

Review Of Models & Techniques For Identification Of Human Health Diseases

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Abstract

Human health diseases are caused due to genetic disorders, environmental conditions, presence of Alpha synuclein bodies, etc. Identification of this disease can be done via estimation of body tremors, slowed movements, fever, change in corpuscles, rigid muscles, impaired posture & balance, pain analysis, loss of automatic movements, speech changes, and writing changes. To estimate these effects, researchers have proposed a wide variety of machine learning techniques that can analyze speech signals, electroencephalogram (EEG) signals, electrocardiogram (ECG) signals, handwriting variations, gait identification & classification, etc. These models are highly variant in terms of their internal operating characteristics, which makes it ambiguous for clinical designers to identify optimal models for their deployments. Furthermore, these models also showcase highly variant performance levels as per their input feature sets. Thus, it is difficult to identify optimal models for a given set of input parameters. To overcome these issues, this paper initially reviews a wide variety of Human Health disease identification models in terms of their contextual nuances, operating advantages, functional limitations, quantitative characteristics, and deployment-specific future scopes. This will assist readers to identify functional models that can be applied for their operation-specific use cases. After referring this comparison, readers will be presented with a comparative analysis of these models in terms of their detection accuracy, classification delay, input datasets, computational complexity, and scalability levels. Based on this comparison, readers will be able to identify optimally performing models as per their qualitative characteristics.

Keywords: Human, Health, Machine, Learning, Bioinspired, Computing, Tremor, Disease, Clinical, Complexity, Cases

1. INTRODUCTION

A neurological condition known as Parkinson's disease (PD) affects 2% to 4% of people over the age of 65% [1]. The fast aging of the global population is projected to be one of the biggest difficulties that not only Europe but the whole globe will face over the next thirty years. Additionally, the number of people afflicted by the neurodegenerative disease will keep growing [2]. The health impairment that patients suffer as a direct consequence of their condition is much less severe as a result of treatment when medication is begun early in the evolution of Parkinson's disease [3]. Because of this, it is critical that this ailment be diagnosed at an early stage. Many other cutting-edge tactics have been developed in recent years with the intention of achieving this objective. Some of them are built on cutting-edge technologies that provide fresh chances for diagnosing Parkinson's disease much more quickly and consequently at an earlier stage [4]. Others are based on revolutionary technology advancements that provide promise for the creation of cutting-edge Parkinson's disease therapies. It is a difficult task given that the condition has for a long time had few obvious symptoms and that the cognitive abilities of a healthy population vary widely based on characteristics like age, education, and other aspects. The procedure is now more challenging than it would otherwise be because of this. Due to these elements, achieving this goal has proved to be fairly challenging. The most accurate imaging methods are magnetic resonance imaging (MRI), position emission tomography (PET), and computer tomography (CT), but since they are also costly, they are seldom utilized as preventative screenings. They are used instead after the illness has reached a more severe stage [5, 6]. It would be advantageous to create and adopt less expensive substitutes as a direct consequence of this. Thanks to technological breakthroughs, it may now be possible to diagnose diseases or track their progression, even when the symptoms at first seem to be of little concern. Even in cases when the sickness hasn't yet shown itself, this is true. This has the potential to significantly improve both the quality of life for those who have Parkinson's disease and the quality of life for their families. It also has the potential to improve communication with the healthcare providers that they see [7]. There is also a chance that the usage of telemedicine solutions might lead to fewer visits to the doctor, which would reduce the amount of money that has to be spent on the healthcare system [7], [8].

A broad number of symptoms that might appear in different ways are common to Human Health diseases. Depending on which parts of the body they affect, these symptoms may be split into two groups: motor symptoms and non-motor symptoms. Symptoms that might be categorized as motor symptoms include dyskinesia, bradykinesia, tremor, freezing of gait, and dysphagia. On the other side, non-motor symptoms might include things like despair, anxiety, restlessness, signs of the urinary system, dysarthria, or hypomimia [9], [10]. In addition to the symptoms already mentioned, hypomimia is distinguished by a limited range of facial expressions and a slower pace of facial movement (facial bradykinesia).

Parkinson's disease patients are said to exhibit facial characteristics like the well-known "poker face" [11]. In addition, one may see the unequal facial muscle action as well as the tightness of the muscles themselves. The main cause of a situation in which a person finds it difficult to express their emotions is these symptoms [9]. A remarkable feature in and of itself is that individuals with Parkinson's disease (PD) are less able than healthy controls (HC) to recognize the emotions and moods of other people. [12] Healthy controls are more likely to be able to accomplish this. Since people may communicate with one another, they can also express their feelings and sentiments in addition to their views and facts [13]. Because Parkinsonism has been shown to have negative effects on the vocal tract (dysarthria) [10], in addition to having an impact on cognitive function [14], this method is hampered in this condition. This is why Parkinsonism impairs this mechanism. Additionally, it has been shown that PD patients' social wellbeing is impacted by communication ability deficits [14]. [Reference required] Due to the challenges involved in trying to use the lips and tongue in the proper way, tongue twisters are among the most challenging speech exercises to pronounce. Dysarthria may occur in patients with Parkinson's disease as a result of the weakening of the articulators, which is more likely to happen while pronouncing tongue twisters.

In the next part, we'll examine a number of machine learning-based approaches for general purpose health disease detection, that are comparable to one another in terms of their quantitative performance measures and their quantitative qualities. A parametric analysis and comparative assessment of the models under consideration will then help determine which models are most suited for the various clinical use cases. A few last thoughts on the investigated models and some suggestions for how to further boost its performance will complete this paper. Finally, some suggestions for more reading and research will be provided to complete this text.

2.IN-DEPTH REVIEW OF DIFFERENT MODELS FOR IDENTIFICATION OF HUMAN HEALTH DISEASE TYPES

A wide variety of diseases are prevalent to the human body, and identification of these diseases is a multidomain task, which is carried out by different researchers via different deep-learning based models & techniques. Blacklegged ticks in eastern North America spread the bacterium *Borrelia burgdorferi*, which causes Lyme disease, to people (*Ixodes scapularis*). Given within 72 hours after a blacklegged tick bite, antibiotic prophylaxis has been found to lower the risk of Lyme disease [1]. Knowing how to recognize a blacklegged tick may improve treatment for Lyme disease. In this research, specialists develop an autonomous system for instantly identifying blacklegged ticks using state-of-the-art computer vision techniques. The taxonomy of tick species is established using trained convolution neural network models. Convolutional neural network (CNN) models are improved by using better knowledge transfer methods. Using their best convolution neural network model, tick species can be predicted with 92% accuracy. With their vision-based technology, finding ticks is simpler than ever, and you can more precisely monitor the spread of illnesses brought on by ticks. Using this approach together with the regions where ticks are most likely to be found, the risk of contracting Lyme disease may be determined. Deep learning has never been used to categorize ticks previously, therefore this is interesting news for the ecology and risk management of illnesses carried by ticks.

