ТЕОРЕТИЧНІ ТА ПРИКЛАДНІ ПРОБЛЕМИ ІНТЕЛЕКТУАЛЬНИХ СИСТЕМ ПІДТРИМАННЯ ПРИЙНЯТТЯ РІШЕНЬ

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A CONCATENATION APPROACH-BASED DISEASE PREDICTION MODEL FOR SUSTAINABLE HEALTH CARE SYSTEM

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Abstract. In the present world, due to many factors like environmental changes, food styles, and living habits, human health is constantly affected by different diseases, which causes a huge amount of data to be managed in health care. Some diseases become life-threatening if they are not cured at the starting stage. Thus, it is a complex task for the healthcare system to design a well-trained disease prediction model for accurately identifying diseases. Deep learning models are the most widely used in disease prediction research, but their performance is inferior to conventional models. In order to overcome this issue, this work introduces the concatenation of Inception V3 and Xception deep learning convolutional neural network models. The proposed model extracts the main features and produces the prediction result more accurately than traditional predictive models. This work analyses the performance of the proposed model in terms of accuracy, precision, recall, and f1-score. It compares the proposed model to existing techniques such as Stacked Denoising Auto-Encoder (SDAE), Logistic Regression (LR), MLP, MLP with attention mechanism (MLP-A), Support Vector Machine (SVM), Multi Neural Network (MNN), and Hybrid Convolutional Neural Network (CNN)-Random Forest (RF).

Keywords: feature extraction, disease prediction, deep learning, Inception V3, Xception.

INTRODUCTION

The World Health Organization defines the health care system as the organization of people that is mainly constructed to maintain, restore, and monitor the health details of the public. The health system improves people's health by providing personal care given by hospitals and doctors. As a result, the primary goal of the healthcare system is to keep people healthy by detecting diseases early and treating them appropriately. Obtaining an efficient health care system provides benefits to maintaining people's health.

In recent years, the development in the medical field has cured patients of various diseases, but still, people are affected by some diseases due to their unpredictable nature, and it causes a severe life-threatening problem for people. The early prediction of those diseases saves the lives of many people. In the health care system, doctors who use computer-aided diagnoses to quickly treat different diseases need to be able to recognize, analyze, and classify data [5]. Thus, the healthcare system requires a well-trained disease predictive model to accurately predict diseases. Based on the predicted disease, doctors can provide the correct treatment and maintain the patient's health. So, this proposed work designs a system that can efficiently determine the condition to predict the disease based on the given input data about the patient's health.

The accuracy of the prediction result depends on the technique used in training the model, and the training depends on the sample data used for training. So, the sufficiency of the data sample is very important in training the model to get a better prediction result. In order to overcome the deficiency of sample data, the transfer learning technique is used in the deep learning model. Deep learning is a subtype of the machine learning approach. The rapid growth of deep learning in various fields proposes various representative techniques. Because of the better ability to learn the features of input data, deep learning has progressively replaced traditional machine learning techniques [6]. Deep learning has the capacity to determine features automatically from a given dataset for each specific application.

Transfer Learning is a kind of deep learning technique that uses pre-trained knowledge from the past to train the new model and deploy the trained features of a large dataset into a small dataset. Hence, using this pre-trained transfer learning technique in the deep learning model will reduce the time taken for the classification and prediction of disease [5]. However, the deep learning technique used by the conventional model has several advantages, but the accuracy performance is not better. So, the main motive of this research work is to improve prediction accuracy by modifying the state-of-the-art method by concatenating networks. This research work uses a concatenation of two different pretrained Convolutional Neural Network (CNN) models called Inception V3 and Xception.

The Inception model consists of multiple convolution filters of various sizes, and hence it can improve the adaptability of the network and extract more copious features of different scales. Simultaneously, by using the Network in Network model, the Inception model can significantly reduce the parameters of the model. Hence, the network can minimize the number of convolution filters as much as possible without losing model feature representation, thus minimizing the complexity of the model [3]. Whereas, in the exception model, the term "exception" refers to an extreme. The exception model takes the rule of the Inception model to an extreme, so it provides the added advantage of feature extraction in a pointwise manner also. The concatenation of two different models makes the proposed system stronger due to the capability of multiple feature extraction [16]. The concatenation model reduces the complexity and provides accurate prediction results based on the given input data, which could be sustainable and reliable for health care.

The research contribution is summarized as follows:

- Presented a sustainable healthcare prediction system using a concatenation of Inception V3 and Xception to predict the disease based on input data.
- Presented an intense experimental analysis to validate the performance of the proposed model using standard benchmark data.
- Presented a comparative analysis of the proposed model with existing prediction models such as MLP, Logistic regression (LR), stacked denoising autoencoder (SDAE) and hybrid Convolutional Neural Network (CNN) – Random Forest (RF) for performance validation.

