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Development of a Temporal Analysis Model Augmented for Disease Progression Identification through Multiparametric Analysis

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Abstract: In the digital era, a hectic lifestyle and a lack of sufficient nutrition need the analysis of disease-specific aspects for the early detection of diseases in the human body. To identify the presence of heart diseases, electrocardiogram (ECG) parameters are analysed, while for identification of mental issues, electroencephalogram (EEG. These parameters' interdependency must be analysed to identify their cross-effects on different organs. For instance, improper heart functioning directly affects the normal functioning of the lungs, kidneys & liver. Continuous dysfunction of an organ indirectly causes other organs to become dysfunctional, thereby causing premature multiple-organ failure. To overcome this problem, anample diversity of algorithmic models has been defined by researchers over the years. These models need improved disease progression analysis and scalability. Inefficient system design causes clinical mistakes and reduces multi-organ analysis efficacy. This study presents an enhanced temporal analysis approach to determine illness development utilizing multiparametric analysis for a high-efficiency multi-organ analytical model. The machine learning algorithm is trained with temporal ECG, EEG, and blood records data. This data is used for building an augmented deep learning stack, which assists in evaluating the patient's current health condition and estimating progressive diseases that might affect other organs. The novelty & critical idea of the proposed model is that it utilizes an augmented combination of VGGNet-19, InceptionNet, and XceptionNet models to evaluate different diseases. Depending upon their disease-specific accuracy, these models are trained using other datasets for maximum performance. For instance, VGGNet-19 & models showcase the highest accuracy for EEG datasets. On the contrary, it has been shown that InceptionNet models exhibit superior performance when applied to electrocardiogram (ECG) signals, whereas XceptionNet is commonly employed for the classification of blood reports owing to its great efficacy in analysing one-dimensional data. These models are integrated to assess illnesses by utilizing immediate readings with a high level of efficiency. Upon collection of successively estimated readings, the model can predict disease progression with over 90% accuracy. This consistent performance across different disease types makes the system applicable for clinical usage. Furthermore, the proposed model is tested on few another dataset, and its performance and efficiency were compared with recent deep learning models, with an average 14% improvement in accuracy, 16% improvement in precision, 12% improvement in recall, and a 6% increase in computational delay was observed. While the model requires a significant training delay, the evaluation delay is moderate due to the disease-specific model design, making the system applicable for real-time clinical usage.

Keywords: *Progressive, Disease, VGGNet, InceptionNet, XceptionNet, Augmentation Learning*

1. Introduction

The utilization and advancement of diverse data mining techniques in various practical domains, including industry, healthcare, and bioscience, have prompted their adoption in machine learning environments. These approaches are employed to extract significant insights from specific datasets within healthcare communities, biomedical categories, and related fields. The correct analysis of medical databases provides advantages in the early prediction of illness, the treatment of patients, and the provision of community services. The methodologies of machine learning have been effectively used in a wide variety of applications, one of which is the prediction of diseases. When a disease manifests within an individual, the human body will initiate a response by exhibiting various indicators such as pain, alterations in physiological parameters, deviations in behavior, and a diverse range of other modifications. The assessment of these qualities is commonly employed to delineate a particular type of sickness. For instance, the detection of diabetes relies on the analysis of fluctuations in blood glucose levels, while the identification of heart-related conditions is facilitated by the examination of alterations in electrocardiogram (ECG) signals. Both of these procedures are employed to diagnose medical diseases. However, it is important to note that various conditions often exhibit a strong association, and the development of a cross-parametric model might potentially enhance the accuracy of diagnoses. Due to the detrimental impact of prolonged glucose consumption on bodily functions and immune response, there is potential for the integration of cancer detection methods with glucose analysis to examine the influence of fluctuations in blood sugar levels. The body's susceptibility to cancer is heightened due to a reduction in red blood cells and

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compromised immune function. Numerous instances of cross-parameter illness detection have been investigated throughout the course of time. The present study presents a methodology for doing a comprehensive cross-analysis on diabetes, cardiovascular disease, and cancer. The initial step involves examining a range of interrelated parameter correlations across various situations. Subsequently, by using these interconnections of cross-body parameters, the effectiveness of a network of neural networks in the classification of diseases is evaluated. In order to ascertain the presence of illnesses within the human body, that is important to assess evidence that is pertinent to the given circumstances.

The detection of diseases through the analysis of scans, test results, and other data sources is a complex work that encompasses several domains. This task necessitates the development of effective architectures for signal processing and image processing. These architectural designs incorporate several components such as signal pre-processing, segmentation, selection, and extraction of features, classification, and also post-processing. Furthermore, the feature extraction, selection, and classification performance of convolutional neural networks (CNN) architectures is notably high, owing to their intricate design. However, the result of the model is constrained to the training and validation data that were utilized for its development. Moreover, post-processing models encompass a wide range of studies due to the numerous potentialities and inferences that may be derived from inter-parameter correlation. Temporal investigation of electrocardiogram (ECG) data can be utilized to estimate the progression of cardiac disorders such as myopathy. The extended duration of this condition has a direct effect on pulmonary function, leading to the development of disorders such as chronic obstructive pulmonary disease (COPD) as a result of inflammatory processes. Hence, there exists a necessity for doing temporal cross-disease analysis, as it may contribute to the enhancement of diagnostic accuracy for various medical disorders through the development of deep-inference model designs.

