Assessing patient similarity through representation learning on medical records

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Patient similarity assessments, which identify patients similar to a given patient, can help improve medical care. They can be performed using electronic medical records (EMRs). This makes it necessary to convert heterogeneous EMRs into comparable formats to calculate their distance. While versatile document representation learning methods were developed in recent years, it is still unclear how complex EMR data should be processed to create the most useful patient representations.

This study presents a new data representation method for EMRs that accounts for information in clinical narratives. To address the limitations of previous approaches, we propose an unsupervised method for building a patient representation that utilizes unstructured data integrated with structured data extracted from patients’ EMR. For modeling extracted data, we employ a tree structure that captures the temporal relations of multiple medical events from EMR. We process clinical notes to extract symptoms, signs, and diseases using different tools such as Medspacy, MetaMap, and Scispacy and map entities to UMLS. After creating a tree data structure, we utilize two novel relabeling methods for the non-leaf nodes of the tree to capture two kinds of temporal aspects in extracted events. By traversing the tree, we generate a sequence that can be used to create an embedding vector for each patient.

We extensively evaluate the proposed method across patient similarity and prediction tasks, and demonstrate that our methodology leads to lower mean squared error (MSE) and higher precisions and normalized discounted cumulative gain (NDCG) relative to baselines.

CCS CONCEPTS • Health informatics • Language models

Additional Keywords and Phrases: Patient similarity analytics, Patient representation learning, Natural language processing

1 INTRODUCTION

Patient similarity assessment identifies patients similar to a given patient. It allows physicians to derive insights from the records of matching patients to provide better treatment [1]. Calculating patient similarity requires measuring the distance among patients within a population [2]. A distance could be calculated based on various structured and unstructured data types in an electronic medical record (EMR).

EMRs can be processed in the same way as general documents modeled as sequences of words. The difference is that EMRs are sequences of patient events such as diagnoses, procedures, and medications. The representation of an EMR is a low-dimension and
fixed-length embedding vector, so it can be used as an indicator to measure similarity between patients, just as a representation of a document can be used to measure similarity between documents.

In previous works on patient representations based on EMRs, some have relied on structured data types [3, 4, 5, 6, 7], while others only used unstructured data [8, 9]. Not many have combined both structured and unstructured data [10, 11]. Structured data types register using controlled vocabulary; on the other hand, unstructured data is written in natural language. Medications and diagnoses are an example of structured data. Clinical notes such as discharge sheets are unstructured data in EMRs. Many valuable patient details such as past illnesses, signs, and symptoms have been recorded only in clinical notes.

A new patient representation model is presented that utilizes structured and unstructured parts of EMRs and captures some aspects of the temporal relationship between extracted medical events from EMRs. This patient representation is tree-structured and is motivated by [7]. We used the tree structure to model the medical events extracted from EMR and to show temporal aspects such as co-concurrency of the medical events. These make it possible to generate rich sequences after traversing the tree, which maintains the temporal relations of medical events at different levels. These sequences are used as input to the document representation algorithm.

In addition to the structured information, we use unstructured information to construct the tree model. The sequences generated from the tree traversal contain valuable information about diseases, signs, and symptoms extracted from clinical notes. Due to using relabeling approaches that we apply to the tree model, the generated sequence preserves co-occurrence medical events. It considers previous diseases detected in past medical history and could affect the current patient’s medical situation. By applying the representation method to the generated document, embedding vectors are created that can be used in downstream processes. We use the embedding vector in the patient similarity task.

In this study, we demonstrate that clinical notes in the representation reduced mean squared error (MSE) and improved precision and normalized discounted cumulative gain (NDCG) compared to when this type of data was not used. Additionally, the results demonstrate the effectiveness of the tree structure method. We summarize the contributions of this study as follow:

1. **UTTTree**: Proposing a new patient representation based on integrating unstructured and structured data in EMR that modeled as a tree-based structure; applying new relabeling approaches on the tree for enriching the resulting sequence generated by traversing the tree.
2. **UTTTree-II**: Enhancing the model by additional temporal aspect by including the extracted medical events from the patient’s past medical history in EMR.
3. **Evaluating** produced embedding on downstream tasks, including patient similarity and prediction tasks.