The further discussions are arranged in the following order: Section two comprises a detailed literature review and section three presents the proposed model, experimental analysis and its results comparisons are presented in section four and the conclusion is presented in the last section.

RELATED WORKS

In this section, research related to the existing disease prediction system was enumerated. Various techniques, feature advantages, and disadvantages are reviewed for investigation, and finally, the limitations are discussed to structure the research motivation. The healthcare system is rapidly becoming a necessary tool for offering a well-rounded chance to meet the requirements of public health. Integration of healthcare with a recommended system to meet the needs of older and chronically diseased people was reported in [1]. Deep learning is a subfield of machine learning that is broadly used in healthcare systems for the classification, identification, and prediction of clinical data. A feature selection algorithm-based prediction model reported in [3] uses a combination of the FCMIM-SVM approach to detect heart disease. The features for the prediction model are obtained using a fast-conditional mutual information feature selection algorithm, and local learning procedures are followed to remove the redundant and irrelevant features. Machine learning techniques have been broadly adopted in various fields, particularly in medical diagnosis. Multi-feature extraction using Inception-V3 and Densnet-201 is achieved to predict the brain tumor [4].

A feature selection algorithm based on Chronic Obstructive Pulmonary Disease prediction is reported in [6] uses an instance-based and feature-based transfer learning Balanced Probability Distribution (BPD) and cross-domain feature filtering algorithm. Various feature selection algorithms like the AdaBoost algorithm, TCA algorithm, and Multi-Task Learning (MTL) algorithm are compared with the BPD algorithm, and the result demonstrates the superior prediction performance of the BPD algorithm. A comparative analysis of machine learning techniques for disease prediction reported in [8] employs decision trees, K-nearest neighbor, and logistic regression algorithms to predict kidney disease. From the findings, it demonstrates that the decision tree approach and logistic regression give better performance in predicting kidney disease. The article [5] investigates the viability and effectiveness of various machine learning algorithms like REP Tree, Random Tree, Linear Regression, M5P Tree, Naive Bayes, J48, and JRIP to predict cardiovascular disease. And from the analysis, the result demonstrates the superior prediction performance of the Random Tree approach.

The computer-aided screening method reported in [17] utilizes a comparison of 13 pre-trained CNN models like AlexNet, GoogleNet, VGG16, VGG19, etc. and three deep learning based classifiers, namely K-Nearest Neighbor, Support Vector Machine, and Naive Bayes for the analysis of Covid19 X-Ray and CT Scan images. The result demonstrates that VGG19 with SVM classifier provides superior performance to other methods. A novel Leaf GAN (Generative Adversarial Network) method reported in [19] utilizes a data augmentation method to identify disease-affected grape leaves. Initially, for training the GAN model, four types of grape leaf disease images are generated using an image generator model, and secondly, to identify original and duplicate images, an image discriminator is used. Finally, a deep regret gradient penalty method is employed for the stabilization of the GAN model.

A combination of convolutional neural networks with recursive neural networks reported in [20] utilizes an automatic prediction method for identifying and categorizing the different kinds of blood cells. Due to a better understanding of the features of blood cell images, accurate prediction and classification of blood cells are attained. The segmentation of breast masses in mammograms reported in [21] utilizes a comparison of various kinds of deep learning models for the segmentation and classification of breast lesions. The result demonstrates that the VGG19 and ResNet50V2 models perform better in the classification of breast lesions than other models.

The identification of the Citrus Disease Severity reported in [19] trains and compares six different types of deep learning models to predict the Citrus Disease Severity. From the analysis, it demonstrates that GAN-based data augmentation with the Inception V3 model provides superior performance. A disease prediction model reported in [2] utilizes a multi-stage model by the combination of co-clustering and supervised machine learning methods to predict the intravenous immunoglobulin resistance in Kawasaki disease. Initially, co-clustering is used to cluster the missing data pattern blocks. Secondly, the selection of data features is obtained by group lasso. Finally, the prediction of immunoglobulin resistance in a patient is obtained using an explainable boosting method. The machine learning approach reported in the article [7] utilizes a cloud-centric IoT system for the prediction of skin disease. This research mainly focuses on the evaluation of six deep learning models, namely VGG16, Inception, Xception, MobileNet, ResNet50, and DenseNet161. Based on this evaluation, the article created a two-phase classification process by the Targeted Ensemble Machine Classification Model (TEMCM).

Apart from the classification of images, CNN are widely used for the segmentation of images. The segmentation model reported in [20] utilized a CNN along with an optimization technique to segment the various types of land in the Amazon. A deep learning model reported in [8] utilizes the fused outputs of ResNet50, Xception, and DenseNet in the FC layer of the super learner model for classifying the type of vehicle. From the above survey, it is observed that the performance of the prediction model depends on the selection of a suitable learning algorithm and classifiers. Various types of machine learning algorithms are mostly used in the research. From the above literature review, it is observed that the Dense Net and ResNet perform well. However, in some of the articles, concatenation of convolutional neural network models was utilized, but the performance can be improved further using novel architectures. In order to extend the performance of the concatenation-based CNN prediction system, a SoftMax discriminator algorithm is used along with the concatenation model, and it is discussed in the following section.