Researchers have built a diverse range of models to serve this objective [1,2,3,4]. The subsequent portion of this work presents an examination of these models, encompassing their intricacies, benefits, constraints, and potential avenues for further research. The survey findings indicate a need for further study in the area of inferred progressive illness categorization. This limitation hinders the practicality of present methods for immediate clinical use. Section 3 of this study suggests the development of an enhanced temporal analysis model for the purpose of identifying illness progression via the use of multi-parametric analysis. The motivation for this proposal is from the aforementioned finding. This section presents a novel approach to designing an improved technique for analysing materials in order to assess the course of diseases. The proposed method utilizes multi-parametric analysis and employs a high-efficiency multi-organ evaluation model. The model is trained utilizing temporal data from many sources, including the patient undergoing electrocardiogram (ECG), blood reports, electroencephalogram (EEG), and social media updates. The provided data is used to develop an advanced deep-learning framework that assists in evaluating the present health condition of the patient and predicting the advancement of illnesses that may impact further bodily organs. The originality of the suggested model is in its evaluation of diverse situations through the utilization of XceptionNet, VGGNet-19, and InceptionNet architectures. To achieve optimal performance, these models undergo training using several datasets that are selected depending on their specific to disease accuracy. The VGGNet-19 model has been seen to exhibit the best level of accuracy when applied to electroencephalogram (EEG) datasets. In contrast, InceptionNet models demonstrate superior performance in evaluation of electrocardiogram (ECG), whereas XceptionNet is employed for the classification of blood reports owing to its exceptional performance in handling single-dimensional data. These algorithms are integrated to effectively estimate illnesses based on real-time readings. The proposed model employs many indicators, including electrocardiogram (ECG), electroencephalogram (EEG), blood reports, and social media activity, predict the health status and progression in diseases of patients. Additionally, this model has the capability to forecast future diseases based on the course of existing diseases. The assessment of this model is conducted in section 4, where a comparison is made between different situations and the performance of progression evaluation using diverse methodologies. In conclusion, this paper presents noteworthy insights into the suggested model and offers recommendations for expanding its scalability and enhancing its performance.

2. Related Work

Researchers suggest numerous methodologies for multiple parametric studies of human health. For example, [5-6] proposes Optimal Wavelet Transform for electroencephalogram (EEG) and Ballistic-Cardiogram Artifact Reduction (BAR) , electrocardiogram (ECG), and other signal categorization with denoising. Similarly, in [7], deep learning models are used to assess the prediction of sleep bruxism utilising electromyography (EMG), power spectrum density (PSD), electrocardiogram (ECG), electroencephalogram (EEG). This model is used for sleep analysis; however, it may be expanded to analyse numerous parameters using dataset augmentation. Deep learning models explained in [8, 9, 10], the papers explains fuzzy feature with, multiple view CNN (MVCNN) and data decomposition, implemented for diabetes prediction from

EEG signals. Such models also gives advantage for enhancing classification efficiency. The research based on transfer learning improves the performance of CNN models, as reported in [11-13], where electroencephalogram (EEG) signals is implemented for various purposes. The model such bidirectional Gated recurrent units (BiGRU) [14] the approaches for implementation of CNN model also shown to be more accurate as compared to linear classification models thus to be employed in clinical investigation. The research with wavelet transform using various CNN architectures (MTCNN) [15], fuzzy classification techniques [16] along with other models are implemented with multilevel weighted feature fusion using CNN [17], along with quality-aware classification methods [18] for disease predictions. To improve the efficiency of classification process, models can be used to remove redundant feature extraction steps. Other description and classification methods, such as those presented in [19-21], which employ GRU-based RNN, Hjorth descriptors, MobileNet, Inception-v3, Xception, and NasNetLarge, might be used to further improve its efficiency. This would be a step in the right direction. Due to a single kind of illness detection and intensity identification, a combination of these models is responsible for high-efficiency classifications while preserving minimal latency. [22-24] describe similar deep learning models for numerous human body characteristics, including LSTM, deep transfer learning, and lightweight deep neural network architectures. Such model have capability to reduce error rate and enhance accuracy during illness prediction by lowering feature variance during classification.

Researchers describe models of deep learning such as ensemble classifier used for implementation of electrocardiogram (ECG) signals [25], also the efficient model such as LSTM model have quantized architecture which is be used to detect numerous organ issues [26], Thalassemia identification is done with the RBC levels by using ensemble classification [27], and for classification of the blood cell CNN with transfer learning is implemented [28]. But such models are accurate for single kind of blood report but does not perform efficiently when applied to analysis several blood issues. As a result, clinical uses for these models are restricted when tried to detect several issues at a time in model. Similarly, [29-31]'s work is very valuable for RBC-based illness diagnosis, blood pressure-based disease categorization, and postural behavior analysis. It is proposed to integrate these models to measure their performance for combined illness categorization and progression detection. Another area of investigation is the categorization of health conditions based on eating habits. This aids in assessing patients' eating patterns in order to diagnose problems such as obesity, lethargy, and so on. In the research referred to [32-34], the authors offer many models for the analysis of egocentric photo streams, an online learning neural network (OLNN) in the detection of human eating activities (HEAR), and an assessment of the healthy eating index through the aggregation of mobile-based data. Similar models are explored in [35-37], where deep learning models are proposed to be used to analyze various illness kinds. To evaluate the influence of further measurements on the complete human body, a mixture of these models must be used. In response to this fact, the section that follows offers an expanded temporal analysis model for diagnosing illness development utilizing multi-parametric analysis.

Several models exist for detecting human body disorders from various data sources, as was discovered in the review employing multi-parametric analysis to identify disease development. Results from a comparison of these models show that convolutional neural network (CNN) based approaches perform the best. These methods included gated recurrent unit (GRU) based long-short-term-memory (LSTM), recurrent neural networks (RNN), and Q-learning models. Further work has to be done to make these models scalable so that they can analyze illness progression accurately. As a consequence, clinical mistakes arise and the efficacy of multi-organ analysis suffers due to inefficient system design. Models such as GoogLeNet, VGGNet-16, Binary RNN, AlexNet, continuous non-linear RNN, ResNet-50, short-term-memory (STM), InceptionNet, Yolo, XceptionNet are constructed utilizing common CNN architectures. Nevertheless, enhanced CNN-based architectures stand out as the most efficient of these models due to their ability to aid in the interpolation of input datasets in order to improve classification performance. Given these findings, this section proposes a multiparametric analysis-based augmented temporal analysis method for tracking the development of a disease. Input datasets such as electrocardiogram (ECG), electroencephalogram (EEG), and blood reports data are shown in Figure 1 as part of a model for the proposed system. The model as a whole is broken down into its constituent parts, which are each addressed in turn below. These sections as a guide while deploying the model in your system, either in part or in whole.

