Journal of Computer Science

Research Article

Web Based Multi Feature Propagation Analysis Model for Efficient Disease Interference and Recommendation Using Deep Learning

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Article history
Received: 08-02-2024
Revised: 17-03-2024
Accepted: 28-07-2024

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Abstract: Accurate prediction of chronic diseases is critical for proactive healthcare management. This paper proposes a Multi-feature Propagation Analysis-based Deep Learning Model (MPADM) to address this challenge. The model integrates diverse patient data, including medical, diagnostic, genetic, and historical features, collected from multiple sources. After preprocessing, the network is trained to calculate distinct Propagation Weights (PWs) for each feature category, Diagnosis Propagation Weight (DPW), Genetic Propagation Weight (GPW), and Historical Propagation Weight (HPW). These weights, estimated across different disease classes, are aggregated to generate a final predictive score for chronic diseases. To support clinical decision-making, the model also computes a Treatment Support (TS) metric, ranking hospitals and medical practitioners for user recommendation. Implemented with a web-based interface for accessibility, the MPADM model demonstrates enhanced efficacy, significantly improving prediction accuracy and the quality of therapeutic recommendations compared to existing benchmarks.

Keywords: Deep Learning, Disease Prediction, Chronic Diseases, Web Inference, Recommendation, MPADM

Introduction

Rapidly evolving modern lifestyles have contributed to an increased prevalence of diverse diseases, placing significant strain on human health and healthcare systems. While some of these conditions are treatable, others remain chronic or incurable. In either case, early and accurate diagnosis is critical, as it enables medical practitioners to administer effective treatments, manage symptoms, and improve patients' quality of life. Diagnosis typically relies on identifying a set of symptoms. However, this process is complicated by symptom overlap, where multiple diseases present with similar clinical signs, making definitive identification challenging. This diagnostic uncertainty underscores the growing need for intelligent decision-support systems. Such systems can analyze patient-reported symptoms and provide data-driven recommendations to assist clinicians in reaching a conclusive diagnosis.

Chronic diseases, such as diabetes, hypertension, and cardiac conditions, are long-term health issues that cannot be cured but can be managed with effective treatment. Diagnosis typically begins with identifying a patient's symptoms, which medical practitioners analyze to reach a clinical conclusion. However, this process is susceptible to human error in classification or prediction. To mitigate this limitation, researchers have developed and implemented clinical decision support systems designed to enhance diagnostic accuracy and consistency.

Various computational techniques have been employed for disease prediction, each with inherent strengths and limitations. Traditional methods include Support Vector Machines (SVM), which classify samples by maximizing the margin between different disease classes, and Genetic Algorithms (GA), which optimize classification by evaluating the fitness value of candidate solutions. Ensemble methods improve robustness by aggregating predictions from multiple models derived from medical records. Furthermore, algorithms such as decision trees, self-organizing maps, and neural networks

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have also been widely applied to this task. However, despite their utility, these existing approaches often struggle to achieve the high levels of classification accuracy and predictive reliability required for robust clinical decision support.

Disease prediction involves identifying potential illnesses by analyzing structured data, such as questionnaire responses collected via online platforms. Numerous computational approaches exist that utilize these user-provided answers to perform diagnostic classification. A key challenge in such systems lies in designing effective symptom inference, as users typically lack technical medical knowledge. For instance, a patient with a bacterial skin infection might only report the symptom of itching. To accurately infer the underlying condition, the system must pose a targeted series of queries, such as the presence of itching, pain, or diarrhea, and then process this textual data to extract meaningful clinical features for prediction.

While traditional machine learning algorithms, such as Support Vector Machines (SVM), Decision Trees, Self-Organizing Maps (SOM), and Genetic Algorithms (GA), can process various datasets, they often struggle with missing features and lack scalability when handling large volumes of data. Model accuracy is highly dependent on sample size, which limits their effectiveness in comprehensive disease prediction. Deep learning architectures offer a robust alternative, as they are inherently suited to managing high-dimensional data and extracting complex patterns. To leverage this capability, this article proposes a deep learning-based system designed for scalable and accurate disease prediction. The system employs a web interface to collect symptom data across diverse geographical locations, utilizing agent containers for efficient and standardized data aggregation. This collected data is merged, preprocessed, and used to extract discriminative features for training a deep neural network. The core of our model lies in its Multi-feature Propagation Analysis, which evaluates how user-reported symptoms propagate across different disease categories to infer the most probable condition. This integrated approach forms the basis of our proposed Web-based Multi-feature Propagation Analysis Model (MPADM) for effective disease prediction and treatment recommendation.