PROPOSED WORK

The proposed predictive model contains a concatenation of Inception V3 and Xception CNN (Fig. 1). The proposed work consists of three stages. The first stage involves Normalizing of the given medical input data. The second stage involves features extraction from the input-data using concatenation approach. The third stage involves the prediction of output using soft max discriminant classifier.

Data Normalizing Stage. This stage starts from the collection of medical datasets. Since the non-standardized input data's take more time for learning process, the data in the dataset are subjected to Normalizing procedure. Based on the type of input data standardization will be applied to every input data to have the same dimension/size.

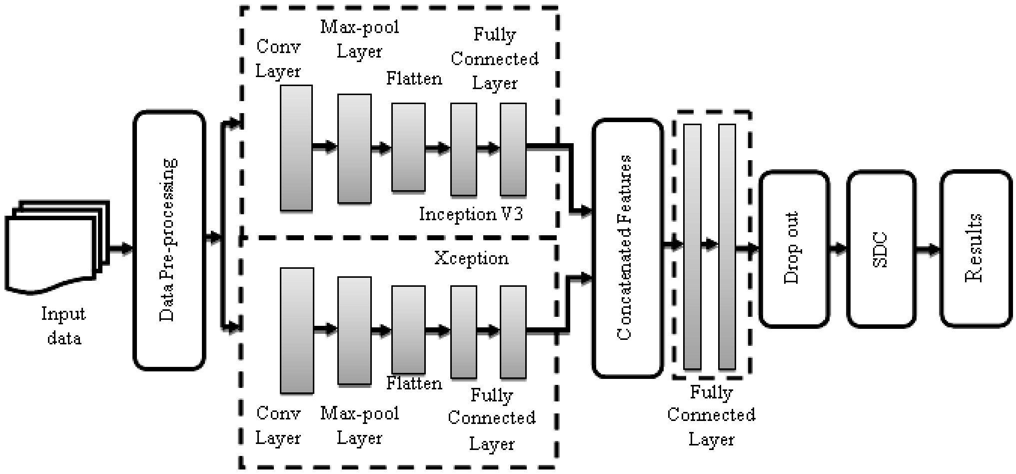

Fig. 1. Architecture of Proposed Concatenation Model

Feature Extraction from the Concatenation Model. Feature extraction is an essential step to be done before predicting the output, which is used to determine knowledge from datasets and it mainly focus on the selection of representative features from the given dataset, which will make the classifier to easily diffirentiate between the various classes. Additionally, it also provide benefit by reducing the computational time for training the classifier. A well-organized feature extraction method will improve the accuracy of predicted output. So, in this work, for attaining better feature extraction parallel deep feature extraction technique based on transfer learning method is applied to the concatenation of Inception V3 and Xception CNN models. The Normalized input data is given to the Xception and Inception V3 CNN model for feature extraction. To improve the quality of resultant feature map, the feature extracted from the two models are combined. Xception model convolutes the input data by both depth wise and pointwise manner (Fig. 2) and Inception model convolutes the input data by depth wise manner (Fig. 3).

Prediction of output using Soft-max Discriminant Classifier (SDC). The correct prediction of the given input data is done by the process of classification. The task of the classifier is to approximate a feature map function from input data to discrete output data. The important function of SDC is to identify the particular class to which the testing data belongs to. This can be done by using the calculation of weighing distance between the test data and train data. In the proposed work, the SDC is used as a binary classifier since it needs only two classes, where class 1 represents abnormal status and the class 2 represents the normal status. The following Figs. 2 and 3 show the architecture of Inception V3 Model and Xception model respectively.

Consider the input medical dataset $D=\{D_1,D_2,\dots,D_n\}$. The normalization of the input data is given by

$$f(D)=x+y\frac{D-\min(D_i)}{\max(D_i)-\min(D_i)},$$

where D_i defines the input medical dataset of D, x and y represents the constant of normalizer.This standardized input datas are further given as input to the training and testing in the model. The standardized input data from the given medical dataset is given as input to both the Xception and Inception V3 model. The feature map expression of g_1 from the pre-trained Inception V3 model is given

