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Disease Diagnosis Systems Using Machine Learning and Deep learning Techniques Based on TensorFlow Toolkit: A review

Firdews A.Alsalman1,*

College of Computer Science and Mathematics Department of Software University of Mosul firdewsalsalman@uomosul.edu.iq

Shler Farhad Khorshid²

Akre Technical College of Informatics Department of Information Technology Duhok Polytechnic University Shler.sulayvani@gmail.com

Amira Bibo Sallow³

Technical College of Administration Department of Information Technology Management Duhok Polytechnic University amira.bibo@dpu.edu.krd

Article information

Article history: Received : 1/1/2022 Accepted : 4/4/2022 Available online : Machine learning and deep learning algorithms have become increasingly important in the medical field, especially for diagnosing disease using medical databases. Techniques developed within these two fields are now used to classify different diseases. Although the number of Machine Learning algorithms is vast and increasing, the number of frameworks and libraries that implement them is also vast and growing. TensorFlow is a well-known machine learning library that has been used by several researchers in the field of disease classification. With the help of TensorFlow (Google's framework), a complex calculation can be addressed effectively by modeling it as a graph and properly mapping the graph segments to the machine in the form of a cluster. In this review paper, the role of the TensorFlow-Python framework- for disease classification is discussed.

Keywords:

machine learning, deep learning, TensorFlow, python, Disease Diagnosis Correspondence: Author : Firdews A.Alsalman1 Email:firdewsalsalman@uomosul.edu.ig

Abstract

I. **INTRODUCTION** Rapid technological advancements have had a major effect on human life. As a result of these advancements, technology and physical computer systems have become indispensable in human life. Humanity is sustained for nearly a lifetime by computers, electronics, applications, and supported devices [1]. In a nutshell, technology is used in every aspect of life. The health and medicine industries are two of these regions. These systems are often used in the stages of disease diagnosis, classification, and treatment (for decision support purposes) [2]. The high number of illnesses, the need for a large volume of data for diagnosis and treatment, and the additional expense of gathering and processing this data have all necessitated the use of computer systems in medicine. For medical scientists, early diagnosis is critical in the treatment of many diseases [3]. Machine learning (ML) and Deep Learning (DL) algorithms are now used in a wide variety of medical applications, including disease detection and classification [4].

Artificial intelligence (AI) and similar technologies are becoming more common in business and society, as well as in healthcare [5]. Many features of patient care, as well as administrative functions within payers, providers, and pharmaceutical companies, could be affected by these technologies. Several studies have already demonstrated that AI can perform as well as or better than humans at critical healthcare tasks such as disease diagnosis. In order to detect malignant tumors and guide researchers on how to develop cohorts for expensive clinical trials, algorithms are now outperforming radiologists. For a variety of reasons, all believe it will be several years before AI changes humans in a variety of medical process domains [6]. This success can be attributed to the creation of extra innovative ML, the accessibility of broad datasets for addressing issues in these fields, and the development of software frameworks that make it simple to use large quantities of computational resources to train models on these massive datasets [7].

Python's popularity in data science has soared, particularly in terms of easily accessible tools and libraries for free. According to a survey conducted by the authoritative site KDNuggets in May 2018, Python is used by 65.2 percent of the approximately 2000 participants in the category "Top Analytics, Data Science, ML Tools," compared to 52.7 percent for RapidMiner and 48.5 percent for R, its two main competitors. In practice, Python has been the programming language of choice for the data science community over the last three years, with R coming in second [8]. Python's popularity is likely due to its relative ease of use (even for non-computer scientists), vast ecosystem of libraries for every field of data science, and support quick implementations of a large number of scientific algorithms written in C and Fortran via NumPy and SciPy wrappers. TensorFlow, a Googledeveloped library of open-source ML tools that allows you to deploy computation in CPU or GPU, uses graphs flow data. PyTorch is a project that uses the Python programming language and has Facebook's support. Theano is a Python library that supports mathematical expressions with tensioners, and CNTK is a collection of Microsoft resources that are accessible to DL code. Keras is a neural network library. TensorFlow is based on our first-generation method, and it has been simplified and generalized to enable researchers to explore a wider range of ideas with relative ease. TensorFlow supports both large-scale training and inference: for quick training, it efficiently uses hundreds of powerful (GPU-enabled) servers, and for inference, it runs classification model in production on a variety of platforms, from large distributed clusters in a datacenter to running locally on mobile devices. Simultaneously, it is adaptable enough to allow for innovation and research into new machine learning models as well as system-level optimizations [9].

