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Research paper

Real-time multi level chronic disease prediction and recommendation model using deep learning

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ABSTRACT

Towards the problem of chronic disease prediction and recommendation, an efficient real-time multi-level chronic disease prediction and recommendation model (RMCDPRM) is presented. The model preprocesses the medical data set and cluster the data set under multiple levels according to the stages of disease. Once the data set is grouped, then the features of the trace are extracted and trained with neural network. At the test phase, the neurons of intermediate layer estimates Class Level Disease Support Value (CLDSV) for various features. This will be measured for all the class of diseases and received at the output layer. Finally, the method computes the value of Disease weight for all the classes. Finally, a class with higher DW is selected as result. Further, the method computes Disease Handling Support (DHS) and Patient Curing Weight (PCW) for various hospitals and medical practitioners. Based on the values of DHS and PCW, the method computes Medical Support MS and ranks them to generate recommendations for the user. The RMCDPRM model hikes the disease prediction accuracy up to 99 %.

1. Introduction

Modern society faces variety of health issues in recent times which are identified in frequent times. The most dangerous disease is the diabetes which is a chronic disease which cannot be reversed till their life. The chronic disease like hypertension, cardiac and diabetes are challenging the person in variety of ways. They introduce other illness like fatigue, paralyze, stroke and so on. Such disease can be managed for their lifetime by diagnose them at the earliest. Also, they can be prevented by taking necessary actions or can be postponed for certain time by diagnose them at the earlier. For example, the upcoming diabetes can be predicted by monitoring the blood sugar, HbA1C, BMI and so on. Similarly, the hypertension can be predicted by monitoring the blood pressure, urea and cholesterol. By predicting the possible diseases, the lifestyle of the person can be changed to avoid the disease.

Disease prediction is the process of identifying the possibility of the disease based on the symptoms and other features. To perform the prediction process, the medical practitioner consider set of features and conclude the possibility of the risk. However, the medical practitioner would not conclude exactly as there will be human error. To support the medical practitioner, there are number of decisive support systems are invented, which takes set of parameters as input and produces a result according to the previous history of various diseases. However, the performance of the system is greatly depending on what parameters are considered and what method is used. For example to predict the diabetes, there are number of approaches available. Among them, some of the methods would consider only the blood sugar and HbA1C where some other method would consider BMI of the person as another input. Similarly, the Genetic algorithm based approaches computes the fitness value for different population produced from the symptom set. On this way, the support vector machine based approach computes the support value for the given sample against various class of samples to identify the possibility of the disease. The naïve Bayes algorithms consider the rules to measure the similarity of the features against various samples of the class. The neural network based approaches computes the weight measure for the test sample in predicting the disease. Similarly, there are number of approaches can be named which uses various features and methods in predicting the disease. However, the methods suffer to

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achieve higher performance in predicting the disease.

In order to improve the accuracy of disease prediction systems, it is necessary to use huge volume of data. The approaches discussed above would miss set of features and does not handle such volume of data. To handle this, the deep learning models can be used and by designing the neural network with much number of layers, the entire features can be considered and would support to achieve higher accuracy in disease prediction.

The recommendation systems are used in various medical problems to support the medical practitioner. By designing effective recommendation system, the medical practitioner would get valuable information about the disease. In this way, the recommendations system can be designed to identify the most effective drug and the hospital in curing the disease. By considering all these, an efficient Real-time Multi Level Chronic Disease Prediction and Recommendation Model have been sketched in this article. The multi-level chronic disease prediction model is designed to handle the features at various levels towards predicting the disease. By handling the features at various levels, the accuracy of disease prediction can be improved.

The article has been structured to present the introduction about the problem in section 1. Section 2 presents the detailed survey of various methods about the problem. Section 3, discusses the detailed working of the proposed approach and section 4 discusses the evaluation results in detail. Section 5, presents the conclusion of the work in detail.