$$q_1(i) = r_1(c_1 = c_{1i} \mid g_1(v_1, b_1)).$$

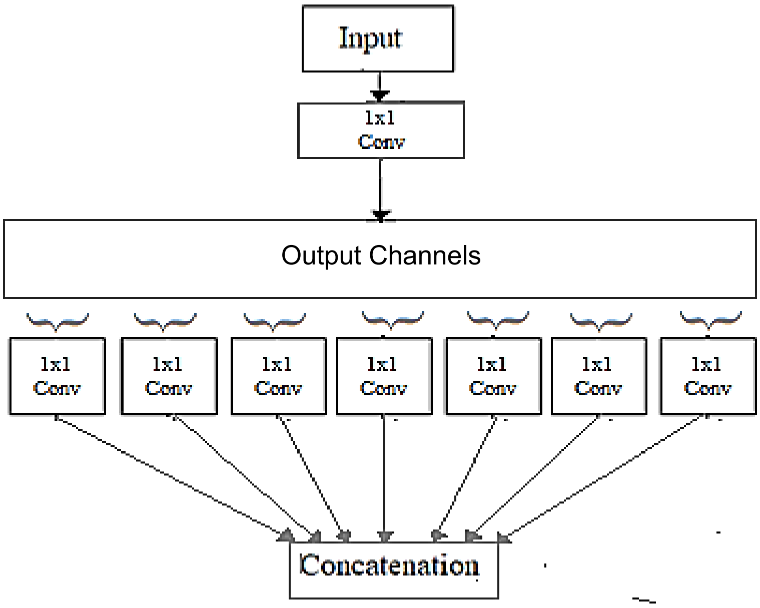

Fig. 2. Architecture of Xception

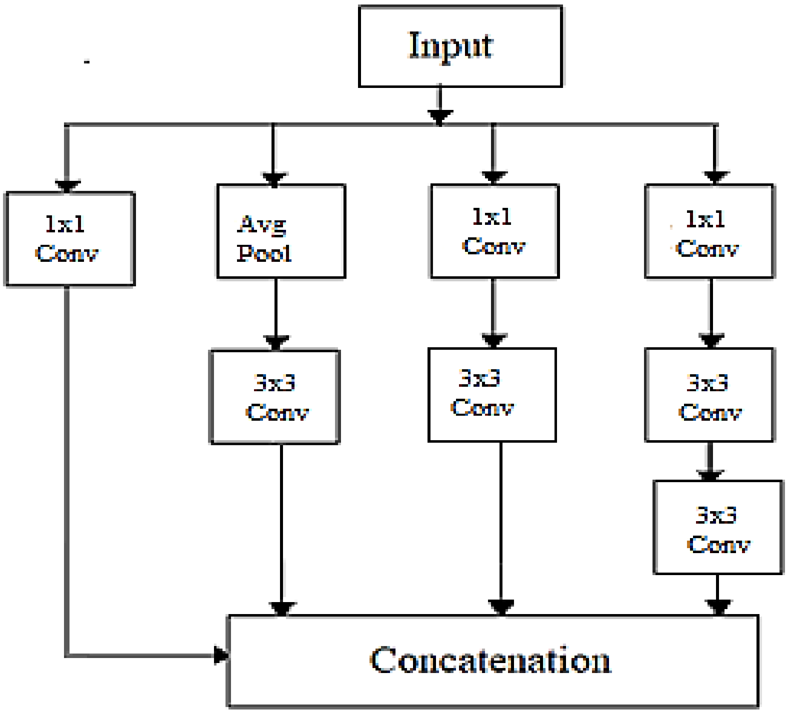

Fig. 3. Architecture of Inception V3

The feature map expression of g_2 from the pre-trained Xception model is given by

$$q_2(i) = r_2(c_2 = c_{2i} \mid g_2(v_2, b_2)),$$

where v_1 and v_2 are the weight vector and b_1 and b_2 are the bias vector of the Inception V3 and Xception model. The final feature map expression of G from the concatenation model is given by

$$Q(i) = R(C = c_i \mid G;(V, B)),$$

where $Q = q_1 + q_2$, $R = r_1 + r_2$, $C = c_1 + c_2$, $G = g_1 + g_2$, $V = v_1 + v_2$ and B=$B = b_1 + b_2$. The final feature map output obtained from the concatenation network is given as input to the FC layer of the proposed mode ,which flattens the input into a fixed length vector form. Next, the output of FC layer is given as input to the drop out layer which is used for regularizing the data by avoiding overfitting in the network. Finally, the output "*s*" from drop out layer is given to the SDC for the classification of data.

Training and Testing of Data's using SDC. Consider the training data set be $S = \{S_1, S_2, S_3, \ldots, S_m\} \in K^{e \times f}$ is determined from the *m* distinct classes:

$S_m = \{S_1^m, S_2^m, S_3^m, \ldots, S_{f_m}^m\} \in K^{e \times f_m}$ represents totally f_m data from the m^{th} class, where $\sum_{i=1}^{m} f_i = f$.