This paper focused on the Tensor flow library it has different features and performance characteristics for disease classification by machine and deep learning algorithms. The remaining part of the review is categorized as follows: Section 2 presents machine learning and deep learning concept in disease classification. Section 3 covers the most popular libraries for machine learning and deep learning. Section 4 covers the related work. The discussion is in section 5. Finally, Section 6 concludes the study.

2. Methods and basic concepts

a) Machine Learning

AI can give a machine the ability to reason. AI enhances the intelligence of a machine. ML is a branch of AI research. Several researchers believe that knowledge cannot be produced without learning. Figure 1 illustrates the various forms of ML Techniques. Reinforcement, Evolutionary Learning, Supervised, Unsupervised, Semi-Supervised. ML approaches include deep learning and reinforcement learning. [10].



Figure 1. types of machine learning algorithms [10]

ML algorithms were created and used to analyze medical data sets. ML now recommends a variety of methods for effective data analysis. The digital revolution has provided comparatively low-cost and accessible means for data collection and storage, especially in recent years. Data collection and examination machines are being installed in new and modern hospitals to allow them to collect and share data in big information systems. Medical data sets were observed using ML algorithms [11]. ML now recommends a variety of methods for effective data analysis. The digital revolution has provided comparatively low-cost and accessible means for data collection and storage, especially in recent years. ML is the study of algorithms and mathematical models that computer systems employ to enhance their performance over time on a given task [12]. Several ML algorithms perform exceptionally well in the diagnosis of heart, asthma, liver, malaria, and hepatitis diseases. The Naive Bayes (NB), Logistic Regression (LR), Support Vector Machine (SVM), Decision Tree (DT) Algorithms are commonly used algorithms for disease detection, according to the literature.

b) Deep Learning

Deep learning (DL) is a data modeling technique that is also known as deep machine learning or hierarchical learning. that employs several processing layers to create a high level of abstraction. In recent years, conventional approaches such as rule-based methods, statistical learning methods, and machine learning methods such as SVM, RF, and NB have been used to diagnose disease. With the advent of DL methods, it is now commonly used by researchers all over the world to identify different diseases. DL has demonstrated significant success in a variety of domains by efficiently capturing extensive range dependencies and constructing dense hierarchal features [13], [14]. DL is based on deep neural networks (the term "deep" refers to networks with more than one hidden layer), which include Convolutional Neural Networks (CNN), Recurrent Neural Networks (RNN). Deep Belief Networks (DBN), Auto-encoder (AE), Artificial Neural Network (ANN), and **a**) more [1].



Figure 2. (a) ANN with two hidden layers. (b) CNN architecture [12].

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3.Deep Learning and machine learning Frameworks for Disease Diagnosis Systems

These libraries' DL and ML models are used to train with the aid of data and model parallelism. The following are some of the most well-known outlets for disease diagnosis:

1) TensorFlow

Conclutor

Is a dedicated framework developed by the Google Brain team in 2011 for tasks involving complex numerical calculations [12]. The source code for this method, previously known as DistBelief, was revised, and it became an application-based library. TensorFlow was renamed in 2015, and Google made it open source. This framework has a Python and C++ interface, and it was released in February 2017 as version 1.0 [15]. Simply put, TensorFlow is a library of machine learning and deep neural networks that can be used to solve extremely complex mathematical problems. It can be thought of as a programming method in which the equations are interpreted as a data flow graph, allowing us to write a program first and then run it in a session. TensorFlow has a number of benefits for an application. A C/C++ backend allows it to run faster than pure Python code. TensorFlow

supports parallel computing, both on the CPU and on the GPU [7].

