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Artificial Intelligence in Diagnosing Tuberculosis: A Review

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***Abstract*— Tuberculosis (TB) is among top ten causes of deaths worldwide. It is the single most cause of deaths by an infectious disease and is ranked 2nd only after the HIV/AIDS. In third world countries, the diagnosis of TB is done through conventional methods. To diagnostic results are obtain from conventional methods such as blood, culture, sputum and biopsies. They are tedious as well as take long time like 1-2 weeks or maybe evenmore. Therefore, to lower the detection time and raise the accuracy of diagnosis several researches have been carried out. In the past fifty years, due to the advanced and sophisticated technologies, in medical as well as computer science fields, have paved a way to utilize the essence of both the areas. In Artificial Intelligence (AI) various Machine Learning (ML) algorithms have furthered the interests in Computer-aided Detection (CADe) and Diagnosis (CADx) methods. These methodologies assist in medical field for diagnosing the diseases through clinical signs and symptoms as well as radiological images of the patient. They have been implemented for the diagnosis of TB. Advances in AI algorithms, has unveiled great promises in identifying the presence and absence of TB. As of late, many attempts have been made to formulate the strategies to increase the classification accuracy of TB diagnosis using the AI and machine learning approach. This review paper, aims to describes the diverse AI approaches employed in the diagnosis of TB.**

***Keywords*— tuberculosis; artificial intelligence; artificial neural network; machine learning; convolution neural networks.**

I. NTRODUCTION

Tuberculosis is an age-old disease. This ancient killer disease has survived for thousands of years. There are quite a few archaeological evidences, found in ancient Egypt, pointing to the existence of this disease. Such as pott's disease (spinal tuberculosis), found in Egyptian mummies [1],[2] . Furthermore, several literary documentations reveal the existence of TB, in ancient India, China and Greece [3], [4]. TB was known by various names, throughout the history. In ancient Greece, it was called "Phthisis" or "consumption" (because of extreme weight loss in patients). During middle ages, scrofula (Mycobacterial cervical lymphadenitis) was popularly believed, to be cured by the royal touch of Kings of England and France. It was known as "King's evil". Later in the 18th century, prevalence of TB was so high, that one in every fourth death was attributed to TB [5]. The term "White plague" was used to describe TB patients, because of inadequate ventilation, overcrowding, malnutrition and accommodation facilities in TB sanatoriums [6].

Robert Koch in 1822, discovered Mycobacterium Tuberculosis, the causative organism of TB [7]. He demonstrated that, due to high lipid content in the cellular wall of the micro-organism, it was difficult to identify using common dyes [8]. The discovery of Bacillus-Chalmette Guerin (BCG) in 1908 [9] and anti-tuberculosis drugs in 1943 gave hope for the elimination of TB disease[10]. Since, the discoveries of vaccines, there was a significant decrease in the TB cases. In 1990s, due to the onset of AIDS pandemic, TB cases rose again drastically with TB resistant strains[11]–[24]. Subsequently, many strategies were developed for the control and prevention of the TB disease. To commemorate the discovery made by Koch, every year 24th March is recognized as "World TB day". TB is still one of the leading cause of deaths in the world. According to World Health Organization (WHO) in 2015, TB was detected in 10.4 million people out of which 1.8 million people succumbed to death from the TB illness [25].

A. Types of TB

TB is an airborne infectious disease. It is caused by bacteria Mycobacterium Tuberculosis (MTB). TB is categorized into two main types, depending on the site which MTB affects. If the bacteria affect lungs and its surrounding regions, then it is called as Pulmonary Tuberculosis (PTB). When the bacteria affects and spreads to other parts of the body then it is called Extra Pulmonary Tuberculosis (EPTB). Few types of PTB are primary Tuberculosis pneumonia, cavity Tuberculosis, Tuberculosis pleurisy, military TB and laryngeal TB. On the other hand, types of EPTB include

Pot's disease, lymph node disease, Tuberculosis meningitis, adrenal Tuberculosis, Tuberculosis peritonitis, Tuberculosis pericarditis, Osteal tuberculosis [26]–[30]. The symptoms of TB and few types of PTB and EPTB are shown in Fig. 1

