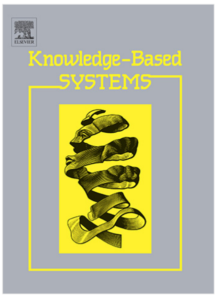

Predicting ICD-9 code groups with fuzzy similarity based supervised multi-label classification of unstructured clinical nursing notes

Tushaar Gangavarapu, Aditya Jayasimha, Gokul S. Krishnan, Sowmya Kamath S.

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Declaration of Interest

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All authors in this research, have participated in:

- conception and design, or analysis and interpretation of the data,
- drafting the article or revising it critically for important intellectual content, and
- the approval of the final version.

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- Tushaar Gangavarapu *(Corresponding author)*,
- Aditya Jayasimha, and
- Gokul S Krishnan.

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We understand that the corresponding author is the sole contact for the editorial process (including editorial manager and direct communications with the office). He is responsible for communicating with the other authors about progress, submissions of revisions, and final approval of proofs. We confirm that we have provided a current, correct email address which is accessible by the corresponding author and which has been configured to accept email from `tushaargvsg45@gmail.com`.

This statement is signed by all the authors to indicate agreement that the above information is true and correct:

Author's name	**Author's Signature**	**Date**
Tushaar Gangavarapu	Tushaar	September 16, 2019
Aditya Jayasimha	Aditya@	September 16, 2019
Gokul S Krishnan		September 16, 2019
Sowmya Kamath S		September 16, 2019

Research Highlights

Manuscript title: Predicting ICD-9 Code Groups with Fuzzy Similarity based Supervised Multi-Label Classification of Unstructured Clinical Nursing Notes.

Highlights of this research include:

- Design of a fuzzy token-based similarity matching approach for unstructured clinical data. This is used for deriving optimal data representations and eliminating anomalous or redundant data, due to which the cognitive burden is reduced, and an improvement in the clinical decision-making process is observed.
- Leveraging vector space and topic modeling to extract the rich patient-specific information available in unstructured clinical nursing notes to predict ICD-9 code groups accurately. Experimental results show that our proposed supervised learning models consistently outperformed the state-of-the-art models built on structured data.
- Design of an approach that utilizes unstructured clinical text for the development of CDSSs, thus eliminating the dependency on the availability of structured EHRs. This can be crucial in countries where structured EHR adoption is not widespread.
- Exhaustive benchmarking experimentation revealed that the proposed fuzzy similarity model consistently outperformed the state-of-the-art structured data based disease prediction model by 7.79% in terms of AUPRC and 1.24% in terms of AUROC.

Predicting ICD-9 Code Groups with Fuzzy Similarity based Supervised Multi-Label Classification of Unstructured Clinical Nursing Notes

Tushaar Gangavarapu[a,1,*], Aditya Jayasimha[b], Gokul S Krishnan[b], Sowmya Kamath S[b]

[a] *Amazon.com, Inc., Bangalore, Karnataka, India*

[b] *Healthcare Analytics and Language Engineering (HALE) Lab,*
Department of Information Technology,
National Institute of Technology Karnataka, Surathkal, Mangaluru, India

Abstract

In hospitals, caregivers are trained to chronicle the subtle changes in the clinical conditions of a patient at regular intervals, for enabling decision-making. Caregivers' text-based clinical notes are a significant source of rich patient-specific data, that can facilitate effective clinical decision support, despite which, this treasure-trove of data remains largely unexplored for supporting the prediction of clinical outcomes. The application of sophisticated data modeling and prediction algorithms with greater computational capacity have made disease prediction from raw clinical notes a relevant problem. In this paper, we propose an approach based on vector space and topic modeling, to structure the raw clinical data by capturing the semantic information in the nursing notes. Fuzzy similarity based data cleansing approach was used to merge anomalous and redundant patient data. Furthermore, we utilize eight supervised multi-label classification models to facilitate disease (ICD-9 code group) prediction. We present an exhaustive comparative study to evaluate the performance of the proposed approaches using standard evaluation metrics. Experimental validation on MIMIC-III, an open database, underscored the superior performance of the proposed Term weighting of unstructured notes AGgregated using fuzzy

[*] Corresponding author.
Email addresses: tusgan@amazon.com (Tushaar Gangavarapu), 15it103.aditya@nitk.edu.in (Aditya Jayasimha), gsk1692@gmail.com (Gokul S Krishnan), sowmyakamath@nitk.edu.in (Sowmya Kamath S)
URL: http://infotech.nitk.ac.in/faculty/sowmya-kamath-s (Sowmya Kamath S)

[1] T. Gangavarapu completed most of this work at Healthcare Analytics and Language Engineering (HALE) Lab, Department of Information Technology, National Institute of Technology Karnataka, Surathkal, Mangaluru, India.

*S*imilarity (*TAGS*) model, which consistently outperformed the state-of-the-art structured data based approach by 7.79% in AUPRC and 1.24% in AUROC.

Keywords: Clinical Decision Support Systems, Disease Prediction, Healthcare Analytics, ICD-9 Code Group Prediction, Machine Learning, Natural Language Processing.

1. Introduction

Disease prediction and quantification of patients' health data have been shown to have significant contributions in improving clinical care and management [70]. Every year, over 30 million patients visit hospitals in the United States alone [22], and 83% of these hospitals utilize the Electronic Health Record (EHR) system [36]. EHRs have seen widespread adoption due to the stipulations of the Health Information Technology for Economic and Clinical Health (HITECH) Act of 2009 [1]. Over recent years, with the rise in EHR implementation in the hospitals of developed countries, application of machine and deep learning models to patient data for the prediction of clinical outcomes such as causal effect inference and survival analysis has sparked widespread interest [100, 81, 28, 92]. Owing to the availability of large, de-identified, public healthcare databases such as MIMIC (Medical Information Mart for Intensive Care II [55] and III [43]), mining patient data to accurately assess the severity of illness and determining diagnostic measures for augmenting healthcare policies has become a prominent area of research [44, 57, 16]. Healthcare data accessible via structured EHRs is widely used in the existing Clinical Decision Support Systems (CDSSs) [10, 46, 67]. However, there is limited adoption of these structured EHRs in developing countries, thus leaving clinicians in such countries with no choice but to resort to manual consumption of available clinical notes for causal effect inference and decision-making [48].

Clinical notes maintained by caregivers like nurses, record subjective assessments and crucial information concerning a patient's state, which is mostly lost when transcribed into structured EHRs [29]. Mining and modeling such nursing notes for extracting rich patient data and utilizing this to predict clinical events and outcomes with machine learning models is a challenging process, owing to their rawness, high-dimensionality, sparsity, complex temporal and linguistic structure, and presence of rich medical jargon and abbreviations [29, 42]. The efficacy of using such raw clinical notes largely depends on the ability to extract and consolidate the information embedded in them effectively [91]. Furthermore, there is often a need for multiple-label assignment (from a large set of potential labels) to a patient record [3] due to the manifold nature of disease symptoms. Disease prediction (ICD-9[2] code group prediction [30]) and risk assessment via nursing notes can help in taking effective measures at the earliest signs of patient distress. Recognition of the onset of disease and the determination of its risk using clinical nursing notes, followed by effective communication and response by interdisciplinary care team members could be both time- and cost-efficient [25], which can also lead to reduced hospital mortality rate [20].

Early works [87, 31, 60, 34, 19] applied machine learning techniques to structure patient data in forecasting the length of stay in Intensive Care Units (ICUs) and mortality prediction. In recent years, practical progress in clinical machine and deep learning is benchmarked using MIMIC databases, for clinical prediction tasks such as in-hospital, short-term, and long-term mortality prediction, length of stay prediction, phenotyping, and ICD-9 code group prediction [35]. Johnson et al. [44] extracted a set of features from the MIMIC-III database for the prediction of ICU mortality and compared several existing works against Logistic Regression (LR) and gradient boosting models. More recently, Purushotham et al. [70] reported their performance on five clinical prediction tasks (on MIMIC-III database) using deep learning models and compared the performance with existing state-of-the-art methods and scoring systems.

Although some state-of-the-art methods benchmark machine and deep learning models for several clinical prediction tasks on MIMIC, they have neglected the rich patient information available in the unstructured clinical nursing notes. In this paper, the applicability of vector space models (with term weighting [80] and Doc2Vec [53]), topic modeling (Hierarchical Dirichlet Process (HDP) [84] and Latent Dirichlet Allocation (LDA) [6] with Topic Coherence (TC) [77]) is studied to model this data. Our objective is to measure their effectiveness in vectorizing and accurately modeling the semantic relationships between the textual features of unstructured nursing notes, for accurately predicting the ICD-9 code groups. A fuzzy similarity based data cleansing approach was designed to derive optimal data representations and eliminate redundant information in the nursing notes, thus improving the causal effect inference. We experimented with eight supervised multi-label classification approaches including K-Nearest Neighbors (KNN), Multi-Layer Perceptron (MLP), One-vs-Rest (OvR) with KNN, OvR with LR, OvR with Support Vector Machines (SVM), Random Forest (RF), Hard Voting Ensemble (HVE), and Stacking Ensemble (SE), to accurately predict the ICD-9 code groups. Furthermore, we present an exhaustive study to evaluate a variety of data cleansing (using similarity) and modeling (using machine learning) approaches across several standard evaluation metrics. The key contributions of our work are summarized below:

[2] International Classification of Diseases, ninth revision.

- Design of a fuzzy token-based similarity matching approach for unstructured clinical data. This is used for deriving optimal data representations and eliminating anomalous or redundant data, due to which the cognitive burden is reduced, and an improvement in the clinical decision-making process is observed.

- Leveraging vector space and topic modeling to extract the rich patient-specific information available in unstructured clinical nursing notes to predict ICD-9 code groups accurately. Experimental results show that our proposed supervised learning models consistently outperformed the state-of-the-art models built on structured data.

- Design of an approach that utilizes unstructured clinical text for the development of CDSSs, thus eliminating the dependency on the availability of structured EHRs. This can be crucial in countries where structured EHR adoption is not widespread.

The rest of this paper is organized as follows: Section 2 provides an overview of the related work and reviews their advantages and limitations. Section 3 describes the MIMIC-III database and the preprocessing steps designed to generate optimal representations from the clinical nursing notes. The experiments, evaluation, and results are discussed in great detail in Section 4. Finally, Section 5 concludes this paper with highlights on future research possibilities.

2. Related Work

An extensive body of research on using machine and deep learning models for clinical predictions is available in the existing literature. In this section, we discuss a few of these works to provide an overview of the existing models and state-of-the-art methods built on large healthcare datasets. In this discussion, we also highlight the importance of accurate ICD-9 code group prediction in modern healthcare systems.

Buchman [9] compared statistical and connectionist models for the prediction of clinical trajectory, including resource and outcome utilization in surgical ICUs. However, much of this work formulated the task of identifying patients at risk as binary classification rather than regression. Other early works [11, 21] showed that machine learning models provide promising results in predicting medical risk, mortality, and in forecasting the length of stay in ICU. Early works [11, 12] also established that feed-forward neural networks almost always outperformed severity scores and logistic regression in mortality risk prediction among hospitalized patients. With recent advances in machine and deep learning, there is widespread interest in applying these models to predict healthcare outcomes accurately [52, 63, 15]. Dabek and Caban [24] reported that several psychological conditions, including depression, post-traumatic stress disorder, and anxiety, could be improved using a neural network model. Che et al. [14] designed a scalable feed-forward deep learning framework for disease diagnosis that learns relevant clinical features based on the prior knowledge from medical ontologies.

Some works that aimed at multi-label prediction of the diagnostic codes from clinical time series used feed-forward neural networks [52], temporal Convolutional Neural Networks (CNNs) [74], and Long Short Term Memory (LSTM) networks [17] to capture the co-morbidities in the hidden layers implicitly. Other recent works [56, 33, 69] modeled clinical time series and disease data by leveraging the power of deep learning approaches. In 2016, novel deep learning architectures were proposed to model survival analysis as a time-to-event regression task [96, 72]. Luo [58] used sentence and segment LSTM models with word embeddings to classify the relations in the nursing notes. More recently, Rajkomar et al. [71] showed that novel neural network based architectures including LSTM perform well in the prediction of an extended length of stay, 30-day unplanned re-admission, inpatient mortality, and diagnoses on general EHR data. Krishnan and Kamath [48] used extreme learning machine architecture with Word2Vec embedding for mortality prediction using unstructured ECG text reports. Khin [45] developed a bi-directional LSTM with deep contextualized word embeddings and variational dropouts, and empirically validated the model's superiority in terms of performance and convergence. These previous works demonstrate the power and efficacy of machine and deep learning models in large healthcare applications.