a) TensorFlow structure

The structure of TensorFlow is based on the execution of a data flow graph. The nodes and edges are the two fundamental units in this last one. The first describes a mathematical procedure, while the second identifies tensors, which are multidimensional arrays. The typical use of TensorFlow architecture, as previously stated, is to run a session after the graph has been formed. The graph computations are converted and sent to the appropriate environment for execution on a GPU or CPU by the session [16]. Figure 3 shows a graph from a TensorFlow session.



Figure 3. TensorFlow work example [17]

Z and Y, for example, are tensors. MatMul will be used in the program (which are processes done for tensors Z and Y), then add, and finally add the result to the tensor X. The outgoing tensors of each working travel through the next one until they reach the desired result W. Finally, the software will create a session in which the graph will be run and the results calculated. So, what does a tensor imply? a tensor seems to be a very general entity in mathematics that has its meaning expressed in a vector space, particularly in multilinear algebra and differential geometry. It can be used to identify multisector or applications that are multilinear. A tensor is a multidimensional array that can be zero, one, two, or more dimensions. Table 1 summarizes the data [18]. Tensors give developers the freedom to shape a dataset in any way they want due to the nature of how information stored in images is encoded. This is particularly useful when working with images

Table 1. Tensor Rank [17]

Dimension	Mathematical Object	In Code
Zero	Scalar	[1]
One	Vector	[1,2,3,4,]
Two	Matrix	$[[1,2,3,4,\ldots],[1,2,3,4,\ldots],[1,2,3,4,\ldots],\ldots]$
Three	Tensor	[[[1,2,],],[[1,2,],],[[1,2,],],]

b)TensorFlow's Structure

TensorFlow was developed to help in the design and implementation of computational graphs using modern machine learning algorithm and optimization techniques. TensorFlow is compatible with Python, C++, and other programming languages. The TensorFlow library, which contains the Core Execution Framework, will be invoked by the language binding. It permitted programmers to use CPUs, GPUs, desktops, servers, and mobile devices to perform extremely complex calculations. This means that programmers can create their software first and then run it on a variety of computers [19]. There are three main phases in the TensorFlow architecture. The first is data processing, which allows programmers to write code in a variety of programming languages, which TensorFlow then translates into hardware instruction sets for CPU, Android, GPU, and other platforms. The second phase is to layer the model. Third phase train and estimate the model, programmers may use Estimator and the Keras model for training and estimating [20].

2) Keras

It's an open-source library written in the Python programming language. As a foundation, it employs TensorFlow or Theano. For DL -related tasks, it is the most commonly used by researchers. It's a lot easier to use and build complete solutions with it. Despite using both Theano and TensorFlow as a backend, the dimensions of input data must be taken into consideration. It has shown great promise in DL tasks like speech recognition, computer vision, and multimedia, classify a variety of diseases ,among others [1].

3) scikit-learn

is the most common Python library for ML. When working on classification problems, the scikit-learn library offers a handy report that gives you a simple understanding of a model's accuracy based on a variety of metrics. The accuracy, recall, F1-score, and support for each class are displayed using the classification report() feature [21].

4. Related Work

Pandey et. al. [22] used the MIT-BIH arrhythmia patientspecific dataset to classified heartbeats into four types: one regular beat and three irregular beats. As part of the data preprocessing, baseline noise reduction, heartbeat separation (which separates the heartbeats within such a window size of 180 based on R-peak). As result of the data pre-processing, baseline noise removal, heartbeat segmentation (which separates the heartbeats within a window size of 180 based on R-peak), and normalization using Z-score were all performed. For model training and tests, scikit-learn and the TensorFlow computational library of Python are used in all experiments. Random forest (RF), SVM, long short-term memory (LSTM), K-nearest neighbours (K-NN), and ensemble of SVMs were used to classify the data. With an overall accuracy of 94.4 percent, an average accuracy of 97.2 percent, sensitivity of 65.26 percent, specificity of 93.35 percent, precision of 69.11 percent, and an F-score of 66.24 percent, the best result was obtained using an ensemble of SVMs.