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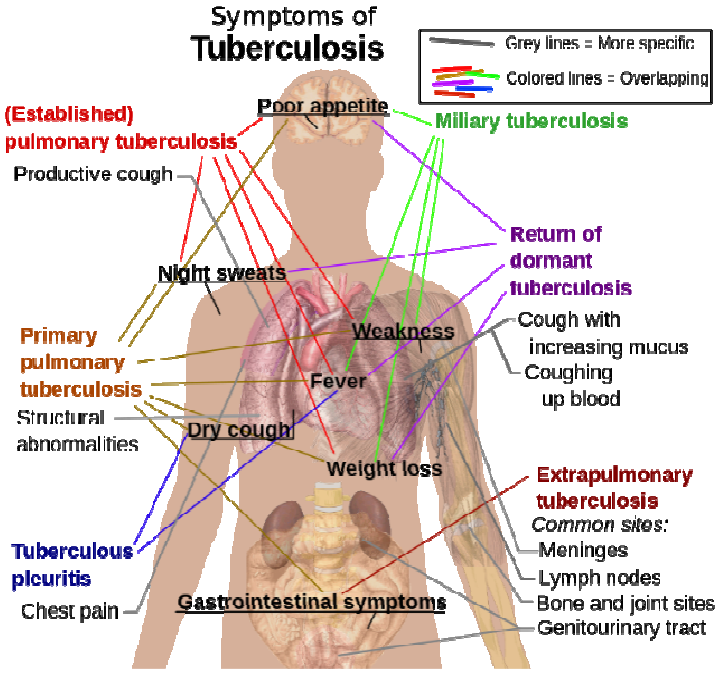

Fig. 1 Types of PTB and EPTB [31]

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B. Co-infection, risk factors and other causes of TB

TB is a common cause of AIDS-defining diseases. It is also a leading cause of deaths in AIDS patients [32]. TB and Diabetes Mellitus (DM) is another common co-infection, the risk of getting TB is higher in patients with diabetes [33]–[39], as the immunity of a diabetes patient is less when compared to a reasonable person [40]. The other risk factors that cause TB are smoking, silicosis, crowding, prisons, substance abuse, alcoholism, end-stage renal diseases and malnutrition [41]–[46],[32].

C. The conventional method of diagnosing TB

The bacterium generally spreads through the air, when a person having TB coughs, sneezes or talks. Air is the major medium for the spreading of MTB. At times TB can spread through Cattle, Monkey's, Sheep's, Goat's, Cat's and Dog's [47]. The bacteria typically affects the lungs, and in a few cases, it might also affect the brain, spine, and kidney [48].

There are two conditions of TB-which are Active Tuberculosis (TB) and Latent Tuberculosis (LTB). Active TB is one where the TB bacteria are active and multiplying in the body. The people having active TB show symptoms of persisting cough for more than two weeks, followed by pain in the chest, loss of appetite, loss of weight, weakness, fatigue, chills, fever, and sweating at night. The diagnosis of the active TB is done either by skin test, blood test, chest X-ray, positive sputum smear culture or combining these tests. In latent TB, the person infected may not show signs and symptoms as in active TB. LTB can stay dormant for many years and may become active when the person's immunity goes down. LTB cannot spread to others; it is usually diagnosed when a person tests positive for TB skin test or TB blood test [48]. Table 1 gives a brief description of the current TB tests, their inference and shortcomings [49].

D. Artificial Intelligence in Medicine (AIM)

The term "Artificial Intelligence" (AI) was coined by John McCarthy [50]. The word "AI," was used for the first time in a workshop organized by McCarty, at Dartmouth College [51]. The workshop included M.L Minsky, N Rochester (IBM), C.E Shannon (Known as "the father of information theory") and other scholars, who were in future to become prominent figures, in the field of AI [52]. Over the last 60 years, the field of AI has been through many ups and downs. M.L Minsky and S.A Papert published a book named "Perceptrons," which describes limitations of two-input perceptron's. Many consider this book to mark the beginning of "AI winter." An era where the funding for AI projects declined drastically [51], [53]. Nevertheless, the field of AI continued with significant progress under a different name called Intelligent Knowledge-Based Systems (IKBS).

In 1975, MYCIN was the first, AI expert system (also known as knowledge-based systems), to provide consultation and diagnosis for Antimicrobial therapy. Edward Shortleaf developed it for his Ph.D. dissertation [54]. The other early expert systems were PIP- Present Illness Program (acquires the diagnosis of patients with renal disease), INTERNIST-1- internal medicine diagnosis by modeling behavior of clinicians[55], CASNET (Casual Associated Network)- for Glaucoma assessment and therapy, PUFF- Pulmonary function test interpretation[56-58]. Miller [59] has done a review on medical expert systems from 1954 to 1993. Shu-Hsien Liao [60], has conducted a review on expert systems from 1995 to 2004. Reference [60] has covered all expert system of one decade, including medical

expert systems. In recent years, there has been a huge advancement in the health care system. The technology has paved a way, for the patients to get an instant diagnosis about their vital health through health apps and wearable [61]. The generated report is maintained in Electronic Health Records. (EHRs) and alerts the doctor about any abnormal condition of the patient.

TABLE I
MAIN SHORTCOMINGS OF TB DIAGNOSTIC TESTS [49].