Consider the test data from the drop out layer as as $s \in K^{e \times 1}$ For representing the test data "*m*" class data's are used and by which a minimum reconstruction error is attained. The distance in between the *m* class data and the testing data helps SDC for classifying the input data. The expression of SDC will be given by the following equations:

$$l(s) = \text{argmax}\, T_s^i;$$

$$l(s) = \text{argmax} \log \left(\sum_{j=1}^{f_i} \exp\left(-\alpha \parallel s - s_j^i \parallel_2\right) \right),$$

where T_S^i, $l(s)$ defines the distance between the i^{th} class and the test data, from this *s* can be identified. α defines the penalty parameter, which can be used when $\alpha > 0$. If "*s*" corresponds to the i^{th} class, then s and s_j^i will have the same features and hence $\left\| s - s_j^i \right\|_2$ will goes to zero. This indirectly indicates that the features of the test data match with the features of the i^{th} class. Therefore T_s^i helps to attain the higher value asymptotically and hence T_s^i is maximized. By this way, SDC learns to predict the corresponding class of the given input data.

The prediction output of the SDC will be represented using binary classification as follows:

$$Output\, Z = \begin{cases} class1 \text{ if } T_s \le 0, \\ class2 \text{ if } T_s > 0. \end{cases}$$

Where *P* defines the decision condition of the SDC, which is predefined during the training period of SDC. *Class 1* defines the abnormal status and *class 2* defines the normal status. The decision condition will get change based on the type of disease.

Pseudocode for the proposed Concatenation of Inception V3 and Xception Model

```
$Input: D = \{D1, D2, D3, \ldots, Dn\}$
$Output: Z = \begin{cases} class1 \text{ if } T_s \le 0 \\ class2 \text{ if } T_s > 0 \end{cases}$
Begin
Initialize data normalization for the given input $f(D)$
  Give the normalized data to both Inception V3 and Xception Pre-trained Model
      Obtain the feature map of Inception V3 model as $q_1$
        Obtain the feature map of Xception model as $q_2$
          Concatenate both pre-trained model and obtain final feature map as $Q$
            Flatten the final feature map using FC layer
              Regularize the FC output data using drop out layer
            Give the regularized data to SDC and obtain the classification
        Obtain the classification of SDC from $l(S) = \text{argmax}\, T_s^i$
   If $T_s \le 0$
     SDC predicts the output as abnormal status
   else
     SDC predicts the output as normal status
   End if
End
```

RESULTS AND DISCUSSION

The proposed Concatenation of Inception V3-Xception prediction model is experimentally validated using MatLab 14.1 installed in an intel i3 processor 2.20 GHZ frequency with 8 GB memory. In order to obtain the accurate prediction of disease, the metrices such as accuracy, precision, recall, and f1-score are evaluated in the proposed work The first data set is collected from the Cardiology Department of Chinese PLA General Hospital [25]. The feature includes demographics, vital signs, lab tests, echocardiography, comorbidities, length of stay, and medications. Total 105 features are obtained from each patient and a total of 736 patient data are used in the dataset. The second data set is collected from the UCI machine learning repository [26]. The dataset includes 76 features which include demographics, vital signs, cholesterol, echocardiography, and medications. The benefit of using this dataset is that it allows investigating the classification with multiple features. The simulation parameters used in the proposed model is listed in Table 1.

Table 1. Simulation parameters

No	Parameter	Range/Value
1	Normalizer constant for input	x=0.1, y=0.7
2	Learning rate	0.9
3	Number of epochs	500

TP means the actual medical data containing abnormal value is correctly predicted as abnormal patient, FN means the actual medical data containing abnormal value is incorrectly predicted as Normal patient, FP means the actual medical data containing Normal value is incorrectly predicted as abnormal patient and TN means the actual medical data containing Normal value is correctly predicted as Normal data. The performance of the proposed work is determined in terms of the following metrices:

$$Recall = \frac{TP}{TP + FN};$$

$$Precision = \frac{TP}{TP + FP};$$

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN};$$

$$\text{F1-score} = \frac{2TP}{2TP + FP + FN}.$$

The Performance metrics of the proposed model is presented in the form of the following Table 2.

Table 2. Performance metrics of proposed model

No	Performance metrics	Dataset 1	Dataset 2
1	Recall	0.993	0.991
2	Precision	0.990	0.987
3	F1-score	0.991	0.914
4	Accuracy	0.985	0.983

Further the performance of the proposed concatenation model has been compared with existing techniques evaluated in Chen et al. [21] research work for dataset 1 and Sudarshan et al. [26] research work for dataset 2. For the data set 1, techniques like stacked denoising auto-encoder (SDAE), logistic regression (LR), MLP, MLP with attention mechanism (MLP-A) and Multi neural networks (MNN) are used to compare with proposed model. For the dataset 2 techniques like support vector machine (SVM), logistic regression (LR), Random Forest (RF), swarm artificial neural network (S-ANN) and multi neural networks are used to compared with proposed concatenation model.

