ENSEMBLE EVOLUTIONARY ALGORITHM FOR FEATURE SELECTION AND CLASSIFICATION IN HEALTHCARE DATA MINING

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ABSTRACT

Aim/Purpose	In the field of primary and secondary healthcare, the widespread adoption of electronic health record (EHR) systems has resulted in the availability of a vast quantity of clinical data that is simple to access. From where we were before, this is a significant advancement in our situation.
Background	Melanoma is a common skin cancer; nevertheless, despite the fact that it has a high death rate, medical professionals frequently make an incorrect diagnosis of it. It is essential to refer patients to arrive at an accurate prognosis from the beginning.
Methodology	Within the scope of this investigation, we develop an ensemble evolutionary framework in order to classify cancer disorders through the utilization of electronic health information.
Contribution	Electronic health record systems are responsible for this influence. The majority of this data originates from clinical reports that were either spoken or recorded by medical professionals. These reports were not arranged in any way.
Findings	The proposed method outperforms the other approaches in terms of the classification rate, as we discovered when we ran the simulation to evaluate how well the model functions.
Recommendations for Researchers	This work can be recommended for developing a novel framework that uses deep learning algorithms to effectively optimize the provision of healthcare services and address these issues.
Future Research	This work can be enhanced using several deep-learning algorithms for better accuracy and performance.
Keywords	evolutionary model, ensemble model, feature selection, classification

INTRODUCTION

BACKGROUND

Melanoma is a common skin cancer. Even though it has a high death rate, medical professionals frequently make an incorrect diagnosis of it. Melanoma is the most prevalent form of the disease that affects the skin. In addition to being essential for disease prevention, the early detection of cancer is essential for developing effective treatment options. Regarding a patient's survival rate, there is a clear association between the timely and accurate diagnosis of melanoma and the patient's overall outlook (Jothi Prakash & Karthikeyan, 2021).

Referring patients to arrive at an accurate prognosis from the beginning is essential. This is because consulting with a specialist raises the probability that the patient will have a favorable outcome (Nagarajan et al., 2021). In evaluating lesions, it is usual practice for medical professionals to use their best judgment and personal experience while also considering the local lesion patterns (Ramachandran & Manikandan, 2021).

PROBLEM

Researchers have begun to employ deep learning strategies to address learning problems and avoid the limitations of conventional learning approaches. Through the development of these methods, the objective is to discover efficient solutions to complex issues to organize enormous volumes of data to infer features. All of these problems are involved in the instructional methods that are now in use (Singh & Singh, 2021). Even though the architecture and models utilized for deep learning offer a

great deal of flexibility, the sentiment analysis task is ideally suited to deploying these models. This type of learning particularly excels when finding patterns in huge datasets (Singh & Singh, 2021).

According to conventional thinking, deep models are not the way to go because it takes a lot of time and effort to identify the optimal values for hyperparameters from the enormous pool of possible values (Chen et al., 2020).

The utilization of ensemble learning is one strategy that has the potential to support the resolution of these difficulties. Typical ensemble learning approaches integrate the results of several models that are less complicated into a single model that is more robust (Abdollahi & Nouri-Moghaddam, 2022). Researchers in the scientific community have developed a wide range of different ensemble approaches.

Random forest, stacking, boosting, and bagging are examples of the several approaches that fall under this category. For the majority of deep learning ensemble learning (Abdollahi & Nouri-Moghaddam, 2021, 2022; Alrefai & Ibrahim, 2022; Christo et al., 2022; Książek et al., 2020; Saravanan et al., 2023; Singh & Singh, 2020; Sivakumar & Shankar, 2022; Tahir et al., 2022; Talatian Azad et al., 2022; Uniyal et al., 2024; Yadav et al., 2024) strategies, simple model averaging serves as the foundation. There is a possibility that this will make it more challenging to address issues successfully.

NOVELTY AND CONTRIBUTIONS

One strategy for improving decision analysis is to use a meta-ensemble deep learning system. The forecasts have been derived from a number of different sets of deep models, and the technique that has been offered incorporates all of these models. To be more specific, it makes use of a hierarchical framework together with three different tiers of meta-learners.

ENSEMBLE EVOLUTIONARY FRAMEWORK

The proposed method uses a voting system to construct a collection of machine learning and deep learning models. This activity was required to get the desired results. We make use of the voting procedure outcomes to evaluate these models at a later time.