Test	Methodology	Interpretations	Shortcomings
1. Chest X-ray	X-ray of chest recorded to detect inflammation in the lungs.	Abnormal shadow visible on X-ray	Cannot exclude extra pulmonary TB
2. TB skin test	Injecting small amount of Tuberculin in the lower arm and observing the swelling.	Bigger the raised area of the swelling, more are the chances of being infected by TB	May give false results if person was infected by some other bacteria. Cannot differentiate between latent TB and active TB.
3. TB Interferon gamma release assays (IGRAs)	Mix blood sample with special substances to identify interferon gamma cytokine.		Blood sample must be instantly examined, laboratory required, test is for detecting latent TB.
4. Sputum smear test	A series of special stains are applied to a thin smear of patient's sputum and it is examined under microscope for signs of TB bacteria.	Morphological characteristics identification to detect presence of *M.tuberculosis*	In cases of HIV and TB co-infection, TB cannot be detected due to low levels of TB bacteria.
5. Fluorescent microscopy	Illumination of patients sputum smear with quartz/high pressure mercury lamp	Morphological characteristics identification to detect presence of *M.tuberculosis*	Expensive and time consuming
6. Culturing bacteria to test	Culture the bacteria from biological sample of patient on *M.tuberculosis* selective media	Detection of presence of bacteria by observing colony characteristics	Time consuming
7. Polymerase chain reaction	The assay targets the KatG gene having unique sequence in TB bacterium.	Presence of the *Mycobacterium tuberculosis* complex will give the test positive.	Expensive
8. GeneXpert test	Identification of DNA present in TB bacteria.	If DNA found, patient if TB positive.	Expensive.
9. Nucleic acid amplification test	Amplification of nucleic acids from biological specimens of suspected patient.	If nucleic acids found, patient is TB positive.	Lower sensitivity for respiratory tract specimens.

II. MATERIAL AND METHOD

In this section, an overview of various AI methodologies, applied in the diagnosis of TB is presented. Several studies have been carried out for the diagnosis of TB implementing AI algorithms. El-Solh et al., [62] claimed that they were the first to implement an AI technique for diagnosing TB. Later, many different approaches were utilized to achieve maximum accuracy to diagnose TB. AI uses predictive algorithms such as Decision Trees, Support Vector Machine (SVM), Naive Bayes Classifier, Genetic Algorithms (GAs), and Fuzzy Algorithms (FA).

A. A ubiquitous method in medical diagnosis using AI

AI is an area of computer science. It helps in the development of computers that, can mimic the human-like thought processing, reasoning and self-correction ability [63]. A rule of thumb has always been followed since AI techniques were applied in diagnosing diseases. The creation of a specific disease database is done by collecting a patient's medical report or Electronic Health Record (EHRs)[64]-[65]. Amato et al.,[66] generalized a few steps involved in the process of diagnosing medical data using ANNs. The essential steps are shown in Figure 2.

Steps are shown in Fig. 2, refer to the training phase (the green color background). This model is acclimatized to recognize the symptoms of the disease. The next stage involves the testing phase (Diagnosis), wherein new records of the patients will be tested against the verified database. The outcome of the diagnosis may be positive, negative or uncertain. This is verified by the doctor as shown in Fig. 2 (blue color background). Based on the prediction accuracy, if the data diagnosed is correct, it is later shifted to training dataset.

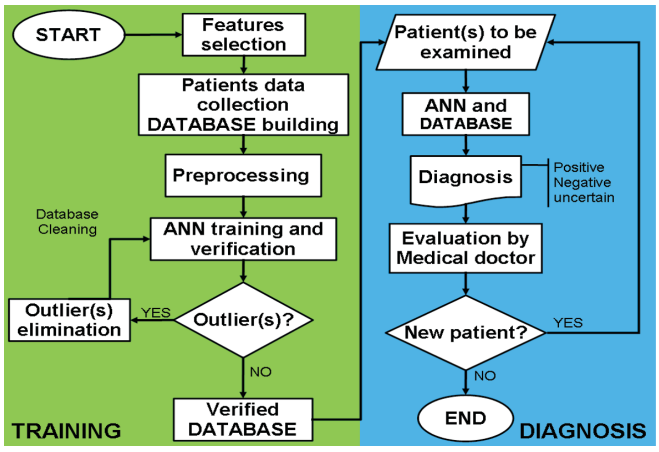

Fig. 2 ANNs -based medical diagnosis[66].

B. Data mining approaches

Rusdah et al.,[67] discussed exclusively on the different data mining approaches implemented for the diagnosis of the TB. The raw data before using for diagnosis must go through the data mining process [67]–[69]. Data mining process involves the pre-processing of the data. Such as data cleaning, data transformation, data integration, and data reduction. In their research, the authors have attempted to classify the PTB and EPTB. In their research, they considered only the physical symptoms of the disease, i.e., duration of a cough, Loss of Appetite, Weight Loss, Hemoptysis (blood in the sputum), and so on. In the preliminary stage of the disease, these symptoms are common in both the cases of PTB and EPTB. Hence, they could not differentiate between PTB and EPTB. Therefore, they discarded all EPTB cases and investigated only PTB cases using ensemble methods on four classifiers. They obtained high accuracy with SVM classifier.