Figs. 4 and 5 presents the precision analysis of proposed model and conventional models for dataset 1 and dataset 2 respectively. From the results, it is clear that the proposed concatenation model exhibits maximum precision which indicates the classification performance of proposed concatenation model has been increased due to the multi feature selection and processing using soft-max Discriminant classifier. Similarly, for dataset 2 the maximum performance is obtained by the proposed concatenation model whereas conventional methods obtain minimum precision values compared to proposed concatenation model. The average precision value attained by the proposed concatenation model for dataset 1 is 0.990 and for dataset 2 the obtained precision is 0.987 which is much better than the conventional methods.

The recall metrics of the proposed model and conventional models for dataset 1 and dataset 2 has been presented in Figs. 4 and 5 respectively.

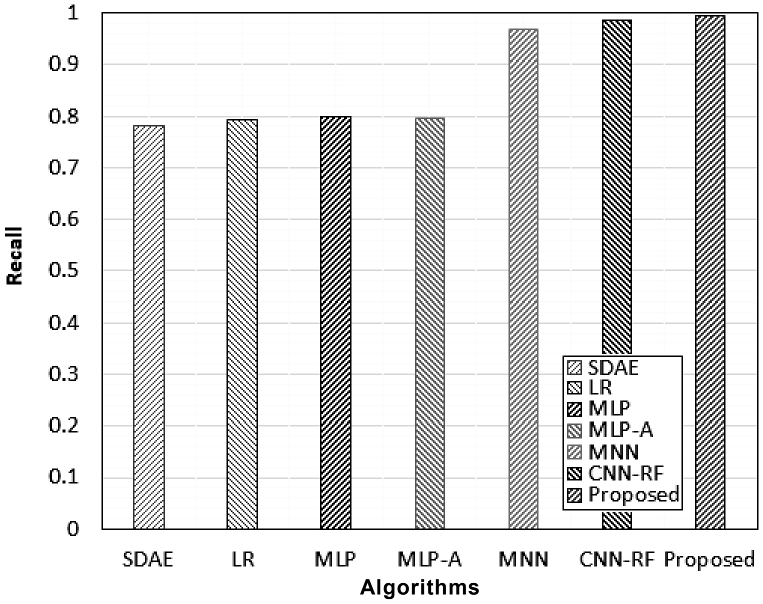

Fig. 4. Recall analysis for dataset 1

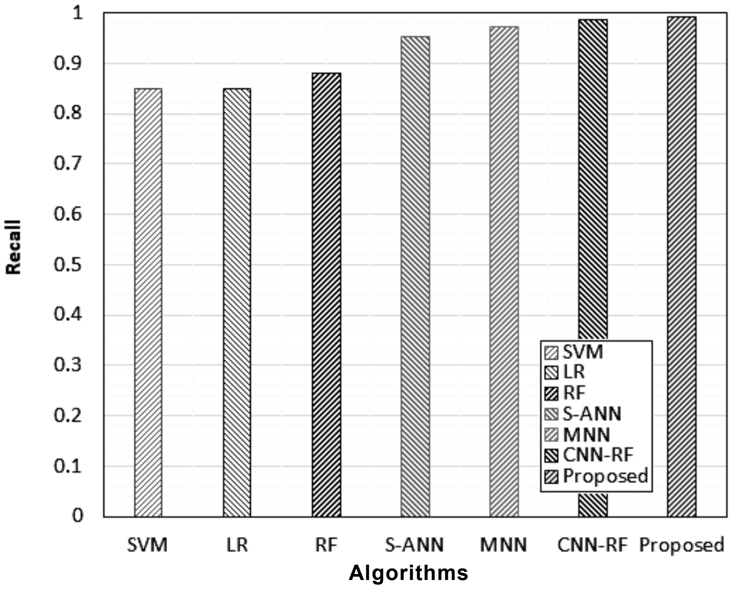

Fig. 5. Recall analysis for dataset 2

Results shows that the maximum recall obtained by the proposed model for both datasets. Though the performance of MNN is much better than other conventional techniques however it is lesser than the CNN-RF model and proposed concatenation model. The average recall value obtained by the proposed model for dataset 1 is 0.993 and for dataset 2 the obtained recall value is 0.991. The F1-score analysis for the proposed model and existing models are comparatively presented in Figs. 6 and 7 for dataset 1 and dataset 2 respectively. Based on the recall and precision values, the f1-score has been obtained and presented. From the results it clear that the maximum score is obtained by the proposed concatenation model when compared to other conventional techniques. The average f1-score obtained by the proposed concatenation model for dataset 1 is 0.991 and 0.914 for dataset 2.