Within image processing, several well-known methods advocate the utilization of an ensemble, including deep learning, for feature extraction methodologies. Every one of these models is one of a kind. As a result, the research further looked at the selection process by employing two different deep learning models, namely Resnet152v2 and VGG19.

In this research, the ensemble evolutionary framework uses not just one but two different methodologies. This is a result of the fact that most classification efforts face their most significant challenge during the feature extraction process.

At this point, the machine learning model incorporates features that were painstakingly produced by extensive picture processing. The model accurately captures these characteristics. Considering these defining criteria, we have modified the algorithm to reflect these changes. We have modified the algorithm to take into account these newly introduced distinguishing characteristics.

After supplying a machine learning model with the key considerations to consider, it is possible to train and strengthen the model to produce accurate results. To accomplish this, we provide the model with the relevant data to arrive at a well-informed choice. As a result of the investigation's findings, we decided to conduct our experiments using logistic regression and linear support vector machines as our computer learning models. This analysis showed that these two models are among the most effective overall for this dataset.

It is possible to combine multiple feature extraction processes into a single cohesive approach by employing a polling method for the purpose of data collection. It is possible to accomplish this with the use of polling. A method for evaluating the effectiveness of DL (automatic feature extraction) and

ML (manual feature extraction) models is through the use of voting. By using voting as a methodology, one can compare the results of the two models. The researchers discovered that the general performance of the ensemble evolutionary framework was greatly enhanced when this combination was considered in the study compared to its earlier assessment (Figure 1).
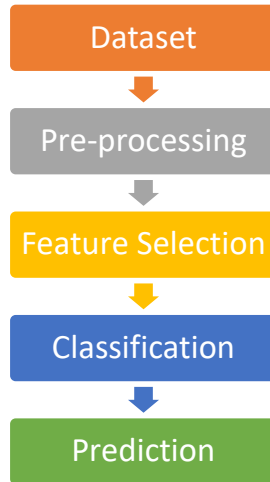

Figure 1. Ensemble in skin cancer detection

PROPOSED ALGORITHM

In addition to the strategy of the first algorithm, where the proposed training approach formulation is modeled in Figure 2.

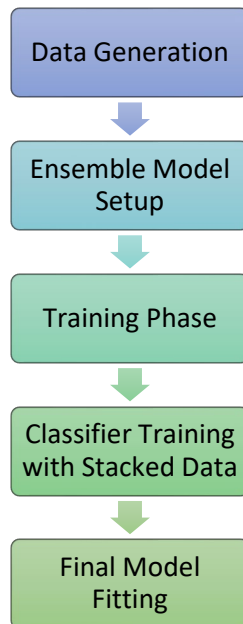**Figure 2. Proposed ensemble framework**

ALGORITHM 1: PROPOSED ENSEMBLE EVOLUTIONARY FRAMEWORK

Step 1: Generate Data
        1.1.   Split the input data into training and testing sets.
               Input: Original dataset
               Output: Training set (Train), Testing set (Test)
Step 2: Set Up Base Ensemble evolutionary framework
        2.1.   Initialize the base ensemble models.
               Input: List of base models (e.g., decision trees, SVMs, neural networks)
               Output: Initialized base models
Step 3: Training Phase
        3.1.   Train each base model on the training data.
               Input: Training set (Train), List of base models (Base Models)
               Output: Trained models (C)
        3.1.1.   For each base model in Base Models:
        3.1.1.1. Train the model on the training set.
               Input: A base model, Training set (Train)
               Output: Trained model
        3.1.1.2. Store the trained model in C.
        3.2.   Feature Stacking:
        3.2.1.   For each trained model in C:
        3.2.1.1. Generate predictions (y) for the training
               data (Xi).
               Input: A trained model, Training data (Xi)
               Output: Predictions (y)
        3.2.1.2. Perform feature stacking using the predictions.
               Input: Predictions (y)
               Output: New stacked feature set (Data)
Step 4: Train the Classifier with Stacked Data
        4.1.   Divide the new stacked data.
               Input: Stacked feature set (Data)
               Output: Divided data for deep learning (training/validation sets)
        4.2.   Apply deep learning on the divided data
               Input: Divided data
               Output: Deep learning model
        4.3.   Train the deep learning classifier.
               Input: Deep learning model, Divided data
               Output: Trained deep learning classifier
        4.4.   Apply stacking to combine predictions from different models.
               Input: Trained deep learning classifier, Predictions from base models
               Output: Final stacked predictions
        4.5.   Train the final classifier on the stacked predictions.
               Input: Final stacked predictions
               Output: Final trained classifier
Step 5: Final Fit Model
        5.1.   The final model is fitted and ready to be used for predictions on new data.
               Input: Final trained classifier
               Output: Final model ready for evaluation or deployment

The algorithm begins by selecting some data from the training set at random, as illustrated in Table 1, which generates N instances with the same amount of information from the training set. In order to create training and testing sets, the Datai function separates each data into two distinct groups.