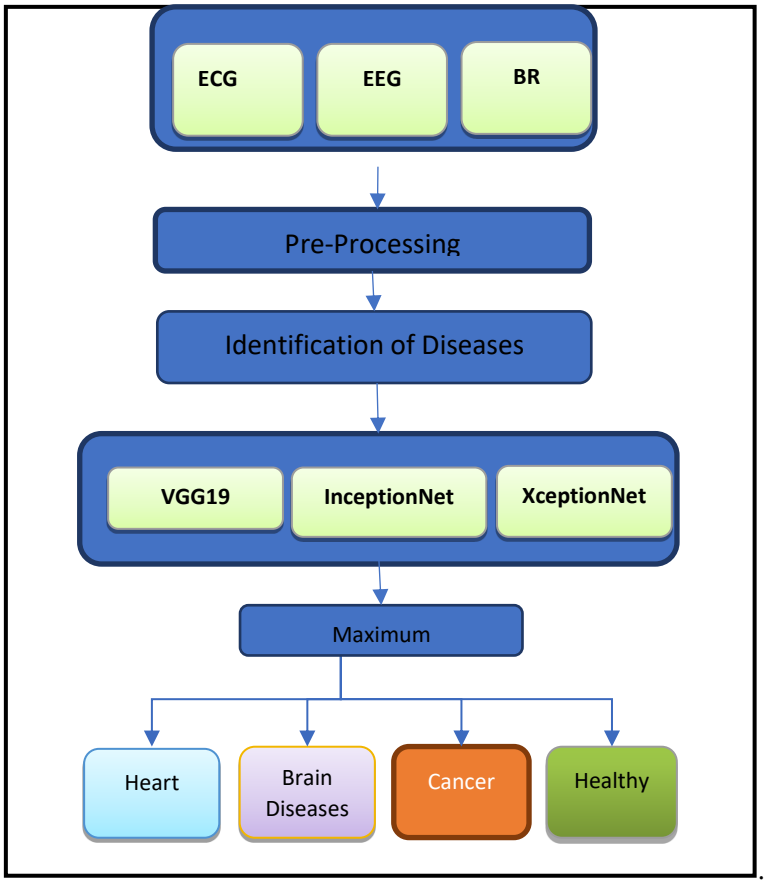

Fig 1. Model for the proposed system

3. Results and Discussions

3.1. Database

The evaluation of the proposed model encompasses various datasets, including the electroencephalogram (EEG) dataset sourced using the Siena Scalp electroencephalogram (EEG), electrocardiogram (ECG) dataset retrieved from the BIDMC Congestive Heart Failure database, and the blood report dataset derived from the NHANES Laboratory. The databases encompass a total of 11,200 items, each about distinct patient categories exhibiting diverse health problems.

3.2. Pre-Processing layer

Converting data from several sources into a standard format facilitates processing. When working with 2D data, CNN models perform better in terms of categorization. Hence, the model makes use of 2D representations of both the electrocardiogram (ECG) and electroencephalogram (EEG) data. But first, an equation 1–based quantization technique is applied to every data sample.

$$Q_{data_i} = round\left[255 \times \frac{(Data_i - \min(Data))}{\max(Data) - \min(Data)}\right] \ldots (1)$$

Where Q_{data_i} represents $the\ i^{th}$ is an instance of quantization input data. The use of the number 255 is employed to transform the data frame into an 8-bit scale, hence enhancing the performance of categorization. Following the algorithm 1 process of quantization, the datasets of the electroencephalogram, or EEG, and electrocardiogram (ECG) are transformed into two-dimensional vectors.

Algorithm-1:Convert the dataset into a 2D vector

1. State 2D empty vector with size 256x256, define col=0, row=0.
2. In all input signal, save the input signal in a row, col position
3. For columns, col=col+1
4. if col=128, then row=row+1, col=0
5. if row=128, then store 2D vector in dataset, name it value of detected disease, continue the process for the next signal
6. For blood reports, convert the data into 1D data.

This approach yields several 2D vectors corresponding to every electrocardiogram (ECG) and electroencephalogram (EEG) data. In a similar manner, one-dimensional signals are obtained for the datasets pertaining to blood reports and dietary habits. Blood reports often include measurements of many parameters such as haemoglobin levels and blood pressure, levels of glucose, vitamin B12 levels, vitamin D3 levels, kidney function test results, liver function test results, blood gas levels, and other relevant indicators. Further pre-processing of the data may involve filtering, normalization, and feature extraction, depending on the problem's specific requirements and the data's characteristics.

3.3. Identification of Diseases

Algorithms 2, 3, and 4 illustrate the three classifiers we suggest merging: VGG19, InceptionNet, and XceptionNet. With a total of 19 layers, VGG19 is indeed a deep neural network with 16 convolutional layers as well as 3 fully connected layers. Frequently utilized in image classification problems, the model accepts as input a 224x224 picture with three colour channels (RGB), and produces a probability distribution more than a thousand classes. Deep convolutional layers define VGG19's architecture, and they are reinforced by max pooling layers that down sampled the feature maps. To do this, the input picture is passed through a series of convolutional layers, each of which is made up of a series of 3x3 filters with such a stride of 1 with padding of 1. The network's final, fully linked layers are responsible for mapping the input characteristics to the desired classes. Our raw data is then sent into VGG19 the general steps of VGG19 is as shown in algorithm 2, Exception, and inception for further processing. In the tensorflow2 code snippet example shown below, VGG19 is employed. Combining the findings from three different CNNs—VGG19, InceptionNet, and XceptionNet—improves accuracy and reduces variation in electroencephalogram (EEG) signals, electrocardiogram (ECG) signals, but only one (1D) blood report data, respectively. Using equation 2, the two models' output classes are merged based on the results of the tests performed on each model.

$$C_{out_{EEG}} = \left[A_{test_{VGG}} \times C_{out_{VGG}}\right] \ldots (2)$$

$A_{test_{VGG}}$represents the testing accuracy of VGGNet 19, while $C_{out_{VGG}}$ represents VGGNet output classes. ECG and blood records are classified using conventional Inception-Net and Xception-Net models. Equations 3 and 4 manage classifier outputs using similar fusion techniques. XceptionNet's operation is explained in the code below.

A distinct classification layer is assigned to each temporal group cluster. The selection of these layers is determined by the efficiency of individual CNN models, as measured by data-based input. During the assessment, it was noted that VGGNet-19 models demonstrate high accuracy in the context of InceptionNet, which is a well-recognized architecture of deep neural networks utilized for image classification applications. Here is a sample code using Keras library in Python to implement nceptionNet. This code defines an inception_module function that creates one block of the InceptionNet architecture.

Algorithm-2: VGG19 Model

The VGG19 architecture is composed of a total of 19 layers, which encompass 16 layers of convolution, 3 layers that are fully connected, and a max pooling operation.