1.1. Problem statement

Predicting chronic disease with existing approaches performed by considering limited features and less volume of data. To achieve higher accuracy in disease prediction, it is necessary to use huge volume of data. The objective of this research is to maximizing disease prediction accuracy by considering huge volume of data with intelligent technique. With the inclusion of deep neural network, the scalability issue can be overridden and supports the maximization of prediction accuracy. With all these intension, this article recommends a novel Real-time Multi Level Chronic Disease Prediction and Recommendation Model (RMCDPRM).

2. Related works

The problem of chronic disease prediction has been approached with number of techniques and this section discusses various approaches related to the problem.

A deep learning model is presented in [1], towards predicting chronic kidney disease which uses laboratory and clinical features. The model uses eight different machine learning models towards predicting the disease. An integrated model is presented towards predicting chronic diseases in [2], which monitors the continuous monitoring of lifestyle and environment factors towards prediction. A multi label neural network based prediction model (ML-NN) [3], predict the disease using multi label learning scheme according to cross entropy function. A comprehensive model is presented in [4], which analyze the performance of different models in early prediction and risk identification. A machine learning model is presented in [5], towards chronic kidney disease prediction which uses UCI data and different machine learning algorithms are used towards classification. A deep belief network (DBN) based model is presented in [6], which predict kidney disease using softmax activation function. A cluster then classify model is presented in [7], which categorize the pain types according to the symptoms and performs classification according to morphological features. An unsupervised framework is presented in [8], which compare the efficacy of different unsupervised algorithm and uses different machine learning algorithms towards classification. A machine learning based hybrid model is presented in [9], which evaluate the performance of various models towards predicting kidney disease. A Blended Ensemble Learning Prediction Model is presented in [10], which uses ensemble learning and optimal classifier towards prediction. A performance evaluation model is presented in [11], to perform risk prediction of pulmonary disease. An artificial intelligence based prediction model is sketched in [12], which perform prediction with Naïve bayes and SVM. A survival prediction model is given in [13], to support intensive care unit which uses different data sets. A CNN based chronic disease prediction model is given in [14], which perform feature extraction using CNN and classification with KNN. The importance of redox system biology in predicting chronic disease is sketched in [15], to predict cardiac necrosis. The performance of N-Acetylcysteine in Chronic Obstructive Pulmonary Disease is analyzed in [16]. The nutritional status of COPD patients and the link between dyspnea and nutritional status is analyzed in [17]. Risk analysis in pulmonary disease is analyzed in [18], which analyze the risk of morbidity and mortality. Apache Spark [19], designed to predict chronic kidney disease with the support of hybrid machine learning. The correlation of serum zinc is analyzed in [20], which consider the blood pressure and end products in risk analysis. A web based prediction model is presented in [21], designed towards predicting CKD which uses clinical features and statistical learning methods. An early detection and prediction model is presented in [22], to support Chronic Obstructive Pulmonary Disease (COPD) prediction.

A CT radiomic nomoram based COPD prediction model is sketched in [23], which applies logistic regression towards classification. A machine learning based CKD prediction model is given in [24], which uses different variables and machine learning classifiers. A detail review of AI models in early prediction of CKD is presented in [25]. A SMOTE based machine learning model is sketched in [26], to predict COPD. A two stage semi supervised K means (SSK-Means) is sketched in [27], towards risk prediction in CVD. The risk prediction on COPD in smokers and non-smokers is sketched in [28], which uses the association of genetic variants to perform prediction.