Rayavarapu et. al. [23] proposed two common machine learning techniques, Voting Classifier and Deep Neural Network (DNN) Classifier to predict cervical growth. By splitting the dataset into training and testing, classifiers such as LR, DT, NB, RF, K-NN, and SVM may generate class labels for unknown samples. The voting classifier receives the final results and, with the help of the majority, assigns class labels to the data. The Voting classifier and DNN classifier are evaluated using datasets from cytology and biopsies. When comparing the accuracy of Voting Classifier and DNN Classifier on cytology and biopsy, Voting Classifier has the highest accuracy (97–99). The proposed DNN classifier is built using the most recent version of TensorFlow.

Segovia et. al. [24] demonstrated several computer-aided diagnosis (CAD) systems depend on Deep Neural Networks that enhance Alzheimer's and Parkinson's disease diagnosis. In attempt to face the minor sample size issue, they test twodimensional reduction techniques based on Principal Component Analysis and Non-Negative Matrix Factorization (NNMF), respectively. TensorFlow is a good tool for developing CAD frameworks for neurodegenerative disorders, according to the findings. When merged with PCA dimensionality reduction, the proposed DNN-based systems obtained an accuracy for three databases.

Rajpurohit et. al. [25] proposed an automated system for detecting Acute Lymphoblastic Leukemia (ALL) from microscopic blood pictures, which would improve accuracy and allow for early detection. Image processing can be used to process the microscopic blood image and extract the required attributes. The accuracy of the CNN classifier model is 98.33 percent, while the SVM, KNN, and Feed Forward Neural Networks models are 91.4 percent, 94.85 percent, and 94 percent, respectively. They used the TensorFlow architecture to implement CNN and FNN; the network has seven convolutional layers, seven pooling layers, two completely linked layers, and one dropout layer. The developed method improves the accuracy of Acute Lymphoblastic Leukemia diagnosis, making it easier to provide early care to patients.

Johri et. al. [26] proposed two neural network-based models, the VGFR Spectrogram Detector and Voice Impairment Classifier, with the aim of assisting doctors and patients in early detection of Parkinson's disease. The data was collected from the UCI ML Repository and the PhysioNet Database Bank. To identify Parkinson's disease patients based on two signs using VGFR Spectrogram Detector using CNN and Voice Impairment using ANN. On the testing dataset, two modules, gait and speech impairment, were implemented with an accuracy of 88.17 percent and 89.15 percent, respectively. the comparison with three major algorithms, SVM, XG Boost, and MLP, found that the proposed model is more efficient and returns better accuracies.

Pash et. al. [27] compared the accuracy levels of various algorithms such as Support Vector Machines (SVM), K-Nearest Neighbor (KNN),, Decision Trees (DT), ANN, and TensorFlow Keras on a heart attack dataset obtained from Kaggle. The researchers analyzed the Kaggle dataset that included attributes related to heart disease such as age, gender, blood pressure, cholesterol, and so on. When using a large dataset, the efficiency and accuracy of algorithms decreases, so they used ANN and Tensor Flow Keras to improve prediction accuracy. The accuracy results were respectively as follows: SVM (81.97%), K-NN (67.2%), Decision Tree (81.97%), and ANN(binary model) (85.24%).

Zhao et. al. [28] presented model based on LR and SVM to classify the Colorectal cancer into abnormal and normal samples. His research could lead to a new approach for developing cancer classification models based on independent factors, demonstrating that risk prediction models that include genetic as well as conventional risk factors can be more useful. Most significantly, the findings show that an integrated model can be used to address the issue of low accuracy and an imbalance between sensitivity and specificity. The results of the logistic regression show that Firmicutes (AUC 0.918), Bacteroidetes (AUC 0.856), BMI (AUC 0.777), and age (AUC 0.710), as well as their combined factors (AUC 0.942), are successful in detecting CRC. RBF is the most accurate kernel kind, with an accuracy of 90.1 percent when k = 5 and 91.2 percent when k = 10. This research introduced a new approach for predicting colorectal cancer risk based on independent risk factors.