Dongardive et al.,[70] utilized classification technique named Identification tree (IDT) to computationally diagnose TB[71]. IDT uses the Average Disorder Score (ADS) and picks the most significant parameter. At first 45 parameters were included in the study, which was later reduced to 19 parameters. The IDT generated a list of 12 rules for TB diagnosis. The accuracy obtained using IDT is 94.50%.

C. Neural Network with Multilayers

A neural network is a computational model which is similar to the human brain. It consists of several interconnected nodes (neurons), which processes the given information with its self-learning ability and generates better results[72]. Figure 3 shows, a simple neural network with one "input layer," two "hidden layer" and an "output layer." Every single layer has neurons, which are connected by weighted connections. The i-th neuron in one layer and j-th neuron in the next layer determine the value of W_{ij}[66].

El-Solh et al.,[62] implemented a General Regression Neural Network (GRNN) algorithm[73], for predicting active pulmonary tuberculosis. The Input pattern was created by using 21 unique parameters. These parameters were differentiated into three main categories viz, demographic, constitutional symptoms, and radiographic findings. The neurons required to form the hidden layer is decided by the number of patterns used while training the dataset. GRNNs requires one neuron per pattern processed. For the assessment of the model, they applied the 10-fold cross-validation method. The diagnosis accuracy of the model was reported to be 92.30% accurate[62].

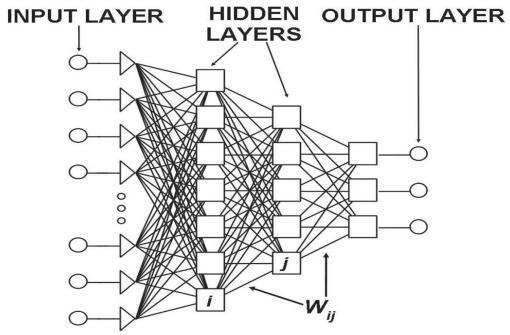

Fig. 3 A simple structure neural network [66].

Santos et al.,[74] utilized ANNs for developing and evaluating a prediction model for the diagnosis of Smear Negative Pulmonary Tuberculosis (SNPT). The authors considered only symptoms and physical signs for designing the neural network. The neural network was implemented using multilayer feedforward method architecture with Back Propagation (BP) algorithm and single hidden layer. The authors reported a 77% accuracy of the model [74].

Er, et al.,[75] in their study choose thirty-eight features to form the patient's medical reports. They used GRNN and BP algorithms and compared with the previous studies on GRNN [62] and BP [74]. They achieved an accuracy of 93.18% compared to 92.30% by [62]. In the case of MLNN with BP (single hidden layer) This study[75], achieved an accuracy of 93.04% relatively higher and more accurate than[74] who reported 77% accuracy. The authors, used a similar structure and same training algorithm as reported by[62] and [74], but the input features selected for diagnosing the tuberculosis disease were much better and may have resulted in higher accuracy.

Furthermore, Er et al. also implemented two different Multilayer Neural Networks (MLNNs) model structures. Levenberg-Marquardt (LM) [76], [77] and Back-Propagation with Momentum (BPwM) algorithm [78] approaches were used for training MLNNs. The LM and BPwM algorithms were implemented on the first model having a single hidden layer and on the second model having two hidden layers. To calculate the performance of their neural network, they used a 3-fold cross-validation method. In this study, 95.08% of classification accuracy was received by the LM algorithm using two hidden layers. The authors claimed that the LM training algorithm converged better than BPwM training algorithm and MLNNs using two hidden layers performed better than those using a single hidden layer.

Er, et al.,[79] conducted another study on diagnosing chest diseases using ANNs. Tuberculosis was also one of the diseases considered in this study. They used the previously applied LM and BPwM algorithm and extended it for few other training algorithms such as Probabilistic Neural Network (PNN), Learning Vector Quantization (LVQ) and Radical Basis Function (RBF). This study [79], reported the LM algorithm obtained the best classification accuracy for diagnosis of tuberculosis disease with two hidden layers.

D. Genetic Algorithm

Genetic algorithms are search algorithms which work by natural selection and natural genetics [80]. Even the simplest of GA's involve three kinds of operators viz, selection, crossover, and mutation [81], [82]. Selection operator chooses the fittest chromosome for reproduction. Crossover operator randomly chooses a point and changes the bits of the chromosomes before and after the point to generate new offspring's. Mutation operator randomly changes few of the bits in a chromosomes [83]. Fig. 4 represents the flow chart of a typical Genetic Algorithm.