A multi biomarker panel is sketched in [29], to predict the events of cardiovascular patients with CKD. The method uses prognostic algorithm to predict CVE. A hybrid model combining multiclass Support Vector Machine (MSVM) and Deep Convolutional Neural Network (DCNN) is sketched in [30], which uses DCNN towards feature extraction and categorize using MSVM. A casual graph ontological framework is presented in [31], towards predicting survival rate of patients. Hybrid Support Vector Machines fine-tuned Spatial Transformer Networks (HSVM+FSTN) is presented in [32], towards cardiac failure prediction. A machine learning based tumor segmentation and classification model is sketched in [33]. Various techniques of predicting heart failure is analyzed in [34]. An ML based scheme towards predicting heart failure in early stage is sketched in [35], which uses various ML techniques towards the issue. A retrospective multicenter study has been enforced by clubbing CKD patients and healthy samples by applying six different ML models to predict CKD [36] an optimized prediction model is presented in [37], which includes disease trajectories and uncover risk factors towards treatment enhancement. A fundamental study on ML towards CKD is presented in [38], towards omic based disease prediction. An ensemble modeling with various ML techniques is presented in [39], towards predicting liver diseases. An hybrid explainable artificial intelligence-based ML (HXAI-ML) model is presented in [40], towards predicting cardio vascular diseases.

All the above discussed approaches suffer to achieve higher performance in predicting the chronic diseases. In overall, the existing approaches suffer with poor disease prediction accuracy as they consider limited features and limited volume of data.

2.1. Real-time multi level chronic disease prediction and recommendation model (RMCDPRM)

The proposed RMCDPRM model uses the medical data set which contains number of features and records. Initially, the data set has been preprocessed with Multi-Level Normalizer. The normalized data set has