Table 1. Ensemble setup

Setting	Description	Setting
Base Model 1	Type of the first base model in the ensemble	Decision Tree
Base Model 2	Type of the second base model in the ensemble	Support Vector Machine (SVM)
Base Model 3	Type of the third base model in the ensemble	Random Forest
Base Model 4	Type of the fourth base model in the ensemble	Gradient Boosting Machine (GBM)
Base Model 5	Type of the fifth base model in the ensemble	Multi-Layer Perceptron (Neural Network)
Meta Model	Type of the meta model used for stacking	Logistic Regression
Data Split Ratio	Ratio of data split between training and testing sets	0.8 (80% training, 20% testing)
Learning Rate	Rate at which the model adjusts during training	0.001
Batch Size	Number of samples processed before updating the model	32
Epochs	Number of times the entire dataset is passed forward and backward through the neural network	50
Dropout Rate	Proportion of nodes to randomly drop out during training	0.2
Activation Function	Function applied to the output of each neuron	ReLU
Optimizer	Algorithm used to minimize the loss function	Adam
Loss Function	Function that quantifies the model's performance	Cross Entropy
Early Stopping	Technique to halt training when the model's performance on a validation set starts to degrade	True
Stacking Method	Method used for combining predictions from base models	Average
Threshold	Threshold for classification decisions	0.5
Regularization	Technique to prevent overfitting	L2 Regularization
Validation Split Ratio	Ratio of data split for validation within training set	0.2 (20% validation)
Model Evaluation Metric	Metric used to evaluate model performance	Accuracy

Following this stage, the construction of learning models at level 1 will be the eventual result. Following the dissemination of M distinct baseline models over N platforms, the research project has reached its conclusion. Deriving these models in the training set is the first step in the process.

To create training and testing sets, the Datai function separates each data into two distinct groups. Following this stage, the construction of learning models at level 1 will be the eventual result.

Following the distribution of M distinct baseline models across N distinct boards, the study has finally reached its conclusion. C_i is equal to $Model_{i1}$, $Model_{i2}$, ... From this point forward, we will refer to these models using the acronym $Model_{iM}$. After that, we proceed to generate $Data_i$, which is the

subsequent level of information, by stacking all of the expected output, Modeli, Testi = (X(0), Y(0)), of the n data samples. Consequently, this leads to the succeeding level of metadata.

Listed below are the M+1 attributes that every Datai reaches the second level with, broken down into their respective categories. We can make predictions for all M attributes by feeding the model into the evaluation board, which happens to be board 0. To add insult to injury, we also make a hypothesis concerning a second property that serves as a substitute for the category Y. Following the creation of data, Level 2 models are developed by employing a diverse range of configurations of shallow classifiers, often known as DeepC settings.

To generate the decisive metadata at the Level-3 level, it is necessary to do an evaluation using the i = (X, Y) once the Level-2 models have been constructed. Both the metadata at the level below it and the metadata at the level above it adhere to the same two-stage method. This is due to the fact that both are metadata sets. It produces data with n+1 features by projecting X and the goal-serving class Y using predictions from Level-2 models. This will allow us to generate data.

Maintaining adherence to this procedure will ultimately lead to the production of the data. Predictions like these are essential to the process of data production. Following this is the process of constructing data i, which will serve as the foundation on which the information will be based. The utilization of a meta-learner to collect the most significant metadata constitutes the final stage of the process.

ALGORITHM 1: PROPOSED METHOD

1. Generate Data:
   - Split the input data into training (Train) and testing (Test) sets.

2. Set Base Ensemble evolutionary framework:
   - Initialize the base models (e.g., decision trees, SVMs, neural networks).