### 2 RELATED WORK

In this section, we provide a classification of patient representation methods based on different perspectives such as data type, information aggregation strategy, time modeling methods, similarity metrics, downstream task type, and technology:

**Data Type**: This category is based on the type of data used for generating patient representations. Some studies used only structured data in EMR, such as diagnostic codes or drugs and laboratories, recorded using terminology systems. Choi et al. [3] used the word2vec method [12, 13] to represent diagnostic codes. Furthermore, Choi et al. [14] combined the vector resulting from the representation of the diagnostic code with the representation of the patient. This model was used to predict heart failure. The representations created by Miotto et al. [11] were based on clinical notes and structured data. Their results outperformed Choi et al. [14] in the disease prediction task. Miotto et al. [11] used the autoencoder method for representation. In contrast, Choi et al. [14] showed that the autoencoder method is not better than other baselines in predicting disease when the structured data is used alone. Using these results, we can infer the importance of clinical notes in creating a patient representation of EMRs.

Alternatively, some studies utilize clinical notes to represent patients. Dligach et al. [15] reported that clinical notes could produce results comparable to other methods. In the TAPER [10], they represent the clinical note with a Transformer model. It was shown that clinical notes used in combination with structured data outperformed clinical notes used alone. These conflicting results suggest the need for further studies on the benefits of combining structured data and unstructured clinical notes.

Previous research used different approaches to clinical notes processing methods can be classified based on involving named entity recognition (NER), annotation, and normalization using UMLS [15, 16, 17, 18] or not using normalization [8, 10]. NER identifies and aligns biomedical entities to knowledge bases, enhancing decision-making efficiency [19]. Previous research has not verified the effects of NER and normalization using UMLS on the patient similarity task.

A variety of text representation methods was used in the studies, such as Doc2vec [7], topic modeling [11], autoencoder [8], and pre-trained BERT [10]. Furthermore, the TAPER [10] method, which uses transformer-based models on clinical notes, shows better results than [11]. However, comparing these results is difficult due to the variety of datasets used, how medical codes are grouped, and the diversity of the tasks and ablation evaluations.
**Fusion strategy:** Data fusion of multiple sources yields more accurate, more consistent, and more helpful information than any single data source can provide. Data fusion processes are often categorized as late and early [20]. The kind of fusion strategy is another issue that has not been discussed in many previous studies [21]. The majority of previous studies employed late fusion. During late fusion, information from different types of data is represented separately. For example, in [10], the resulting vectors are merged to form the patient representation. Then the resulting embedding vectors are merged to form patient representation. By contrast, data in early fusion is integrated before being represented. Henriksson et al. [16] determined that an early fusion strategy performed better than late fusion for ADR identification.

**Time modeling methods:** Regardless of the type of data and fusion strategy, modeling time data is one of the essential aspects we evaluated in previous studies. Based on how they are modeled in the time dimension, studies can be divided into four categories: 1- Studies that use medical events regardless of their timing ([8, 11, 15]). 2- Studies that take into account the chronological order of events. 3- Studies that take into consideration time irregularities along with chronology by accounting for a time window [7, 5, 22, 23, 24, 25, 26]. Windows intervals vary from five minutes to one year. 4- Studies that give importance to recent events [23]. The first group cannot provide a comprehensive case explanation regarding the importance of prioritization and latency in medical decision-making. In the second group of studies, the interval between events is not taken into account. The third group uses a time window and normalizes the event duration based on its length. As a result of the wide range of time intervals (from five minutes to one year), a comparison is impossible. There is no consideration of some chronic or effective diseases that have occurred in the past and can influence the patient’s present condition.

**Similarity metrics:** The patient representation has been applied to a wide range of applications and downstream tasks. One such task is patient similarity. We explore how patient similarity is measured in previous research in this sub-section. Methods in which similarity was determined by measuring the distance between embedding vectors of different data types can be found in studies like [27, 28, 29, 30, 31]. However, determining patient similarity based on patient representation has received less attention. Pokharel et al. [7] used a combination of structured data in a tree model. They presented a method for evaluating based on final diagnoses. This evaluating method is inspired by Gottlieb et al. [28]. However, the priority of the final diagnosis recorded for the patient is considered in it. We have followed the same approach in this study. The most used similarity metric was the calculation of cosine distance [11, 7], Euclidean [32], and Mahalanobis [33]. Comparing the performance of different metrics in the patient similarity tasks requires further investigation.

According to a review of the methods, it is evident that representing patient information is receiving attention from researchers. Aside from the aspects mentioned above, the studies differ in the downstream tasks and the technology used. However, variations in datasets and different experimental designs make it difficult to compare the reported results. Table 1 presents some characteristics of studies in this area.