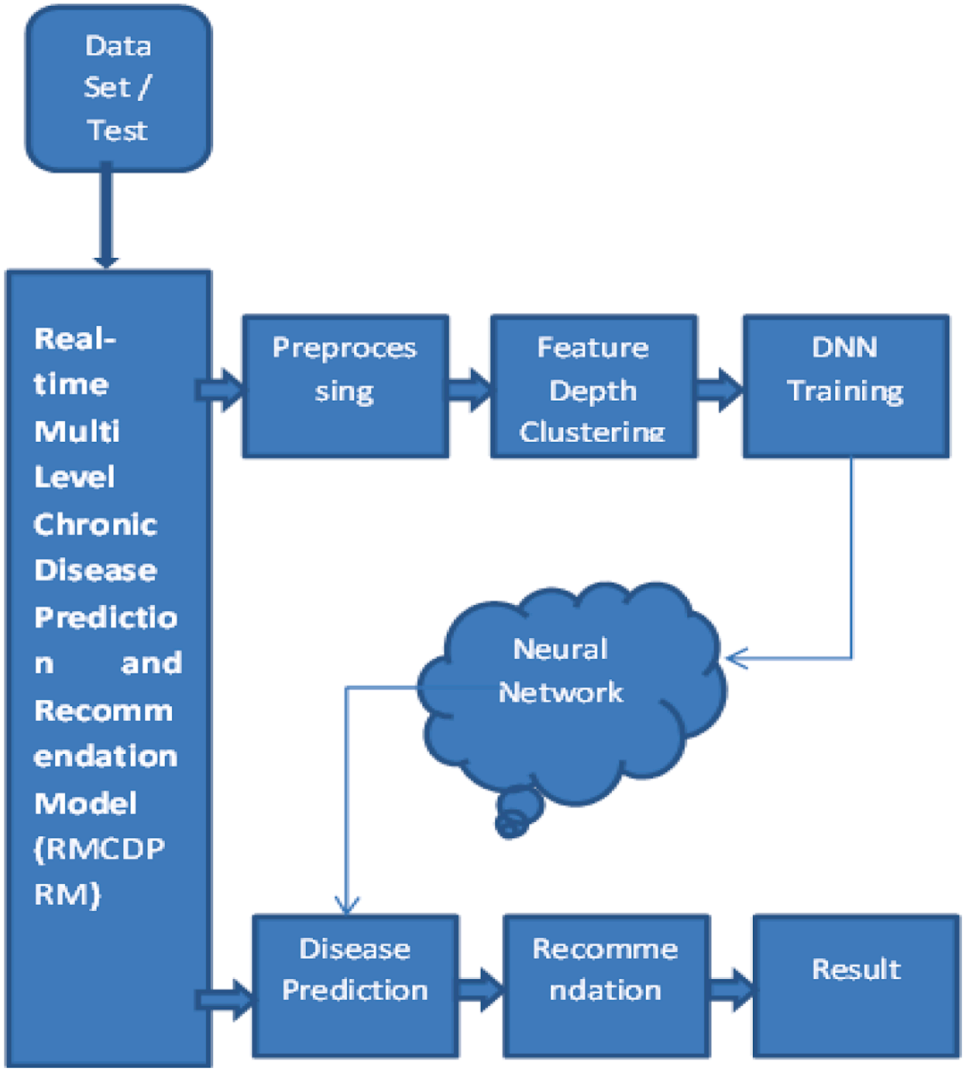

Fig. 1. working model of RMCDPRM Prediction Model.

been clustered Feature Depth Clustering. The Feature depth clustering algorithm groups the data according to the stages of disease. Once the data set is grouped, then the features of the trace are extracted and trained with neural network. At the test phase, the neurons of intermediate layer estimates Class Level Disease Support Value (CLDSV) for various features. This will be measured for all the class of diseases and received at the output layer. Finally, the method computes the value of Disease weight for all the classes. Finally, a class with higher DW is selected as result. Further, the method computes Disease Handling Support (DHS) and Patient Curing Weight (PCW) for various hospitals and medical practitioners. Based on the values of DHS and PCW, the method the method computes Medical Support MS and ranks them to generate recommendations for the user.

The working model proposed RMCDPRM system is presented in Fig. 1, and the working model is discussed in detail in this section.

2.2. Preprocessing

The medical data set given has been read and set of features and dimensions present in the tuples are identified. According to the dimensions set of various tuples, the method generates the set of ensemble set. With the dimensions identified and ensemble set generated, the method reads each tuple and verifies the presence of dimensions at various ensembles. Fi the dimensions set match with any of the ensemble set, and then the feature values are identified. If any of the tuple identified with null value, then it has been removed from the data set. The preprocessed set has been used towards further processing.

Algorithm:

Given: Medical data set Ms.
Obtain: Preprocessed set Ps.
Start
Read Medical data set Ms.
Initialize ensemble set Es.
For each tuple T
Identify feature set Fes $= \sum Features \in T$
For each ensemble E
Compute Feature Match Measure FMM.

$$FMM = \frac{\sum_{i=1}^{Size(E)} Count(E(i) \in T)}{size(E)}$$

If FMM==1 then
Known Feature sample.
For each feature f in E
If T(f)==Null then
Remove the trace from set Ms.
Break.
End
End
Ps $= \sum (T \in Ps) \cup T$
Else

(continued on next page)

(*continued*)

Generate Ensemble $E = \bigcup_{i=1}^{size(T)} E \cup T(i)$
Add to ensemble set Es $= \sum (Ensemble \in Es) \cup E$
End
End
End
Stop

The preprocessing algorithm identifies the features and dimensions to identify the noisy records. The noise removed data set has been used to perform disease prediction.

2.3. Feature depth clustering

The feature depth clustering algorithm groups the tuples of the data set according to the stage of the disease. The data set has number of records belongs to various diseases with the stage label. According to the stage label, the method computes the Depth Class Similarity (DCS) value. The DCS value has been measured according to the number of features the tuple has and number of features the samples of the class have. Also, the method computes the average feature similarity value (AFSV). The value of AFSV is measured according to the similarity of the feature values between the given sample and the samples of the class. According to the DCS value measured, the method identifies the group and stage class of the tuple. The feature depth clustering algorithm clusters the traces in more accurate way to support effective disease prediction.