Yilmaz et. al. [29] proposed ML approaches such as LR, k-NN, SVM, DT, RF, and eXtreme Gradient Boosting (XGBoost) to find binary classification as regular and abnormal cervical cells. XGBoost and k-NN classifiers, among others, provide better performance, with an accuracy of 85 percent. In the second sample, the same dataset is used for a deep learning model focused on CNN. As a result, the training and test datasets have accuracy rates of 99 percent and 93 percent, respectively. Without a label or a function dataset, the CNN model derives its features from raw data. t. It takes 50 epochs in this model to achieve these accuracies in under 20 minutes of computation time.

Gupta et. al. [30] used various machine learning algorithms to predict the tumor stage of colon cancer using the Tumor Aggression Score (TAS) as a prognosis. The performance of various machine learning algorithms was assessed using fivefold cross-validation, which is a powerful method of model validation. When the Tumor Aggression Score was considered as an attribute alongside the standard attributes usually used for TNM stage prediction, the Random Forest model had an F-measure of 0.89. They also discovered that the RF algorithm outperformed all other algorithms for predicting the five-year disease-free survival (DFS), with a precision of about 84 percent and a region under the curve (AUC) of 0.82.

Qanbar et. al. [31] presented deep learning image recognition techniques to diagnose malaria. CNN techniques were used in the research for image classification. Various methods for improving the efficiency of CNN methods for increasing the accuracy rate in the estimation process have been established. The Residual Attention Network is the most widely used of these techniques (RAN). The estimation processes performed using the (RAN deep learning model yielded a 95.79 percent accuracy rate for image classification. The estimation processes performed by the SVM model had an accuracy rate of 83.33 percent. As a result, it is thought that combining the RAN model with deep learning approaches in the diagnosis of malaria produced more successful results. The study concluded that the pretrained CNN methods VGG16, MobilenetV2, Resnet50, and AlexNet have advantages and disadvantages when compared to each other. As a result, VGG16 obtained 95.04 percent, ResNet50 obtained 94.37 percent, MobileNetV2 obtained 93.69 percent, and AlexNet obtained 92.64 percent training accuracy score.

Wanjale et. al. [32] introduced the feedforward neural network, or ANN. When compared to other regression models, it has been found to have excellent results in predicting the severity of Parkinson's disease. They compared ANN to six traditional machine learning models, including DT, RF, SVM, and Multiple Linear Regression. The proposed model comparison shows that ANN is a better ML model for detecting and predicting Parkinson's disease, with precision of 83.56 percent for total UPDRS and 85.135 percent for motor UPDRS, which are the scales for calculating the intensity elaborated further. To implement all of the machine learning models, they used the python AI libraries "Sklearn", "TensorFlow", and "Keras". Finally, the proposed model generates an accuracy of 84.45%.

Iradukunda et. al. [33] presented a suitable model to aid in the accurate detection of malaria. The used dataset came from the National Institute of Health in the United States and consisted of 27,560 images of infected and uninfected red blood cells (RBCs). The Extreme Learning Machine (ELM) model was used to identify and forecast whether a patient was infected with malaria or not using a single hidden layer feedforward neural networks methodology. ELM has been compared to other machine learning methods such as K-NN, SVM, CART, CNN, RF, VGG16, RESNET, and DENSENET, and it has outperformed them all with 99 percent accuracy, 28 seconds cost time, 0.0095 Misclassification Error, and 98 percent precision, demonstrating its effectiveness in the application of malaria cell detection scenarios.