Related Works

This section reviews relevant computational approaches for disease prediction and recommendation. Akter et al. (2021) proposed a computer-aided diagnostic system based on deep learning to predict Chronic Kidney Disease (CKD) using various clinical features. Similarly, Ge et al. (2020) introduced a multi-label neural network (ML-NN) model that applies multi-label learning techniques for chronic disease prediction. These studies demonstrate the growing application of neural networks in medical diagnostics but primarily focus on single data sources or specific learning paradigms.

Vasquez-Morales et al. (2019) proposed a neural network classifier for assessing Chronic Renal Disease (CRD) risk, integrating demographic and medical data through a Case-Based Reasoning (CBR) framework. Similarly, Wu et al. (2021) designed a mobile-based medical system that employs a Combined Sparse Autoencoder (CSAE) algorithm for classification, leveraging multiple data sources within a deep neural network architecture. For handling data imbalance and cross-domain challenges, Wang et al. (2020) introduced a Balanced Probability Distribution (BPD) scheme, which utilizes instance-based cascaded transfer learning for weight distribution and incorporates a cross-domain feature filtering algorithm. Comparative analyses have also been conducted, such as the work by Antony et al. (2021), which evaluates the performance of unsupervised methods like K-means clustering and DBSCAN. Further advancing predictive modeling, Wang et al. (2021) developed a tensor factorization model that integrates clinical and sequential factors from electronic health records to uncover latent patterns for chronic disease prediction. Complementing this, an adaptive group regularization scheme by Faruqui et al. (2021b) employs Gaussian Mixture Model (GMM) clustering to learn underlying data structures, thereby enhancing disease prediction accuracy.

Yang et al. (2021) presented a predictive analysis model designed to forecast Multiple Chronic Conditions (MCC) specifically within working populations. In a related approach, Bravo et al. (2021) proposed a holistic data mining scheme that incorporates user feedback features to enhance disease prediction accuracy.

An experimental analysis of various machine learning algorithms for Chronic Kidney Disease (CKD) classification was conducted by Khan et al. (2020), using a labeled kidney patient dataset. Shifting focus to continuous monitoring, Wu et al. (2022) proposed a scheme employing wearable devices to track lifestyle and environmental factors in both indoor and outdoor settings. In the realm of neural network-based prediction, Parab et al. (2020) introduced a back-propagation artificial neural network (BP-ANN) model, integrating partial least squares regression for classification. For dynamic and temporal data modeling, Faruqui et al. (2021a) developed a dynamic functional continuous-time Bayesian network, utilizing tensor-based control charts derived from multilinear principal component analysis. To leverage diverse data sources, Chen et al. (2021) proposed a Hybrid Deep Transfer Learning model for stroke risk prediction (HDTL-SRP), which integrates knowledge structures collected from various origins. Finally, Bashir et al. (2021) presented a comprehensive unsupervised

framework that employs multiple machine learning models for predictive analysis.

Alanazi (2022) presented a chronic condition prediction model that combines Convolutional Neural Networks (CNN) for feature extraction with K-Nearest Neighbors (KNN) for classification, utilizing lifestyle-related features. Rajeashwari and Arunesh (2022) conducted a comparative analysis of machine learning algorithms across multiple datasets to identify an optimal model for effective chronic disease prediction. Debal and Sitote (2022) proposed a multi-classification framework employing Random Forest (RF), Support Vector Machine (SVM), and Decision Tree (DT) as base classifiers. Further refining ensemble methods, Kavi Priya and Saranya (2022) introduced a hybrid approach integrating a Multi-Objective Firefly Optimization Algorithm (MOFFA) with Random Forest to generate heterogeneous decision trees. Advancing into relational data modeling, Lu et al. (2021) developed a Graph Neural Network (GNN) model that constructs a weighted patient network for feature extraction before applying GNN for disease prediction. In parallel, clinical and epidemiological studies have provided critical data and perspectives: Molla et al. (2022) conducted an institutional cross-sectional study for detailed analysis of heart failure patients, while Ibrahim and Lawrence (2022) performed a service evaluation using monthly random sampling. Zheng et al. (2021) specifically investigated the impact of epidemiologic features, including behavioral and demographic factors, on prediction accuracy. For specialized conditions, Sampath et al. (2021) designed a region-based deep learning model for Alzheimer's stage prediction using volumetric brain features. Complementing data-driven approaches, Ramkumar et al. (2021) proposed a healthcare monitoring scheme that leverages IoT devices for continuous patient health tracking to aid in early disease prediction.