Algorithm:

Given: Preprocessed set Ps, Disease set Ds.
Obtain: Cluster set Cs.
Start
Read Ps, Ds.
Initialize Cluster set Cs.
For each disease class Di
For each stage class *Sc*
Initialize Cluster $C = \bigcup_{i=1}^{size(k)} Find\ Random\ samples\ (Ps, Di, sc)$
End
End
For each tuple T
For each disease class Di
For each stage class sc
Compute Dimensional Match Measure (DMM).

$$DMM = \frac{\sum_{i=1}^{size(T)} Count(T(i))}{\sum_{i=1}^{size(sc)} Count\left(\sum Features \in sc(i)\right)/size(Sc)}$$

Compute Average Feature Mean Value AFMV.

$$AFMV = \frac{\sum_{j=1}^{size(sc)} \left(Count\left(\sum Sc(i) \equiv T(j)\right)/size((T))\right)}{\sum_{i=1}^{size(T)} Size(Sc)}$$

Compute DCS = DMM×AFMV
End
End
Class *c* = Choose the class with maximum DCS.
Index T to the selected class.
End
Stop

The feature depth clustering algorithm groups the records of the data set by computing DCS value according to the DMM and AFSV values. The organized data set has been used to perform disease prediction.

2.4. DNN training

The proposed model trains the neural network according to the clustered data set. The method generates the neural network with number of diseases and sub classes. The network has been generated with number of intermediate layers according to the number of disease classes and sub classes. For each tuple of a class of a disease, the method generates a layer with number of neurons where each neuron has been initialized with the features of the tuple given. The neurons of the layer are designed to compute the class level disease support value (CLDSV) which is being measured with one to one samples of the training class and test sample. Using the CLDSV value, the intermediate neurons computes the disease weight (DW) and returns the value at the output layer. The trained network has been used to perform disease prediction.

2.5. Disease prediction

The test phase involve in passing the test sample to the trained network. The neurons of intermediate layer estimates Class Level Disease Support Value (CLDSV) for various features. This will be measured for all the class of diseases and received at the output layer. Finally, the method computes the value of Disease weight for all the classes. Finally, a class with higher DW is selected as result.

Algorithm:

Given: Trained Network TDnn, Test sample T.
Obtain: Disease Class Dc
Start
Read TDnn and T.
Pass T to the network TDnn.
The intermediate neurons performs the following:
For each intermediate layer l
For each neuron n
Compute class level disease support value (CLDSV).

$$CLDSV = \frac{\sum_{j=1}^{size(T)} Dist(T(j), N(i)(j))/size(T)}{Size(T)}$$

End
Compute Disease Weight $DW = \sum_{j=1}^{size(NN)} CLDSV(NN(j))/NN$
Forward DW to next layer
End

$$Dc = \max_{i=1}^{size(Disease\ Classes)} (Dw(i))$$

Stop

The above disease prediction algorithm computes the class level disease support value for the test sample against various neurons at different intermediate layer. Based on the value of CLDSV, the method computes the value of DW and identifies the class with maximum disease weight as result.

2.6. Recommendation

The model maintains the data set with the traces of treatment provided for various patients with different disease classes. The proposed model produces recommendation according to the performance of the medical unit. TO perform this, the method computes Disease Handling Support (DHS) and Patient Curing Weight (PCW) for various hospitals and medical practitioners. Based on the values of DHS and PCW, the

method computes Medical Support MS and ranks them to generate recommendations for the user.

Algorithm:

Given: Preprocessed set Ps, Disease class c
Obtain: Recommendation R
Start
Read Ps, C.

$$\text{Identify the medical units Mu} = Mu \cup \left(\left(\sum_{i=1}^{Size(Ps)} MedicalUnits \in Ps(i)\right) \ni Mu\right)$$

For each medical unit m

$$\text{Compute Disease Handling Support DHS} = \frac{\sum_{i=2}^{size(Ps)} Count(Ps(i).Disease == C \;\&\&\; Ps(i).unit == m)}{\sum_{i=2}^{size(Ps)} Count(Ps(i).unit == m)}$$

Compute Patient Curing Weight PCW.

$$PCW = \frac{\sum_{i=2}^{size(Ps)} Count(Ps(i).Disease == C \;\&\&\; Ps(i).unit == m \;\&\&\; PS(i).state == Cured)}{\sum_{i=2}^{size(Ps)} Count(Ps(i).Disease == C \;\&\&\; Ps(i).unit == m)}$$

$$\text{Compute Medical Support MS} = \frac{PCW}{DHS}$$

End
Recommendations R = Sort Medical units with MS.
Stop

The above algorithm produces recommendation by computing medical support for various units and sorts them to produce recommendation.