The availability of large public healthcare databases such as MIMIC-II and MIMIC-III has enabled healthcare researchers to benchmark the developed machine and deep learning models in the effective prediction of clinical events and outcomes. In 2016, Pirracchio [66] presented that the super learner algorithm which is an ensemble of various machine learning models outperforms severity scores such as SOFA (Sepsis-related Organ Failure Assessment) [89], SAPS-II (Simplified Acute Physiology Score) [54], and APACHE-II (Acute Physiologic Assessment and Chronic Health Evaluation) [47] in ICU mortality prediction. The author's work underscored the superiority of machine learning models over traditional prognostic scores but the author did not benchmark the obtained results against most recent machine and deep learning models.

Recently, Johnson et al. [44] presented a case study on clinical mortality prediction task, highlighting the challenges in replicating results reported by related and recent publications on MIMIC-III. They reviewed 28 key existing works and compared the reported performance against LR and gradient boosting models using an extracted set of features from MIMIC-III. Furthermore, the authors stressed the need for an improvement in the way of reporting the performance of clinical prediction tasks, to account for the substantial heterogeneity in the studies and to ensure fairer comparison among approaches. Harutyunyan et al. [35] proposed a comprehensive deep learning approach using multitask Recurrent Neural Networks (RNNs) and empirically benchmarked their outcomes using four different clinical prediction tasks on the MIMIC-III database. Their work showed promising results for using deep learning models in clinical prediction. However, the authors only compared their obtained results against standard LR model and LSTM deep learning model [38], and excluded the comparison with machine learning models (specifically, super learner) or severity scoring systems. Purushotham et al. [70] presented an exhaustive set of benchmarking results on several clinical tasks including the length of stay, phenotyping, multiple versions of in-hospital mortality predictions, and ICD-9 code group predictions using the MIMIC-III database. They used LSTM-based deep architectures and compared their performance with traditional machine learning approaches and severity scoring systems on these tasks.

In 2019, Krishnan and Kamath [50] proposed a novel hybrid metaheuristic approach with genetic algorithm and extreme learning machine for patient-specific mortality prediction that outperformed various severity scoring systems and machine learning models. However, their study uses large-scale structured lab event data for the clinical prediction task. In a parallel work [49], ICU mortality prediction task was performed using Word2Vec, Glove, and FastText embeddings of MIMIC-III nursing notes. They used the RF classifier, and their data processing and feature extraction are quite different from the approaches followed in this paper. Stone [83] discussed the opportunities of improving the triage accuracy in CDSSs, to effectively assist the medical personnel in drawing inferences in high-pressure situations with many distractions, where the patient history concerning the sustained trauma is limited. This work extends the efforts of the author by utilizing the patient-centric information to identify high-risk patients, thus aiding the underlying CDSS with increased triage accuracy, optimized patient outcomes, and minimized risk of clinical deterioration. To automate the process of ICD-9 coding, Zeng et al. [97] proposed a multi-scale deep neural transfer framework which employs the transfer of (Medical Subject Headings (MeSH) domain knowledge to improve the coding process. Huang et al. [40] employed state-of-the-art deep neural models, including CNN, LSTM, and Gated Recurrent Unit (GRU) to predict (top-10) ICD-9 code categories. However, these works utilize discharge summaries of the MIMIC-III database rather than the nursing notes—clinician's notes are more rich, informative, and patient-centric. Moreover, modeling nursing notes can facilitate reliable billing, effective clinical decision support, and revising healthcare policies, while modeling discharge summaries is only useful only in billing.

Table 1: Comparison of this work with the state-of-the-art works in the prediction of clinical outcome(s) using the MIMIC-III database.

Work	**Data**			**Approach(es)**	**Modeling and classification**			**Performance evaluation**	
	Data source(s)	**Structure**	**Volume**		**Classification type(s)**	**Feature modeling**	**Classifier(s)**	**Comparison**	**Evaluation metric(s)**
Harutyunyan et al. [35]	Chart and lab events data	Structured	42, 276 ICU stays	In-hospital mortality prediction, decomposition prediction, length of stay prediction, and phenotyping	Mortality: binary; decomposition: binary; length of stay: multi-class; phenotyping: multi-label	17 selected clinical variables (1)	Deep supervision, multitask standard LSTM, and multitask channel-wise LSTM (3)	LR, standard LSTM, and channel-wise LSTM (3)	AUROC, AUPRC, Kappa, and mean absolute difference (4)
Purushotham et al. [70]	Lab, input, output, and chart events data, and prescriptions	Structured	35, 627 admissions	In-hospital mortality prediction, short- and long-term mortality prediction, length of stay prediction, phenotyping, and ICD-9 code group prediction	Mortality: binary; length of stay: multi-class; phenotyping: multi-label; ICD-9 code group: multi-label	Three feature sets of 17, 20, and 135 features respectively (3)	MLP, multimodal deep learner, and RNNs (2)	Scoring methods and super learner (2)	AUPRC and AUROC (2)
Huang et al. [40]	Discharge summaries	Unstructured	59, 652 summaries	Prediction of (top−10) ICD-9 code categories using state-of-the-art deep learning models	Multi-label classification via deep learning approaches	TF-IDF, Word2Vec, and word sequencing with an embedding matrix (3)	CNN, LSTM, and GRU (3)	Prakash et al. [68], LR, RF, and MLP (4)	ACC, micro F1, AUPRC, precision@5, and hamming loss (5)
Zeng et al. [97]	Discharge summaries	Unstructured	58, 929 summaries	ICD-9 code assessment via deep transfer learning framework	Multi-label classification via deep neural networks	Word embeddings (1)	Transferring MeSH domain knowledge with sequential CNN (1)	Hierarchy-based SVM, flat SVM, and segmented CNN (3)	Micro-average precision, micro-average recall, and micro-average F-measure (3)
This work	Nursing notes	Unstructured	223, 556 notes	Term weighting of voluminous nursing notes aggregated using the fuzzy similarity of the raw clinical text for effective ICD-9 code group assessment	Multi-label classification via machine learning approaches	Term weighting, Doc2Vec (500 and 1, 000), HDP with BoW, HDP with term weighting, and LDA with TC (6)	KNN, MLP, KNN as OvR, LR as OvR, SVM as OvR, RF, HVE, and SE (8)	Purushotham et al. [70], Doc2Vec (500 and 1, 000), HDP with BoW, HDP with term weighting, and LDA with TC (and their respective variants of naive aggregation) (12)	Accuracy, MCC, AUROC, AUPRC, F1, CE, and LRL (7)

Many hospitals in developed countries, including the United States, employ ICD-10 diagnostic coding systems, and hence there is a need for the translation of legacy ICD-9 codes into more specific ICD-10 concepts. Hernandez-Ibarburu et al. [37] studied the incompatibilities between ICD-9 and ICD-10 coding schemes. They presented a way of improving the translation of legacy data (that employs ICD-9 codes) with an extended version of ICD-10 codes generated using selected ICD-9 codes, in turn improving the mapping reliability. To achieve the mapping, they employed general equivalence mappings and integration of certain ICD-9 concepts within the hierarchical relations of ICD-10 codes. Angiolillo et al. [2] also studied the effect of coding terminology transitions on healthcare quality analysis. They reported that the legacy metrics across ICD generations could be bridged through equivalence mapping of ICD-9 concepts. Furthermore, they hypothesized that developing novel metric definitions could mitigate the complexity arising from equivalence mapping.

Our work explores a much-neglected, but an abundant source of patient information, i.e., unstructured clinical notes, and advances the state-of-the-art methods in the literature by using the rich information present in them, which is so often lost in the structured EHR generation process. By utilizing the patient-centric information to identify high-risk patients, this work enhances the underlying CDSS with optimized patient outcomes, increased triage accuracy, and minimized risk of clinical deterioration. Furthermore, our work presents an exhaustive comparative study to evaluate the performance of various data cleansing and modeling approaches across a variety of machine learning models in the multi-label prediction of ICD-9 code groups. Table 1 shows a detailed comparison of our proposed work with the state-of-the-art works in the area of prediction of clinical outcome(s) using the MIMIC-III database.

2.1. Motivation

In hospitals, especially in ICUs, a high patient-to-staff ratio and advanced medical equipment are utilized for continuous support and monitoring of critically ill patients. However, critical care patients are often susceptible to varied complications arising from advanced medical interventions, that can adversely affect their mortality and morbidity [85]. Common infections include central line-related bloodstream infection, ventilator-related pneumonia, and catheter-related urinary tract infection, that arise from the usage of invasive devices in ICUs. Surgical site infections resulting from prior procedures performed on patients and acute renal failure due to unrecognized drug interactions are also potential risks [85]. Ventilator support provided to critical care patients is often related to several complications including barotrauma, short and long-term intubation, weaning errors, and gastrointestinal tract bleeding [94]. Additionally, ICU patients pose a risk of acid-base problems, nutritional complications, and psychological disturbances [94]. Furthermore, ICU survivors are known to suffer from neuro-psychiatric, quality of life, and long-term physical impairments [27]. The minute variations in the condition of ICU patients is recorded and monitored regularly by the trained nursing staff. Hence, nursing notes are very data-rich voluminous resources containing continuously documented subjective and objective assessments concerning a patient's state. Effective modeling of such clinical text to aid in the early identification of high-risk patients is of utmost importance, to provide prioritized care and prevent further complications.

Due to practical constraints, the availability of resources including medical equipment and staff in ICUs is, more often than not, limited [32]. There is often a lack of accurate knowledge of the etiology of ICU complications, leading to the inability of accurate risk assessment and prevention of resulting complications; as a result of which, in most cases, adequate clinical care can only be provided after a complication develops. ICD-9 codes are designed to code diseases into categories, essential in epidemiological studies [73], cost-effectiveness analysis, and determining healthcare policies [18]. ICD-9 code group prediction is a preliminary step to ICD-9 code prediction, requiring high prediction performance. Since the patient encounters are grouped by diagnoses, ICD-9 code groups facilitate research, along with tracking and billing, by reporting on severity, symptoms, and use of resources across agencies. Furthermore, disease-specific staging systems could be beneficial towards capturing the severity, symptoms, and use of resources within a single code group. However, the existing state-of-the-art model [70] built on structured EHR data reported modest performance in ICD-9 code group prediction with an AUROC score of 0.7772 and AUPRC score of 0.6008. Thus, there is a need for the development of an effective modeling strategy to facilitate accurate ICD-9 code group prediction, in turn aiding in the accurate determination of ICD-9 codes.

3. Materials and Methods

In this section, we first discuss in brief, the statistics of the MIMIC-III database. The detailed overview of the Natural Language Processing (NLP) pipeline architecture used in the task of ICD-9 code group prediction is shown in Figure 3. Then, we elucidate on the preprocessing steps employed to extract features for ICD-9 code group prediction as a multi-label classification task.

3.1. Dataset Description and Cohort Selection

MIMIC-III is a freely accessible large database developed by the Massachusetts Institute of Technology Lab for Computational Physiology. It encompasses di-

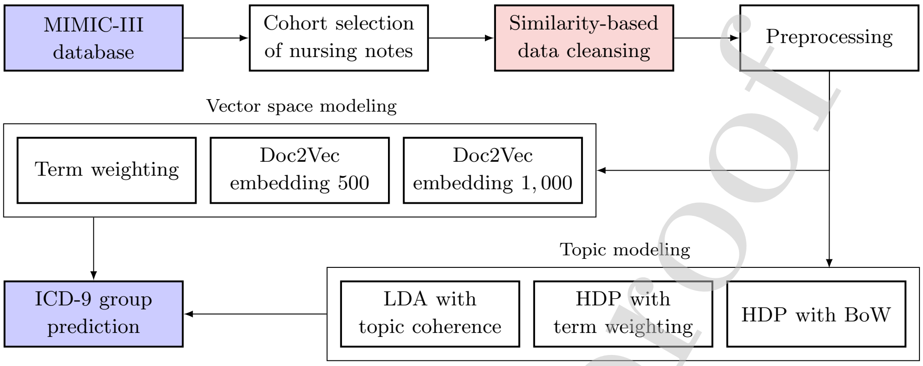


Figure 1: NLP pipeline used to predict the ICD-9 code group using unstructured clinical nursing notes.

verse and comprehensive de-identified health-related data of over $40,000$ critical care patients at the Beth Israel Deaconess Medical Center, Boston, Massachusetts between June 2001 to October 2012. The database contains crucial patient information including vital sign measurements, demographics, laboratory test results, medications, procedures, imaging reports, caregiver (nursing) notes, and in and out of hospital mortality.