Research Gap

The literature review reveals several persistent limitations. Existing models, such as the KNN-CNN hybrid, rely on narrow feature sets (e.g., lifestyle or clinical data alone), while multi-classification approaches often use limited classifiers. Critically, no existing framework integrates the comprehensive range of diagnostic, clinical, and lifestyle features necessary for robust prediction. Furthermore, these models are typically trained on limited datasets, which constrains their predictive accuracy and recommendation utility. To address these gaps, this research is motivated to develop a model trained on a large-scale, multi-feature dataset collected via a web-based platform with agent support. Our objective is to enhance both disease prediction performance and the quality of clinical recommendations.

Materials and Methods

Design and Implementation of MPADM

The proposed Multi-feature Propagation Analysis Deep Learning Model (MPADM) follows an integrated workflow for chronic disease prediction and treatment recommendation. The architecture begins by ingesting two primary data streams: a historical medical dataset and real-time symptom inputs collected through a web interface. To ensure comprehensive and geographically diverse data, mobile software agents are deployed to gather records from distributed sources. The aggregated data is first preprocessed using a feature discrimination normalizer to standardize and clean the inputs. From this refined dataset, four key feature categories are extracted: medical, diagnostic, genetic, and historical.

These features are used to train a deep neural network, where individual neurons are initialized to represent specific elements of the feature set. The core innovation of MPADM lies in its propagation analysis. During inference, the model calculates distinct, learnable Propagation Weights (PWs) for each feature category: a Diagnosis Propagation Weight (DPW), a Genetic Propagation Weight (GPW), and a Historical Propagation Weight (HPW). Each neuron estimates unique sets of DPW, GPW, and HPW across different disease classes. These weights are subsequently aggregated to compute a final composite PW for each potential chronic disease, enabling the prediction.

Beyond prediction, the model generates a practical Treatment Support (TS) metric. This metric evaluates and ranks hospitals and medical practitioners based on the specific predicted condition and relevant patient features. The final output presented to the user comprises both the disease prediction and a ranked list of recommended healthcare providers. The following sections detail each architectural component shown in Figure 1.

Data Collection

This component is responsible for aggregating medical data from distributed sources. The system employs a mobile agent framework, guided by a predefined data taxonomy. This taxonomy serves as a metadata schema that maps specific data types to their storage locations. Based on this mapping, the system dynamically generates and deploys a corresponding number of software agents to each identified source.

These mobile agents are then dispatched to their respective remote locations. Upon arrival, each agent autonomously accesses, reads, and securely retrieves the relevant data records, transmitting them back to a central repository for consolidation.