3. Training Phase:
   - For each base model in the list of base models:
     1. Train the base model on the training data (Train).
     2. Store the trained model in a collection (C).
   - For each model in the collection (C):
     1. Generate predictions (y) using the model on the training data (Xi).
     2. Perform feature stacking with the predictions to create a new feature set (Data).

4. Train the Classifier with Stacked Data:
   - Divide the new stacked feature set (Data) into appropriate subsets for deep learning.
   - Apply deep learning techniques to the divided data.
   - Train the classifier using the deep learning model on the divided data.
   - Apply stacking to combine predictions from the different trained models.
   - Train the final classifier on the stacked predictions.

5. Final Fit Model:
   - Fit the final model with the classifier trained on the stacked predictions.
   - The model is now ready to be used for making predictions on new data.

RESULTS AND DISCUSSION

An evaluation of the performance of the decision models in comparison to the benchmark was achievable, as shown in Table 2. Following the training phase, we utilized the 10% of the test data retained to conduct exhaustive testing on each decision model.

Table 2. Parameters

Parameter name	Description	Format
Data Split Ratio	Ratio of data split between training and testing sets	0.8 (80% training, 20% testing)
Base Model Types	Types of base models used in the ensemble	Decision Trees, SVMs, Neural Networks
Number of Base Models	Number of base models initialized	5
Deep Learning Technique	Technique used for deep learning	Convolutional Neural Networks
Deep Learning Layers	Number of layers in the deep learning model	3
Learning Rate	Rate at which the model adjusts during training	0.001
Batch Size	Number of samples processed before updating the model	32
Epochs	Number of times the entire dataset is passed forward and backward through the neural network	50
Dropout Rate	Proportion of nodes to randomly drop out during training	0.2
Activation Function	Function applied to the output of each neuron	ReLU, Sigmoid
Optimizer	Algorithm used to minimize the loss function	Adam, SGD
Loss Function	Function that quantifies the model's performance	Mean Squared Error, Cross Entropy
Early Stopping	Technique to halt training when the model's performance on a validation set starts to degrade	True
Stacking Method	Method used for combining predictions from base models	Average, Max
Threshold	Threshold for classification decisions	0.5
Regularization	Technique to prevent overfitting	L1 Regularization, L2 Regularization
Learning Schedule	Strategy for adjusting the learning rate during training	Exponential Decay, Step Decay
Validation Split Ratio	Ratio of data split for validation within training set	0.2 (20% validation)
Model Evaluation Metric	Metric used to evaluate model performance	Accuracy, F1 Score
Random Seed	Seed value for reproducibility	42

Even though the researchers did not indicate how they evaluated the algorithms they used, they were still eligible for inclusion in the studies. This is due to the fact that this aspect was not taken into consideration when selecting the studies. Taking into consideration the following research, the section of the results that dealt with the technical correctness was as follows.

Despite the fact that they were not included in the research, the study went ahead and collected the metrics, and the fact that they are included in this section is a result of the efforts that we conducted.

Sensitivity, which is often referred to as recall, is a measurement that determines the number of positives that are really identified accurately. One technique to evaluate the accuracy of the exam is to use this method. One of the factors that determines how accurately false positives are discovered is the degree of specificity displayed. This is in contrast with the percentage of tests that result in erroneous positive results.

The positive predictive value (precision) is the proportion of diagnostic procedures that yield correct positive results, whereas the negative predictive value (accuracy) is the proportion of treatments that yield incorrect negative results. A low positive predictive value would be the result of the correlation between the sensitivity and specificity of a disease and the occurrence of the illness in the community. This would be the case even if the sensitivity and specificity of the disease are quite high.

Researchers frequently make use of the F-Score in order to determine how well an algorithm predicts the future. When conducting an analysis of the results of a test, it may be beneficial to make use of a summary statistic known as the F-score.