Chron's disease and ulcerative colitis are two instances of inflammatory bowel illnesses, according to [2]. (IBDs). Cardiovascular events, such as stroke and ACS, are more likely to occur in patients with inflammatory bowel illness. By using computational data mining technology, patients with inflammatory bowel disease (IBD) may be able to quickly and affordably get insightful information about their risk of vascular disease from their electronic medical records. The research of 90 IBD patients also included 30 people with vascular disease. To establish the capability of predicting arterial events and the most important elements of the whole dataset, researchers looked at 30 patients with IBD and arterial disease. Their findings demonstrate that machine learning (ML) is capable of accurately classifying the most crucial clinical variables in a dataset and predicting the occurrence of an arterial event and its type (stroke or acute coronary syndrome) from medical records. They may change treatment regimens as a result of their novel results, which may provide physicians more resources to aid patients.

Utilizing human-curated illness ontologies aids in diagnosis, therapy, cross-time data comparability, and improved clinical decision-making [3]. Such ontologies make the classification of illnesses based on common anatomical or histological traits. Despite developments in molecular biology, the majority of ontologies still represent a "reductionist" viewpoint. By looking at the proximity links between disease modules (DMs) in the human interactome network, it is possible to detect illnesses that are patho-biologically similar and to help in drug discovery and repurposing. To evaluate the validity of similarity linkages created by structural closeness of DMs, disease-gene connections and clinical trial reliability have certain drawbacks. This work investigates the relationship between the structural closeness of related DMs in the interactome and the category closeness of illnesses in human-curated ontologies in order to provide light on the commonalities across diseases. Researchers provide a technique (and related algorithms) for automatically building a hierarchical structure using DM proximity interactions, which they then compare to a human-curated illness taxonomy. The studies presented here show that the suggested method can be used to evaluate structural and categorical similarities of human diseases, support the expansion and improvement of human disease categorization systems, and identify promising network regions for discovering novel disease-gene relationships.

The findings of [4] study indicate use of multimodal pictures, such as those produced by magnetic resonance imaging (MRI) and positron emission tomography (PET), may help in the diagnosis of Alzheimer's disease (AD). Oftentimes, PET is either unavailable or too expensive in multimodal imaging. The majority of approaches in use today overlook missing data, which reduces sample sizes. Even with the advancements, it is still difficult to mix and extract information from

many data sources. The authors discuss a deep learning architecture that addresses these issues by combining a TPA-GAN with a PT-DCN for the imputation and categorization of multimodal brain images. The team first introduces a TPA-GAN that, by fusing pyramid convolution, attention, and illness categorization, fills in the gaps in PET data from an MRI scan. To learn and incorporate multimodal input for illness classification, the next stage is to build a deep convolutional network with path wise transfer blocks. Their strategy outperforms state-of-the-art approaches for both picture imputation and the diagnosis of brain disorders when applied to the ADNI-1/2 datasets.

According to [5], Parkinson's disease (PD) is an irreversible neurological condition that affects the motor system. Early identification and therapy may dramatically decrease the course of Parkinson's disease. This study proposes an extensible unsupervised feature selection method using longitudinal multimodal data and manifold learning. Classification and clinical score prediction assist in the early detection of PD. The suggested method takes use of unified embedding and sparse regression (UESR) to adaptively identify similarity matrices and discriminative features. To learn about multimodal data structures, researchers use sparse adaptive control with the $l_{2,p}$ norm and subject similarity restrictions. To tackle this issue, an iterative optimization technique is used. On the PPMI dataset, researchers put the suggested method to the test. Their method is superior to existing methods for regressing clinical ratings and categorizing longitudinal data.

EHRs could be a useful information source, according to [6]. Specialists in clinical documentation examine the report, keep track of all the previous procedures and examinations, and code the electronic health record (EHR) in accordance with the International Classification of Diseases (ICD) (ICD). Coding electronic health records makes it easier to extract data and share information. Here, we look at multi-label classification using computers. NLU for clinical text mining has advanced, although it hasn't been used with additional languages yet. On display are the contextual dependencies of Contemporary Transformers (CT) models. In order to take use of the Language Model's unannotated corpus of internal, in-domain, and closely related EHRs for the downstream job, the team has chosen to concentrate on Spanish EHRs for this research. Although the International Classification of Diseases coding system contains a hierarchy, the upper levels seldom rarely use it. Researchers develop and implement a hierarchical head for multi-label categorization using the ICD's multi-task classification hierarchy.

Work in [7] claims that a potential new field of study is the application of artificial intelligence and neuroscience to identify brain disorders. Functional connectivity (FC) studies are often used to quantitatively analyze fMRI data in search of diagnostic biomarkers. In the past, studies have often classified brain disorders using low-order FC traits while neglecting high-order functional connections across different brain areas. A multi-tiered MFC was used in this work to identify neurological diseases. Researchers created a DNN model to learn abstract FC feature representations. During the training of the DNN model, which included both supervised and unsupervised learning stages, prototype learning was included into supervised fine-tuning to enhance intra-class compactness and inter-class separability. The researchers next trained an ensemble classifier using hierarchical stacking learning to take into consideration all of the abstract FC traits they had learnt at various levels. Two large fMRI datasets were subjected to systematic analyses. The suggested MFC model's strong classification performance across diverse pre-processing pipelines, brain parcellations, and cross-validation techniques demonstrated its efficacy and generalizability. This work combines low- and high-order FC patterns to classify neurological illnesses in a more precise manner.

Alzheimer's disease (AD) is a degenerative brain ailment that may have negative long-term effects. sMRI may be used to characterize the cortical atrophy linked to Alzheimer's disease in its early phases. Cognitive performance may be predicted using a broad range of sMRI morphological features. 3D sMRI may provide more information than cognitive testing. Only a tiny portion of the literature may be able to predict with accuracy certain brain MRI results in the future. Using a 3D multi-information generative adversarial network (mi-GAN) [8] to predict the general state of a patient's brain over time and a 3D Dense Net-based multi-class classification network optimized with a focal loss to identify the actual clinical stage, this article proposes a framework for predicting the clinical stage of a disease. Mi-GAN can produce high-quality individual 3D brain MRI images as long as 3D brain sMRI and multi-information are provided as a starting point. The ADNI conducts scientific studies (ADNI). Their mi-GAN exhibits excellent performance with a state-of-the-art SSIM of 0.943 between genuine MRI pictures and generated ones. Instead of utilizing conditional GAN and cross entropy loss, Mi-GAN and focused loss increase the accuracy of pMCI relative to sMCI by 6.04%.

Numerous neurological conditions, according to [9], cause a progressive loss of brain structure and function. Researchers were able to predict diagnosis using huge longitudinal MRI datasets utilizing machine learning and deep neural networks, suggesting deterioration. Convolutional Neural Networks (CNN) are used to extract pertinent information from each longitudinal MRI visit, while recurrent neural networks are used to classify visits (RNNs). However, this form of modelling produces classifications that are not supported by clinical data since it disregards the illness's natural history. Experts advocate demanding categorization homogeneity between visits in accordance with illness progression and integrating variables across visits using an unique longitudinal pooling layer to get around this problem. The effectiveness of the suggested approach is evaluated using longitudinal structural MRIs from three neuroimaging datasets (Alzheimer's Disease Neuroimaging Initiative, N=404), 274 healthy controls, 329 AUD patients, and 255 adolescents from the National Consortium on Alcohol and Neurodevelopment in Adolescence (NCANDA). For longitudinal categorization across all three tests, their approach surpasses the most widely used algorithms, enabling more precise monitoring of brain states

across a variety of circumstances.