1. To mathematically model VGG19. Let's call this function f. f(input) = output_vector
2. The function f consists of several layers that perform different operations on the input image.
3. The initial layer of the VGG19 architecture consists of a convolutional layer, which employs a collection of filters to process the input picture and extract relevant characteristics, say as layer L1. The output of L1 is a set of feature maps. f(input) = L1(input)
4. The subsequent layer in VGG19 consists of max pooling layer, which serves to decrease spatial dimension of feature maps. Let's call this layer L2. f(input) = L2(L1(input))
5. Fully connected layer VGG19 take outcome of the convolutional layers and produce a probability

The create_inception_net function then uses this block to create a full InceptionNet model with the specified number of classes also shown in equation3.

C_(out_BR)=[A_(test_Inception)×C_(out_Inception)]…(3)

$$C_{out_{ECG}} = \left[A_{test_{Xception}} \times C_{out_{Xception}}\right] \dots (4)$$

The XceptionNet architecture is comprised of 36 convolutional layers including 3 fully linked layers, resulting in a total of more than 20 million parameters. Experimental research has demonstrated that this approach attains exemplary performance on many computer vision research, encompassing picture categorisation, object identification, and also semantic segmentation. The output the XceptionNet using ECG can be shown in equation4.

The electroencephalogram (EEG) classification yields results about certain categories of brain disorders, encompassing diseases such as Parkinson's, Alzheimer's, epilepsy, and Parkinson's. The categorization of electrocardiogram (ECG) findings in heart disease categories, such as cardiac arrhythmia coronary artery disease (CAD), as well as deep vein thrombosis, is accompanied by a categorization of blood reports, which yields outputs related to cancer illnesses. Convolutional neural networks (CNNs) are advantageous in the categorization of electrocardiogram (ECG), electroencephalographic (EEG), and blood report data due to their ability to process a substantial volume of input samples. This characteristic enables these networks to effectively analyze extensive characteristics, hence facilitating accurate classification. The electroencephalogram (EEG), and electrocardiogram (ECG), with blood reports were provided to the progressive analysis and correlation engine for further examination. The subsequent part describes the design of the engine, which facilitates the temporal evaluation of the specified user health classes.

3.4. Progressive Evaluation & Correlation Mechanism

As mentioned in section 3.2, in the health category classification process execution occurs for each individual data cluster. As a result, an assessment is conducted to determine the illness type and severity for each user. This aids in the assessment of temporal health issues for every individual user. The assessment of illness development is contingent upon the temporal conditions associated with each specific disease type. Such progression (P_{D_p}) is calculated for each patient as shown in equation 5.

$$P_{D_p} = \frac{\left(\sum_{i=1}^{N-1} S_{D_i} - S_{D_{i+1}}\right)}{N-1} + S_{D_N} \dots (5)$$

S_D represents the severity of disease D, while N represents temporal assessments conducted for the specific disease. Progression value denotes the rate at which the illness exhibits growth or advancement over a certain period. The previously mentioned value is assessed for each neurological disorder, cardiovascular condition, and malignant neoplasm. Following the assessment of these disorders, they are subjected to analysis by a correlation engine, wherein the course of each condition is evaluated against established clinical guidelines. The guidelines encompass the influence of the advancement of heart disease and kidney disease on pulmonary function, as well as the effects of brain disease and heart diseases on blood pressure regulation, among other factors. In order to assess the link between the standard clinical recommendations and the progression level of each illness, equation 6 is employed for comparison purposes.

$$Corr_{D_B} = \frac{\sum_{i=1}^{N} P_{D_i} - CR_{D_B}}{\sqrt{\sum_{i=1}^{N} (P_{D_i} - CR_{D_B})^2}} \dots (6)$$

CR_{D_B} indicate clinical reference for disease D on the body structure B, while $Corr_{D_B}$ signifies the current patient's correlation among disease D and body part B. This correlation value estimates the chance of illness D occurring on the individual's body part B can be utilized to make a further clinical diagnosis. Therefore, this method may be employed by medical professionals to assess the impact of various illnesses on individual organs and their subsequent development. The outcomes of this progression identification are seen across a diverse range of patients and assessed on the basis of accuracy, precision, memory, and computational latency.

Algorithm-3: InceptionNet

Consider input image with x and the output each layer as h(i), where i is the layer number. Output of this layer can be represented as: h(1) = f(W(1)*x + b(1)) where f is the activation function, W(1) is the set of convolutional filters, and b(1) is the bias term.

The second layer of InceptionNet consists of numerous filters with diverse sizes (1x1, 3x3, 5x5). The output of each filter can be represented as: h(2,1) = f(W(2,1)*x + b(2,1)), h(2,2) = f(W(2,2)*x + b(2,2)), h(2,3) = f(W(2,3)*x + b(2,3)) where W(2,i) and b(2,i) are the filters and bias terms for the i-th filter, correspondingly. The outcome of the second layer is obtained by concatenating the outputs of each filter: h(2) = concatenate(h(2,1), h(2,2), h(2,3)).

The third layer of InceptionNet is another set of filters with different sizes, followed by a concatenation operation, comparable to the second layer. The outcome of this can be represented as:
h(3,1) = f(W(3,1)*h(2) + b(3,1)), h(3,2) = f(W(3,2)*h(2) + b(3,2))
h(3,3) = f(W(3,3)*h(2) + b(3,3)), h(3) = concatenate(h(3,1), h(3,2), h(3,3))

The fourth layer is a pooling layer that decreases the size of the output by taking the maximum value within a small window of the output. The output of the fourth layer represented in: h(4) = maxpool(h(3))

The fifth layer is a fully connected layer that takes the outcome of the previous layer and produces a set of features for classification. The outcome of the fifth layer indicated as: h(5) = f(W(5)*h(4) + b(5))
Finally, the last layer is another fully connected layer which produces the final result. The output of last layer indicated as: h(6) = softmax(W(6)*h(5) + b(6)) where softmax is the activation function used for multi-class classification tasks

Algorithm-4: XceptionNet

XceptionNet model can be represented as a series of depthwise separable convolutional layers sequence by a set of fully connected layers for classification. Input image indicated as x and output of each layer as h(i), where i is the layer number.