Khanam et. al. [34] proposed method that has a high degree of accuracy in predicting diabetes. Using the WEKA method, first preprocessed the data, then tested seven different machine learning algorithms on the PIDD to forecast diabetes, including DT, NB, K-NN, RF, LR, SVM and AB and calculate the performance of each algorithm. With an accuracy rate of around 86 percent for all epochs, the NN with two hidden layers is the most efficient and promising of all the developed models for analyzing diabetes (200, 400, 800). The accuracy of logistic regression (78.8571%), random forest (77.3429%), Naive Bayes (78.2857%) and ANN (88.57%) was discovered.

Jakhar et. al. [35] proposed chest X-ray image reports are used to train a powerful deep machine learning forecasting model for predicting pneumonia in patients. Since deep learning is efficient in image data processing, it makes this task more successful. Deep learning algorithms in Python were used to create an effective model that will aid doctors in detecting this deadly disease. As compared to state-of-the-art machine learning approaches, the proposed system is found to be more effective in prediction, with an average accuracy of 84 percent, which is better than all other classifiers.

Sharma et. al. [36] Presented model for predicting heart disease. Heart disease is one of the main areas where DNN can be used to increase the overall efficiency of heart disease classification. The classification can be done in a number of ways, including KNN, SVM, NB, and RF. The UCI dataset for heart disease have been used to show that Talos Hyper-parameter optimization is more effective than other methods. In DNN, Talos optimization is a modern optimization strategy. Other optimizations have a lower accuracy than Talos and provide better accuracy (90.76%). It is tested on datasets related to heart disease in order to determine a successful predictor.

Muthalagu et. al. [37] proposed a method for distinguishing five different types of skin diseases. To improve the diagnostic accuracy of multi-species vaccine uptake, it is important to abandon conventional methods and implement automated methods. Melanoma, Psoriasis, Rosacea, Vitiligo, and Xanthelasma were classified as five forms of skin diseases in this study. Because of the similar effects and symptoms that the patient experiences, this project will benefit a wide segment of society and address the problem of difficulty in recognizing the types of skin diseases to which the human is exposed, and will undoubtedly lead to the early and faster detection of skin diseases. They achieved the five main basics of classifying images using the TensorFlow module and SVM algorithm and predicting the disease each time an image is loaded in the testing system and a training model has been successfully compared the testing image with the trained model and the accurate results.

Salehi et. al. [38] proposed CNN for using MRI images to diagnose and classify Alzheimer's Disease (AD) earlier. With a total of 1512 mild, 2633 regular, and 2480 AD images, the ADNI 3 image class was used. The model performed well when compared to many other related works, with a significant accuracy of 99 percent.

Smaida et. al. [39] introduced a component of deep learning techniques for performing multi-class classification in order to classify eye diseases. They compared three CNN models, CNN, Vgg16, and InceptionV3, in order to assess their output using bagging ensemble in this analysis. In their work, they use Python to deploy a DL convolutional network based on Keras and TensorFlow for image classification. A variety of medical images were used as a data set to identify eye diseases, which included four common diseases: diabetic retinopathy, glaucoma, myopia, and normal vision. It has been shown that using a bagging ensemble produces better predictive performance than classification methods alone.

Ajagbe et. al. [40] proposed using magnetic resonance images (MRI) to classify Alzheimer's disease (AD) images using deep convolutional neural network (DCNN) involving CNN and transfer learning (Visual Geometry Group (VGG)16 and VGG19) and extend the evaluation metrics because the weaknesses and ability of algorithms cannot be exposed by a few metrics. Neurologists classify Alzheimer's disease images into four categories, and the findings are evaluated using a variety of metrics. For the test, six metrics were used: accuracy, area under curve (AUC), F1-score, precision, recall, and computational time. In three of the categories, VGG-19 was the best, CNN was the best in two, and VGG-16 was the best in one.

Kundaram et. al. [41] suggested the use of magnetic resonance imaging (MRI) samples to train a DCNN for Alzheimer's disease classification. The suggested approach divides There are three types of Alzheimer's disease (AD), moderate cognitive impairment (MCI), and normal regulation (NC). To model DCNN, researchers used Spyder tools from the Anaconda package, which includes the Keras library and the TensorFlow backend on GPU. In comparison to other tests, the ADNI dataset and performance classification result showed 98.57 percent accuracy. Their framework also allows us to extend this technique to predict disease stages at a higher level.