Work in [10] claims that one of the worst neurological conditions in the world is Alzheimer's disease (AD). An ensemble

of Deep Learning (DL) models may be used to learn complex patterns from MRI images and utilize those patterns to

detect AD. Since Deep Transfer Ensemble (DTE) is an ensemble of DL-architecture-neutral deep neural networks trained using transfer learning, classifying AD with it is computationally simple. DTE makes advantage of the distinctive and complementary perspectives offered by the many locally optimal solutions used by various networks. DTE obtains a 99.05% and 85.27% accuracy for NC and AD classification using two distinct datasets. For MCI and Alzheimer's illness, DTE obtains split accuracy rates of 98.71 percent and 83.11 percent, respectively. It also performs wonderfully when there are 50 samples in the class. The small dataset showed 85% accuracy for NC vs AD. It performed better than other deep models examined in the past, including snapshot ensembles.

Work in [11] provides an overview of recent research on quantitative gait analysis in neurodegenerative diseases. Technological developments could help in clinical diagnosis and severity grading of some illnesses. This gait analysis difficulty examination examines pertinent sensors, characteristics, and processing techniques. First, we discuss the typical gait cycle and any deviations that might result from neurodegenerative illnesses. The most well-known feature extraction, classification, clustering, and selection methods are then thoroughly explained. Finally, we discuss some of the open issues and potential directions.

Researchers advocated for in [12] Although machine learning has the potential to enhance dementia diagnosis, it is not always possible to put study findings into practice. The feature-selection based optimization for dementia diagnosis does not take into account the time spent doing diagnostic assessments. Researchers are examining the effect of evaluation time as a practical restriction on feature selection for Alzheimer's disease diagnosis. Scientists employ a trio of feature selection techniques to choose assessment items for dementia patients from a large dataset that is readily accessible to the public. The objective of cost-sensitive feature selection is to decrease evaluation time and increase diagnostic accuracy without breaking the bank. Researchers created a toolkit that resembles a sandbox with a graphical user interface to study user-selected subsets of assessment items in order to promote clinical use and further examination of their recommended accuracy-vs-cost optimisation methodologies. Subsets of accuracy-cost optimized assessment items may perform better than the majority of traditional tests in terms of diagnostic accuracy and/or overall assessment time. Overall, their evaluation and sandbox tool may help clinical users and other stakeholders analyze and evaluate if items on dementia diagnostic assessments are helpful and may lead them to reconsider dementia diagnostic evaluations. By increasing diagnosis accuracy and assessment time, researchers produce predictive and effective dementia diagnostic exams and provide a sandbox interface for doctors and non-specialists.

The JHCPMMP was purportedly employed in the binary classification research for Alzheimer's disease [13]. The study's objective was to create a classification system that could take the complexity and variety of brain networks into consideration. In this study, subclass weighted logistic regression is suggested (SWLR). HC against AD accuracy was 95.8%, HC vs EMCI accuracy was 91.6%, HC vs LMCI accuracy was 93.7%, EMCI vs LMCI accuracy was 89.5%, and LMCI vs AD accuracy was 91.6%. The results show that distinct regions of the brain experience core decline at various stages of Alzheimer's disease. These brain areas constantly rotate counter clockwise in two-dimensional imagery.

The authors of [14] devise a unique method for producing synthetic Photoplethysmogram (PPG) data, which is then utilized to enhance classifier performance. They do this by using a physical model of the cardiovascular system. computer modelling of the electrical activity, blood flow, and blood pressure of the heart. The cardiac model creates PPG time-series that are both healthy and CAD by altering pathophysiological factors using a small sample of real PPG data. VAE may be used to create statistical feature space for CAD. using both (i) entire data and (ii) artificially abbreviated real disease data. When trained on synthetic data, the classifier's performance (sensitivity, specificity) improves from (0.65, 1) to (1, 0.9) and from (1, 0.95) to (1, 0.9). (1, 1). Physical modelling and statistical feature space selection function better than the standard Generative Adversarial Network (GAN) architecture when it comes to producing realistic PPG data with pathophysiological interpretation. This technique may be used to train machine learning algorithms for heart healthcare applications using huge datasets.

Parkinson's disease is a multisymptomatic neurodegenerative condition that is treated with levodopa (PD). Motor function testing is crucial for determining how much levodopa to provide. Speech impairment is a warning indication of Parkinson's disease that requires attentive observation. Levodopa's effects on speech have been the subject of studies in the past, with varying degrees of success. To ascertain the impact of treatment on three sustained phonemes, 24 PD patients were interviewed during medication on and off phases, along with 22 healthy volunteers. A Support Vector Machine was used to categorize the characteristics (SVM). The findings demonstrate that the timing, amplitude, and harmonics of the levodopa-sensitive phoneme /m/ are influenced by medication. It was similarly successful to distinguish PD-off from control recordings using /m/ and /o/. The phonemes /a/, /o/, and /m/ were used in a support vector machine (SVM) classification for drug effect and differentiating PD from control speech to get the best results. The SVM [15] was successful in differentiating between PD-off and PD-on instances with an AUC of 0.81. The automatic speech analysis in PD should make use of several phoneme recordings. Their results may be used to the tele-monitoring of levodopa response and the early diagnosis of parkinsonian dysarthria. In the healthcare sector, which gathers and retains enormous volumes of data, artificial intelligence has shown to be a priceless tool. Chronic obstructive pulmonary disease, often known as COPD, is a complicated syndrome with several interconnected symptoms. Results, difficulties, and potential applications of AI in COPD research are reviewed. The research team searched PubMed and DBLP for relevant papers up to the year 2020 and discovered 156. The resultant papers were analyzed and divided into four major contextual groups using qualitative and quantitative criteria: I, "COPD diagnosis," II, "COPD prognosis," III, "Patient categorization," and IV, "COPD treatment." To make sense of the enormous volumes of complicated data created by COPD, more sophisticated techniques and the ongoing use of AI are required.

Early detection of mild cognitive impairment (MCI) and the prodromal stage of Alzheimer's disease are crucial since some people with MCI will go on to acquire Alzheimer's disease. A multi-stream deep convolutional neural network may be used by researchers to distinguish between MCI that is stable and MCI that is developing [16]. Researchers first contrast MRI scans of individuals with Alzheimer's disease with those of individuals with normal cognition in order to detect anatomical features. These landmarks are used by a convolutional neural network (CNN) to extract patches from MRI data and categorize them. After that, they train the architecture using images of people with Alzheimer's disease and people with cognitively normal conditions to make up for the absence of increasing MCI training data. The suggested architecture is then adjusted using progressively deteriorating MCI data using the weights from the trained model. With an F1-score of 84.96%, their strategy exceeds other MCI classification techniques.

According to studies reported in [17, 18], because to developments in deep learning and medical imaging technologies, researchers may now utilize CNN to categorize instances of Alzheimer's disease (AD) and forecast clinical scores. The Principal Component Analysis Network (PCANet) binarizes and generates blockwise histograms for image properties using PCA to construct multilevel filter banks for centralized sample learning. PCANet's flexibility is restricted by the extraction of tens of thousands to hundreds of thousands of features and the creation of multilayer filter banks that depend on sample data. This study presents the nonnegative matrix factorization tensor decomposition network to handle these problems (NMF-TDNet). Researchers design multilayer filter banks for sample learning using NMF instead of principal component analysis; they then use the learned information to build a higher-order tensor and use tensor decomposition (TD) to reduce data dimensionality, producing final picture features. In order to aid in the diagnosis of AD and the prediction of clinical scores, these characteristics are fed into a support vector machine (SVM). The methods ADNI-1, ADNI-2, and OASIS are used to assess their approach. The experimental findings demonstrate that NMF-TDNet outperforms PCANet in terms of input characteristics and data dimensionality reduction.