The initial layer of XceptionNet is standard convolutional layer with a set of filters with size 3x3. The output of this layer can be represented as: h (1) = f(W (1)*x + b(1)), where f is the activation function, W(1) is the set of convolutional filters, and b(1) is the bias term.

The second layer XceptionNet is a depthwise separable convolutional layer

h (2) = f(W(2,2) *f(W(2,1)*x) + b(2)), where W(2,1) and W(2,2) are the sets of filters for the depthwise and pointwise convolutions, respectively, and b(2) is the bias term.

The 3rd layer in XceptionNet is a depthwise differentiated convolutional layer like the second. Layer output can be represented as: h(3) = f(W(3,2)*f(W(3,1)*h(2)) + b(3))

The fourth layer output of each residual module can be represented as:

h(4,i) = f(W(4,i,2)f(W(4,i,1)(h(4,i-1) + h(4,i-2))) + b(4,i)), where W(4,i,1) and W(4,i,2) are the sets of filters for the depthwise and pointwise convolutions, respectively, and b(4,i) is the bias term.

The final layer of XceptionNet is a set of fully connected layers that take the output of the previous layer and produce a set of features for classification, h(5) = f(W(5)*h(4,N) + b(5)), where N is number of residual modules in model, W(5) is the set of weights for the fully connected layers, and b(5) is the bias term.

Finally, the last layer is another fully connected layer that produces the final classification result. The output of the last layer is indicated as: h (6) = softmax(W(6)*h(5) + b(6)), where softmax is the activation function used for multi-class classification tasks.

4. Result

The model proposed is assessed using various datasets, including the electroencephalogram (EEG) dataset obtained from the Siena Scalp EEG database, which is accessible on Kaggle. Additionally, the electrocardiogram (ECG) dataset from the BIDMC heart failure congestive database and the blood report dataset from the NHANES Laboratory are also utilized for evaluation purposes. The databases encompass a total of 11,200 entries, each representing distinct patient types exhibiting diverse health problems. The data is partitioned in 70:30 ratio for training and testing. The testing set is subjected to parametric analysis, wherein the accuracy (A), recall (R), precision (P), and delay values are calculated. This analysis is conducted subsequent to training the model using the provided training sets. The Figure2 indicate the loss and accuracy of the model, for few epoch such as 3-4 epoch, as the epoch increases the accuracy can be stabilize for the model. MVCNN [10], PSD [7], MTCNN [15], as well as the proposed model are all calculated for the above-mentioned variables of accuracy, recall, precision, and latency. The parameters are tested in a variety of scenarios to help estimate how they would behave in real-world situations. Table2 displays, for example, the accuracies (A) for a variety of test set sizes (TSS). According to Figure 3, we evaluated the model by raising the tss, and the model's accuracy remained steady and

improved upon relative to that predicted by the baseline model.

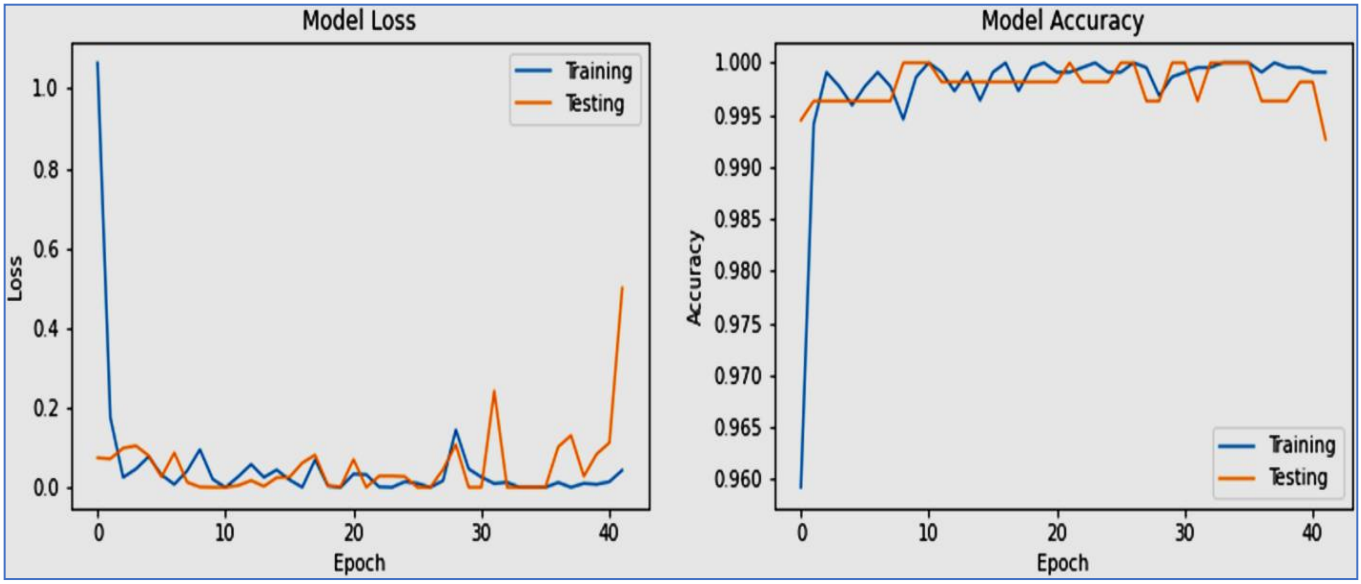

Fig 2: Loss and Accuracy for the proposed model

Table 2: Accuracy Comparison

TSS	PSD [7]	MV [10]	MT [15]	Proposed Model.
100	77.84	61.29	63.27	96.23
200	78.57	61.86	63.86	97.12
300	78.72	61.98	63.99	97.32
400	79.05	62.24	64.25	97.71
500	79.21	62.36	64.38	97.91
750	79.30	62.43	64.45	98.02
1000	79.30	62.43	64.45	98.02
1200	79.31	62.44	64.46	98.03
1400	79.31	62.45	64.47	98.04
1600	79.31	62.45	64.47	98.04
1800	79.32	62.45	64.47	98.05
2000	79.32	62.45	64.47	98.05
2200	79.32	62.45	64.47	98.05
2400	79.33	62.46	64.48	98.06
2600	79.33	62.46	64.48	98.06
2800	79.66	62.72	64.74	98.46
3000	79.72	62.77	64.80	98.55
3100	79.79	62.83	64.86	98.64
3200	79.86	62.88	64.91	98.72
3300	79.93	62.93	64.97	98.81