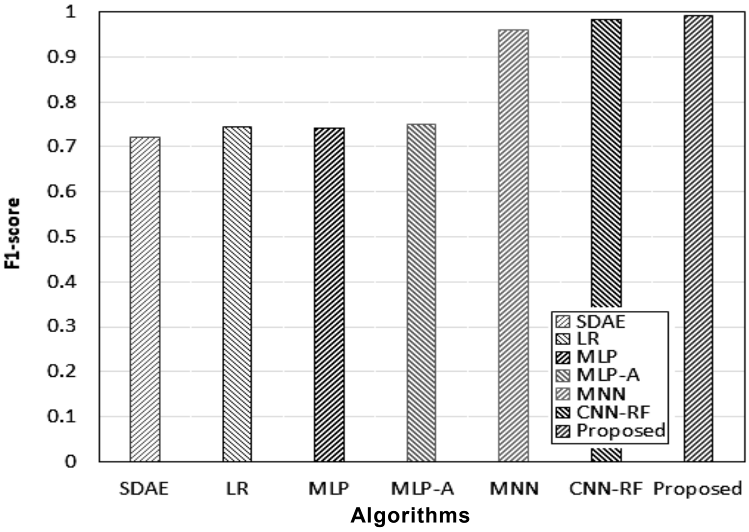

Fig. 6. F1-score analysis for dataset 1

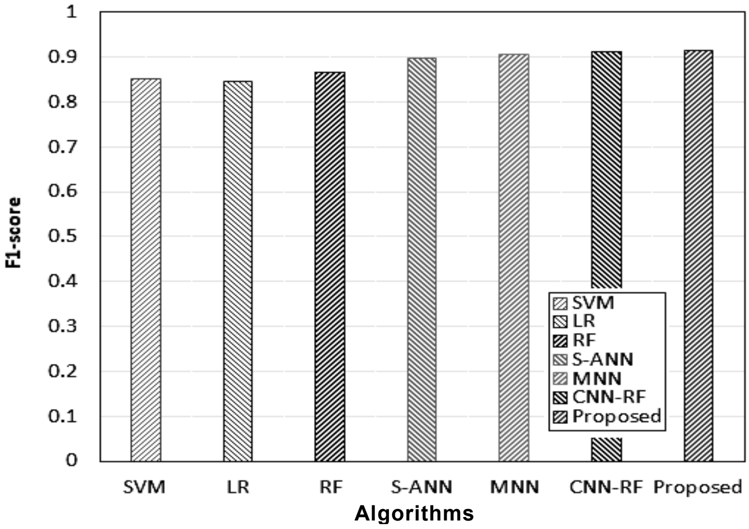

Fig. 7. F1-score analysis for dataset 2

The accuracy of the proposed concatenation model and conventional models are comparatively analyzed and depicted in Figs. 8 and 9 for dataset 1 and dataset 2 respectively. It can be analyzed from the results; the maximum accuracy is determined by the proposed concatenation model for both datasets whereas the performances of conventional models are lesser than the proposed model accuracy values. The maximum accuracy obtained by the proposed model is 0.985 for dataset 1 and 0.983 for dataset 2. The accuracy obtained by MNN for dataset 1 is 0.966 and dataset 2 is 0.968 which is nearly 2% lesser than the proposed concatenation model. The accuracy obtained by CNN-RF for dataset 1 is 0.973 and dataset 2 is 0.978 which is also nearly 1% lesser than the proposed concatenation model. The multi feature selection using concatenation model and prediction using SDC increases the prediction accuracy of the proposed model. Whereas conventional model performs less due to the improper feature selection and classification process.

Table 3 shows the performance comparative analysis of proposed concatenation model and conventional models in terms of accuracy, recall and precision. The average values from the results of dataset 1 and dataset 2 are presented in the tabulation. It can be observed from the results the performance of proposed concatenation model is much better than the conventional techniques. Thus, it is clear that the proposed concatenation model can be used for predicting disease in health cares to attain sustainable development.