3. Results and discussion

The performance of real-time multi-level chronic disease prediction and recommendation model (RMCDPRM) model is evaluated and presented in this section. To evaluate the performance, the model considered number of features and data tuples obtained from various data sets. The data set is fabricated by collecting from different data sources like Kaggle and Chronic Disease Indicator (CDI). The data set is fabricated to cover 30 features with 1 million records of data. The excessive features from various data set has been eliminated and only required features are collected to frame the data set. It includes age, gender, bmi, blood_pressure, cholesterol_level, glucose_level, physical_activity, smoking_status, alcohol_intake, family_history, biomarker_A, biomarker_B, biomarker_C, biomarker_D, and target.

The key factors considered for performance analysis is displayed in Table 1, which has been measured for various metrics towards analysis.

3.1. Disease prediction accuracy

The disease prediction accuracy represents the performance of the model in predicting the exact disease. It is measured with the number of predictions performed and number of correct predictions made. It has been measured as follows:

$$DPA = \frac{TP + TN}{TOtal\ Prediction} \times 100$$

Where TP-true positive and TN-True negative.

Table 1
Evaluation details.

Key	Detail
Data sets	Kaggle, CDI
Total Features	15
No of Locations	10
Total Tuples	1 million

The performance of methods in predicting the disease is evaluated and plotted in Table 2, where the RMCDPRM model introduces higher prediction accuracy.

The accuracy of methods in predicting the possible disease is encountered and sketched in Fig. 2, where the RMCDPRM model introduces higher prediction accuracy.

False Prediction Ratio:

The false prediction ratio shows the rate of false prediction produced by any approach. The FPR is measured with number of false positive and false negative predictions made by any approach.

$$FPR = \frac{FP + FN}{Total\ Prediction} \times 100$$

Where FP-false positive and FN – false negative.

The false prediction ratio introduced by various models are measured and plotted in Table 3, where the RMCDPRM model introduces less false prediction ratio.

The false prediction factor generated by the methods are counted and given in Fig. 3. The proposed RMCDPRM model introduces less false prediction compare to others.

Time Complexity:

The time complexity is the performance metric which shows the time taken by the model in predicting the disease.

$$\text{Time Complexity} = \frac{Sum\ of\ all\ time\ taken\ for\ prediction}{TOtal\ Prediction} \times 100$$

The time complexity incur by the methods is counted and given in Table 4, where the proposed RMCDPRM model introduces less time complexity compare to others.

The time complexity is measured for various methods and presented in Fig. 4. The proposed RMCDPRM model introduces less time complexity compare to others.

4. Conclusion

This paper presented a RMCDPRM model towards chronic disease prediction. The model uses the medical data which has been preprocessed with Multi-Level Normalizer. The normalized data set has been clustered Feature Depth Clustering. Once the data set is grouped, then the features of the trace are extracted and trained with neural network. At the test phase, the neurons of intermediate layer estimates Class Level Disease Support Value (CLDSV) for various features. This will be measured for all the class of diseases and received at the output layer. Finally, the method computes the value of Disease weight for all the classes. Finally, a class with higher DW is selected as result. Further, the method computes Disease Handling Support (DHS) and Patient Curing Weight (PCW) for various hospitals and medical practitioners. Based on the values of DHS and PCW, the method the method computes Medical Support MS and ranks them to generate recommendations for the user. The proposed model improves the performance of disease prediction up to 99 % with less time complexity. In future, the mode can be further tuned to consider more features and include data from many locations which would support the achievement of higher prediction accuracy.

Table 2
Accuracy in disease prediction.