# R	Year	Dataset	Focused Disease(s)	Methods used	Framework	Result
[23]	2018	Cervical cancer dataset	Cervical Cancer	Voting classifier DNN	TensorFlow	Cytology (voting classifier): 97% Biopsy (voting classifier): 99%
[24]	2018	Tc-ECD SPECT database DaTSCAN database F-DMFP-PET database 8F-FDG-PET database	Alzheimer's disease Parkinson's disease	DNN NB DT SVM	TensorFlow	mTc-ECD SPECT (DNN): 83.51% DaTSCAN (SVM): 91.53% F-DMFP-PET (DNN): 70.11% F-FDG-PET (DNN): 96.16%
[25]	2018	images from IDB1 dataset	Acute Lymphoblastic Leukemia	CNN SVM K-NN Feed forward NN	TensorFlow	98.33% 91.4% 94.85% 94%
[35]	2018	X-Ray images	Pneumonia diseases	DCNN SVM RF DT LR NB	Keras	84% 76% 82% 77% 77% 72%
[26]	2019	VGFR Dataset Voice Impairment Dataset	Parkinson Disease	ANN CNN SVM XG BOOST MLP	TensorFlow Keras library	VGFR dataset (ANN): 89.15% (MLP): 87.79% Voice Impairment dataset (MLP): 85.60%
[28]	2019	Dataset from NCBI website	colorectal cancer	LR+RF LR+SVM LR+ANN LR+K-NN LR+NB	TensorFlow	87.3% 90.1% 88.4% 84.5% 80.7%
[30]	2019	Data from Chang Gung Memorial Hospital,	Colon Cancer	RF SVM LR MLP K-NN Adaptive Boosting	Scikit-learn TensorFlow	RF: 84%
[31]	2019	Malaria Cell Images Dataset	Malaria Diseases	RAN VGG16 Mobile NetV2 ResNet 50 AlexNet SVM	TensorFlow, Keras scikit-learn libraries	95.51% 94.94% 50.00% 78.16% 93.55% 83.30%
[33]	2019	blood cell (RBC) images from National Institute of Health in USA	Malaria Disease	SVM K-NN CART RF CNN VGG16 RESNET DENSENE	Keras TensorFlow	ELM: 99%

Table 2. Summary of Review Papers Based on Disease Diagnosis

# R	Year	Dataset	Focused Disease(s)	Methods used	Framework	Result
[22]	2020	MIT-BIH arrhythmia datasets	Cardiovascular disease	Ensemble SVM SVM RF K-NN LSTM	scikit-learn TensorFlow	94.40% 90.09% 93.45% 72.56% 92.16%
[27]	2020	dataset from Kaggle	Cardiovascular disease	SVM K-NN DT ANN	TensorFlow Keras library	81.97% 67.2% 81.97% 85.24%
[29]	2020	images from Herlev dataset	Cervical cancer	LR K-NN SVM NB DT RF XGBoost CNN	scikit-learn and Keras library TensorFlow	83% 85% 83% 80% 83% 83% 85% 99%
[32]	2020	from the UCI- Machine Learning repository	Parkinson's Disease	ANN DT RF SVM Multi linear model	Sklearn TensorFlow "Keras	ANN: 84.45%
[36]	2020	Heart Disease UCI dataset	Heart Diseases	LR K-NN SVM NB Talos RF	Keras	85.25% 90.16% 81.97% 85.25% 90.78% 85.15%
[38]	2020	OASIS dataset	Alzheimer Disease	CNN	TensorFlow	99%
[39]	2020	Dataset from Kaggle	Eye Disease	CNN VGG16 InceptionV3	Keras TensorFlow	71.57% 83.86% 87.71%
[34]	2021	Pima Indian Diabetes (PID) dataset	Diabetes Disease	LR K-NN SVM NB DT RF AB ANN	Keras TensorFlow	ANN: 88.57%
[37]	2021	Images from Dermnet, DermWeb	Skin Disease	SVM	Keras TensorFlow	91%
[40]	2021	Medical Image from Kaggle	Alzheimer Disease	CNN VGG-16 VGG-19	Keras TensorFlow	71% 77% 77%
[41]	2021	dataset neuroimaging initiative (ADNI)	Alzheimer Disease	DCNN	Keras TensorFlow	98.57%