Due to excessive consumption and deadly overdoses of the drug, researchers in the United States came to the conclusion that opioid addiction and overdose had become a public health hazard [19]. A one-size-fits-all prescription regimen may leave patients with significant leftovers in situations of persistent and severe pain, which might result in abuse and overdosage. Consider the history of opioid usage for each patient to lower the chance of overprescribing and overdose. The objective of this project is to create a machine learning model that can precisely forecast a patient's level of opioid use within the first two weeks after discharge. Electronic health records, prescription history, and consumption questionnaires are used to collect information on short-term opioid use after joint replacement surgeries. Non-responses jeopardize the validity of survey findings. By using fictitious labels created via Bayesian regression, a semi-supervised learning strategy gets around this issue. This method's main objective is to give missing information from opioid survey responses priority. To further simplify categorization based on the prediction, pseudo labels are introduced. Extensive testing demonstrates that a semi-supervised learning (SSL) model performs statistically better than a supervised one for categorizing patients. This method allows doctors to tailor each patient's opioid dose to meet their unique requirements, resulting in more efficient pain management and less opioid use.

Work in [20] asserts that improvements in machine learning methods have benefited models for representation learning, classification, and prediction created from EHR data. The effectiveness and readability of the models have improved, especially when it comes to decision-making and policy-making. The authors of this paper construct a temporal deep learning model for depression diagnosis using EHR sequences and a transformer architecture. To make predictions regarding chronic illnesses, this model can combine data from five distinct high-dimensional EHR data sources across time. Researchers conducted pretraining and fine-tuning on EHR data in order to beat the existing state-of-the-art in chronic illness prediction and uncover the underlying relationship between EHR codes. The model increased the precision-recall area under the curve (PRAUC) for depression prediction from 0.70 to 0.76. Self-Attention Weights (SAW) in each sequence, which quantified the relationship between codes, improved the model's interpretability. These findings show the model's capability to interpretably and effectively predict depression using a variety of EHR data, which may help in the future screening and early identification of chronic diseases.

Parkinson's disease (PD) patients and healthy controls may be distinguished from one another using a realistic and unbiased technique, which was found in [21]. (HC). Researchers developed PD-ResNet, a model based on residual network (ResNet) architecture, to explore the differences in gait between PD and HC as well as between PD severity levels. Using a polynomial enhanced dimensions approach, the gait characteristics of the input are given larger dimensions. The information is then transformed into a three-dimensional image for PD-ResNet to utilize. To enhance generalization, SMOTE, data augmentation, and early halting are used. To train PD-ResNet to concentrate on difficult situations while eliminating outliers to increase classification accuracy, a special loss function is created. Their suggested model performs with 95.51% accuracy, 94.44% precision, 96.59% recall, 94.44% specificity, and an F1-score of 95.51% on the clinical gait dataset.

According to [22], heart disease has a detrimental influence on people's lives since it often results in hospitalizations and fatalities. Early diagnosis and treatment depend on accurate prognosis. AI and IoMT aid in the monitoring, prediction, and diagnosis of cardiac disease. Most of the disease forecasting models in use today only provide prognoses. The authors provide predictions about heart disease using machine learning in two different binary and multicategory contexts. In order to simplify the data and increase the generalizability of the binary classification prediction, they first recommend utilizing a Fuzzy-GBDT approach. Bagging is used with fuzzy-GBDT to reduce overfitting. The bagging fuzzy GBDT approach may be used to estimate the severity of heart disease. Bagging-Fuzzy-GBDT excels in accuracy and stability for predictions based on binary and multiple classifications.

AI is often employed to solve healthcare difficulties, claims [23]. Researchers have classified the severity of Chikungunya cases using deep learning. Overfitting and unnecessary parameter tinkering plague these algorithms. This research recommends employing a cyber-physical system based on artificial intelligence to categorize instances of the Chikungunya disease (CPS). CPS is a strategy that improves outcomes by combining computational and physical components. The severity model for the Chikungunya illness employs random forest (RF). Due to complicated designs and high link weights, RF suffers from overfitting and slow computing. An adaptive crossover-based genetic method is used to generate a changing RF model (ACGA). For speedier outcomes, ACGA may be used to improve the RF design. The Chikungunya illness data collection is widely used. The findings show that, in terms of F-measure, accuracy, sensitivity, and specificity, ACGA-RF surpasses competing models. The planned CPS system may discourage patients from traveling near hospitals.

The investigation detailed in [24] Membranous nephropathy is diagnosed based on clinical symptoms, serology, and an obvious kidney biopsy (MN). Optical examination may provide false-positive results, and the failure to detect biochemical alterations hinders the study of the disease process. Although hyperspectral microscopy has the ability to provide information on immune complex components, the high dimensionality of the pictures produced makes it more challenging to analyze and diagnose disorders. This paper proposes a unique classification technique for the intelligent diagnosis of MN using a microscopical hyperspectral pathology dataset. SSDP uses clustering density peaks to produce maps that show the spectral and spatial properties of MHSI. By compressing spatial-spectral local intra-class pixels and separating spectral inter-class pixels, graph embedding creates low-dimensional features with essential diagnostic information in the immune complex. SVMs categorize pixels in low-dimensional space in order to recognize MN. Two instances of experimentally established facts are MN connected to the hepatitis B virus and MN associated to primary MN. The suggested SSDP is therapeutically useful for MN diagnostic automation with a sensitivity of 99.36%.

According to [25], comprehensive automated algorithms are needed for categorizing retinal pictures. There are little publicly accessible data on diabetic retinopathy (DR) and age-related macular degeneration (AMD), two retinal illnesses, and the cost of expertly annotated photos is significant (AMD). Despite the fact that DR and AMD share characteristics like haemorrhages and exudation, as established by a number of studies, most classification algorithms only train disease models separately when just one picture label is available. Learning from several sources at once to build a more reliable model. Synergic adversarial label learning (SALL) uses retinal illness labels as extra signals in semantic and feature space to collaboratively train a model via knowledge distillation. The study team discovered that using the suggested strategy increased model accuracy for categorizing DR and AMD fundus images by 5.91 and 3.66%, respectively. Additional testing validates the accuracy and readability of SALL in medical imaging environments.

Among the clinical indicators used to determine if someone has Parkinson's disease are dyskinesia, rigidity, and resting tremor (PD). When using clinical rating scales to assess PD symptoms, there may be discrepancies amongst observers. The authors of this paper outline an automated deep learning-based movie-based PD detection system. Researchers describe a 3D convolutional neural networks (CNN) ability to categorize the severity of PD [26]. The severity of PD may be identified through non-medical transfer learning, according to research, despite the paucity of clinical data in this area. Researchers created a Temporal Self-Attention (TSA) mechanism to help the network concentrate on tiny temporal visual signals, such tremor frequency, in order to bridge the gap between medical and non-medical datasets. The patient exhibits bradykinesia and postural tremors on seven of the MDS-UPDRS part III evaluations. Task-assembling is used by researchers to give a multi-domain learning approach for predicting the severity of PD. On their PD video dataset, researchers do experimental testing for TSA and task-assembling. For binary task-level classification, researchers acquire an MCC of 0.55, while for three-class patient-level classification, they reach an MCC of 0.39.