**Table 1:** Comparative table of the number of studies in the field of patient representation

| Reference Number | Year | Unstructured data | Unsupervised (U) | Supervised (S) | Learning manner | Method | Downstream Tasks (Evaluation metric, result) | Time order based | UMLS alignment | Fusion strategy |
|------------------|------|------------------|------------------|----------------|----------------|--------|---------------------------------------------|----------------|---------------|----------------|
| [22]             | 2015 | S                |                  |                |                | Deep Boltzmann machine | Prediction: (Disease, only utilizes 70 most frequent ICD-9 codes) | ✓              | ×             | L              |
| [11], Deep Patient |      |                  |                  |                |                | Autoencoder | Prediction: (Disease, AUC=0.773) | ×              | ×             | L              |
| [14], Med2vec    | 2016 | S                | ✓                | ✓              |                | Word2Vec | AUC = 0.93, Accuracy = 0.84 | ×              | ×             | L              |
| [23]             | 2016 | U                | ✓                | ✓              | ✓              | Word2Vec | Prediction: (Disease, on 80 diagnosis AUC =0.67) | ✓              | ×             | E              |
| [34]             |      | U                | ✓                | ✓              | ✓              | Word2Vec | Prediction: (Disease -heart failure, AUC =0.82) | ✓              | ×             | L              |
| [16]             |      | U                | ✓                | ✓              | ✓              | Word2Vec | Prediction: (ADE-related diagnoses, AUC=0.93, Accuracy = 0.84) | ✓              | ×             | L              |
| [25]             |      | U                | ✓                | ✓              | ✓              | CNN Based | Prediction: (Readmission, AUC =0.750) | ✓              | ×             | L              |
| [35]             | 2017 | U                | ✓                | ✓              | ✓              | RNN-Based | Prediction: (Disease (heart failure), AUC =0.883) | ✓              | ×             | L              |
| [15]             |      | S                |                  |                |                | Autoencoder | Prediction: (Billing code, Precision=0.709, Recall=0.725, F1=0.715) | ✓              | ✓             | L              |
The review of previous studies’ findings motivates us to use clinical texts in modeling and measuring patient similarity and, therefore, current study design by focusing on the most meaningful use of clinical notes and considering the relationship of this information with a structured data time dimension. Due to some contradictory results in previous studies, we have tried to design the experiments to compare the effect of each of the characteristics preserved in the model’s design.

3 METHODOLOGY

This work proposes a new patient representation (UTTree) based on integrating structured and unstructured parts of EMR. Fig. 1 shows the workflow of the proposed method.

3.1. The UTTree

This workflow takes as input a database containing the various types of information recorded in the EMRs of several patients, and its output is the degree of similarity between both patients. According to the proposed algorithm, the degree of similarity is calculated by comparing the cosine distance of the embedded vectors generated for each patient. To evaluate the accuracy of the obtained similarity scores, we recorded the final diagnoses for each patient to create a gold standard described in section 3.3. The output of the proposed algorithm is compared with the ideal similarity scores. This section continues with an explanation of the different parts of the workflow. This workflow consists of five main steps, which are described below:
Figure 1 - Overview of the proposed method. First, EMR data for each patient is taken from the dataset (1-a). After that, structured and unstructured data are preprocessed separately (1-b). For homogenizing the preprocessed data, we use a data structure called the quadruple (1-c). To develop a tree structure, we apply quadruples (2-a). Next, we conduct a relabeling process for creating compound information in non-leaf nodes (2-b). As a result of traversing the tree (3-a), rich sequences are obtained (3-b), which are used as inputs for the document representation algorithm (4-a) to generate embedding vectors for patients (4-b). Finally, the cosine distance between the vectors is considered as a similarity score. For each patient, k patients that are most similar are returned (5).

**Data Preprocessing:** In the first phase, the goal is to identify a person's previous and current illnesses from the descriptions written in clinical texts. Since signs and symptoms describe the diseases in medical texts, all terms related to diseases, signs, and symptoms are extracted and grouped according to their sections in medical notes. After grouping, using alignment, a suitable diagnostic code is provided for each expression. Also, information about prescriptions and laboratory tests is extracted. We use a quadruple data structure to homogenize the structure of information extracted from structured and unstructured sources that provide the basis for combining information.