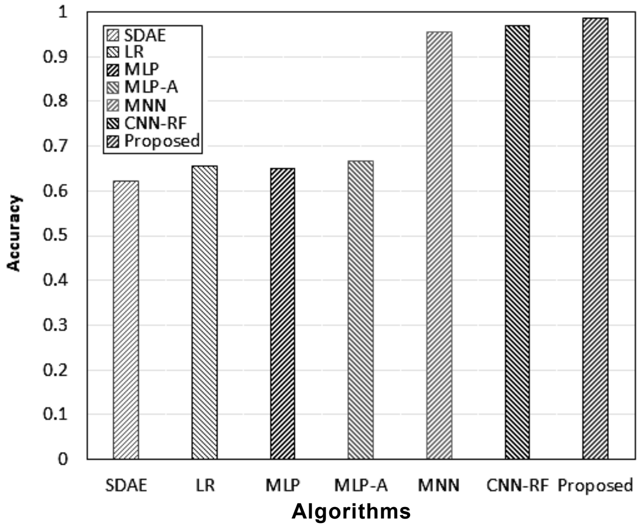

Fig. 8. Recall analysis for dataset 2

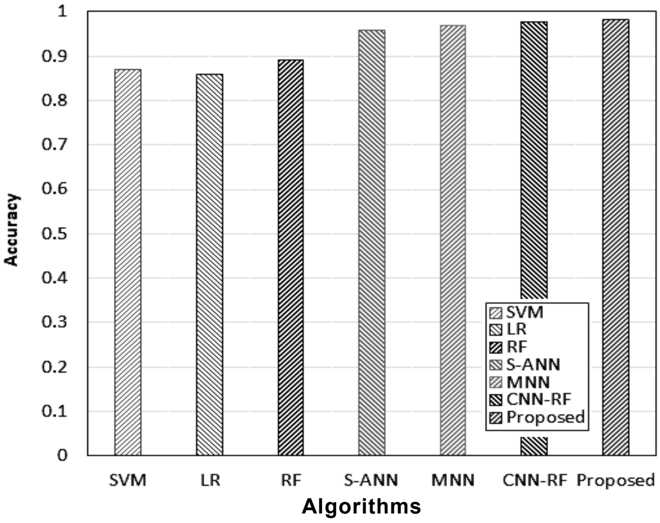

Fig. 9. Accuracy analysis for dataset 2

Table 3. Performance comparative analysis

No	Method	Accuracy	Precision	Recall
1	Stacked denoising auto-encoder (SDAE)	0.623	0.670	0.782
2	Logistic regression (LR)	0.655	0.700	0.792
3	MLP	0.651	0.692	0.799
4	MLP with attention mechanism	0.667	0.710	0.795
5	SVM	0.87	0.85	0.85
6	Logistic regression	0.86	0.84	0.85
7	Random forest	0.89	0.88	0.88
8	Swarm-ANN	0.957	0.952	0.952
9	MNN	0.966	0.962	0.97
10	CNN-RF	0.973	0.982	0.987
11	Proposed Inception V3 – Xception -SDC	0.985	0.988	0.992

CONCLUSION

A concatenation model for disease prediction in healthcare system is presented in this research work using InceptionV3-Xception model and Soft-max Discriminant Classifier. The proposed architecture utilizes the multi-features extracted from concatenation model and classify the data using Soft-max Discriminant Classifier. The novelty in the architecture enhances the classification performance of data analysis system compared to conventional CNN model. Standard healthcare datasets are used for experimentation and verified through performance metrics like accuracy, recall, precision and f1-score.To demonstrate the better performance, conventional techniques like stacked denoising auto-encoder (SDAE), logistic regression (LR), MLP, MLP with attention mechanism (MLP-A), support vector machine (SVM), Random Forest (RF), swarm artificial neural network (S-ANN) ,multi neural networks and Convolutional Neural Network-Random forest (CNN-RF) are compared with proposed concatenation model. Experimental results depicts that the performance of proposed model is much better than the conventional approaches. However, the performance of proposed concatenation model has several benefits, the prediction result is possible only for binary classes whether the data is normal or abnormal, that is considered as a minor limitation of this work. Further this research work can be extended using multi classification to identify the particular stage of the disease.

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МОДЕЛЬ ПРОГНОЗУВАННЯ ЗАХВОРЮВАННЯ НА ОСНОВІ ПІДХОДУ КОНКАТЕНАЦІЇ ДЛЯ СТІЙКОЇ СИСТЕМИ ОХОРОНИ ЗДОРОВ'Я / К. Тарагесварі, Н. Мохана Сундарам, Р. Сантош

Анотація. У сучасному світі внаслідок багатьох факторів, таких як зміни навколишнього середовища, стилі харчування та життєві звички, на здоров'я людей постійно впливають різні захворювання, що призводить до того, що в системі охорони здоров'я потрібно керувати величезною кількістю даних. Деякі захворювання створюють небезпеку для життя, якщо їх не вилікувати на початковій стадії. Для системи охорони здоров'я це робить складним завданням розробити добре навчену модель прогнозування захворювань для точної їх ідентифікації. Моделі глибокого навчання найбільш широко використовуються в дослідженнях прогнозування захворювань, але їх продуктивність поступається звичайним моделям. Щоб вирішити цю проблему, у роботі подано конкатенацію моделей згорткових нейронних мереж глибокого навчання Inception V3 і Xception. Запропонована модель виділяє основні ознаки та створює результат прогнозу точніше, ніж інші традиційні моделі прогнозування. У роботі аналізується продуктивність запропонованої моделі з точки зору точності, прецизійності, запам'ятовування та F1-міра, порівнюються моделі з існуючими методами, такими як стековий автоматичний кодувальник (SDAE), логістична регресія (LR), MLP, MLP з механізмом уваги (MLP-A), опорна векторна машина (SVM), мультинейронна мережа (MNN), гібридна згорткова нейронна мережа (CNN), випадковий ліс (RF).

Ключові слова: вилучення функцій, прогнозування захворювань, глибоке навчання, Inception V3, Xception.