Disease Prediction Accuracy %			
	3 lakh	5 lakh	1 million
ML-NN	65	73	78
CNN	71	77	81
DBN	75	82	85
CNN-KNN	82	86	94
BADLM	85	90	96
Proposed	89	93	99

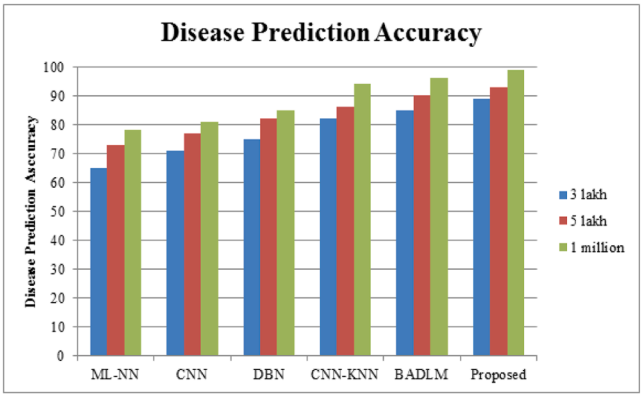

Fig. 2. Accuracy in disease prediction.

Table 3
False prediction ratio.

False Prediction Ratio %			
	3 lakh	5 lakh	1 million
ML-NN	35	27	28
CNN	29	23	19
DBN	25	18	15
CNN-KNN	18	14	6
BADLM	15	10	4
Proposed	11	7	1

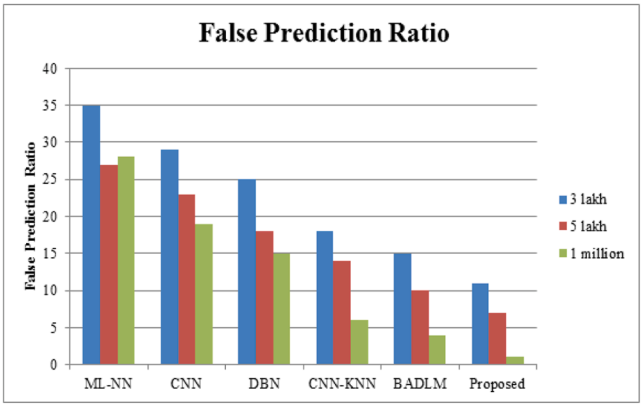

Fig. 3. False prediction ratio.

Table 4
Time complexity in seconds.

Time Complexity in seconds			
	3 lakh	5 lakh	1 million
ML-NN	68	79	91
CNN	65	76	85
DBN	56	69	81
CNN-KNN	37	53	67
BADLM	26	41	55
Proposed	21	32	45

CRediT authorship contribution statement

M Manoj Kumar: Writing – original draft, Visualization, Validation, Software, Methodology, Investigation, Formal analysis, Data curation. **R Siva:** Writing – review & editing, Supervision, Project administration, Conceptualization. **M Baskar:** Writing – review & editing, Validation, Investigation, Formal analysis.

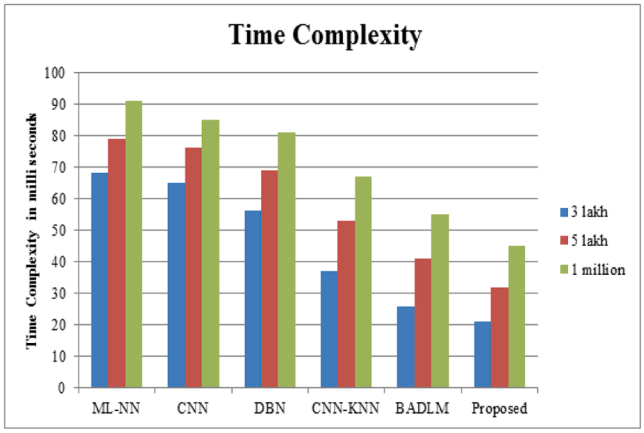

Fig. 4. Time complexity.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

Data will be made available on request.

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