DOI: 10.3844/jcssp.2025.2726.2734

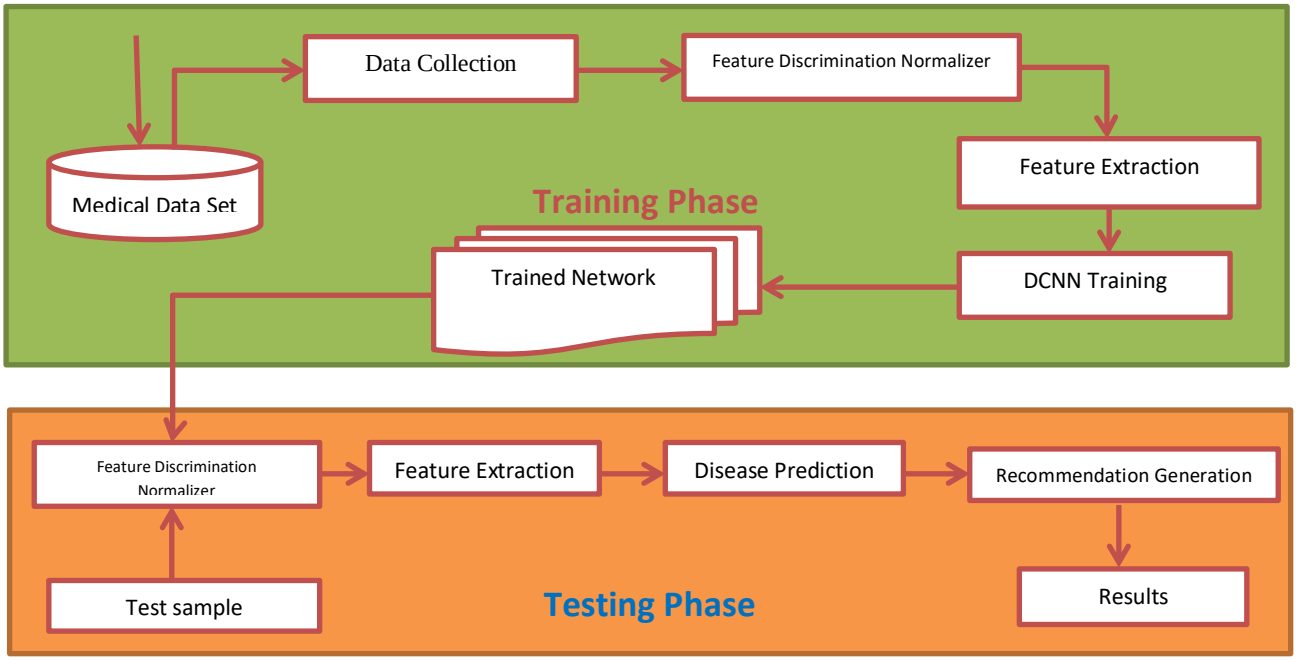

Fig. 1: Working structure of MPADM model

Algorithm 1

Inputs:

- *DaT*: Data Taxonomy
- *Mda*: Local Medical Data Repository

Outputs:

- *Mda*: Updated Medical Data Repository

Procedure:

1. **Fetch** *DaT*, *Mda*.
2. **Identify** all unique source locations from DaT.
   Let $Ls = \{location_1, ..., location_n\}$ where $n = |DaT|$.
3. **For each** remote location *l* in *Ls*:
   1. **Initialize** a mobile agent *Mag* with parameters: (Target_Location = *l*, Home_Address).
   2. **Migrate** Mag to the target remote location l.
   3. **Extract** all relevant medical data tuples from *l*.
      Let $Da = \{tuple_1, ..., tuple_k\}$ be the dataset retrieved from *l*.
   4. **Return** *Mag* (with *Da*) to the Home_Address.
   5. **Merge** the retrieved data **Da** with the central repository.
4. End
5. Release the updated *Mda* repository.

Feature Discrimination Normalizer

The Feature Discrimination Normalizer (FDN) algorithm serves as a preprocessing module designed to enhance data quality for downstream prediction tasks. It operates by first scanning the entire input dataset to identify all unique features present. Subsequently, it evaluates each data tuple's relevance and consistency through a Tuple Fitness Score (TFS). This score quantitatively assesses a tuple's suitability. considering factors such as completeness, outlier status, and coherence with the overall dataset distribution. Tuples falling below a predefined TFS threshold are filtered out, while those meeting the criteria are retained. The output is a normalized, high-fidelity dataset primed for effective model training and robust disease prediction. Selected tuples selected are utilized for feature extraction.

Algorithm 2

Inputs:

- *Ms*: Raw Medical Dataset
- *TH*: Fitness Threshold

Outputs:

- *Pmd*: Preprocessed Medical Dataset

Procedure:

1. **Load** the raw dataset *Ms*.
2. **Extract** the global feature set
   Let $Fes = \{f_1, ..., f_n\}$ be the set of all unique features present in *Ms*.
3. **For each** tuple *T* in *Ms*:
   1. **Calculate** Tuple Fitness Score (TFS)
      $$\frac{\sum_{i=1}^{size(Fes)} Fes(i) \in T}{Size(T)} \times \frac{\sum_{i=1}^{size(T)} T(i) != null}{Size(T)}$$
   2. **If** *TFS* > *TH* **then**
      Add tuple T to the preprocessed dataset *Pmd*
      End
4. End
5. **Return** *Pmd*.

Feature Extraction

The proposed model integrates a multi-source feature vector composed of four categories: medical, diagnostic, genetic, and historical features. These features are systematically extracted from the preprocessed dataset to

form a comprehensive input representation for the prediction model.