Work in [27] claims that one of the most expensive and quickly spreading illnesses in the world is Alzheimer's disease. Everyone engaged in care, including patients, caregivers, nurses, and family members, is impacted. Patients find MRI and PET scans to be cumbersome when it comes to monitoring the development of an illness. Predicting the illness's stage and halting its progress need a more clever and effective strategy. Machine learning and S-parameter data from six antennas placed around the head allowed for the non-invasive recording of Alzheimer's disease-related brain alterations. Nine models' heads' circumferences were measured. Utilizing machine learning methods, the data was examined. Each algorithm's prediction and accuracy scores were calculated and compared to discover which may better categorize the phases of Alzheimer's disease. The logistic regression (LR) model's overall accuracy and effectiveness in differentiating between the 4 phases of Alzheimer's disease was 98.97%. In order to forecast the start of Alzheimer's disease in the brain, the results provide a unique approach for clinics and monitoring systems that combines machine learning with non-invasive microwave medical sensors and devices.

According to [28]'s research, breakthroughs in the personalized treatment of chronic illnesses have been made possible by systems biology, the Internet of Things, and AI. In the EU and the US, chronic illnesses cost C=700 billion and \$3.5 trillion in healthcare expenses, respectively. The likelihood of both ineffective therapy and excessive prescription usage is increased when acute pain episodes caused by chronic illnesses are treated according to broad clinical recommendations that fail to take into account the particulars of each episode, such as its severity or length. Knowing the circumstances of each patient's suffering can let the doctor provide pain medicine for each patient and emergency with impartiality. The authors of this work make symptomatic crisis predictions based on ambulatory data for individuals with chronic illnesses. Researchers categorize pain based on patient descriptions of it. They tested their plan on people who had migraines. Migraines are one of the most expensive neurological illnesses for both commercial and public healthcare systems, affecting around 12% of the world's population. Real-time pain curve analysis is used in this work to classify pain episodes. Pain kinship curves are a physical characteristic. These variables are taken into account by machine learning algorithms

while classifying different types of pain episodes. Modelling and clustering are used to describe how bouts of chronic pain develop. Using a Logistic Model Tree (LMT) technique, 51 migraine sufferers can be accurately categorized into 4 pain clusters based on 4 morphological criteria.

Work in [29] asserts that Alzheimer's disease (AD) is a neurological condition that degenerates over time. To investigate brain activity, find biomarkers for AD, and diagnose the disease's early stages, resting-state functional magnetic resonance imaging (MRI) must first build the brain's functional connection network (BFCN) (rs-fMRI). The techniques used to label rs-fMRI data currently only take into account one time point. More data points are usually preferable when doing longitudinal analysis to identify brain illnesses. To detect EMCI and LMCI in patients, researchers integrate the FSN model with PFC learning and employ numerous rs-fMRI time points. Following selection of the FSN architecture, researchers create several time-point BFCNs. Through the use of multitask learning in the prefrontal cortex, longitudinal investigations of EMCI and LMCI are carried out. Working together, researchers may eventually learn about all of BFCN's unique characteristics. The suggested PFC technique finds a balance between particular and generic properties discovered from data points over time. SNF integrates traits from many places of time. Their approach is assessed using the ADNI-2 data set. Experiments demonstrate that their strategy outperforms the prevailing best practices.

One of the deadliest coronavirus pandemics in recorded history will occur in 2019 (COVID-19). The use of automated lung infection categorization using CXR pictures may improve COVID-19 diagnosis. COVID-19 classification from pneumonia CXR images is challenging because to common geographic traits, significant feature diversity, and contrast variety. Deep learning models are only capable of a certain amount of work since it is impractical to gather a vast quantity of data about a particular ailment. With MAG-SD [30], COVID-19 in CXR pictures of pneumonia is automatically labelled. Utilizing MAG-SD, MA-Net creates prediction vectors from multiscale feature maps. We use attention directed augmentations and soft distance regularization to strengthen trained models and make them less susceptible to noise. They were successful in improving the CXR categorization for pneumonia using their multiscale attention model. Studies show that for identifying pneumonia, MAG-superior SDs outperform cutting-edge models.

According to research, one's judgment deteriorates under stress [31]. Doctors can make better choices if they are able to identify stress symptoms early on. fNIRS may be used to detect stress. The majority of earlier research classified single fNIRS data without taking channel correlations into account, which might provide differentiating traits. Here, a fNIRS method based on the idea of joint-channel connection is described for detecting stress during decision-making. This approach combines feature selection and classifier modelling into a sparse model using intra- and inter-channel regularizer. In this work, decision-making under stress was simulated using the Trier Social Stress Test and the Balloon Analog Risk Task, and the subsequent changes in brain hemodynamic signals were recorded using fNIRS. Their improved approach was supported by experiments, which had an accuracy of 0.961%. Prior research has supported the validity of their technique and given guidance for improving the fNIRS channel settings by confirming the stress correlation and connectivity of brain areas assessed by feature selection. According to our knowledge, this is the first study to apply a sparse model for stress detection that analyzes data sparsity and correlation across brain areas at the same time. The suggested approach could help medical professionals spot stress while making clinical decisions.

Work in [32] asserts that telemedicine has altered patient care by making better health analytics tools, more readily accessible remote healthcare, fundamental diagnoses of medical conditions, etc. available. The usage of IoT and AI enhances the health advantages of telemedicine. Telemedicine is opening up new channels for integrating cyber-physical systems into medical treatment with the emergence of artificial intelligence (AI) and the Internet of Things (IoT), enabling remote patient monitoring and interactive assistance. With 7.4 million victims globally, atrial fibrillation (AF) was the most common reason for cardiac arrhythmia-related deaths. Between 2050 and 2060, between 12 and 17.9 million persons in the United States and Europe are predicted to have AF. Since AF is a cardiovascular illness, it is of great importance for overall public health. Here, we examine the most recent developments in the recording of cardiac rhythms, the detection of arrhythmias, the internet-connected heart, and data visualization. By analysing the current literature on CNN and IoT devices in the diagnosis of cardiac disease, researchers present an overview of the major research gaps and recommend future study subjects.

Auscultation is a crucial method for checking for anomalies in the respiratory system, according to [33]. Automated analysis of lung auscultation sounds may be helpful in low-resource healthcare settings with a shortage of doctors. For application in the diagnosis of respiratory disorders from individual breath cycles, a lightweight CNN architecture based on a hybrid scalogram of lung sound properties is presented. EMD and CWT are used in the suggested feature set (CWT). The train-validation-test set of the ICBHI 2017 lung sound dataset, which excludes any patient-specific information, is used to evaluate the suggested technique. The suggested framework obtains weighted accuracy ratings of 98.92% for three-class chronic classification and 98.70% for six-class pathological classification when compared to the well-known and much bigger VGG16. The suggested CNN model performs better than comparable lightweight alternatives.