Elveren et al.,[85] used a Multilayer neural network with two hidden layers and a Genetic Algorithm (GA) for training the algorithm. Reference[85], created a data set of 150 patient's samples, which was divided into two classes, one class with 50 patients who had TB, another class with 100 patients who had non-TB diseases.

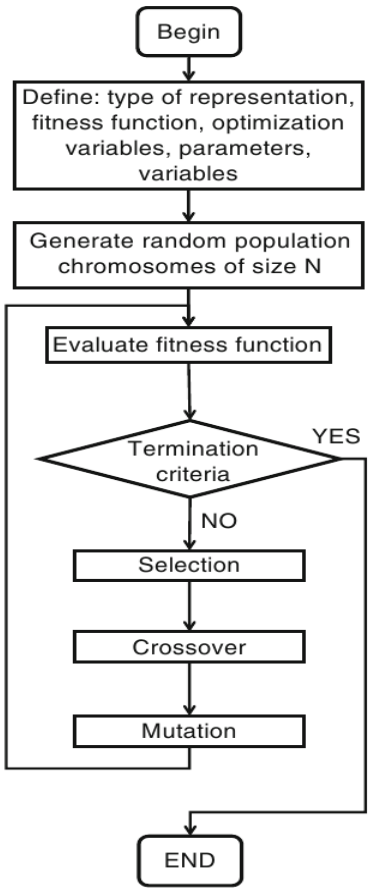

Fig. 4 Genetic algorithm flow chart [84].

The feature selection for the input layer and estimation of the performance of the neural network is similar to[75]. The hidden layers consisted of 50 neurons on each layer. One single neuron at the output layer, where the output diagnosis value 1 represents no TB and 2 represents TB. The results obtained showed a classification accuracy of 94.88% in predicting the TB cases. The authors compared their results with previous studies of [62] and [74], who have reported accuracy of 92.30% and 77% respectively. The results of [85] were better than [75], a study on BPwM with two hidden layers classification, which reported accuracy of 93.93%. Reference [85] could not compare their result with [75] on Levenberg-Marquardt (LM) algorithm, because of the complexity of the algorithm. The authors concluded that their classification accuracy for diagnosing TB with GA's is better than previous studies. Training of MLNN with GA takes too much time. However, they are also an effective way to diagnose TB.

E. Fuzzy Logic

The simple framework of the Fuzzy Logic Controller (FLC) [86],[87] is shown in Figure 5. The FLC accepts crisp input values, which are in the form of degree of Membership Function (MF), between 0 and 1. These MFs are described in linguistic labels (very cold, cold normal, hot, very hot), it is known as fuzzification. The inference engine runs on a set of rules. Finally, the rules are defuzzified into crisp output[88].

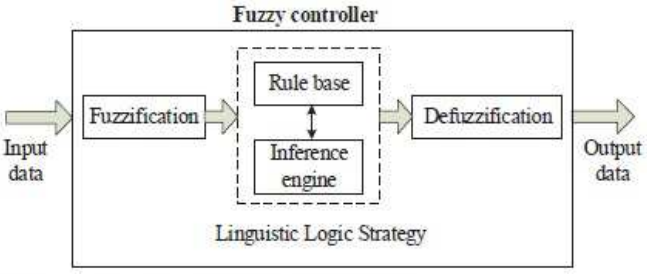

Fig. 5 The Fuzzy Logic Controller [89].

Ansari et al.,[90] used a neuro-fuzzy system to diagnose TB. A rule-based fuzzy system, it is an intelligent technique. The five inputs were given to the fuzzy inference system, as the risk factors to detect TB. The neuro-fuzzy integrated system, consist of six layers. It uses the backpropagation algorithm that adjusts the membership function and optimizes fuzzy rule for each variable. Their proposed model gave good results and agreed with the doctor's opinion [90].

Omisore et al.,[91] applied the Genetic Neuro Fuzzy inferential method for detecting TB. The components of their system's architecture are Knowledge Base, Genetic-Neuro-Fuzzy Inference System (GENFIS) Engine and Decision Support Engine. The database consists of structured data (facts and rules for diagnosing TB), unstructured data (experience, good practice, guesses, and judgments). The GENFIS is comprised of GA, NN, and FL. It uses a feed forward propagation learning technique. It is created using seven layers of neurons. Only hidden and output layers have active nodes and are involved in the computation, whereas the nodes at the input are passive. Each preceding layer acts as an input to the next layer. Fuzzification of the variables is done using triangular membership function. It gives output in linguistic terms, which describe the severity of the disease. There are twenty-four diagnostic parameters in the neural network, which are divided into five categories. The neural network is trained with a back-propagation algorithm with a sigmoid function. Genetic Algorithm (GA) use fitness function to obtain the optimal value of parameters. The accuracy of the GENFIS was reported to be 70% [91]. The low classification accuracy is due to insufficient TB patient records.