MIMIC-III database contains $2,083,180$ note events, of which $223,556$ are nursing notes of $7,704$ distinct ICU patients (subjects). Details of the nursing note text corpus are summarized in Table 2. At present, we considered two criteria to select the MIMIC-III subjects in the preparation of our datasets. Firstly, the subjects with age less than 15 (neonates) were identified using the age at the time of admission to the ICU. Based on the existing literature [44, 70], only adult subjects (age 15 or above) are considered for the study. Secondly, for each MIMIC-III subject, only their first admission to the hospital was considered, and all later admissions were discarded. This was done to ensure the prediction with the earliest detected conditions (faster risk prediction), to avoid any information loss, and to ensure similar experimental settings as in existing literature [44, 70, 48]. Figure 2c outlines the distribution of the number of code group mismatches across patients' first admission to their later admissions. From Figure 2c it can be observed that the code groups in the later admissions of over 94% of the patient nursing notes are the same as those occurring in their first hospital admission. Owing to this, we decided to consider only the first admission of a MIMIC-III subject to a hospital, with no loss of information.

Table 2: Statistics of the clinical nursing note text corpus.

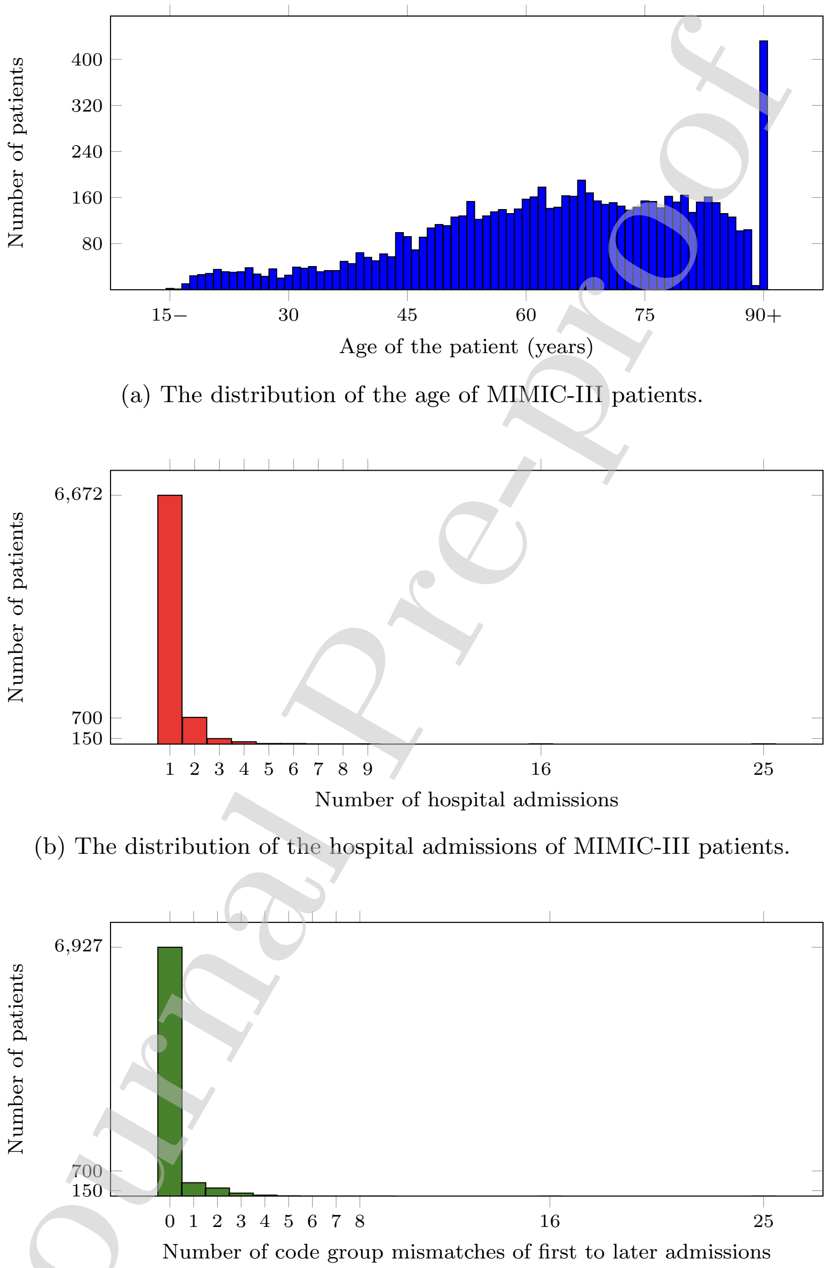
Parameter	Total	Average
Clinical nursing notes	$223,556$	–
Sentences in the nursing notes	$5,244,541$	23.46
Words in the nursing notes	$79,988,065$	357.80
Unique words in the nursing notes	$715,821$	3.20

3.2. Data Extraction

The MIMIC-III (v1.4) database consists of 26 relational tables in total. For the purpose of this study, the following four tables were used to extract the selected cohort data: ***noteevents*** consisting of several kinds of reports and notes including ECG reports, radiology reports, nursing notes, and discharge summaries in an unstructured text form; ***admissions*** reports information concerning the patient's admission to the hospital and is used for the time of the subject's admission to the ICU; ***patients***, containing the charted data for all critical patients, from which the patients' date-of-birth is obtained for the computation of the age of patients; ***diagnoses_icd***, comprises the ICD-9 diagnoses of the patients. Most relevant healthcare features and data is present in these tables, and therefore these tables are selected to prepare datasets for the task of ICD-9 code group prediction. The statistics of the data extracted from the MIMIC database is shown in Figure 2. With the patient cohorts presented in Section 3.1, the dataset extracted from the selected tables contained nursing notes corresponding to $7,638$ patients with the median age of 66 years (Quartile $Q_1 = 52$ years, Quartile $Q_3 = 78$ years).

3.3. Data Cleansing, Aggregation, and Preprocessing

Due to various factors including outliers, noise, missing values, incorrect or duplicate records, and others, the data extracted from the MIMIC-III database has erroneous entries. The following three issues with the extracted data were identified and handled accordingly. Firstly, the erroneous entries in nursing notes with the *iserror* attribute of the ***noteevents*** table set to one were identified and removed. Secondly, some subjects that had duplicate records were identified, and the duplicate entries were deduplicated. The resulting data obtained by handling erroneous entries corresponded to $6,532$ MIMIC-III subjects. Finally, a MIMIC-III subject had multiple nursing notes with different ICD-9 code groups, which were merged or purged using a fuzzy token-based similarity approach.



(a) The distribution of the age of MIMIC-III patients.

(b) The distribution of the hospital admissions of MIMIC-III patients.

(c) The distribution of the code group mismatches across MIMIC-III patients' first and later admissions.

Figure 2: Statistics of the data extracted from the MIMIC-III database.

3.3.1. Fuzzy Token-based Similarity Merging

Multiple nursing notes of a MIMIC-III subject have to be merged to enable multi-label ICD-9 code group classification. Figure 3 shows the heavy-tailed distribution of nursing notes across various patients. It can also be observed that the extracted MIMIC-III patient cohort has an average of 176.49 nursing notes per patient, with $4,183$ patients having more than fifty nursing notes composed of over $17,890$ words on an average. Such voluminous nursing notes often include many similar terms which could significantly affect the vector representations. To handle the voluminosity and near-duplicate nursing notes of a patient, Monge-Elkan (ME) [61], a token-based fuzzy similarity scoring scheme is integrated with Jaro [41] internal scoring scheme and used as a decision-making mechanism. ME similarity is used to handle clinical abbreviations, alternate names, and medical jargon. Jaro similarity is used as an internal scoring scheme to handle typographical errors and to obtain a normalized similarity score between 0 and 1. Given two nursing notes η_i and η_j with $|\eta_i|$ and $|\eta_j|$ tokens ($\mathcal{C}_k^{(i)}$s and $\mathcal{C}_l^{(j)}$s) respectively, their ME similarity score with Jaro is,

$$\text{ME}_{\text{Jaro}}(\eta_i, \eta_j) = \frac{1}{|\eta_i|} \sum_{k=1}^{|\eta_i|} \max \left\{ \text{Jaro}(\mathcal{C}_k^{(i)}, \mathcal{C}_l^{(j)}) \right\}_{l=1}^{|\eta_j|} \tag{1}$$

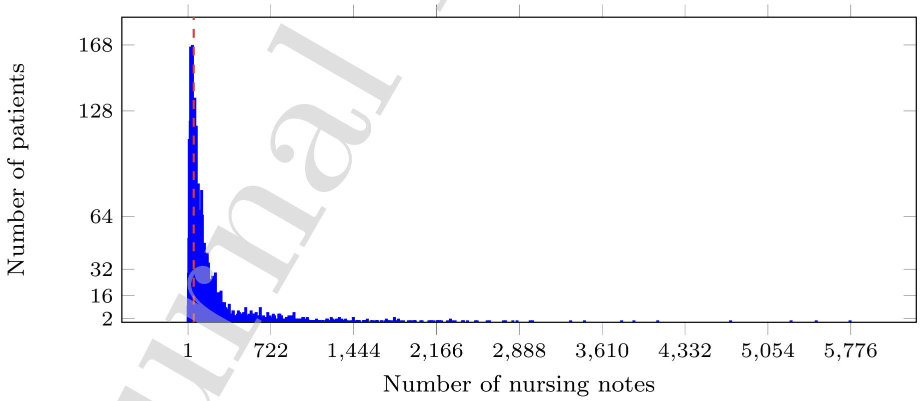


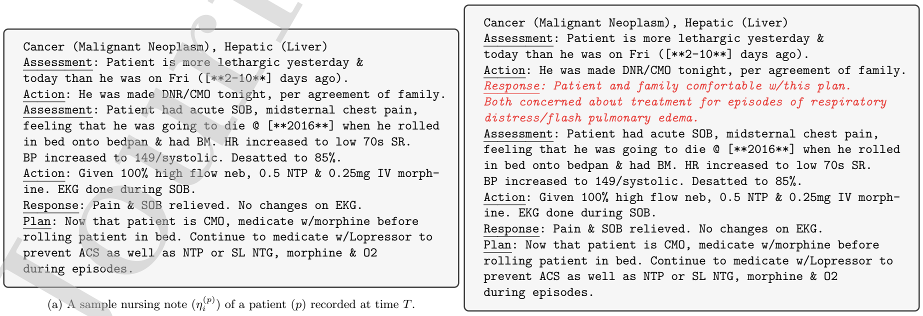
Figure 3: The distribution of nursing notes across various MIMIC-III subjects (red dashed line exhibits the distribution at 50 nursing notes).

where the Jaro similarity score of two given clinical terms (tokens) $\mathcal{C}_i$ of length $|\mathcal{C}_i|$ and $\mathcal{C}_j$ of length $|\mathcal{C}_j|$ with m matching characters and t transpositions is,

$$\text{Jaro}(\mathcal{C}_i, \mathcal{C}_j) = \begin{cases} 0, & \text{if } m = 0 \\ \frac{1}{3}\left(\frac{m}{|\mathcal{C}_i|} + \frac{m}{|\mathcal{C}_j|} + \frac{2m-t}{2m}\right), & \text{otherwise} \end{cases} \tag{2}$$

The nursing notes of a patient are processed in the order of oldest to the most recent. Based on the predetermined similarity threshold (θ) ranging between 0 and 1, a pair of nursing notes ($\eta_i^{(k)}$, $\eta_j^{(k)}$) corresponding to a patient ($\mathcal{P}^{(k)}$) are merged only if $\text{ME}_{\text{Jaro}}(\eta_i^{(k)}, \eta_j^{(k)})$ is less than θ, else $\eta_j^{(k)}$ is retained and $\eta_i^{(k)}$ is purged, thus maintaining only the latest of the two nursing notes. Note that, similarity merging and purging applies only to nursing notes and not to the ICD-9 code groups. Corresponding ICD-9 codes across various nursing notes of a patient are merged to enable multi-label classification. The resultant nursing note for a patient $\mathcal{P}^{(k)}$ after merging is hereafter referred to as the *aggregate nursing note* of that patient. For the purpose of this research, we have empirically determined the fuzzy-similarity θ to be 0.825 using grid search.