The finger tapping test (FTT) is crucial for diagnosing Parkinson's disease (PD) [34], however manual visual assessments might result in score discrepancies owing to clinician subjectivity. The need for direct physical touch with wearable sensors may interfere with how persons with Parkinson's disease move. A depth camera and spatial-temporal 3D hand pose estimation are used to record and examine the 3D hand movements of PD patients. The technique's usage of a temporal encoding module, an addition to A2J's deep learning architecture, reduces pose jittering, and the technique's posture refining method reduces the requirement for vast quantities of data. Clinical settings are used to annotate the first vision-based 3D PD hand dataset, which consists of 112 hand samples from 48 PD patients and 11 control volunteers. When identifying real-world data, the new technology performs better than human physicians with an accuracy of 81.2%.

Work in [35] claims that PAD is an artery disease that progresses over time and causes considerable morbidity and death. For PAD detection techniques, invasive, costly, or time-consuming equipment and specialized personnel are often needed. Researchers employ a cuff to characterize the circulatory system and provide a special automated, non-invasive, and simple method to detect PAD. The superimposition of arterial and venous pressure was discovered, and it was modelled as a function of cuff pressure. Analysing the mathematical models' parameters led to the creation of a feature-based learning approach that could recognize PAD patterns. The evolutionary algorithm and principal component analysis were used to choose the traits that were most effective in predicting PAD. A neural network-based RUSBoost ensemble model was utilized to diagnose PAD. Data collected from 14 patients with PAD and 19 controls were used to verify the suggested technique. It correctly detected PAD 91.4% of the time, with 90% sensitivity and 92.1% specificity. Sadly, the confusing influence of age was not taken into consideration.

Work in [36] states that Alzheimer's disease is the most prevalent kind of cognitive impairment, yet the suggested approach provides a non-invasive and precise PAD diagnosis and may be integrated into oscillometric blood pressure readings that are already used. The area of computer-assisted Alzheimer's disease diagnosis and prognosis has recently made strides. Graph neural networks (GNNs) have attracted a lot of attention recently due to their ability to accurately recreate sample correlation and integrate multimodal data in an efficient manner. The complete dataset is used by a large number of GNNs for node classification, creating a massive fixed-graph structure that makes it impossible to assess each GNN separately. Researchers propose an auto-metric GNN (AMGNN) model for AD diagnosis as a solution to this problem. In the beginning, we provide a meta-learning technique based on measurements for inductive learning via several node classification tasks. Tiny graphs may be used in meta-tasks to make the model agnostic to sample size, enhancing performance with fewer samples. The probability restriction in AMGNN allows for node similarity metric learning and multimodal data fusion. On the TADPOLE dataset, the model was tested for early AD diagnosis and MCI conversion prediction. The accuracy of the average and median models is 94.44% and 87.50%, respectively. Their approach promotes the adoption of graph-based deep learning algorithms for illness detection since it enhances classification performance and flexibility.

However, [37] found that based just on symptoms, it might be difficult to distinguish between unipolar and bipolar depression. Measuring functional connectivity (FC), particularly dynamic FC, offers one potential way to distinguish BD from UD. The bulk of study used statistics at the FC and group levels, however they may not be sensitive enough to pick up on minute variations in FC dynamics between BD and UD. A more precise depiction of individual differences is possible because to the application of machine learning and the HOFC network across the brain. We employed HOFC, which recognizes temporal synchronization across dynamic FC time series, to categorize 52 BD, 73 UD, and 76 controls (HC). With a success rate of 70%, it was able to discern between BD and UD. The systems of olfaction, vision, and hearing were connected in a coordinated and adaptable manner by the motor and cognitive processes. While the connectomes of BD and UD show distinct FC synchronization patterns, they both exhibit comparable deficits in cognitive and emotional functioning. While communication between the ventral attention and frontoparietal cortices is compromised in BD, there are flawed connections between the visual and somatosensory cortices in UD. It was discovered that the length of a patient's illness had an effect on the ability to distinguish between BD and UD, with more severe symptoms making the diagnosis harder to make as time went on. It's probable that BD and UD have different neurological causes and similar causes.

Work in [38] describes the strategy for illness prediction using genetic and imaging data. Researchers provide a multilayer survival model to predict the onset of severe illness in patients with intermediate symptoms. It is a multi-layered model of how genes and scans are connected to one another. As a consequence, it may be essential to eliminate particular modalities from consideration in traditional additive models when their contributions are disproportionate. The fixed time period of earlier classification-based techniques has limits; this issue is resolved by switching to a survival model. Researchers have also suggested data-specific penalties, such as the group lasso penalty for genetic data and the l2-penalty for imaging data. Finally, a proximal gradient-based optimization (PGO) technique is described. Combining genetic (single nucleotide polymorphisms, or SNPs) and imaging (anatomic MRI measurements) data from the ADNI database, the technique successfully predicted AD in patients with MCI. Experimental results demonstrated the method's efficacy in predicting AD conversion. It proved the accuracy of genetic variations and anomalies in brain imaging in predicting health status. The general approach could be able to predict the appearance of new illnesses.

Fusion analysis of multi-modal data is becoming feasible for treating complex brain illnesses [39]. Due to the low volume and high dimension of multi-modal data, present machine learning algorithms are sadly unable to effectively conduct high-veracity fusion feature selection. In order to find early-onset mild cognitive impairment risk genes and disease-related brain areas, this study presents the genetic-evolutionary random forest (GERF) technique (EMCI). Using conventional correlation analysis, fusion features are created to look into the relationship between brain areas and genes. By using genetic-evolutionary theory, classification and feature extraction are improved. The ADNI database was used to evaluate the recommended GERF technique, and the findings indicate that classification accuracy in small sample learning is promising. Researchers contrast GERF with other approaches to demonstrate its advantages. The researchers also provide a paradigm for identifying pathogenic characteristics that might be used to the study of multimodal data in EMCI and other disorders. The new knowledge from this study may be utilized to improve the effectiveness of electric shocks used in transcranial magnetic stimulation and to help clinical medicine control the progression of illness.

In [40], it was suggested that auscultation data analysis may be done using a deep learning model. Here, breathing recordings are utilized to categorize irregularities in a person's respiratory cycle and identify a medical explanation. Front-end feature extraction creates a spectrogram from the auditory data. The background spectrogram characteristics are

classified using a deep learning network (DLN). Three important improvements to respiratory-sound analysis have been validated by experiments using the ICBHI benchmark dataset. First, it is examined how different spectrogram types, spectral-time resolution, overlapping/non-overlapping windows, and data augmentation affect prediction accuracy. As a result, we describe a ground-breaking deep learning system that can compete with and even outperform the leading techniques now used in the industry. Researchers combine Teacher-Student technique sets to find a balance between model performance and complexity for real-time applications.

According to [41], patient feedback and medical professionals' evaluations of motor function are used to gauge how well people with Parkinson disease respond to therapeutic interventions. The possibility of rating scale differences among ratters may have an influence on the subjectivity and inter/intra-ratter reliability of these sources. By doing this trial, they intended to determine what impact wearable electronics and data analysis would have on the levodopa therapy. Wearable electronics were used to evaluate the motor abilities of 36 patients. It was assessed at time 0 (T0), time 1 (T1), and time 12 (T12) after the start of treatment (T2). The three-axis accelerometer, three-axis gyroscope, and microcontroller that performed statistical tests such analysis of variance, Pearson correlation, and support vector machine (PC SVM) based classification made comprised the inertial measurement equipment. There is a low dose-response association for levodopa, and certain symptoms (such bradykinesia) react well to the drug while others (like tremor) do not. Technology may allow for the exact measurement of levodopa treatment efficacy. If a clinical examination and patient feedback were integrated, the evaluation of motor function may be more accurate.