F. Artificial Immune System (AIS)

"AIS is adaptive systems inspired by the biological immune system and applied to problem-solving"[92]. When a pathogen attacks the immune system, some of the immune cells can detect the attack [93]–[95]. As soon as they detect the foreign body (antigen), the immune system starts to make multiple similar antibodies. This is called clonal expansion. This expansion produces a large number of antibodies, which are specific to the antigen. They either neutralize or kill the antigen. These antibodies remember the antigens in their immunological memory. So that they can respond faster if the same pathogen attacks again [96].

Er, et al., [97] used an Artificial Immune System (AIS) for diagnosing TB. The authors used their previous dataset for the comparative study. Here they applied the AIS algorithm for the detection of TB. The classification accuracy was reported to be 90%, which is exactly same accuracy achieved by using the LM algorithm with two hidden layers [97].

Shahaboddin et al, [98] used an Artificial Immune Recognition System (AIRS)[99],[100] to diagnose TB. They chose twenty features from the 175 medical reports. The selected features were classified using both Fuzzy Logic Controller (FLC) and the Artificial Immune Recognition System (AIRS). They used 10-fold cross-validation. The authors reported a 99.14% classification accuracy.

Saybani et al., in 2015[101] incorporated support vector machine (SVM) into AIRS (SAIRS2) to diagnose TB. They conducted their study using the dataset from [98]. They used a machine learning software called Waikato Environment for Knowledge Analysis (WEKA), to develop the SAIRS2 classifier. To assess the performance of SAIRS2, they utilized different built-in algorithms (classifiers) present in WEKA for a comparative study on the same TB dataset. To validate the performance, they used a 10-fold cross-validation method. They reported a 100% classification accuracy.

Sayabani et al., in 2016[102]combined Real World Tournament Selection (RWTS) with AIRS (RAIRS2) to diagnose TB. Tournament Selection (TS) is one of the strategical selection method in Genetic Algorithms (GAs) [103]. They used the same dataset and performance evaluation method as of [101]. A comparative study was made on built-in WEKA algorithms and one other study [98]. They reported a 100% classification accuracy.

G. Convolutional Neural Networks

The field of AI has progressed into a new era of Deep Learning. In particular, CNN, which is a class of deep learning, which uses a feed-forward artificial neural network for analyzing visual imagery. They have become the most preferred technique for analyzing medical images. Currently, they are considered as state of the art for image classification. For the understanding of the CNN, a simple illustration is represented below in Fig. 6.

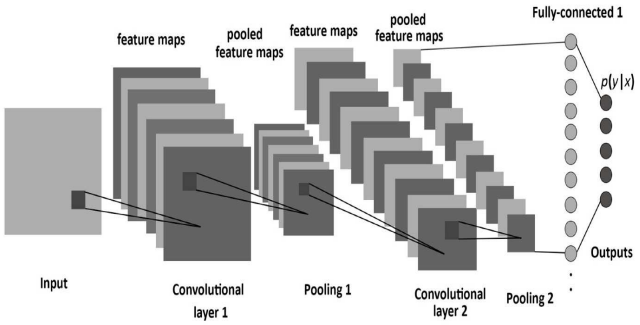

Fig. 6 A basic structure of Convolutional Neural Network (CNN)[104].

CNN consists of many layers, of which few basic are mentioned here. Convolutional layer, Pooling layer, and Fully-connected (FC) layer. The convolutional layer computes a dot product between the small region of the input layer and the weights. The pooling layer reduces the spatial size of the image, without changing the depth of the image. The FC layer as the name implies connects to each neuron of one layer to each neuron of another layer.

Few studies have been carried out for the detection of Tuberculosis using the CNN methodology. The main reason for the dramatic surge in the use of CNN is due to non-requirement of the domain knowledge. The CNN model extracts and learns meaningful features on its own. It segregates the target classes during the training phase.

Hwang et al.,[105] were the first to propose the implementation of CNN for the detection of tuberculosis. They modified the AlexNet[106] architecture as per their preferences. AlexNet uses general image recognition (256x256 size image). In this study, the authors added an extra convolutional layer (C1 at the beginning) for feature extraction, to support their high-resolution CXR images (500x500). The number of hidden nodes in the fully connected layer was reduced as less number of training images and classes were used. The model was trained with two weights: First, with randomized initialized weights and second with pretrained convolutional parameters (ImageNet classification dataset). The result of applying random weights was unsatisfactory with AUC=0.82 & Accuracy=0.77. In the case of pretrained weights, the results were much better AUC=0.96 & Accuracy=0.90. The pretrained model was implemented on the classification of the Montgomery and Shenzhen data sets respectively. The result obtained in case of Montgomery dataset were reasonable with AUC=0.88 & Accuracy=0.67, while in the case of Shenzhen dataset the results were impressive with AUC=0.93 & Accuracy=0.84.