Consider two sample nursing notes ($\eta_i^{(p)}$ and $\eta_j^{(p)}$) of a patient (p) extracted from the MIMIC-III database, recorded at times T (shown in Figure 4a) and $T' > T$ (shown in Figure 4b) respectively. It can be observed that both the recorded nursing notes are quite similar—the nursing note recorded at time T' records all the details in nursing note $\eta_i^{(p)}$, along with additional 'response' concerning the patient's state. To handle the voluminosity of the nursing notes and delete the near-duplicate nursing notes, we compute the ME similarity (with internal Jaro similarity scoring) score using Equation 1. The nursing notes shown in Figure 4 have an ME similarity score of 0.85, which is higher than the preset threshold



Cancer (Malignant Neoplasm), Hepatic (Liver)
Assessment: Patient is more lethargic yesterday & today than he was on Fri ([**2-10**] days ago).
Action: He was made DNR/CMO tonight, per agreement of family.
Assessment: Patient had acute SOB, midsternal chest pain, feeling that he was going to die @ [**2016**] when he rolled in bed onto bedpan & had BM. HR increased to low 70s SR. BP increased to 149/systolic. Desatted to 85%.
Action: Given 100% high flow neb, 0.5 NTP & 0.25mg IV morphine. EKG done during SOB.
Response: Pain & SOB relieved. No changes on EKG.
Plan: Now that patient is CMO, medicate w/morphine before rolling patient in bed. Continue to medicate w/Lopressor to prevent ACS as well as NTP or SL NTG, morphine & O2 during episodes.

(a) A sample nursing note ($\eta_i^{(p)}$) of a patient (p) recorded at time T.

Cancer (Malignant Neoplasm), Hepatic (Liver)
Assessment: Patient is more lethargic yesterday & today than he was on Fri ([**2-10**] days ago).
Action: He was made DNR/CMO tonight, per agreement of family.
Response: Patient and family comfortable w/this plan. Both concerned about treatment for episodes of respiratory distress/flash pulmonary edema.
Assessment: Patient had acute SOB, midsternal chest pain, feeling that he was going to die @ [**2016**] when he rolled in bed onto bedpan & had BM. HR increased to low 70s SR. BP increased to 149/systolic. Desatted to 85%.
Action: Given 100% high flow neb, 0.5 NTP & 0.25mg IV morphine. EKG done during SOB.
Response: Pain & SOB relieved. No changes on EKG.
Plan: Now that patient is CMO, medicate w/morphine before rolling patient in bed. Continue to medicate w/Lopressor to prevent ACS as well as NTP or SL NTG, morphine & O2 during episodes.

(b) A sample nursing note ($\eta_j^{(p)}$) of a patient (p) recorded at time T' ($> T$).

Figure 4: Two sample de-identified nursing notes from the MIMIC-III database. The two nursing notes are quite similar, while the only new content is the updated response (indicated as red italicized text).

of 0.825. Thus, note $\eta_j^{(p)}$ is retained, and note $\eta_i^{(p)}$ is purged.

3.3.2. Preprocessing

The next phase in the NLP pipeline is to preprocess the nursing notes to achieve data (text) normalization. Transformation of text into a canonical form allows for the separation of concerns and helps maintain consistency. Preprocessing essentially includes tokenization, stopword removal, and stemming/lemmatization. First, multiple spaces, special characters, and punctuation marks are removed. During tokenization, the clinical notes' text is split into several smaller tokens (words). Stopwords from the generated tokens are removed using the NLTK English stopword corpus [5]. Furthermore, character case folding is performed, and references to images (file names such as '*scanImage.png*') are removed. It is to be noted that, token-length based token removal was not performed to avoid the loss of important medical information (such as '*CT*' in '*CT Scan*'). Finally, stemming was performed for suffix stripping, followed by lemmatization to convert the stripped tokens to their base forms. To eliminate overfitting and lower the computational complexity, the tokens appearing in less than ten nursing notes were removed before any further processing.

3.4. Feature Extraction

Let $\mathcal{P}$ be the set of all patients. A patient ($\mathcal{P}^{(k)} \in \mathcal{P}$) has a sequence of nursing notes, $\mathbb{S}^{(k)} = \{\eta_i^{(k)}\}_{i=1}^{N^{(k)}}$, with $N^{(k)}$ total nursing notes ($\eta_i^{(k)}$s).

Each nursing note constitutes a variable length of tokens from a sizeable vocabulary $\mathbb{V}$, and each patient has a variable number of such notes, thus making $\mathbb{S}^{(k)}$ very complex. Thus, the transformation (T) of unstructured clinical text ($\mathbb{S}^{(k)}$) into an easier-to-use form (such as fixed length vector of tokens) is critically important. Thus, an effective mapping from the $\mathbb{S}$ space to $\mathbb{R}$ is attempted.

$$T : \mathbb{S}^{(k)} \longrightarrow \mathbb{R}^d \tag{3}$$

The patient information is transformed into a machine processable form, $\mathcal{P}^{(k)} = T(\mathbb{S}^{(k)})$, $\mathcal{P}^{(k)} \in \mathbb{R}^d$. To tackle the curse of dimensionality [4], usually $d \ll |\mathbb{V}|$. Although traditional dictionary and rule-based NLP transformations show good performance in certain applications, they are not automated and need manual effort to adapt them in various domains [48]. To improve the performance and effectiveness of the classification models, optimized vector representations of the underlying corpus is mandatory. To enable an exhaustive comparative study, we use six data modeling approaches as described below.

3.4.1. Vector Space Modeling of Aggregated Clinical Notes

A prominent transformation of the Bag of Words (BoW) that weighs each token in an unsupervised way, is the term weighting scheme. It is a numerical statistic that captures both the importance and specificity of a term in the given vocabulary. The weight ($W_m^{(i)}$) of a term $w_m^{(i)}$ (of total $|w^{(i)}|$ terms) in a nursing note η_i (of total N nursing notes) occurring $f_m^{(i)}$ times is given by,

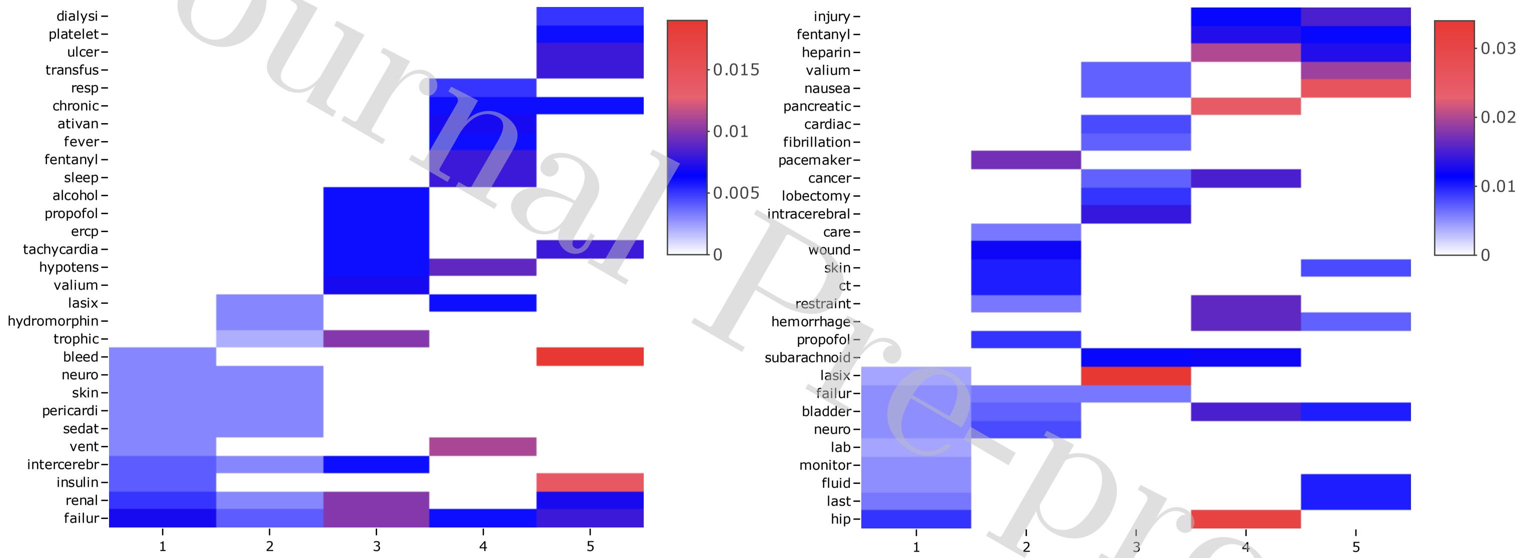
$$W_m^{(i)} = \begin{cases} \left(1 + \log_2 f_m^{(i)}\right)\left(\log_2 \frac{N}{|w^{(i)}|}\right), & \text{if } f_m^{(i)} > 0 \\ 0, & \text{otherwise} \end{cases} \tag{4}$$

The weight of every term in a patient's aggregate nursing note ($\mathcal{P}^{(k)}$) is computed to obtain a vector $\mathcal{V}^{(k)} \in \mathbb{R}^{|\mathbb{V}|}$. Now, the patient information in machine processable form, $\mathcal{P}^{(k)}_{\text{term\_weighting}} = \mathcal{V}^{(k)}$.

Due to the one-hot encoding of every word in BoW models, the resulting models suffer from high dimensionality and sparsity. Moreover, BoW models do not capture the intuition of semantically similar nursing notes having similar representations. For example, two terms with a close semantic relationship (as in '*Cancer*' and '*Melanoma*') could be mapped to two entries with large distance. Vector space embeddings cope with these shortcomings by efficiently learning the term representations in a data-driven manner. An influential work in this domain is the Doc2Vec or Paragraph Vector (PV) network. Doc2Vec aims at numerically representing variable length documents as fixed length low dimensional document embeddings (vectors). Doc2Vec is essentially a neural network with one shallow hidden layer that learns the distributed representations, to provide a content-related measurement. It incorporates semantic textual features obtained from the nursing notes text corpus. The PV Distributed Memory (PV-DM) variant of Doc2Vec was chosen over PV Distributed BoW (PV-DBoW) due to its ability to preserve the word order in the nursing notes and its comparatively superior performance [53]. The implementations in the Python Scikit-learn [65] and Gensim packages [75] were used to extract term weighting and Doc2Vec style textual features on the transcribed clinical words (extracted from aggregate nursing notes). For an exhaustive analysis, Doc2Vec dimension sizes of 500 (trained for 25 epochs) and $1,000$ (trained for 50 epochs) were used.

3.4.2. Topic Modeling of Aggregated Clinical Notes

Topic modeling can be used for finding a set of terms (topics) from a collection of documents that best represents the documents in the corpus. Traditional models of information retrieval such as Latent Semantic Analysis (LSA) [93]



(a) HDP modeled using BoW.

(b) LDA with TC modeled using BoW.

Figure 5: Correlations between top ten terms' membership in $d = 5$ topic modeling clusters obtained using aggregated nursing notes (using fuzzy similarity $\theta = 0.825$).

use a low approximation of BoW/term weight matrix by calculating the singular value decomposition of the matrix. Such models usually deal with complex matrix computations. A variant of the LSA is the probabilistic LSA [39] that combines co-existing and implicit topic data into probabilistic statistics to find potential relationships among terms.

A popular cluster analysis approach, LDA is a generative topic model based on the Bayesian framework of a three-layer structure (documents, topics, and terms). LDA generates a soft probabilistic and flat clustering of terms into topics and documents into topics. LDA posits that each (aggregate) nursing note $\eta_i^{(k)}$ of a patient $\mathcal{P}^{(k)}$ and each term belongs to a set of d ($\ll |\mathbb{V}|$) clusters (topics) $\mathcal{T}$, with some probability ρ. Thus, each nursing note is transformed as,

$$\eta_i^{(k)} \longrightarrow \mathcal{T}_i^{(k)} \in \left[\rho_{ij}^{(k)}\right]_{j=1}^{d} \text{ where } \sum_{j=1}^{d} \rho_{ij}^{(k)} = 1 \text{ and } \rho_{ij}^{(k)} \geq 0 \ \forall j \tag{5}$$

Similar to other clustering approaches, there is no simple way to determine the correct number of d LDA clusters. To cope with this issue, more complex models such as Hierarchical Bayesian Non-parametric (HDP) which automatically determine the number of clusters through posterior inference can be used. HDP is a hierarchical Bayesian non-parametric model that can model mixed-membership data with potentially infinite terms, in an unsupervised way. In LDA, only the mixture of topics is drawn from the Dirichlet distribution, while in HDP, a Dirichlet process is used to capture the uncertainty in the number of terms. For the ease of interpretation, the top ten terms' membership with five HDP clusters is shown in Figure 5a.

