
5	Number of training data pairs	300
6	Number of checking data pairs	0
7	Number of fuzzy rules	64
8	Number of Epochs	40

Source: Field Survey, 2022

5. Result and Discussion

The test result is the outcome of the tested software system based on the input data. This helps in phase validating the code effectiveness and correctness. The system was tested to found out how it could be used to diagnose tuberculosis. Table 7 shows the results obtained after testing the system using the test plan and test data. In the course of the testing the actual and expected results were compared to ascertain they produced the same result or there is a difference.

Table-7. Comparison between Actual and Expected Results

S/N	**Actual values**	**Predicted values**	**S/N**	**Actual values**	**Predicted values**	**S/N**	**Actual values**	**Predicted values**
1	severe	severe	44	Moderate	Moderate	87	Moderate	Moderate
2	severe	severe	45	Severe	Severe	88	Severe	Severe
3	severe	severe	46	Severe	Severe	89	Moderate	Moderate
4	Moderate	Moderate	47	Severe	Severe	90	Mild	Mild
5	Severe	Severe	48	Mild	Mild	91	Mild	Mild
6	Mild	Mild	49	Moderate	Moderate	92	Mild	Mild
7	Moderate	Moderate	50	Severe	Severe	93	Severe	Severe

8	Mild	Mild	51	Mild	Mild	94	Severe	Severe
9	Moderate	Moderate	52	Severe	Severe	95	Moderate	Moderate
10	Mild	Moderate	53	Mild	Mild	96	Mild	Mild
11	Moderate	Moderate	54	Mild	Mild	97	Severe	Severe
12	Severe	Severe	55	Moderate	Moderate	98	Severe	Severe
13	Moderate	Moderate	56	Severe	Severe	99	Mild	Mild
14	Severe	Severe	57	Mild	Mild	100	Moderate	Moderate
15	Severe	Severe	58	Severe	Severe	101	Mild	Mild

Source: Field work, 2022

5.1. Model Performance Evaluation and Interpretation of Results

This subsection provides results and evaluation of the developed ANFIS based Tuberculosis Diagnostic model on the test data. Table 7 shows the predicted and desired values from the test dataset. Table 8 shows the confusion matrix outcomes. Table 9 shows the computation of developed model performance such as the precision, accuracy, specificity, sensitivity, and F1-Measure of the developed model. Table 25 shows the summary of the result based on each fuzzy linguistic value is presented instances.

Table-8. Confusion Matrix of Developed Model on Test Data

		Predicted Class			
		Mild	Moderate	Severe	Total
Actual Class	Mild	**42**	0	0	42
	Moderate	0	**34**	0	34
	Severe	0	0	**53**	53
Total		42	34	53	**129**

Source: Field work, 2022

Table-9. Summary of Model Result

Binary Breakdown per Label	**Positive label**		
Statistic	**Severe**	**Moderate**	**Mild**
True Positives	53	32	42
True Negatives	76	95	87
False Positives (Type I Errors)	0	0	2
False Negatives (Type II Errors)	0	2	0
Accuracy	100%	99%	99%
Precision	100%	100%	100%
Sensitivity	100%	100%	100%
Specificity	100%	100%	100%
F-measure	1	1	1

Source: Field work, 2022

The confusion matrix in Table 8 shows that all instances in each target class were accurately classified with not misclassified cases. True positive was rate for severe 100% (without type 1 or type II errors) while moderate and mild 99%. The accuracy is 100%; the precision is 100% for severe, while moderate, and mild cases have 99%. The specificity for all categories is very severe which implies an insignificant false positive rate (FPR) and severe true positive rate (TPR). Also, the F-measure on the average is 1. The result of accuracy, precision, sensitivity, specificity, and F-measure prove that the model is efficient and effective for classification and prediction of the degree of tuberculosis. Figure 9 shows numbers of accurate predictions.

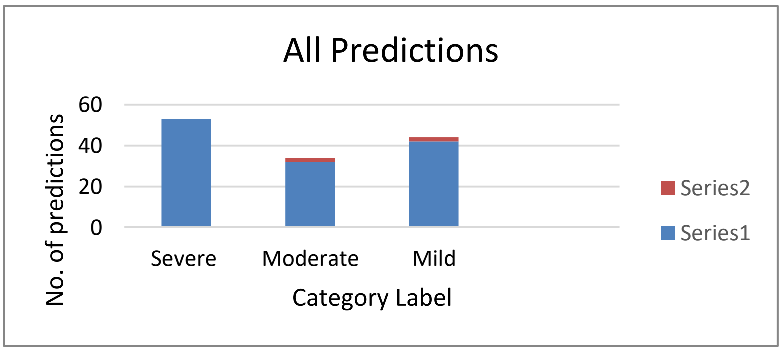


Figure-8. Graph Showing Numbers of Accurate Predictions

In Figure 8, the patterns leading to severe and mild have 100% correct prediction. None of the instance was wrongly predicted. Table 9 shows the comparison of crisp output of domain expert and the new system for ten patients

Table-9. Comparison of Crisp Output of Domain Expert and the new System for Ten Patients

S/N	Patient No.	% Possibility Domain Expert	Diagnosis	% Possibility Developed System	Diagnosis
1	202119	59	Moderate	59	Moderate
2	9000087	91	Severe	91	Severe
3	2201421	48	Moderate	48	Moderate
4	9100182	56	Moderate	56	Moderate
5	8700008	12	Mild	12	Mild
6	2301694	62	Severe*	48	Moderate*
7	2101387	62	Severe	62	Severe
8	8900021	29	Mild	27	Mild
9	9300201	87	Severe	87	severe
10	2201450	33	Mild	33	Mild

Source: Field work, 2022

In summary, the diagnosis system was tested to ensure that it met the aim and objectives of the research. From the analysis of the attributes and the comparison of the crisp output of domain expert, it shows that the new model is reliable, by having 90% accuracy prediction in the ten (10) cases predicted. Likewise, the statistical model analysis showed precision, sensitivity, and specificity to be 100%, while the F-measure is 1 for the severity (mild, moderate and severe) of tuberculosis. In addition, the analysis shows that all the attributes of the disease contribute to the degree of the disease severity. Thus it will be a good tool that will assist medical personal.

6. Conclusion

In conclusion all the stated objectives of the research were achieved in which the developed system enables users to determine and select relevant features or symptoms of tuberculosis for accurate and easy prediction using genetic algorithm. This new system equally designed an adaptive neuro-fuzzy inference system (ANFIS) based diagnostic system using selected features by the genetic algorithm. Also, the genetic-neural-fuzzy medical diagnostic system was implemented after the design to assist in diagnosis of tuberculosis. Finally, performance evaluation of the new system was done based on standard performance metrics.

Among other tasks the system reported is capable of performing are:

1. Rank symptoms of tuberculosis based on their influence on the degree of tuberculosis infection
2. Build ANFIS for tuberculosis diagnosis based on symptoms
3. Extract frequent patterns and build fuzzy rules
4. Diagnose tuberculosis and report severity of the disease.

The solution hence was seen to have eliminated the stated problems. The artifact produce at the end of the research is very efficient and is highly recommended for health centers that manage tuberculosis.

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