Researchers are already utilizing deep learning algorithms to identify eye problems thanks to the development of CAD technology [42]. In this article, we examine the accuracy with which AMD, glaucoma, and cataracts may be detected using deep learning. Any modification to the retina's structure is a sign of a potentially dangerous eye condition. It's probable that existing deep learning algorithms can't accurately analyze fundus pictures because of data imbalance and outliers. Robust deep learning techniques (RL) may be able to increase the effectiveness of detection. In this study, researchers used retinal fundus colour images to automatically detect eye issues by fusing deep learning with a brand-new mixture loss function. Researchers use these two losses in a deep neural network model to boost the effectiveness of biological classifier recognition. This is because complicated datasets with class imbalance and outliers may be dealt with by focused loss and corr-entropy-induced loss functions with good generalization and durability. An empirical real dataset from the area of ophthalmology is used to test the theory. The baseline performance of a model and the performance of a model trained using deep learning utilizing their suggested loss function are assessed using accuracy, sensitivity, specificity, kappa, and AUC. In experimental situations, the algorithm's efficacy and resilience have been shown.

Experts' results on [43] indicate that it is difficult to predict the outcome of cardiac disease. Sequential feature selection, LDA, RF, GBC, DT, SVM, and KNN were used to predict heart disease. The method of system verification employs K-fold cross-validation. For our comparative study, we used six different methodologies. It was examined using the Heart Statlog Cleveland Hungary, Switzerland, Long Beach V, and Hungary databases. On the Hungary, Switzerland, Long Beach V, and Heart Statlog Cleveland Hungary Datasets, respectively, the Deep Forest (DF) Classifier sfs (100%, 99.40%, and 100%) and the Decision Tree Classifier sfs (100%, 99.76%) demonstrated the best performance. Analysis in the context of earlier cardiac prognostic studies. The project aims to develop the model to a level where it may be used with other feature selection techniques, such a random forest classifier. This inquiry suggests a fresh strategy for developing the model and streamlining its application in the real world in an attempt to build on earlier investigations.

According to studies in [44], the medical industry is increasingly using wireless connection and the Internet of Things. Biomedical image processing may be used to find disorders in biomedical pictures. Tongue diagnosis is an inexpensive, non-invasive method that supports fundamental healthcare systems all over the world. Depending on their experience, doctors examine the tongue often. Quantitative analysis may be used to remove the qualitative features of imaged tongues, producing an illness detection technique that harms patients as little as possible. To analyze photos of the tongue and diagnose illnesses, automatic deep learning (DL) models must be created. This paper builds a synergic deep learning tongue color image analysis model for IoT-enabled disease detection and classification. The ASDL-TCI paradigm includes data collection, pre-processing, feature extraction, classification, and optimization. People's tongues are photographed by IoT devices and sent to the cloud for analysis. Additionally, feature extraction and picture augmentation are used. In order to identify conditions, deep neural network (DNN) classifiers are used. The parameters may be changed to improve the accuracy of the diagnosis based on EBWO. Using common tongue photos as benchmarks, a series of simulations were used to assess the efficacy of the ASDL-TCI model. The ASDL-TCI model had maximum precision, recall, and accuracy of 0.984, 0.973, and 0.983, respectively, in the simulation result, proving its superior diagnostic performance over the other options.

Work in [45] asserts that echocardiogram (echo) is crucial for determining the presence of cardiovascular disorders. The diagnostic and prognostic significance of echo images is still manually assessed and interpreted by echocardiographers. Several applications use machine learning and signal processing to evaluate medical ultrasound data. Utilizing these methods made automated echo analysis and interpretation possible. Automation of image measurement minimizes effort and human error. The most current techniques for automatically evaluating echocardiogram data are examined by experts. Researchers analyze the effectiveness of current techniques for classifying views, segmenting boundaries, and diagnosing illness. We go through the fundamentals of Doppler, M-mode, and B-mode. Investigated are problems, limitations, and unrealized promise in the approaches now in use. This research examines the current state of automated echo analysis as well as the challenges that must be overcome in order to develop workable systems for in-clinic or on-the-spot diagnostics. A spike in interest in EEG-based wearable emotion classifiers has recently occurred due to the possibility for real-time

monitoring of patients with neurological illnesses like ALS, ASD, or Alzheimer's. Wearable emotion classifiers have the potential to enhance patient outcomes in healthcare and promote social integration. Despite the significance of emotion classification to neuro-medicine, emotion classification hardware platforms have limitations in their approaches to emotion classification in a healthcare environment. The authors of this study [46] address wearable emotion classification (EC) algorithms, feature extraction methods, and practical implementation using electroencephalogram (EEG) data. We present a neuroscience-based analysis of current hardware emotion classifier accelerators in this paper and use it to identify several potential research areas, including multi-modal hardware platforms, accelerators with tightly-coupled cores operating consistently near/supra-threshold, and pre-processing libraries for common EEG-based datasets.

Work in [47] asserts that the future of healthcare is being impacted by the development of new technology. Testing new remedies may result from understanding the causes of depression. Alarming numbers of individuals experience depression globally. In order to determine how depression impacts a person's quality of life, this article uses machine learning techniques to evaluate and examine a variety of data. The experiment mainly consists of two sections. Data integration is described in the first section. With the help of the Secure Hash Algorithm, data connections are monitored. By using hashing, information objects may be found and indexed. In Part 2, a model using both supervised and unsupervised machine learning was suggested. The creation and verification of the research idea both included consolidations. To evaluate the effectiveness of the posterior probability multi-class SVM, classification tasks from the clustered data were chosen. It was disheartening when expectations for a sample were not realized. The suggested approach allowed us to boost categorisation accuracy to 91.16 percent.

Traditional machine learning has made strides in the last few years, which has allowed for the application of phonocardiography for the non-invasive detection of coronary artery disease (CAD) [48]. (PCG). Performance metrics could be enhanced by deep learning that combines many representations. Researchers suggest multiple kernel learning (ML) to merge deep embeddings from pre-trained convolutional neural networks (CNN). The suggested MKL has the least amount of overlap with other base kernels and the maximum degree of similarity to the ideal kernel. There are 960 PCG epochs altogether (from 40 CAD and 40 control patients) that may be examined. Kappa = 0.7850 for the transferred embeddings suggests an accuracy of 89.25%. The accuracy is then increased to 91.19 percent with a kappa of 0.8238 in MKL by mixing them with features that were produced by humans. The results of this research show the potential of PCG signal in the creation of a highly accurate CAD identification system.

FoG is a typical motor impairment in PD, claims [49]. FoG makes it difficult to walk, which makes accidents from falling more likely. It may be quite beneficial to have a gadget that keeps an eye out for FoG and gives them external signals to assist them get over their frozen. Preventative cueing is made possible by the capacity to anticipate FoG. Both detection and forecasting face difficulties. Patient-independent models have shown good sensitivity but low specificity in the absence of FoG data for a particular patient. Ankle inertial measurement units were used to monitor the gait of seven persons with PD, and researchers explored data augmentation, extra pre-FoG segments, and transfer learning to enhance the accuracy of Deep Gait Anomaly Detector's (DGAD) FoG recognition. The DGAD algorithm has a sensitivity of 63.0% and a specificity of 98.6%, which is 3.2% higher than the greatest specificity reported in the literature. Target models were demonstrated to be able to anticipate 87.4% of FoG onsets. The results of this investigation show that their system can accurately recognize FoG and offer cues in patients with little FoG data.