Probabilistic models are commonly evaluated by measuring the log-likelihood of unseen documents. As an alternative to HDP, the methods of average similarity, perplexity [90], and TC between topics can also be used to derive the optimal number of topics. Perplexity measures the quality and generalization ability of the model. However, perplexity may not always correlate with human judgment and some times the two are anti-correlated [13]. TC is a way to evaluate topic models with a much greater guarantee of human interpretability. In this paper, we adopt LDA with TC as it accounts for the semantic similarity between high scoring terms. C_v, a variant of coherence measurement is used in this study, as it accounts for high correlation with all the available human ranking data [77]. First, C_v segments each of the topic's top K tokens into token pairs. Then, it incorporates a Boolean sliding window approach in which for every window of size s sliding at one token per step, a virtual document is created. Token or token pair probabilities are computed from the total count of virtual documents. To some degree, the sliding window approach captures the proximity between tokens. Then, a confirmation (similarity) measure is used to quantify how strongly a token set supports another token set. Normalized point-wise mutual information [7] is used in this paper as a confirmation measure due to its high correlation with human interpretability. All the confirmation measures are averaged to obtain the final coherence score. The higher the coherence value, the stronger is the model's human interpretability and generalization ability. For the ease of interpretation, the top ten terms' membership with five LDA (with TC) clusters is shown in Figure 5b.

The implementations available in the Python Gensim package were used to implement LDA with TC and HDP models. To provide exhaustive analysis, HDP with truncation level set to 150 was modeled with both BoW and term weighting. Alternatively, LDA (set to 100 topics) with TC was modeled with BoW representations. Furthermore, the number of LDA topics was determined by comparing the TC scores of several LDA models obtained by varying the number of LDA topics from 2 to 500 in the increments of 100.

4. ICD-9 Code Group Prediction

ICD-9 codes are a taxonomy of diagnostic codes that are used by doctors, public health agencies, and health insurance companies across the world to classify diseases and a wide variety of infections, disorders, symptoms, causes of injury, and others. Owing to the high granularity of ICD-9 codes, researchers suggested differentiating between category-level (group) predictions and full-code predictions [51]. Each ICD-9 code group includes a set of similar diseases, and almost every health condition can be represented with a unique ICD-9 code group. In this study, we focus on ICD-9 code group predictions as a multi-label classification problem, with each patient's nursing note mapped to more than one group. All the ICD-9 codes assigned to a patient's admission are grouped into 19 diagnosis classes[3]. In this study, the Ref and V codes are classified into the same code group to lower the computational cost of training. Table 3 presents the statistics of ICD-9 code group labels extracted from MIMIC-III nursing notes.

4.1. ICD-9 Disease Code Group Prediction

In this section, we discuss the prediction algorithms employed to achieve the task of ICD-9 code group multi-label classification. We experimented with eight different prediction models conforming to various algorithmic classes including

[3] `http://tdrdata.com/ipd/ipd_SearchForICD9CodesAndDescriptions.aspx`.

Table 3: Statistics of the ICD-9 code group labels extracted from MIMIC-III nursing notes.

ICD-9 group	**ICD-9 code range**	**Diagnosis**	**#Patients (out of 6,532)**
1	001 – 139	Parasitic and infectious diseases	1,856
2	140 – 239	Neoplasms	1,319
3	240 – 279	Endocrine, immunity, metabolic, and nutritional	4,785
4	280 – 289	Blood-forming organs and blood	2,705
5	290 – 319	Mental disorders	2,614
6	320 – 389	Sense organs and nervous system	2,611
7	390 – 459	Circulatory system	5,393
8	460 – 519	Respiratory system	3,301
9	520 – 579	Digestive system	2,903
10	580 – 629	Genitourinary system	2,912
11	630 – 677	Childbirth, pregnancy, and puerperium	31
12	680 – 709	Subcutaneous tissue and skin	781
13	710 – 739	Connective tissue and musculoskeletal system	1,637
14	740 – 759	Congenital anomalies	269
15	780 – 789	Symptoms	2,432
16	790 – 796	Nonspecific abnormal findings	647
17	797 – 799	Unknown or ill-defined causes of mortality and morbidity	299
18	800 – 999	Poisoning and injury	2,978
19	Ref and V codes	Reference codes and supplemental V codes	4,853

algorithm adaptation based, problem transformation based, and ensemble models. The implementations available in the Python Scikit-learn package were used to make predictions.

4.1.1. Algorithm Adaptation Classification Models

The models in this class adapt existing machine learning algorithms for the task of multi-label classification. We used two models including K-Nearest Neighbors (KNN) and Multi-Layer Perceptron (MLP), for the prediction of ICD-9 code groups. KNN [99] is a non-parametric instance-based (non-generalizing) lazy learner used in regression and classification tasks. In KNN classification, the output class membership is determined by the majority vote of its K closest neighbors. In the sense of multi-label classification, KNN first identifies the K

closest neighbors and then, based on the statistical inferences gained from the neighboring class label sets, maximum a posteriori principle is used to determine the class label set of an unseen instance. Let $\mathbb{S} = \{\eta^{(i)}\}_{i=1}^{|\mathcal{P}|}$ be the set of all aggregate notes of $|\mathcal{P}|$ patients, and $\mathbb{Y}$ denote the set of all possible class labels. Each nursing note $\eta^{(i)}$ is mapped to a class label set $\mathcal{Y}^{(i)} \subseteq \mathbb{Y}$. For an unseen instance $\eta^{(m)}$, let $K(m)$ denote the K closest neighbors. Membership counting function for c^{th} class label ($c \in \mathbb{Y}$), based on K-closest neighbors can be computed as,

$$\text{Count}_m(c) = \sum_{n=1}^{K(m)} \mathcal{Y}^{(n)}(c), \text{ where } \mathcal{Y}^{(n)}(c) = \begin{cases} 1, & \text{if } c \in \mathcal{Y}^{(n)} \\ 0, & \text{otherwise} \end{cases} \tag{6}$$

Let $E(\text{Count}_m(c))$ denote the event ($E(\cdot)$) that $\text{Count}_m(c)$ neighbors of $\eta^{(m)}$ belong to the c^{th} class. Then, using the maximum a posteriori principle, we obtain the membership of a class label (c) as,

$$\mathcal{Y}^{(m)}(c) = \underset{s\in\{0,1\}}{\arg\max}\ \mathbf{P}(H_s^{(c)}|E(\text{Count}_m(c))),\ H_s^{(c)} = \begin{cases} E(c \in \mathcal{Y}^{(m)}), & \text{if } s = 1 \\ E(c \notin \mathcal{Y}^{(m)}), & \text{otherwise} \end{cases} \tag{7}$$

Thus, finding all class membership values will help in obtaining the multi-label classification of an unseen nursing note. In our work, 15 closest neighbors were considered (empirically determined using grid search), where closeness is weighted as the inverse of the distance between instances.

MLP (vanilla neural network) [98] is a feed-forward neural artificial network with an input layer, one or more hidden layers, and one prediction layer at the top, for classification. The first layer takes $\eta^{(m)}$ with p' clinical terms as the input and uses the output of each layer as the input to the following layer. The transformation from a layer l with the output $\mathcal{O}^{(l)}$ to the following layer with weights $W^{(l+1)}$ and biases $b^{(l+1)}$ can be represented as,

$$\mathcal{O}^{(l)} \longrightarrow W^{(l+1)}\mathcal{O}^{(l)} + b^{(l+1)} \longrightarrow \mathbf{g}(W^{(l+1)}\mathcal{O}^{(l)} + b^{(l+1)}) \longrightarrow \mathcal{O}^{(l+1)} \tag{8}$$

where $\mathbf{g}$ is a non-linear activation function such as a tanh, logistic sigmoid, or ReLU [62]. In training, to update the weights and biases, MLP uses a supervised approach called Backpropagation (BP) [78]. BP is used to calculate the gradient of the loss function to update weights, which aids the MLP to learn the internal representations, allowing it to learn any arbitrary mappings within the network. In the case of multi-label classification, while the forward pass remains the same, the classical BP algorithm uses a global error function that addresses the dependencies between the class labels. Figure 6 shows a one hidden layer feed-forward MLP network for multi-label classification. In this study, we use vanilla neural networks with one hidden layer of 75 nodes and a ReLU activation function, empirically determined using grid search.

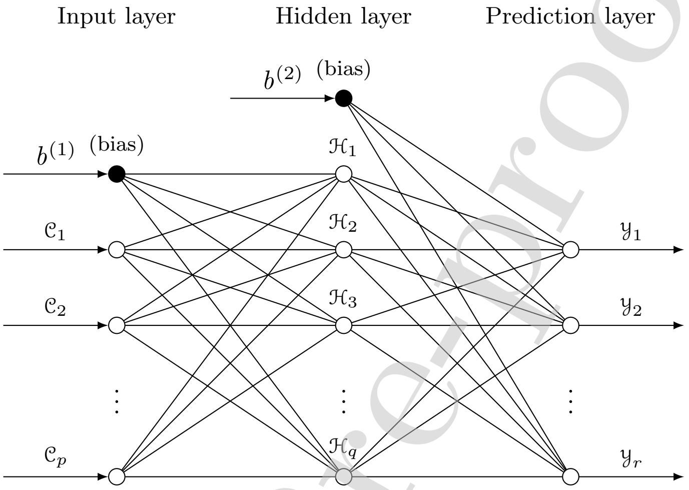


Figure 6: Multi-label classification neural network model with p input clinical terms ($\mathcal{C}_i$s), a hidden layer with q nodes ($\mathcal{H}_i$s), and r possible ICD-9 code groups ($\mathcal{Y}_i$s).

4.1.2. Problem Transformation Classification Models

These classification models aim at transforming an existing multi-label task into one or more single-label regression or classification tasks. Three classifiers including KNN, LR, and SVM were utilized as OvR classifiers in the prediction of ICD-9 diagnosis code groups. LR or maximum-entropy classification [23] is a discriminative model that models the probabilities of possible outcomes using a logistic function. The model posits that,

$$\mathbf{P}(\mathcal{Y}^{(i)}|\rho^{(i)}) = {\rho^{(i)}}^{\mathcal{Y}^{(i)}}(1-{\rho^{(i)}}^{1-\mathcal{Y}^{(i)}}), \text{ where } \rho^{(i)} = \frac{1}{1+\exp(-x_i\beta)} \tag{9}$$

where $\mathcal{Y}^{(i)}$ is a single outcome variable corresponding to x_i and following a Bernoulli probability distribution, that draws a value of 1 with ρ_i probability. The unknown parameter $\beta = (\beta_0, {\beta_1}')'$ is an $(m \times 1)$ vector, where β_0 is the scalar intercept (constant term), and β_1 is an $(m-1 \times 1)$ vector with elements corresponding to $m-1$ explanatory variables of x_i. To achieve fast convergence to the optimal solution, we used the stochastic average gradient solver.

SVM [88] is also a discriminative approach that classifies by constructing hyperplane(s) in a high-dimensional space. For a given set of linear separable training instances, SVM finds a linear rule that maximizes (optimizes) the geometric margin (street width). In practice, most of the training sets are not usually linearly separable. Now, a trade-off between minimizing prediction error and maximizing the geometric margin must be incorporated. Kernels such as tanh, sigmoid, Radial Basis Function (RBF) [64], and others are generally used to transform from the linearly inseparable space to a higher dimensional space where the points could be separated. The RBF kernel on two samples $\eta^{(i)}$ and $\eta^{(j)}$ can be defined as,

$$\mathbb{K}_{\text{RBF}}(\eta^{(i)}, \eta^{(j)}) = \exp(-\gamma \|\eta^{(i)} - \eta^{(j)}\|^2) \tag{10}$$

where γ measures the spread of the kernel. The RBF kernel defines a space that is larger than linear or polynomial kernels and has properties such as being stationary, isotropic, and infinitely smooth. Thus, in this analysis, we used SVM with an RBF kernel with γ set to 1/#features.

OvR [76] prediction strategy essentially transforms the multi-label classification problem into multiple binary relevance tasks. OvR trains a classifier for each class ($c \in \mathbb{Y}$), with the samples (aggregate nursing notes, ($\eta^{(i)}$, $\mathcal{Y}^{(i)}$)) of that class as positive ($c \in \mathcal{Y}^{(i)}$) and the remaining samples as negative ($c \notin \mathcal{Y}^{(i)}$). The base classifiers produce a real-valued confidence score for the prediction decision. Then, for an unseen instance, the combined model predicts all the class labels for which the corresponding base classifiers predicted a positive result.