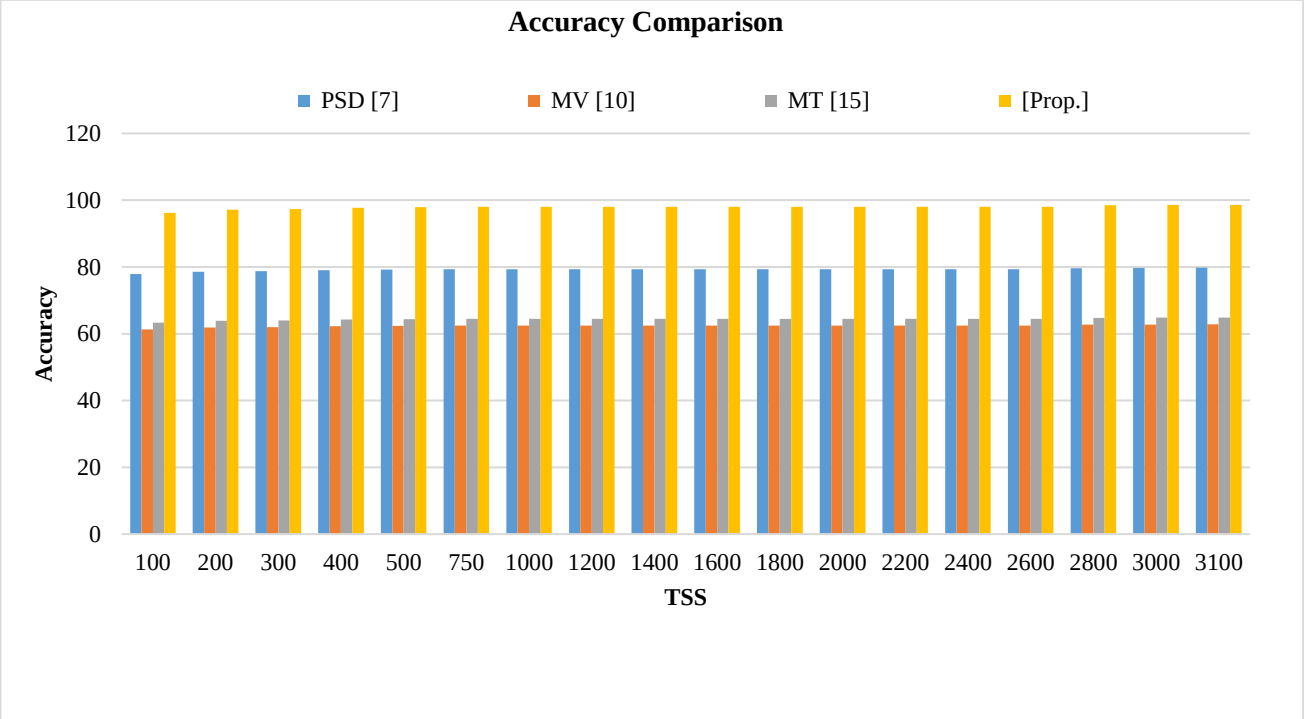

Fig 3: Accuracy Comparison Graph

Figure4 displays the accuracy results, which reveal that the proposed system is 26% more accurate in its progression prediction than MVCNN [10], and 19% more accurate than MTCNN [15]. Table3 below shows similar findings for precision (P) values.

Table 3. Precision Comparison

TSS	PSD [7]	MV[10]	MT[15]	Proposed Model
100	52.39	48.44	40.62	64.76
200	52.88	48.89	41.00	65.36
300	52.98	48.99	41.09	65.50
400	53.20	49.19	41.25	65.76
500	53.31	49.29	41.33	65.89
750	53.37	49.34	41.38	65.96
1000	53.37	49.34	41.38	65.96
1200	53.37	49.35	41.38	65.97
1400	53.38	49.35	41.38	65.98
1600	53.38	49.35	41.38	65.98
1800	53.38	49.36	41.39	65.98
2000	53.38	49.36	41.39	65.98
2200	53.38	49.36	41.39	65.98
2400	53.39	49.36	41.39	65.99
2600	53.39	49.36	41.39	65.99
2800	53.61	49.57	41.56	66.27
3000	53.66	49.61	41.60	66.32
3100	53.70	49.65	41.64	66.38