Lakhani and Sundaram[107]implemented AlexNet[106] and GoogLeNet [107] to classify CXR's from pulmonary TB or as healthy, from four different datasets. These two DCNN's models were divided into pretrained and untrained models. The pretrained model was trained using ImageNet. All the CXR images were randomly augmented with 227x227 pixel. The DCNNs, when pretrained on ImageNet were named AlexNet-TA and GoogLENet-TA (TA-Trained Augmented) and when untrained they were named AlexNet-UA and GoogLeNet-UA (Untrained augmented). The data was divided into training, validation and testing. Accuracies of AlexNet-TA=93.3%, GoogLeNet-TA=95.3%, Ensemble=96.0% and Radiologist augmented=98.7%. Out of 150 test cases, GoogLeNet-TA and AlexNet-TA were able to correctly classify 137 cases trained radiologist classified the remaining 13 cases.

Lopes and Valiati[109] employed three different approaches, such as simple feature extraction, Bag of words and ensemble using pretrained CNN. Each of the approaches utilized all three different architectures (GoogLenet, ResNet and VggNet). They implement SVM classifier at the end, to detect if the images contain TB or not. The Ensemble approach obtained the highest accuracy on the Shenzhen dataset. Both simple feature and bag of words in ensemble achieved the same accuracy=0.846, whereas the AUCs were 0.926 & 0.910 respectively.

Islam et al.,[110] employed CNN's to detect abnormalities in the CXRs. They implemented various networks such as AlexNet, VGG-16, VGG-19, ResNet-50, ResNet-101, ResNet-152 and an ensemble. In their research, the detection of TB was carried out as one of the chest abnormalities. They have not mentioned the detailed procedure for detecting TB. However, they have disclosed the accuracy, AUC, sensitivity, and specificity obtained.

Alcantara et al.,[111] in their research implemented GoogLeNet model from the cafe, pre-trained on ImageNet for the classification of the CXRs. Their dataset consisted of

4701images, which were used for finetuning. The images were divided into normal (453 images) and abnormal (4248 images). For the binary classification, the accuracy was 89.6%. They considered accuracy to be good, as they did not use any pre-processing techniques. The abnormal CXRs had various TB manifestation sites. The same method and model was executed for multi-class classification. For the multi-class classification, the abnormal images were categorized into four classes. It achieved an accuracy of 62.07%.

III. Results and discussion

The MLNNs with the 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, noticeable in [75] and [79]. GAs are metaheuristic in nature. Concepts of GAs are easy to understand and implement. However, MLNNs with GAs is computationally expensive, as seen in [85]. FL is helpful in the differential diagnosis of the disease and also when a disease has intermediated stages. They are suitable in situations describing a nonlinear relationship between the input and output states of a system. Such as intensity, preciseness, the vagueness of a disease. The output results are mentioned linguistically. However, FL algorithms are incapable of learning on their own and are hardcoded to the defined rules. Therefore, [90] and [91] have used FL in differentiating the intensity of the disease using linguistic labels. Due to the disadvantage of hard code rules in FL. They have combined NN with FL, as NN it gives better flexibility in classifying, predicting and pattern recognition. AIRS has multiple domain application, and decision making in medical diagnosis is one of them. They have been proven to be powerful in classification problems, resulting in highly accurate models. The accuracy of the model directly depends on the parameter or the feature selection in cases of manual selection. Therefore, in studies such as [98], [101] and [102], 100% accurate results were obtained. The methods mentioned above have been effective in identifying PTB using mostly clinical symptoms.

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. Hence, the application of CNN in the field of medicine seems inevitable and promising. In the case of CNN, a feature selection of the images is done automatically. However, the selection of hyper parameters such as some epochs, batch size, activation function, etc, have to be defined manually. It is apparent, from the present literature that the pre-trained network with transfer learning, along with ensemble classification achieved the highest accuracies [105],[107] and [110] in case of binary CXR classification. However, which was not the case in[109], ensemble classifier.

Table 2 summarises, comparison of datasets, features, methods, training algorithm and classification accuracy obtained using clinical symptoms and radiological images.

TABLE II
COMPARISON OF VARIOUS AI ALGORITHMS USED FOR DIAGNOSING TUBERCULOSIS (TB).