4.1.3. Ensemble Classification Models

Ensemble learning approaches help in the improvement of the prediction performance by combining several learning models. Three ensemble prediction approaches including Random Forest (RF), Hard-voting Ensemble (HVE), and Stacking Ensemble (SE) were employed in the classification of ICD-9 diagnostic code groups. RF or decision tree ensembles [8] predict by constructing multiple Classification And Regression Trees (CARTs) during training and predict the output class as a function of the outputs of individual trees for the test data. At each node of the CART, a random subset of input parameters (usually of size $\sqrt{\#\text{features}}$) are chosen, and the best feature is selected based on the splitting condition. The splitting conditions are based on the threshold which is determined by optimizing a cost function (such as information gain or Gini index). In multi-label classification, multiple labels are present in the tree leaves, and the entropy is calculated as the sum of entropies of each label,

$$\text{Entropy} = -\sum_{c \in \mathbb{Y}} \rho_c \log_2(\rho_c) + (1 - \rho_c) \log_2(1 - \rho_c) \tag{11}$$

where ρ_c is the probability of class c ($\in$ the set of possible labels ($\mathbb{Y}$)). The predictions of multiple base CARTs are combined using a simple voting scheme (such as probability distribution or majority vote). In this research, we use RF with 100 CARTs of maximum depth 2, and bagging was used to obtain diversity among the base CARTs.

HVE aggregates the predictions of multiple diverse classifiers using a majority rule. Given a set of diverse classifiers (N_is) with prediction sets $\mathcal{Y}_i s$, where each $\mathcal{Y}_i$ a subset of $\mathbb{Y}$ (set of all class labels), then the presence of a class (c) in an unseen instance ($\eta^{(m)}$) can be estimated as,

$$\mathcal{Y}^{(m)}(c) = \begin{cases} 1, & \text{if } \sum\limits_{i=1}^{N} \mathcal{Y}_i^{(m)}(c) > \lceil \frac{N}{2} \rceil \\ 0, & \text{otherwise} \end{cases} \tag{12}$$

Thus, using the majority voting principle, the possible class label set for the unseen instance can be predicted. Many variations on the classifiers used in HVE were tried, starting with KNN, MLP, LR, LR as OvR, SVM as OvR, and KNN as OvR. After much experimentation, only MLP, LR as OvR, and SVM as OvR were used, due to their superior performance. Additionally, the plurality voting scheme was also tested; however, the majority voting scheme outperformed the plurality voting scheme. In this paper, we only present the performance recorded using the majority voting scheme.

SE [95] also combines discrete learning algorithms using a meta-classifier. In the first phase, all the base classifiers (N_is) are applied to the training data which generate the predictions ($\mathcal{Y}_i$s). Then, in the second phase, a meta-level dataset is created by replacing every trained record ($\eta^{(k)}$) with the predictions for that record $(\mathcal{Y}_i^{(k)})_{i=1}^{N}$. Then, another learning algorithm (L) is used to classify the meta-level dataset. On an unseen testing instance η_m, the predicted class set is $L(\mathcal{Y}_i^{(m)})_{i=1}^{N}$. In this study, MLP, LR as OvR, and SVM as OvR are used as first-level classifiers, and MLP is used as the second-level classifier. In contrast to voting, SE learns at the meta-level, when combining multiple classifiers.

4.2. Experimental Validation and Discussion

To validate the proposed approach, we performed extensive experiments over the nursing notes data obtained from the MIMIC-III database. The primary challenge is the multi-label classification, where a set of ICD-9 code groups are predicted for a given nursing note. Let $\mathbb{Y}$ denote the set of all possible labels, $\mathcal{Y}_{\text{true}}$ denote the ground truth class labels, $\mathcal{Y}_{\text{pred}}$ denote the predicted class labels, and $\mathcal{Y}_{\text{score}}$ denote the target scores which are either confidence values or probability estimates of the true class or binary decisions ($\mathcal{Y}_{\text{pred}}$). In this work, binary predictions were used as the target scores, where, pairwise comparison of predicted values and true values is performed. Seven standard evaluation metrics were used to assess the performance of each prediction algorithm with reference to each data modeling approach.

Accuracy (ACC): This metric computes the average number of correct predictions over given samples. In the case of multi-label classification, the function uses a pairwise label matching to estimate the accuracy, as per Equation 13.

$$\text{ACC}(\mathcal{Y}_{\text{true}}, \mathcal{Y}_{\text{pred}}) = \frac{1}{s}\sum_{i=1}^{s} I(\mathcal{Y}_{\text{true}_i}, \mathcal{Y}_{\text{pred}_i}) \tag{13}$$

where s is the total number of samples, and $I(x, y)$ is the indicator function and returns one only when $x = y$.

Area Under the ROC Curve (AUROC): The ROC curve is a graphical plot created by plotting sensitivity against the fall-out ($1 -$ specificity). The AUROC metric [26] indicates the probability that a prediction model will rank a randomly chosen true instance higher than a randomly chosen false instance. A greater AUROC score indicates greater performance.

Area Under the Precision-Recall Curve (AUPRC): The PR curve is a graphical plot created by plotting precision against the recall. When dealing with highly skewed datasets, the AUPRC [26] metric provides a more informative insight into the performance of the prediction algorithm. Higher the AUPRC, the better is the model's performance.

MCC Score: The Matthews correlation coefficient (ϕ-coefficient) [59] presents the essence of the correlation between the observed and the predicted binary classifications. It is a balanced score that takes into account the true/false positives and negatives. The higher the MCC score, the better the prediction is (Range $= [-1, 1]$).

F1 Score: Balanced F-measure or F1-score [82] is an indicator of the prediction accuracy, interpreted as a weighted average of precision and recall. F1 score reaches a perfect recall and precision at 1 (Range $= [0, 1]$) and is computed as,

$$\text{F}_\beta = (1+\beta^2)\frac{\text{Recall} \cdot \text{Precision}}{\text{Recall} + \beta^2 \cdot \text{Precision}}, \text{ where } \beta = 1 \tag{14}$$

Coverage Error (CE): This metric [86] evaluates the average number of labels to be included in order to cover all the true labels of the instance. It can be related to precision at the level of perfect recall, and the lesser the value of CE, the better the performance. CE is calculated as,

$$\text{CE}(\mathcal{Y}_{\text{true}}, \mathcal{Y}_{\text{score}}) = \frac{1}{s}\sum_{i=1}^{s} \max_{j:\mathcal{Y}_{\text{true}ij}=1} rank_{ij} \tag{15}$$

where s is the total number of samples, and $rank_{ij} = |\{k : \mathcal{Y}_{\text{score}ik} \geq \mathcal{Y}_{\text{true}ij}\}|$ ($|\cdot|$ is the cardinality of the set).

Label Ranking Loss (LRL): LRL [86] computes the average number of label pairs that are incorrectly ordered. The lower the LRL, the better the performance (Min = 0). LRL can be computed as,

$$\text{LRL}(\mathcal{Y}_{\text{true}}, \mathcal{Y}_{\text{score}}) = \frac{1}{s}\sum_{i=1}^{s} \frac{|(j,k) : \mathcal{Y}_{\text{true}ij} = 1, \mathcal{Y}_{\text{true}ik} = 0, \mathcal{Y}_{\text{score}_{ik}} \geq \mathcal{Y}_{\text{score}ij}|}{\|\mathcal{Y}_{\text{true}i}\|_0(|\mathbb{Y} - \|\mathcal{Y}_{\text{true}i}\|_0|)} \tag{16}$$

where s is the total number of samples, $|\cdot|$ denotes the cardinality of the set, and $\|\cdot\|_0$ denotes the l_0 norm.

4.3. Experimental Results

In this section, we report an exhaustive comparative study of the performance of various data and modeling approaches on the nursing notes of the MIMIC-III database. For the prediction task of ICD-9 code group classification, 10-fold cross-validation was performed. Furthermore, the mean and standard errors (of the mean) of the performance scores are presented. Table 4 shows the performance of all data modeling approaches and all prediction models using

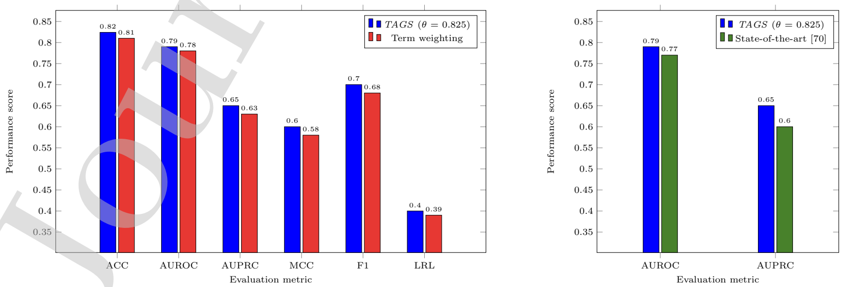


Figure 7: Comparative evaluation of the best performing models (with and without fuzzy similarity modeling) and the state-of-the-art model.

Table 4: ICD-9 code group prediction using nursing notes of MIMIC-III (using fuzzy similarity with $\theta = 0.825$).