3200	53.75	49.70	41.67	66.44
3300	53.80	49.74	41.71	66.50

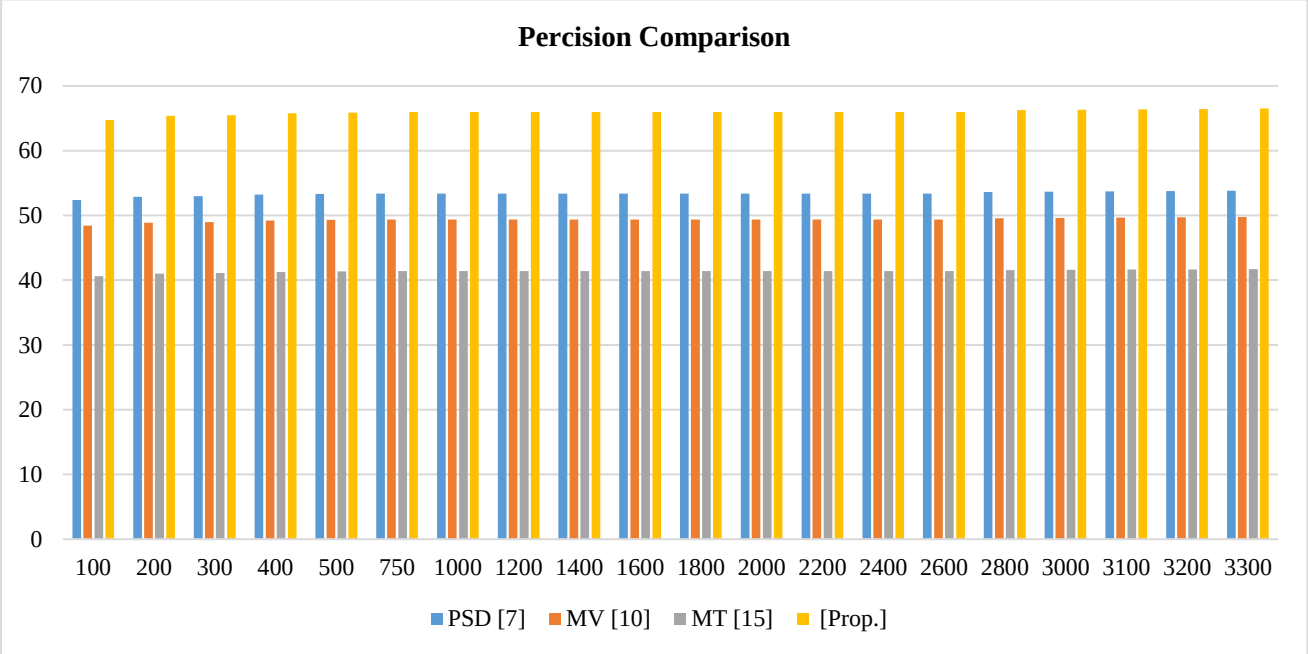

Fig 4: Precision Comparison Graph

As can be shown in Figure 4, the suggested model has a precision that is 12 percentage points higher than PSD [7], 16 percentage points higher than MVCNN [10], and 25 percentage points higher than MTCNN [15]. This makes it suitable for high-precision clinical applications. You may see the same patterns in Table 4, which displays recall (R) values.

Figure 5 shows that the suggested model is 14% more effective than PSD [7], 16% more effective than MVCNN [10], and 24% more effective than MTCNN [15] in terms of recall, making it suitable for high recall clinical applications. Delay in examination results in similar conclusions, as seen in Table 5.

Table 4. Recall Comparison

TSS	PSD [7]	MV[10]	MT[15]	Proposed Model
100	51.73	47.85	40.12	63.96
200	52.23	48.27	40.47	64.57
300	52.33	48.37	40.58	64.66
400	52.54	48.56	40.75	64.95
500	52.65	48.66	40.83	65.09
750	52.71	48.75	40.86	65.15
1000	52.71	48.74	40.86	65.15
1200	52.72	48.75	40.86	65.16
1400	52.72	48.75	40.86	65.17
1600	52.72	48.75	40.86	65.17
1800	52.73	48.76	40.89	65.17
2000	52.74	48.76	40.89	65.17
2200	52.73	48.76	40.89	65.17
2400	52.74	48.76	40.89	65.18

2600	52.73	48.76	40.89	65.18
2800	52.94	48.95	41.04	65.45
3000	52.99	48.99	41.09	65.51
3100	53.04	49.04	41.13	65.56
3200	53.08	49.08	41.15	65.61
3300	53.13	49.12	41.19	65.67

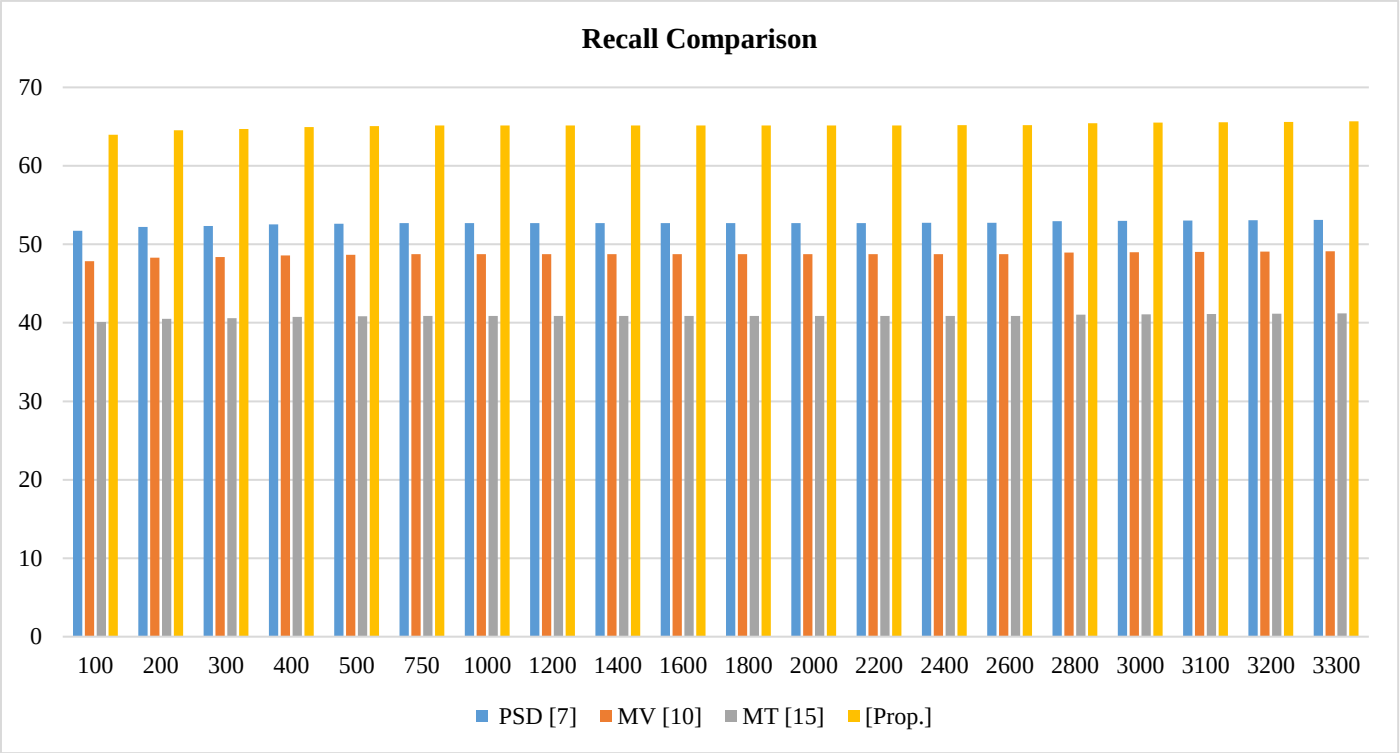

Fig 5: Recall Comparison Graph

Table 5. Delay Comparison

TSS	PSD [7]	MV [10]	MT [15]	Proposed Model
100	0.50	0.48	0.41	0.52
200	0.50	0.49	0.41	0.52
300	0.50	0.49	0.41	0.52
400	0.50	0.49	0.41	0.52
500	0.50	0.49	0.41	0.52
750	0.50	0.49	0.41	0.52
1000	0.51	0.50	0.42	0.52
1200	0.51	0.50	0.42	0.52
1400	0.51	0.50	0.42	0.52
1600	0.51	0.50	0.42	0.52
1800	0.51	0.50	0.42	0.52
2000	0.51	0.50	0.42	0.52
2200	0.51	0.50	0.42	0.52