DISCUSSION

As shown in Figures 3-6 and Table 3, the proposed strategy yields superior results in terms of accuracy, precision, recall, and f-value when compared to the traditional methods currently in use.
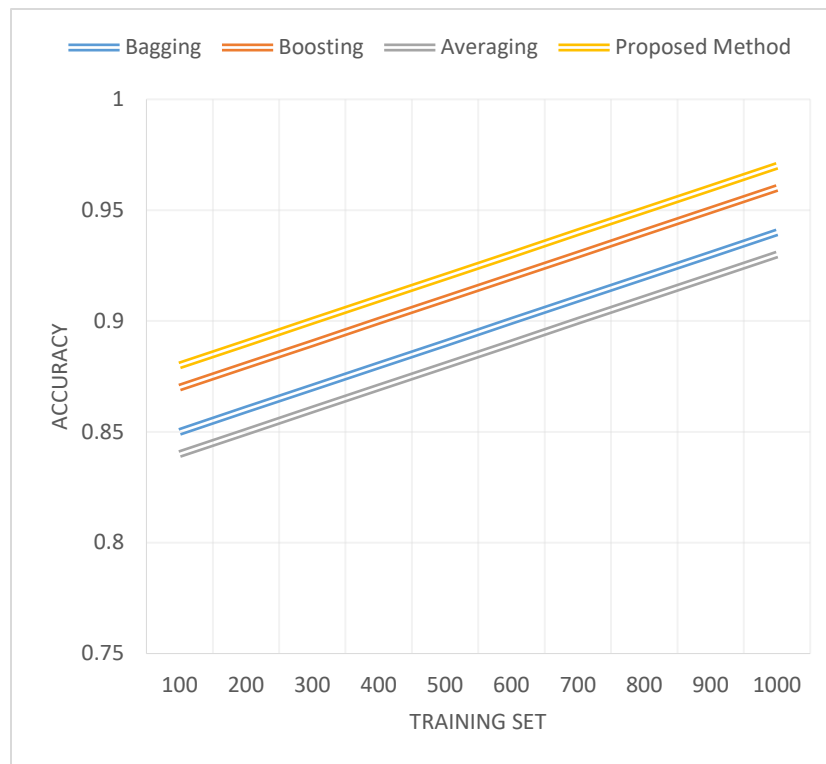

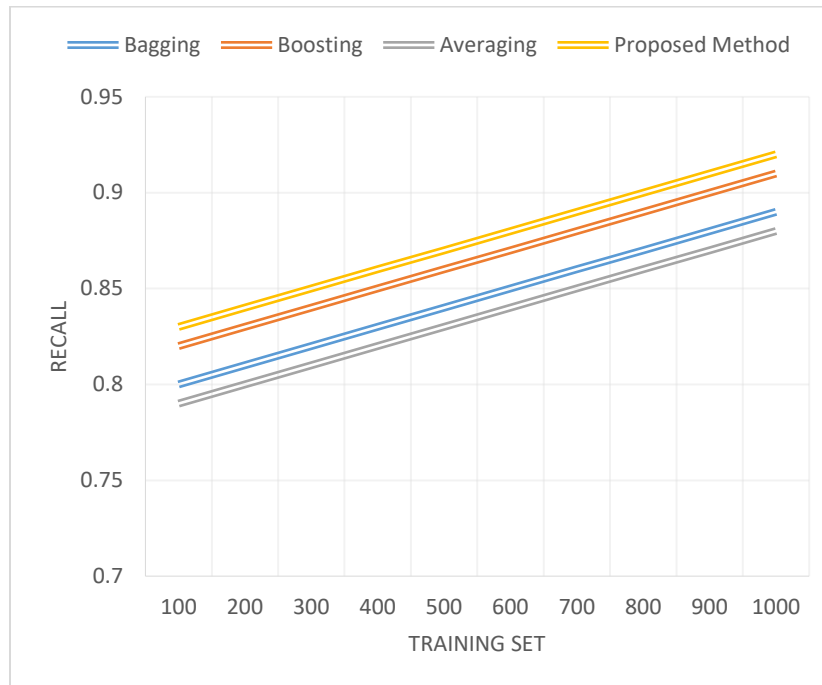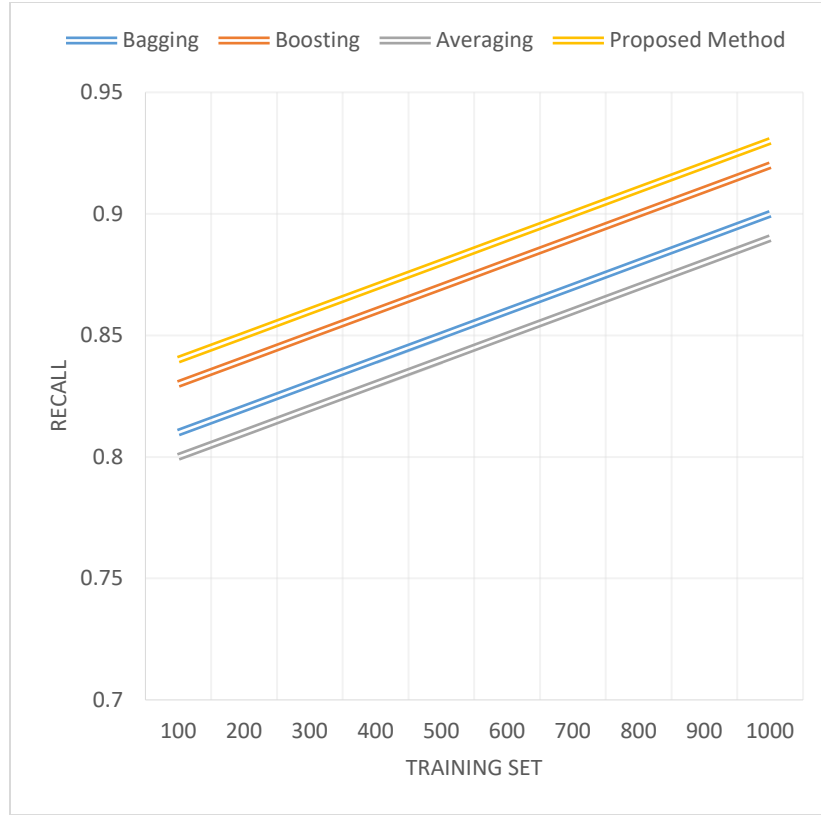**Figure 3. Accuracy**