For instance, diagnostic features are extracted for each patient tuple *T* as a vector comprising six key clinical indicators:

$$Diagnostic\ Features = [\text{BMI}, \text{BS}, \text{HbA1C}, \text{Pr}, \text{Col}, \text{Cr}]$$

Where:

- **BMI**: Body Mass Index
- **BS**: Blood Sugar (fasting)
- **HbA1C**: Glycated Hemoglobin (3-month average blood sugar)
- **Pr**: Blood Pressure (systolic/diastolic)
- **Col**: Cholesterol level
- **Cr**: Creatinine level

Similarly, genetic features are captured as a vector representing familial medical history:

Genetic Features = [PD, PH, PC]

Where:

- **PD**: Parental History of Diabetes
- **PH**: Parental History of Hypertension
- **PC**: Parental History of Cardiac Disease

These feature vectors are subsequently standardized and concatenated to form the complete input for the deep neural network.

Finally, the model extracts historical features by identifying consistent clinical patterns preceding a disease diagnosis. These features are derived from the sequences of medical indicators recorded prior to the onset of a condition.

For example, for diabetes prediction, a historical pattern is defined by a vector of clinical markers observed together in past cases, along with the eventual diagnosis {BMI, BS, HbA1C, Pr, Col, Cr, Disease_Status}.

A feature is considered historically significant if it appears consistently across confirmed cases of the disease. To quantify this, a Feature Frequency Score (FFS) is calculated for each candidate feature *f*. The FFS represents the proportion of disease-positive records in the preprocessed dataset *Pmd* in which the feature is present:

$$FFS = \frac{\sum_{i=1}^{Size(Pmd)} Pmd(i).f == True}{Size(Pmd)}$$

Features exceeding a predefined FFS threshold are retained as validated historical indicators. By encoding these recurrent, pre-diagnostic patterns, the model leverages longitudinal evidence to improve the robustness of its predictions.

DCNN Training

The proposed method processes the multi-dimensional feature vectors generated during the feature extraction phase. These vectors encapsulate distinct sets of medical, diagnostic, genetic, and historical features. A deep neural network architecture is constructed with *n* intermediate (hidden) layers, each containing *k* neurons. Each neuron is initialized to correspond to specific features within the input vector. The core function of these neurons is to compute specialized disease propagation weights that quantify the influence of their respective features. Finally, neurons in the output layer aggregate these weighted signals to produce a comprehensive propagation score for each target disease class, enabling the final prediction.

Disease Inference

The proposed model generates disease predictions by synthesizing several specialized weight metrics. The process begins by extracting feature vectors from the input sample or reported symptoms. These features are propagated through the neural network, where hidden layer neurons compute category-specific propagation weights: Diagnosis Propagation Weight (DPW) from diagnostic features, Genetic Propagation Weight (GPW) from genetic features, and Historical Propagation Weight (HPW) from historical patterns. The output layer neuron aggregates these individual weights to calculate a final, composite Propagation Weight (PW) for each potential disease class. The class with the highest PW value is subsequently identified as the model's prediction.

Algorithm 3

Inputs:

- *DCNN*: Trained Deep Convolutional Neural Network
- *Ss*: Input sample

Outputs:

- *Dc*: Disease Class

Procedure:

1. **Propagate** the sample *Ss* through the network *DCNN* to obtain the feature embeddings at each layer.
2. **For each** layer *l*:
3. **For each** neuron *N*:
4. **For each** neuron *Dc*:
5. **Compute** the **Diagnosis Propagation Weight (DPW)** as the product of normalized inverse distances for key diagnostic features:

$$\frac{\frac{\sum_{i=1}^{Size(DC)} Dist(Dc(i).BMI,SS.BMI)}{Size(DC)}}{\frac{\sum_{i=1}^{Size(DC)} Dist(Dc(i).BS,SS.BS)}{Size(DC)}} \times \frac{\frac{\sum_{i=1}^{Size(DC)} Dist(Dc(i).HbA1c,SS.HbA1c)}{Size(DC)}}{\frac{\sum_{i=1}^{Size(DC)} Dist(Dc(i).Cr,SS.Cr)}{Size(DC)}} \times \frac{\frac{\sum_{i=1}^{Size(DC)} Dist(Dc(i).Pr,SS.Pr)}{Size(DC)}}{\frac{\sum_{i=1}^{Size(DC)} Dist(Dc(i).Col,SS.Col)}{Size(DC)}}$$