Data model	Classifier	Performance scores						
		ACC	AUROC	AUPRC	MCC	F1	CE	LRL
TAGS $(6,532 \times 14,650)$	KNN	0.7857 ± 0.0011	0.7681 ± 0.0010	0.5904 ± 0.0016	0.5286 ± 0.0019	0.6688 ± 0.0017	18.0936 ± 0.0501	0.4181 ± 0.0018
	MLP	0.7947 ± 0.0009	0.7677 ± 0.0013	0.5987 ± 0.0018	0.5366 ± 0.0020	0.6664 ± 0.0018	18.2327 ± 0.0574	0.4226 ± 0.0024
	KNN as OvR	0.7725 ± 0.0018	0.7645 ± 0.0011	0.5738 ± 0.0021	0.5108 ± 0.0024	0.6619 ± 0.0017	**17.9385 ± 0.0791**	0.4204 ± 0.0020
	LR as OvR	**0.8239 ± 0.0011**	**0.7868 ± 0.0011**	**0.6476 ± 0.0011**	**0.5953 ± 0.0018**	**0.6981 ± 0.0016**	18.2849 ± 0.0643	**0.3978 ± 0.0021**
	SVM as OvR	0.7413 ± 0.0014	0.6801 ± 0.0011	0.5249 ± 0.0014	0.4007 ± 0.0024	0.5207 ± 0.0019	19.5542 ± 0.0206	0.5880 ± 0.0018
	RF	0.7630 ± 0.0012	0.6926 ± 0.0009	0.5486 ± 0.0014	0.4388 ± 0.0022	0.5450 ± 0.0016	19.5678 ± 0.0238	0.5728 ± 0.0014
	HVE	0.8171 ± 0.0010	0.7781 ± 0.0007	0.6367 ± 0.0007	0.5786 ± 0.0007	0.6837 ± 0.0009	18.5659 ± 0.0614	0.4132 ± 0.0014
	SE	0.7972 ± 0.0009	0.7698 ± 0.0015	0.6027 ± 0.0021	0.5421 ± 0.0016	0.6701 ± 0.0017	18.2673 ± 0.0630	0.4195 ± 0.0029
Doc2Vec 500 $(6,532 \times 500)$	KNN	0.7399 ± 0.0020	0.6628 ± 0.0027	0.5247 ± 0.0021	0.3949 ± 0.0041	0.4802 ± 0.0055	19.5644 ± 0.0278	0.6363 ± 0.0058
	MLP	0.7368 ± 0.0009	0.7102 ± 0.0012	0.5240 ± 0.0020	0.4150 ± 0.0023	0.5911 ± 0.0021	18.8039 ± 0.0450	0.5078 ± 0.0021
	KNN as OvR	0.7377 ± 0.0016	0.6674 ± 0.0024	0.5206 ± 0.0015	0.3888 ± 0.0030	0.4902 ± 0.0052	19.5144 ± 0.0269	0.6197 ± 0.0055
	LR as OvR	0.7950 ± 0.0013	0.7579 ± 0.0011	0.5970 ± 0.0018	0.5262 ± 0.0023	0.6607 ± 0.0017	**18.6491 ± 0.0375**	0.4400 ± 0.0019
	SVM as OvR	**0.8059 ± 0.0013**	**0.7666 ± 0.0010**	**0.6184 ± 0.0012**	**0.5514 ± 0.0022**	**0.6743 ± 0.0015**	18.7379 ± 0.0462	**0.4273 ± 0.0017**
	RF	0.7484 ± 0.0013	0.6787 ± 0.0010	0.5356 ± 0.0010	0.4142 ± 0.0021	0.5190 ± 0.0018	19.6208 ± 0.0225	0.5991 ± 0.0019
	HVE	0.8013 ± 0.0014	0.7636 ± 0.0011	0.6084 ± 0.0016	0.5407 ± 0.0024	0.6691 ± 0.0012	18.6652 ± 0.0149	0.4312 ± 0.0015
	SE	0.8047 ± 0.0014	0.7652 ± 0.0011	0.6164 ± 0.0008	0.5482 ± 0.0023	0.6715 ± 0.0014	18.7367 ± 0.0483	0.4296 ± 0.0017
Doc2Vec 1,000 $(6,532 \times 1,000)$	KNN	0.7322 ± 0.0018	0.6543 ± 0.0030	0.5104 ± 0.0016	0.3741 ± 0.0036	0.4650 ± 0.0062	19.6614 ± 0.0478	0.6494 ± 0.0072
	MLP	0.7458 ± 0.0011	0.7170 ± 0.0013	0.5307 ± 0.0011	0.4291 ± 0.0025	0.5989 ± 0.0015	18.8467 ± 0.0374	0.4988 ± 0.0021
	KNN as OvR	0.7376 ± 0.0017	0.6712 ± 0.0029	0.5189 ± 0.0013	0.3883 ± 0.0035	0.5020 ± 0.0057	19.5014 ± 0.0415	0.6074 ± 0.0068
	LR as OvR	0.7735 ± 0.0015	0.7414 ± 0.0017	0.5667 ± 0.0015	0.4845 ± 0.0030	0.6374 ± 0.0019	18.7376 ± 0.0526	0.4623 ± 0.0029
	SVM as OvR	**0.8067 ± 0.0012**	**0.7693 ± 0.0013**	**0.6187 ± 0.0012**	**0.5542 ± 0.0021**	**0.6762 ± 0.0016**	**18.6286 ± 0.0472**	**0.4227 ± 0.0023**
	RF	0.7464 ± 0.0012	0.6760 ± 0.0010	0.5334 ± 0.0014	0.4102 ± 0.0020	0.5136 ± 0.0018	19.6269 ± 0.0248	0.6045 ± 0.0020
	HVE	0.7904 ± 0.0015	0.7562 ± 0.0018	0.5922 ± 0.0017	0.5201 ± 0.0033	0.6566 ± 0.0022	18.6607 ± 0.0545	0.4413 ± 0.0033
	SE	0.8052 ± 0.0015	0.7680 ± 0.0013	0.6164 ± 0.0009	0.5510 ± 0.0025	0.6738 ± 0.0016	18.6683 ± 0.0402	0.4249 ± 0.0023
HDP with BoW $(6,532 \times 150)$	KNN	0.7718 ± 0.0009	0.7422 ± 0.0009	0.5723 ± 0.0017	0.4892 ± 0.0018	0.6318 ± 0.0014	18.7632 ± 0.0514	0.4629 ± 0.0014
	MLP	**0.7912 ± 0.0011**	**0.7557 ± 0.0012**	**0.5974 ± 0.0014**	**0.5255 ± 0.0019**	**0.6502 ± 0.0019**	**18.6689 ± 0.0330**	**0.4464 ± 0.0022**
	KNN as OvR	0.7682 ± 0.0008	0.7397 ± 0.0010	0.5661 ± 0.0019	0.4822 ± 0.0018	0.6275 ± 0.0014	18.7482 ± 0.0380	0.4666 ± 0.0016
	LR as OvR	0.7815 ± 0.0010	0.7417 ± 0.0011	0.5850 ± 0.0014	0.5017 ± 0.0020	0.6251 ± 0.0016	18.9294 ± 0.0476	0.4729 ± 0.0020
	SVM as OvR	0.7511 ± 0.0011	0.6875 ± 0.0008	0.5410 ± 0.0015	0.4245 ± 0.0019	0.5284 ± 0.0017	19.4253 ± 0.0279	0.5827 ± 0.0015
	RF	0.7574 ± 0.0015	0.6915 ± 0.0014	0.5486 ± 0.0017	0.4359 ± 0.0028	0.5412 ± 0.0023	19.5291 ± 0.0314	0.5751 ± 0.0026
	HVE	0.7826 ± 0.0013	0.7404 ± 0.0015	0.5869 ± 0.0008	0.5029 ± 0.0022	0.6229 ± 0.0020	18.9688 ± 0.0626	0.4767 ± 0.0029
	SE	0.7851 ± 0.0008	0.7453 ± 0.0008	0.5874 ± 0.0014	0.5083 ± 0.0013	0.6317 ± 0.0006	18.7915 ± 0.0498	0.4660 ± 0.0014
HDP with term weighting $(6,532 \times 150)$	KNN	0.7116 ± 0.0015	0.6723 ± 0.0018	0.4887 ± 0.0023	0.3479 ± 0.0034	0.5254 ± 0.0031	19.3027 ± 0.0297	**0.5724 ± 0.0028**
	MLP	0.7409 ± 0.0016	0.6779 ± 0.0027	0.5245 ± 0.0014	0.3997 ± 0.0028	0.5158 ± 0.0056	19.5698 ± 0.0277	0.5940 ± 0.0069
	KNN as OvR	0.7076 ± 0.0014	0.6689 ± 0.0018	0.4842 ± 0.0024	0.3399 ± 0.0034	0.5213 ± 0.0031	**19.2999 ± 0.0269**	0.5764 ± 0.0028
	LR as OvR	0.7458 ± 0.0014	0.6780 ± 0.0010	0.5310 ± 0.0019	0.4082 ± 0.0027	0.5161 ± 0.0017	19.5929 ± 0.0258	0.5987 ± 0.0019
	SVM as OvR	0.7413 ± 0.0014	0.6801 ± 0.0011	0.5249 ± 0.0014	0.4007 ± 0.0024	0.5207 ± 0.0019	19.5542 ± 0.0206	0.5880 ± 0.0018
	RF	**0.7557 ± 0.0010**	**0.6880 ± 0.0008**	**0.5376 ± 0.0012**	**0.4257 ± 0.0017**	**0.5359 ± 0.0015**	19.4695 ± 0.0268	0.5800 ± 0.0015
	HVE	0.7414 ± 0.0017	0.6801 ± 0.0013	0.5249 ± 0.0015	0.4007 ± 0.0029	0.5207 ± 0.0023	19.5542 ± 0.0083	0.5880 ± 0.0022
	SE	0.7414 ± 0.0017	0.6801 ± 0.0013	0.5249 ± 0.0015	0.4007 ± 0.0029	0.5207 ± 0.0023	19.5542 ± 0.0083	0.5880 ± 0.0022
LDA with TC $(6,532 \times 100)$	KNN	0.7883 ± 0.0016	0.7512 ± 0.0015	0.5939 ± 0.0014	0.5201 ± 0.0029	0.6440 ± 0.0021	18.7220 ± 0.0465	0.4554 ± 0.0025
	MLP	**0.8037 ± 0.0010**	**0.7657 ± 0.0014**	**0.6181 ± 0.0016**	**0.5544 ± 0.0021**	**0.6663 ± 0.0020**	**18.5933 ± 0.0463**	**0.4341 ± 0.0026**
	KNN as OvR	0.7838 ± 0.0012	0.7479 ± 0.0010	0.5859 ± 0.0008	0.5098 ± 0.0017	0.6389 ± 0.0015	18.7532 ± 0.0544	0.4593 ± 0.0019
	LR as OvR	0.8018 ± 0.0010	0.7644 ± 0.0012	0.6157 ± 0.0014	0.5505 ± 0.0019	0.6624 ± 0.0017	18.6514 ± 0.0467	0.4361 ± 0.0023
	SVM as OvR	0.7773 ± 0.0014	0.7272 ± 0.0013	0.5852 ± 0.0016	0.4949 ± 0.0026	0.5999 ± 0.0021	19.1559 ± 0.0464	0.5087 ± 0.0025
	RF	0.7569 ± 0.0014	0.6945 ± 0.0011	0.5531 ± 0.0013	0.4415 ± 0.0023	0.5462 ± 0.0019	19.4421 ± 0.0404	0.5694 ± 0.0022
	HVE	0.8018 ± 0.0011	0.7633 ± 0.0011	0.6160 ± 0.0011	0.5498 ± 0.0017	0.6607 ± 0.0012	18.6970 ± 0.0587	0.4384 ± 0.0020
	SE	0.7983 ± 0.0012	0.7570 ± 0.0010	0.6096 ± 0.0012	0.5408 ± 0.0017	0.6504 ± 0.0013	18.7473 ± 0.0621	0.4513 ± 0.0017

nursing notes processed using fuzzy token-based similarity with $\theta = 0.825$. Table 5 tabulates the performance of all data modeling approaches and all prediction models using nursing notes processed without similarity. We observe that the Term weighting of unstructured (nursing) notes AGgregated using fuzzy Similarity ($TAGS$) model, modeled with LR as OvR, consistently outperforms more complex vector space and topic models. Furthermore, it can be observed from Figure 7 that, the model's performance is higher when nursing notes are processed with similarity, than when processed without similarity.

Table 5: ICD-9 code group prediction using nursing notes of MIMIC-III (without similarity modeling).