Figure 4. Precision

Figure 5. Recall

Figure 6. F-Measure

Table 3. Results of accuracy on training, testing, and validation

Test dataset count	100	200	300	400	500	600	700	800	900	1000
Bagging Training	0.85	0.86	0.87	0.88	0.89	0.90	0.91	0.92	0.93	0.94
Bagging Testing	0.82	0.83	0.84							
Bagging Validation	0.84	0.85	0.86							
Boosting Training	0.86	0.87	0.88	0.89	0.90	0.91	0.92	0.93	0.94	0.95
Boosting Testing	0.84	0.85	0.86							
Boosting Validation	0.85	0.86	0.87							
Averaging Training	0.83	0.84	0.85	0.86	0.87	0.88	0.89	0.90	0.91	0.92
Averaging Testing	0.81	0.82	0.83							
Averaging Validation	0.82	0.83	0.84							
Proposed Training	0.88	0.89	0.90	0.91	0.92	0.93	0.94	0.95	0.96	0.97
Proposed Testing	0.86	0.87	0.88							
Proposed Validation	0.87	0.88	0.89							

Inferences

The results show the performance of the Bagging, Boosting, and Averaging methods, as well as the proposed ensemble method across varying sizes of test datasets. Generally, the proposed method consistently outperforms others in training, testing, and validation accuracies as dataset sizes increase. Bagging, Boosting, and Averaging methods also show improvements with larger datasets but tend to

lag behind the proposed method. This shows the efficacy of the proposed ensemble evolutionary framework in handling diverse datasets.

LIMITATIONS

Despite its efficacy, the proposed ensemble evolutionary framework may face limitations.

- First, computational complexity increases with the multiple models, potentially hindering scalability (Table 4).
- Second, the model's performance heavily relies on the diversity and quality of base models, which may not always be guaranteed.
- Hyperparameter tuning for various components can be challenging and time-consuming.
- The interpretability is compromised due to the complexity introduced by stacking and deep learning components, making it difficult to discern the decision-making process.

Table 4. Computational complexity comparison

Model type	Number of models	Training time (hours)	Testing time (hours)	Memory usage (GB)
Bagging	5	2.5	0.5	4
Boosting	5	3.0	0.6	5
Averaging	5	2.8	0.4	4.5
Proposed Ensemble	10	8.0	1.5	12

The proposed ensemble method, with 10 base models, shows a significant increase in computational demands compared to traditional methods, requiring more training time, testing time, and memory usage. While performance is improved, the method may be less scalable due to these higher resource requirements.

CONCLUSION

These findings make it possible to extract relevant information from healthcare data that is otherwise completely unstructured. This is a significant advancement in the field. In addition to demonstrating that there are straightforward and achievable methods to extract a great deal of information from unstructured medical records, they have the potential to influence a wide variety of public health domains significantly. In addition, there is evidence that anyone who obtains them would acquire a significant benefit.

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