6. **Compute** the **Genetic Propagation Weight (GPW)** using genetic features:

$$\frac{\sum_{i=1}^{Size(DC)} Dist(Dc(i).PD, SS.PD) \Big/ Size(DC)}{\sum_{i=1}^{Size(DC)} Dist(Dc(i).PH, SS.PH) \Big/ Size(DC)} \times \sum_{i=1}^{Size(DC)} Dist(Dc(i).PC, SS.PC) \Big/ Size(DC)$$

7. **Compute** the **Historical Propagation Weight (HPW)** based on historical pattern similarity:

$$\frac{\sum_{i=1}^{Size(DC)} Dist(Dc(i).HP==, SS.HP) \Big/ Size(DC)}{Size(DC)}$$

8. **Compute** the neuron's composite **Propagation Weight (PW)** for disease class *Dc*:
9. End For
10. End For
11. End For
12. Disease class *DC* = Populate class with Max *PW*

Recommendation

Following disease class identification, the model generates personalized recommendations by computing a Treatment Support (TS) metric for relevant hospitals and medical practitioners. The TS value is derived from historical treatment data, quantifying the documented success rates of each provider for the specific predicted condition. Healthcare providers are then ranked in descending order of their TS scores. This ranked list is presented to the user as an actionable set of recommendations, facilitating informed decisions about subsequent care.

Algorithm 4

Inputs:

- *Mds*: Medical Dataset

Outputs:

- *Rs*: Ranked list of healthcare providers for the predicted disease class, sorted by Treatment Support (*TS*) score

Procedure:

6. **Load** the medical dataset *Mds*.
7. **Extract** the unique set of healthcare providers for the predicted disease class:

$$HPS = \sum_{i=1}^{Size(Mds)} (Mds(i).Hospital \ni Hps) \cup HPS$$

8. **For each** provider *H* in *Hps*:
   Compute Treatment Support *TS*

$$\frac{\sum_{i=1}^{Size(Mds)} Count(Mds(i).Hospital==H \;\&\&\; Mds(i).Status==Success)}{\sum_{i=1}^{Size(Mds)} Count(Mds(i).Hospital==H)}$$

9. End
10. Recommendation *Rs* = Rank the hospitals according to *TS*.

Results and Discussion

The MPADM model was implemented in Python and its performance was rigorously evaluated using standard predictive metrics. To ensure a robust assessment, the evaluation was conducted on a composite dataset formed by merging three publicly available sources: the UCI Machine Learning Repository, Chronic Disease Data (CDC), and relevant datasets from Kaggle. Details of these datasets, including their size, features, and origin, are provided in Table 1. The subsequent analysis measures the model's efficacy across several key performance indicators.

Table 1: Evaluation Details

Key	Detail
Data sets	Multiple Sources (UCI, CDC, Kaggle)
Total Features	30
No of Locations	10
Total Tuples	1 million

Disease Prediction Accuracy

The model's prediction accuracy is measured using classification accuracy, calculated as the ratio of correct predictions to total predictions made:

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

Where:

- **TP**: True positive
- **TN**: True negative

As shown in Table 2, the MPADM model demonstrates superior predictive accuracy. Its architecture, which facilitates the collection and integration of large-scale, geographically diverse datasets, directly contributes to this enhanced performance.

Table 2: Disease Prediction Accuracy

Model	Samples		
	300,000	500,000	1 million
CSAE	67	74	79
HDTL-SRP	72	78	82
MOFFA	76	81	86
MPADM	83	87	93

As shown in Fig. 2, the MPADM model demonstrates superior prediction accuracy.

False Prediction Ratio

The False Prediction Ratio (FPR) quantifies an algorithm's error rate, calculated as the proportion of false positive and false negative predictions relative to the total predictions.

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

Where:

- **FP**: False positive
- **FN**: false negative

As shown in Table 3, the MPADM model yields a significantly lower False Prediction Ratio (FPR) compared to other approaches. This improved reliability is attributed to the model's capacity to integrate large-scale, diverse datasets via mobile agents, reducing uncertainty and classification error.