Data model	**Classifier**	**Performance scores**						
		ACC	**AUROC**	**AUPRC**	**MCC**	**F1**	**CE**	**LRL**
Term weighting (6, 532 × 14, 665)	KNN	0.7866 ± 0.0012	0.7689 ± 0.0016	0.5920 ± 0.0025	0.5306 ± 0.0032	0.6697 ± 0.0021	18.0463 ± 0.0691	0.4168 ± 0.0027
	MLP	0.7962 ± 0.0011	0.7694 ± 0.0015	0.6009 ± 0.0026	0.5400 ± 0.0029	0.6685 ± 0.0024	18.2134 ± 0.0530	0.4199 ± 0.0026
	KNN as OvR	0.7741 ± 0.0017	0.7662 ± 0.0014	0.5764 ± 0.0027	0.5144 ± 0.0032	0.6639 ± 0.0020	**18.1744 ± 0.0644**	0.4179 ± 0.0023
	LR as OvR	**0.8143 ± 0.0014**	**0.7804 ± 0.0017**	**0.6378 ± 0.0032**	**0.5845 ± 0.0035**	**0.6874 ± 0.0030**	18.2934 ± 0.0389	**0.3985 ± 0.0030**
	SVM as OvR	0.7414 ± 0.0015	0.6801 ± 0.0015	0.5249 ± 0.0026	0.4007 ± 0.0036	0.5207 ± 0.0028	19.5542 ± 0.0368	0.5880 ± 0.0024
	RF	0.7653 ± 0.0011	0.6951 ± 0.0013	0.5517 ± 0.0024	0.4449 ± 0.0031	0.5484 ± 0.0023	19.5449 ± 0.0387	0.5695 ± 0.0022
	HVE	0.8064 ± 0.0014	0.7782 ± 0.0014	0.6369 ± 0.0031	0.5788 ± 0.0032	0.6832 ± 0.0026	18.5193 ± 0.0489	0.4132 ± 0.0023
	SE	0.7971 ± 0.0013	0.7693 ± 0.0018	0.6017 ± 0.0032	0.5412 ± 0.0034	0.6682 ± 0.0029	18.2290 ± 0.0363	0.4207 ± 0.0030
Doc2Vec 500 (6, 532 × 500)	KNN	0.7134 ± 0.0013	0.5986 ± 0.0021	0.4719 ± 0.0024	0.3111 ± 0.0040	0.3323 ± 0.0059	19.9011 ± 0.0208	0.7824 ± 0.0048
	MLP	0.7370 ± 0.0011	0.7081 ± 0.0017	0.5217 ± 0.0022	0.4113 ± 0.0029	0.5885 ± 0.0026	18.8870 ± 0.0421	0.5113 ± 0.0028
	KNN as OvR	0.7177 ± 0.0013	0.6091 ± 0.0020	0.4783 ± 0.0020	0.3167 ± 0.0035	0.3627 ± 0.0054	19.8782 ± 0.0171	0.7533 ± 0.0048
	LR as OvR	0.7970 ± 0.0007	0.7586 ± 0.0009	0.5999 ± 0.0020	0.5291 ± 0.0016	0.6659 ± 0.0016	**18.6661 ± 0.0346**	0.4382 ± 0.0017
	SVM as OvR	**0.8068 ± 0.0010**	**0.7678 ± 0.0012**	**0.6206 ± 0.0024**	**0.5527 ± 0.0025**	**0.6774 ± 0.0018**	18.7267 ± 0.0269	**0.4245 ± 0.0021**
	RF	0.7490 ± 0.0014	0.6801 ± 0.0016	0.5351 ± 0.0027	0.4142 ± 0.0037	0.5232 ± 0.0029	19.6314 ± 0.0357	0.5942 ± 0.0027
	HVE	0.8011 ± 0.0006	0.7627 ± 0.0008	0.6083 ± 0.0024	0.5387 ± 0.0013	0.6701 ± 0.0011	18.6705 ± 0.0216	0.4318 ± 0.0014
	SE	0.8054 ± 0.0009	0.7659 ± 0.0010	0.6179 ± 0.0028	0.5489 ± 0.0022	0.6740 ± 0.0018	18.7635 ± 0.0400	0.4279 ± 0.0018
Doc2Vec 1, 000 (6, 532 × 1, 000)	KNN	0.7141 ± 0.0016	0.6058 ± 0.0026	0.4754 ± 0.0028	0.3192 ± 0.0045	0.3520 ± 0.0069	19.8945 ± 0.0179	0.7643 ± 0.0058
	MLP	0.7442 ± 0.0011	0.7159 ± 0.0017	0.5312 ± 0.0024	0.4270 ± 0.0030	0.5995 ± 0.0027	18.8172 ± 0.0321	0.4992 ± 0.0028
	KNN as OvR	0.7162 ± 0.0018	0.6112 ± 0.0034	0.4781 ± 0.0037	0.3219 ± 0.0058	0.3671 ± 0.0091	19.8661 ± 0.0200	0.7493 ± 0.0076
	LR as OvR	0.7749 ± 0.0005	0.7425 ± 0.0007	0.5698 ± 0.0018	0.4864 ± 0.0017	0.6418 ± 0.0015	18.7278 ± 0.0397	0.4592 ± 0.0010
	SVM as OvR	**0.8071 ± 0.0009**	**0.7684 ± 0.0012**	**0.6194 ± 0.0027**	**0.5528 ± 0.0026**	**0.6768 ± 0.0022**	18.6731 ± 0.0429	**0.4239 ± 0.0020**
	RF	0.7455 ± 0.0014	0.6760 ± 0.0014	0.5313 ± 0.0023	0.4077 ± 0.0032	0.5138 ± 0.0025	19.6283 ± 0.0375	0.6034 ± 0.0025
	HVE	0.7915 ± 0.0009	0.7559 ± 0.0014	0.5943 ± 0.0037	0.5200 ± 0.0035	0.6588 ± 0.0029	**18.6419 ± 0.0225**	0.4410 ± 0.0022
	SE	0.8061 ± 0.0011	0.7674 ± 0.0013	0.6179 ± 0.0035	0.5508 ± 0.0032	0.6750 ± 0.0025	18.6649 ± 0.0241	0.4256 ± 0.0022
HDP with BoW (6, 532 × 150)	KNN	0.7778 ± 0.0011	0.7505 ± 0.0014	0.5792 ± 0.0024	0.5033 ± 0.0027	0.6407 ± 0.0019	18.5832 ± 0.0558	0.4502 ± 0.0024
	MLP	**0.7946 ± 0.0013**	**0.7574 ± 0.0016**	**0.6026 ± 0.0031**	**0.5336 ± 0.0036**	**0.6518 ± 0.0028**	18.6202 ± 0.0417	**0.4467 ± 0.0028**
	KNN as OvR	0.7733 ± 0.0013	0.7476 ± 0.0017	0.5726 ± 0.0030	0.4949 ± 0.0037	0.6367 ± 0.0026	**18.5783 ± 0.0456**	0.4536 ± 0.0027
	LR as OvR	0.7878 ± 0.0016	0.7453 ± 0.0020	0.5932 ± 0.0030	0.5183 ± 0.0042	0.6307 ± 0.0033	18.7679 ± 0.0444	0.4723 ± 0.0033
	SVM as OvR	0.7623 ± 0.0014	0.6926 ± 0.0017	0.5510 ± 0.0029	0.4450 ± 0.0038	0.5411 ± 0.0032	19.5415 ± 0.0398	0.5776 ± 0.0029
	RF	0.7619 ± 0.0015	0.6982 ± 0.0017	0.5535 ± 0.0029	0.4468 ± 0.0039	0.5563 ± 0.0030	19.5531 ± 0.0314	0.5606 ± 0.0030
	HVE	0.7886 ± 0.0011	0.7438 ± 0.0016	0.5941 ± 0.0027	0.5183 ± 0.0029	0.6286 ± 0.0024	18.8647 ± 0.0482	0.4759 ± 0.0031
	SE	0.7886 ± 0.0006	0.7431 ± 0.0011	0.5935 ± 0.0023	0.5172 ± 0.0017	0.6288 ± 0.0018	18.8853 ± 0.0417	0.4766 ± 0.0022
HDP with term weighting (6, 532 × 150)	KNN	0.7108 ± 0.0010	0.6718 ± 0.0018	0.4885 ± 0.0025	0.3476 ± 0.0030	0.5262 ± 0.0026	**19.3230 ± 0.0378**	**0.5728 ± 0.0027**
	MLP	0.7413 ± 0.0014	0.6783 ± 0.0016	0.5253 ± 0.0029	0.4009 ± 0.0037	0.5167 ± 0.0033	19.5623 ± 0.0396	0.5934 ± 0.0046
	KNN as OvR	0.7067 ± 0.0012	0.6685 ± 0.0020	0.4837 ± 0.0028	0.3393 ± 0.0036	0.5221 ± 0.0029	19.3410 ± 0.0392	0.5767 ± 0.0030
	LR as OvR	0.7455 ± 0.0016	0.6779 ± 0.0016	0.5301 ± 0.0030	0.4072 ± 0.0041	0.5161 ± 0.0030	19.5868 ± 0.0369	0.5984 ± 0.0026
	SVM as OvR	0.7414 ± 0.0015	0.6801 ± 0.0015	0.5249 ± 0.0026	0.4007 ± 0.0036	0.5207 ± 0.0028	19.5542 ± 0.0368	0.5880 ± 0.0024
	RF	**0.7559 ± 0.0012**	**0.6862 ± 0.0018**	**0.5386 ± 0.0030**	**0.4259 ± 0.0039**	**0.5313 ± 0.0033**	19.4848 ± 0.0370	0.5854 ± 0.0030
	HVE	0.7444 ± 0.0023	0.6789 ± 0.0012	0.5286 ± 0.0038	0.4058 ± 0.0049	0.5179 ± 0.0023	19.5742 ± 0.0588	0.5948 ± 0.0031
	SE	0.7413 ± 0.0016	0.6800 ± 0.0010	0.5248 ± 0.0025	0.4007 ± 0.0031	0.5206 ± 0.0024	19.5566 ± 0.0507	0.5882 ± 0.0015
LDA with TC (6, 532 × 100)	KNN	0.7872 ± 0.0011	0.7517 ± 0.0012	0.5937 ± 0.0023	0.5197 ± 0.0027	0.6449 ± 0.0024	18.7065 ± 0.0454	0.4539 ± 0.0020
	MLP	**0.8039 ± 0.0011**	**0.7669 ± 0.0014**	**0.6182 ± 0.0025**	**0.5547 ± 0.0028**	**0.6681 ± 0.0023**	**18.5665 ± 0.0489**	**0.4311 ± 0.0025**
	KNN as OvR	0.7824 ± 0.0008	0.7482 ± 0.0013	0.5851 ± 0.0022	0.5087 ± 0.0026	0.6392 ± 0.0021	18.7217 ± 0.0364	0.4581 ± 0.0021
	LR as OvR	0.8018 ± 0.0013	0.7639 ± 0.0014	0.6152 ± 0.0027	0.5497 ± 0.0033	0.6626 ± 0.0025	18.6916 ± 0.0466	0.4367 ± 0.0024
	SVM as OvR	0.7778 ± 0.0016	0.7297 ± 0.0015	0.5858 ± 0.0028	0.4961 ± 0.0036	0.6050 ± 0.0027	19.1415 ± 0.0275	0.5024 ± 0.0025
	RF	0.7587 ± 0.0015	0.6962 ± 0.0013	0.5527 ± 0.0027	0.4424 ± 0.0032	0.5487 ± 0.0024	19.4452 ± 0.0393	0.5655 ± 0.0022
	HVE	0.8009 ± 0.0009	0.7613 ± 0.0009	0.6141 ± 0.0022	0.5469 ± 0.0020	0.6584 ± 0.0018	18.7753 ± 0.0523	0.4423 ± 0.0019
	SE	0.7975 ± 0.0011	0.7566 ± 0.0013	0.6078 ± 0.0027	0.5388 ± 0.0023	0.6509 ± 0.0025	18.7774 ± 0.0599	0.4510 ± 0.0029

4.4. Discussion

In clinical tasks such as disease prediction, capturing true/false positives and true/false negatives is of utmost importance, due to the critical nature of the task itself. As can be seen from the results in Tables 4 and 5, the AUROC metric captures the hit and miss rates, while AUPRC captures the number of true positives from positive predictions. AUPRC, unlike AUROC, varies with the change in the ratio of target classes in the data, and hence is more revealing while evaluating imbalanced data [79]. From Table 3, it can be observed that the dataset is highly class imbalanced, and hence AUPRC is more informative than AUROC. It can be seen that our approach outperforms the existing state-of-the-art method [70] in these metrics, indicating the significant decrease in the false positives and false negatives. F1-measure captures both precision and recall of the prediction, while MCC score serves as a balanced measure even with class imbalance, as it takes into account true positives, false positives, and false negatives. More specifically, in healthcare applications like disease or diagnosis prediction, false negatives (prediction miss, i.e., a disease which is present, but not diagnosed) are likely to cause more harm than false positives (false alarm) and CE captures these false negatives. LRL performs a pairwise label comparison to determine the loss of prediction. Existing works have benchmarked their performance using only AUROC and AUPRC metrics. Since all the metrics used in this research are very relevant and essential in understanding the proposed model's predictive power, we benchmark these promising results for MIMIC-III database.

Furthermore, the state-of-the-art work by Purushotham et al. [70] is built on structured EHRs that are modeled in the form of feature sets to make clinical predictions. It is a fact that the richness and abundance of information captured by unstructured nursing notes are often lost in the structured EHRs coding process [29]. Our proposed *TAGS* model combines the fuzzy similarity based data cleansing and aggregating approach with a term weighting scheme that captures the importance and rarity of clinical concepts, to model the informally written clinical nursing text into a clinically relevant and usable format effectively. From the results, it can be seen that more complex data modeling approaches such as Doc2Vec and HDP, in contrast to the *TAGS* model, fail to capture all the discriminative features of the clinical nursing notes needed for the machine learning classifier to learn and generalize. We observe that using the *TAGS* model, risk stratification can be achieved well in advance, with an overall accuracy of 82.4%. Also, it can be noted that token-based similarity processing of nursing notes yields higher performance in comparison to that processed without similarity. These promising results emphasize the need for reduction in redundancy and anomalous data for relieving the cognitive burden and improving the clinical decision-making process. CDSSs built on the predictive capabilities of *TAGS* could be suitable for patient-centric and evidence-based treatments, resulting in reduced mortality rates and better risk assessment.

5. Concluding Remarks

In this paper, vector space and topic modeling approaches for multi-label classification of unstructured nursing notes were presented, which capture the semantic information in the nursing notes effectively and leverage such information for disease prediction. The nursing notes were aggregated using a fuzzy token-based similarity matching approach, on which several classification models were built. Exhaustive benchmarking experimentation results on the nursing notes of the MIMIC-III database were presented. We demonstrated that fuzzy token-based similarity processing of nursing notes provides optimal data representation and eliminates anomalous and redundant data, in turn, improving the clinical decision-making process. Furthermore, we observed that the *TAGS* model consistently outperformed other complex vector space and topic modeling approaches by effectively capturing the discriminative features of the nursing notes. The *TAGS* model also achieved superior predictive performance when benchmarked against the state-of-the-art method with 7.79% improvement in terms of AUPRC and 1.24% improvement in terms of AUROC.

The improvement in prediction accuracy though small, is still significant, as our model utilizes unstructured clinical text, in contrast to the state-of-the-art model. Thus, the dependency on availability of structured EHRs for building CDSSs can be eliminated, which is advantageous in countries with low EHR adoption rates. The experimental results highlight the richness of information that our model was able to capture from the clinical nursing notes, highlighting the viability of using unstructured clinical data in disease prediction applications. As a part of future work, we intend to validate the proposed *TAGS* model on real-time clinical data and enhance the prediction capabilities further, focusing on the need for time-aware prediction architectures in hospital scenarios. Furthermore, we aim at exploring the power of deep learning architectures in clinical prediction tasks such as disease prediction, length of stay prediction, hospital readmission, and phenotype classification.

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