Author and Year	**Dataset**	**Features/Parameters**	**Method**	**Training algorithm**	**Classification accuracy in (%)**
El-Solh et al., 1999	563 patients	21 parameters	GRNN (1 hidden layer)		92.30
Santos et al., 2007	136 patient's medical reports, University Hospital, Rio de Janeiro, Brazil	26 clinical variables	MLNN with BP (1 hidden layer)		77.00
Er, Temurtas et al., 2010	150 patient's medical report, Diyarbakir chest Diseases Hospital, Turkey.	38 features	GRNN (1 hidden layer)		93.18
			MLNN (1 hidden layer)	BPwM	93.04
				LM	93.42
			MLNN (2 hidden layers)	BPwM	93.93
				LM	95.08
Er, Yumusak & Temurtas 2010	150 patient's medical report, Diyarbakir chest Diseases Hospital, Turkey.	38 features	MLNN (1 hidden layer)	BPwM	84.00
				LM	84.00
				PNN	88.00
				LVQ	84.00
				GRNN	86.00
				RBF	86.00
			MLNN (2 hidden layer)	BPwM	84.00
				LM	90.00
Elveren & Yumusak 2011	150 patient's medical report, Diyarbakir chest Diseases Hospital, Turkey.	38 features	MLNN (2 hidden layers)	Genetic Algorithm (GA)	94.88
Dongardive et al., 2011	250 sample reports,T.B Hospitals, Mumbai	19 features	Decision Tree	Identification Tree (IDT)	94.50
Ansari et al., 2012		5 features	Neuro-Fuzzy	BP	96.00

Omisore et al., 2015	10 TB patients from St. Francis Catholic Hospital. (Delta State, Nigeria)	24 parameters	MLNN	Genetic Algorithm + Neural Network + Fuzzy Logic	70.00
Er et al., 2012	50 TB patient's medical report, Diyarbakir chest Diseases	38 features	Artificial Immune System(AIS)		90.00
Shahaboddin et al., 2014	175 patient medical report from Pasteur Laboratory, North Iran	20 features	Fuzzy Logic Controller (FLC) with Artificial Immune Recognition System (AIRS)		99.14
Saybani et al., 2015	175 patient medical report from Pasteur Laboratory, North Iran	20 features	Support Vector Machine (SVM) with AIRS	SAIRS2	100.00
				AIRS2	100.00
				MLP	100.00
				Naïve Bayes	100.00
				J48	100.00
				KNN, K=7	100.00
				RBF classifier	100.00
				Hierarchal LVQ	94.83
				Spegasos	99.82
				Random Forest	99.43
				Ridor	99.43
				Lib Linear	98.33
				Random Tree	98.21
				LVQ with kNN	97.13
				Multi pass LVQ	95.98
				LVQ	94.83
				CLOANALG-CSCA	93.68
				CLONALG	92.52
				SMO	89.66
				Zero R	65.49
				Lib SVM	65.49
Saybani et al., 2016	175 patient medical report from Pasteur Laboratory, North Iran	20 features	Real World Tournament Selection (RTWS) with AIRS	RAIRS2	100.00
				AIRS2	100.00
				MLP	100.00
				Naïve Bayes	100.00
				J48	100.00
				KNN, K=7	100.00
				RBF classifier	100.00
				HierarchalLVQ	94.83
				Spegasos	99.82
				Random forest	99.43
				Ridor	99.43
				LibLinear	98.33
				Random tree	98.21
				LVQ K-Nearest Neighbor	97.13
				MultipassLVQ	95.98
				LVQ	94.83
				CLOANALG-CSCA	93.68
				CLONALG	92.52
				SOM	89.66
				ZeroR	65.49
				LibSVM	65.49
Hwang et al.,2016	Private Dataset, Montgomery County (MC)and Shenzhen Datasets	CXRs	CNN	Modified AlexNet	90.00
Lakhani and Sundaram 2017	Montgomery County (MC), Shenzhen, Thomas Jefferson University Hospital and Belarus Tuberculosis Portal	CXRs	CNN*	Ensemble	96.00
				Radiologist augmented	98.70
Lopes and Valiati	Montgomery County (MC),	CXRs	CNN*	Ensemble	84.60

2017	Shenzhen,				
Islam et al., 2017	Shenzhen Dataset	CXRs	CNN*	Ensemble	90.00
Alcantara et al., 2017	5,000 CXRs from Partners In Health at Peru and various other image DB's	CXRs	CNN	Binary classification	89.60
				Multi-class classification	62.07

IV. Conclusion

Many predictive algorithms have been implemented in Machine Learning to diagnose Tuberculosis. These algorithms have been used to detect and increase the accuracy of the models. Different combinations of multilayer neural network, decision trees, fuzzy logic, genetic algorithms, and artificial immune system have been implemented.

However, there is a specific limitation present in NNs. Such as over fitting, at times network, has to be designed by trial and error method, they are "Black-Box" in nature, i.e.: there is no explanation as to how they work, and at present, there is an of lack accurately curated and annotated medical image databases.

Nonetheless, there have been few outstanding research in the medical field using CNN. The future work is to use CNN's for differential diagnosis. As in the cases of tuberculosis, there are various manifestation sites. Therefore, multi-class classification, immediate recognition and the differentiation of percentage of the disease progress will be an immense boon to the medical community. Deployment of the mobile application appears to be cost-effective and timesaving.

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