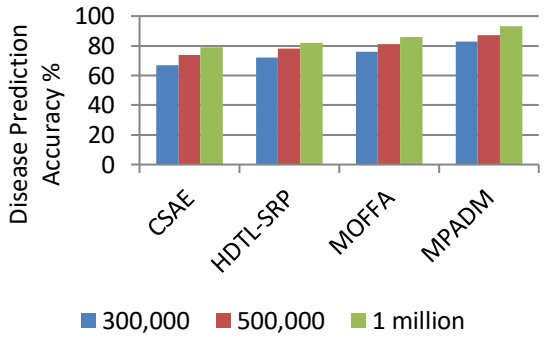

Fig. 2: Disease Prediction Accuracy

Table 3: False Prediction Ratio

Model	Samples		
	300,000	500,000	1 million
CSAE	33	26	21
HDTL-SRP	28	22	18
MOFFA	24	19	14
MPADM	17	13	7

As shown in Fig. 3, the MPADM model achieves a lower false prediction ratio than all other benchmark models.

Time Complexity

The average inference time measures the computational efficiency of a model, calculated as the total time taken for all predictions divided by the number of predictions.

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

As shown in Table 4 and Fig. 4, the MPADM model achieves a lower average inference time than the benchmark models, indicating faster prediction.

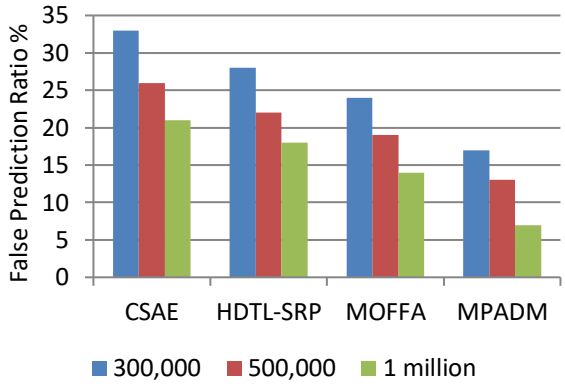

Fig. 3: False Prediction Ratio

Table 4: Time Complexity in seconds

Model	Samples		
	300,000	500,000	1 million
CSAE	68	79	91
HDTL-SRP	65	76	85
MOFFA	56	69	81
MPADM	37	53	67

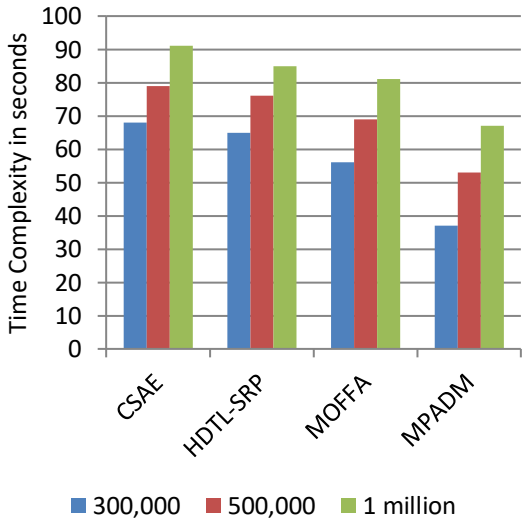

Fig. 4: Time complexity

Conclusion

This article presented the Multi-feature Propagation Analysis Deep Learning Model (MPADM) for chronic disease prediction and treatment recommendation. The model aggregates medical data from distributed sources via mobile agents, preprocesses it using a feature discrimination normalizer, and extracts diagnostic, genetic, and historical features. These features are used to train a deep neural network, which, during inference, calculates specialized propagation

weights, Diagnosis Propagation Weight (DPW), Genetic Propagation Weight (GPW), and Historical Propagation Weight (HPW). These weights are synthesized into a final Propagation Weight (PW) to identify the most probable disease class. Additionally, the model provides actionable recommendations by ranking healthcare providers based on a Treatment Support (TS) metric. Evaluation results demonstrate that MPADM achieves a prediction accuracy of 93% with low computational latency. Future work may enhance the model by incorporating region-centric demographic and lifestyle features to further improve prediction personalization and accuracy.

Funding Information

The authors received no specific funding for this study

Author's Contributions

M. Manoj Kumar: Conceptualization, Methodology, Data curation, Formal analysis, Writing – original draft.

R. Siva: Supervision, Validation, Writing – review & editing, Project administration.

Ethics

This article is original and contains unpublished material. The corresponding author confirms that all of the other authors have read and approved the manuscript and no ethical issues involved.

Conflicts of Interest

The authors declare they have no conflicts of interest to report regarding the present study.

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