2400	0.51	0.50	0.42	0.52
2600	0.52	0.51	0.43	0.53
2800	0.52	0.51	0.43	0.53
3000	0.52	0.51	0.43	0.53
3100	0.52	0.51	0.43	0.53
3200	0.52	0.51	0.43	0.53
3300	0.52	0.51	0.43	0.53

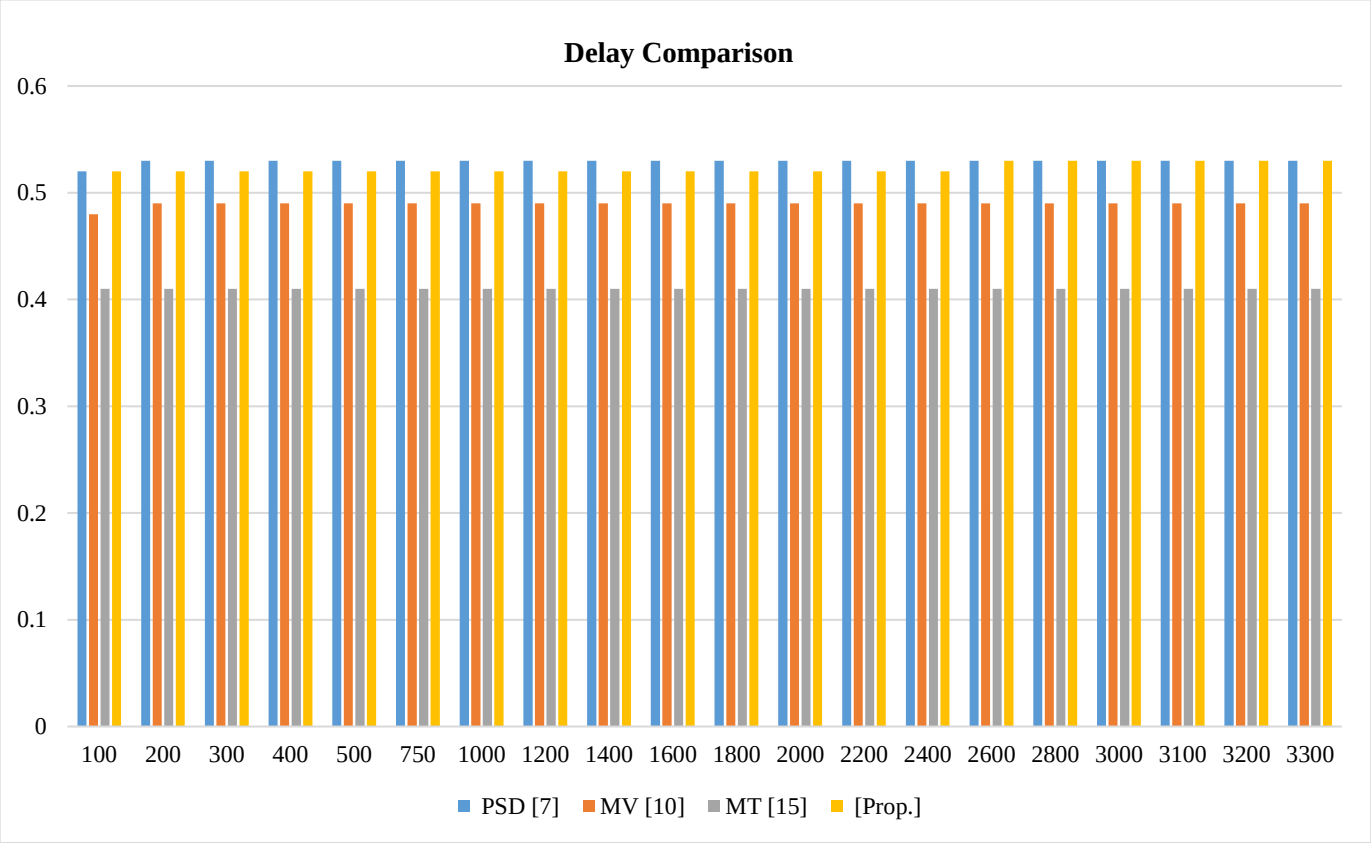

Fig 6: Delay Comparison

It is shown in Figure 6 that the suggested model is 10% slower than MVCNN [10], and 15% slower than MTCNN [15], due to model's usage of numerous training and evaluation phases, but it achieves the same performance as PSD [7] on the presented datasets. Due to the fact that the suggested model only requires a little additional amount of time for computation, it has been found useful in the medical field. It may be employed in situations requiring high precision, high accuracy, and high recall in real-time illness progression diagnosis.

5. Conclusion

Our proposed approach of augmented temporal analysis in illness progression identification utilizes a variety of characteristics to conduct the study. The parameters encompass many types of data, including the results of electroencephalogram (EEG) data, electrocardiogram (ECG) data, blood report facts, including diet information, all pertaining to individuals within the same category. Several different kinds of convolutional neural networks including linear classification models are utilized to classify each parameter. In terms of progression detection, Since classifiers are chosen based on their performance for different data sets, the recommended model is 19% more effective than PSD [7], 26% more accurate than MVCNN [10], but 24% more accurate than MTCNN [15]. Due to the delay in validation and training of this collection of classifiers, the proposed model is 10% slower than MVCNN [10] as well as 15% slow than MTCNN [15] but performs similarly to PSD [7] on the presented datasets. The suggested approach is still widely useful for a variety of clinical application situations, even after the delay has been increased. Q-learning, reinforcement learning, and enhanced deep-learning methods will allow researchers to gradually boost the anticipated model's performance in the future.

Additionally, redundancy elimination during categorisation and progression prediction using efficient feature selection techniques and their implementation on bigger dataset is required to lessen the suggested model's lag time.

Conflicts Of Interest

No conflict of interest

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