Work in [50] asserts that the use of deep learning may significantly benefit in the early diagnosis of Alzheimer's disease. (AD). In order to diagnose MCI and AD, we present a tensorizing GAN with high-order pooling. One way the suggested model may exploit the brain's architecture is by tensorizing a three-player cooperative gaming framework. Given that the classifier incorporates high-order pooling, it is feasible that the suggested model will employ second-order MRI statistics (MRI). They assert that THS-GAN represents the first attempt to categorize MR images for AD diagnosis. The proposed THS-GAN outperforms state-of-the-art techniques, and extensive experimental findings on the ADNI dataset suggest that tensor-train and high-order pooling may improve classification performance. It is evident from visualization that the suggested model can provide trustworthy samples for semi-supervised learning in a range of contexts. Thus, it can be observed that a wide variety of models are proposed by researchers for identification of different disease types. Each of these models vary in terms of their internal operating characteristics, and external requirements under different use cases. An empirical comparison of these models is discussed in the next section of this text, which will assist in identification of optimal models for different scenarios.

3. STATISTICAL ANALYSIS

Based on the review, it was observed that a wide variety of models are proposed by researchers for identification of different disease types. In this section, these models are compared in terms of their accuracy (A), precision (P), delay (D), computational complexity (CC), and scalability (S), metrics, which will assist readers to identify optimum models for their performance-specific use cases. While absolute values for accuracy & precision were available, other metrics like delay, complexity and scalability were evaluated in terms of fuzzy range sets of Low (L), Medium, High (H), and Very High (VH), which were decided based on their internal configurations and performance across different scenarios. Based on this strategy, table 1 showcases parameters for these models,

Model	A	P	D	CC	S
CNN [1]	92.50	85.55	H	VH	M
ML [2]	91.80	84.10	H	H	H
DM [3]	85.40	84.50	H	VH	H
TPA GAN [4]	99.50	86.52	VH	H	H
UESR [5]	75.80	86.39	M	L	H
CT [6]	85.40	89.61	L	H	H
MFC [7]	83.50	91.16	H	H	M
MI GAN [8]	94.30	90.76	VH	VH	VH
RNN [9]	97.90	89.24	H	VH	H
DTE [10]	98.70	89.50	M	H	H
JHCP MMP [13]	95.80	88.71	H	L	VH
GAN [14]	95.00	88.18	VH	H	H
SVM [15]	81.00	85.11	L	L	M
CNN [16]	84.90	87.45	H	M	H
PCA NET [17]	99.50	88.58	M	H	VH
NMF TDNet [18]	93.80	88.10	H	H	H
SSL [19]	92.50	88.98	H	M	H
SAW [20]	76.00	89.24	H	H	H
PD Res Net [21]	95.50	92.98	VH	VH	VH
Fuzzy GBDT [22]	91.90	93.53	M	H	H
ACGA [23]	96.50	92.56	H	H	H
SSDP [24]	99.30	92.73	L	VH	H
SALL [25]	94.10	92.73	H	H	VH
TSA CNN [26]	99.20	92.31	H	H	H
LR [27]	98.90	90.95	L	M	H
LMT [28]	85.90	90.95	M	H	H
BFCN [29]	97.50	90.19	M	H	M
MA Net [30]	99.30	89.32	H	VH	H
fNIRS [31]	91.50	88.53	H	H	H
CNN [32]	90.80	88.53	H	H	H
CWT [33]	98.90	88.69	VH	H	VH
3D CNN [34]	81.20	86.52	VH	VH	VH
RUS Boost [35]	92.10	88.97	H	H	H
AM GNN [36]	94.40	89.68	VH	H	H
HOFC [37]	91.50	90.45	H	H	H
PGO [38]	91.80	91.77	H	H	VH
GERF [39]	85.40	92.84	H	VH	VH
DLN [40]	96.40	93.65	H	H	H
PC SVM [41]	96.50	92.81	H	M	H
RL [42]	99.20	92.00	H	H	VH
DF [43]	99.70	90.10	H	VH	M
DNN EWBO [44]	98.40	90.06	VH	H	VH
EC [46]	90.40	89.49	H	M	VH
SVM [47]	91.20	90.22	M	L	H
ML [48]	91.50	90.84	H	H	H
DG AD [49]	87.40	91.43	H	H	H
THS GAN [50]	99.50	92.69	VH	VH	VH

Table 1. Comparative analysis of different disease identification models in terms of empirical parameter sets

Based on this analysis, it can be observed that DF [43], TPA GAN [4], PCA NET [17], THS GAN [50], SSDP [24], MA Net [30], TSA CNN [26], and RL [42] showcase high accuracy, while DLN [40], Fuzzy GBDT [22], PD Res Net [21], GERF [39], PC SVM [41], SSDP [24], SALL [25], THS GAN [50], ACGA [23], TSA CNN [26], and RL [42] showcase high precision, which makes them useful for a wide variety of real-time clinical use cases.

In terms of complexity, CT [6], SVM [15], SSDP [24], and LR [27] are able to achieve better performance, while in terms of delay, UESR [5], JHCP MMP [13], SVM [15], and SVM [47] are able to showcase faster performance, thus can be used for high-speed clinical deployments. While, MI GAN [8], JHCP MMP [13], PCA NET [17], PD Res Net [21], SALL [25], CWT [33], 3D CNN [34], PGO [38], GERF [39], RL [42], DNN EWBO [44], EC [46], and THS GAN [50] showcase high scalability, thus can be used for identification of large number of diseases in clinical scenarios.

4. CONCLUSION AND FUTURE SCOPE

In this research, a broad array of disease detection models that make use of machine learning-based approaches for large-scale clinical application use cases were analyzed and discussed. According to the findings of the study, it was found that researchers have offered a broad range of distinct performance models for the detection of various disease kinds. The analysis of these models showed that DF [43], TPA GAN [4], PCA NET [17], THS GAN [50], SSDP [24], MA Net [30], TSA CNN [26], and RL [42] showcase high accuracy, whereas DLN [40], Fuzzy GBDT [22], PD Res Net [21], GERF [39], PC SVM [41], SSDP [24], SALL [25], THS GAN [50], ACGA [In terms of complexity, CT [6], SVM [15], SSDP [24], and LR [27] are able to achieve higher performance. On the other hand, in terms of delay, UESR [5], JHCP MMP [13], SVM [15], and SVM [47] are able to display quicker performance, and hence may be utilized for high-speed clinical deployments. While models such as MI GAN [8], JHCP MMP [13], PCA NET [17], PD Res Net [21], SALL [25], CWT [33], 3D CNN [34], PGO [38], GERF [39], RL [42], DNN EWBO [44], EC [46], and THS GAN [50] exhibit high scalability, these models cannot be utilized for the identification of a large number of diseases in clinical settings. In the future, researchers will be able to improve the performance of these models by fusing them together, and they will also be able to apply hybrid bioinspired methodologies for ongoing improvements of real-time situations.

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