5. Comparison and discussion

The table above compares various machine learning and deep learning methods for disease classification across various datasets. It can be noted that most works have been done on the detection of different diseases. For some parameters, such as accuracy, all classifiers produce good results. All of the models had an accuracy of more than 70%. For the purpose of disease classification, "Machine Learning" and "Deep Learning" algorithms with TensorFlow, Keras, and Scikitlearn libraries were utilized. From the findings we noted that CNN has been used for classification and yielded a high accuracy of over 99% in several works. TensorFlow and Keras have large communities, whereas scikit-learn has a very small community. It should also be mentioned that TensorFlow has the best documentation, which is intuitive for usage.

6. Conclusion

In summary, different research papers were reviewed based on disease detection and classification using various Machine Learning and Deep Learning algorithms to categorize subjects as normal or suspicious based on a variety of symptoms, which depicted a good prediction by using a TensorFlow. The accuracy figures of Convolutional Neural Networks, for classifying Alzheimer's Disease, were high (99%). These results were found to be better than all other classifiers, which used TensorFlow to develop the classification model. In a single machine, researchers prefer the TensorFlow model, as it is more flexible and makes better memory usage.

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أنظمة تشخيص الأمراض باستخدام التعلم الالى

وتقنيات التعلم بعمق: ورقة مراجعة

فردوس عدنان عبدالقادر Firdewsalsalman@uomosul. edu.iq كلية علوم الحاسوب والرياضيات، جامعة الموصل، الموصل، العراق شلير فرهاد خورشيد أميرة بيبو سلو amira.bibo@dpu.edu.krd <u>Shler.sulayvani@gmail.com</u> كلية التقنية الادارية

جامعة البوليتكنيك، دهوك، العراق

تاريخ استلام البحث 2022/1/1 تاريخ قبول البحث 2022/4/4 الخلاصة:

أصبحت خوارزمية التعلم الألي والتعلم بعمق Machine learning ذات أهمية متزايدة في المجال الطبي وخاصة لتشخيص (Machine learning ذات أهمية متزايدة في المجال الطبي وخاصة لتشخيص الامراض باستخدام قواعد البيانات الطبية . التقنيات المطورة في هذين المجالين تستخدم الان لتصنيف الامراض المختلفة . على الرغم من أن عدد خوارزميات معتخدم الان لتصنيف الامراض المختلفة . على الرغم من أن عدد خوارزميات معتخدم الان لتصنيف الامراض المختلفة . على الرغم من أن عدد خوارزميات معتخدم الان لتصنيف الامراض المختلفة . على الرغم من أن عدد خوارزميات معتخدم الان لتصنيف الامراض المختلفة . على الرغم من أن عدد خوارزميات كبير ومتزايد أيضا. الاداة Tensor Flow هي مكتبة معروفة في خوارزمية تصنيف الامراض بمساعدة الاداة Tensor Flow، حيث يمكن معالجة عملية حسابية معقدة بشكل فعال عن طريق نمذجتها كرسم بياني وتعيين أجزاء الرسم البياني بشكل صحيح على الجهاز في شكل مجموعة . في ورقة المراجعة هذه ، تمت مناتين بشكل صحيح على الجهاز في شكل مجموعة . في ورقة المراجعة هذه ، مت من مناتين الرجم قرار المراحل المواحل المواحل المعادين الواحل معادة المواحل معاد .

الكلمات المفتاحية: النعلم الالي ، النعلم بعمق، Python ، Tensor Flow، مكتبة Google.