**Creating the tree structure and relabeling:** we apply the quadruples in developing a temporal tree model. We create a subtree for each time window. There are branches for each datatype (disease, prescription, laboratory tests). In each branch of each subtree, the medical events related to that time window and datatype are used as leaf nodes. In the tree’s construction, a modified model of the Weisfeiler-Lehman graph kernels [38] relabeling method has been used to compare graphs that capture topological and label information. Using these kernel co-occurrences, the relation between leaves in each subtree (medical events) converts to rich compounds in non-leaf nodes. In this step, we used two relabeling methods. In the first method, the extracted medical events related
to the same visit are used in relabeling non-leaf nodes. In the second method described in section UTTree-H, data related to the patient’s medical history are also used.

**Traversing the tree:** In the third step, traversing the temporal tree yields sequences used as input of embedding algorithm to represent patient information as vectors.

**Document Representation:** The result of tree traversal is a sequence of components. i.e., a new document for a patient. This document serves as the input of the representation algorithm. In this study, the Doc2Vec algorithm is used. The Doc2Vec model is used to create a vectorized representation of a group of words taken collectively as a single unit. It does not only give the simple average of the words in the sentence.

**Downstream task:** the embedding vectors are fed as input to the patient similarity assessment model. It works based on the cosine distance between patient embedding vectors and the gold standard to measure model accuracy. The results obtained from this method are compared with several baselines. In the continuation of this section, the details of each stage will be presented.

### 3.1.1 Data preprocessing

**Unstructured data processing:** We define the process of automatically extracting clinical concepts from unstructured clinical notes in EMRs. A large amount of the information in an electronic patient record system is unstructured in the form of free text [39]. Clinical text is written by various professionals such as physicians, nurses, physiotherapists, and psychologists. It is often written under time pressure and contains misspellings, non-standard abbreviations and jargon, and incomplete sentences, and is therefore difficult to process for natural language processing (NLP) tools which are mainly developed for other text types [40].

Clinical notes in EMRs contain different text types such as discharge notes, nursing reports, pharmacy notes. Each standard clinical note, mainly discharges note, consists of several components or sections [41]. However, there is significant variation in the number of sections and the descriptive phrases in section headers. This challenge in clinical notes NLP is flexible formatting [42],[39]. In this study, we considered the effect of the patient’s medical history in interpreting their new clinical condition. Therefore, it is essential to differentiate between the patient’s medical history (previous active or resolved medical condition) and new findings in the first step. After sectionizing each note by Medspacy [43], we enter the next step, which is named entity recognition (NER). In this step, medical named entities such as diseases are recognized from medical texts. This step is necessary for representing a complete overview of a patient’s medical history and current significant findings. We use MetaMap [44], cTAKES [45], and scispaCy [46] for this step. After that, we carry out a negation detection step by employing Negspacy [47] to determine whether specific findings are reported as present or absent. Finally, we performed concept encoding to map the extracted terms and mentions to terms in standard terminologies.

A doctor may express the same disease in different ways, so this is a crucial task. In this step, different forms of one disease are automatically mapped to one preferred name. In this process, related concepts are retrieved and sorted according to their degree of similarity with the searched term. We used the output of MetaMap to do this step. We used the concept at the top of the retrieved list with the highest similarity score. Lastly, we sorted the extracted concepts by time. As a result, input notes during this phase will be batched into a set of records. The original word, note type (discharge, nursing, reporting.), section, registered time, negation tag, type, and concept ID of the word are listed for each record. The tools and libraries that list in Appendix 1.

### Structured data processing:

EMRs contain several structured data types. In this study, we use data on prescriptions, laboratories, and procedures. Structured data types are captured using controlled vocabularies rather than narrative text. Healthcare providers usually use the LOINC1 standard for identifying laboratory tests or the RxNorm2 standard for identifying clinical drugs. Lab test results are usually documented too. Based on age, gender, and some other features, this result is interpreted as low, usual, or high. In this study, we use these categories rather than the original values. The name of the original clinical drugs are used for prescriptions and the name of the procedure for procedures.

**Harmonize extracted data:** To harmonize extracted information from clinical notes and structured parts of EMR, we introduce a flat format called quadruple. The quadruple data structure format consists of four components listed in Table 2: Time (t), Event-Type (y), Event (e), and value (v), which are represented by \( \{t_i, y_i, e_i, v_i\}, 1 \leq i \leq n \). The number of quadruples can be different between patients.

| Component          | Definition                                                                 |
|--------------------|-----------------------------------------------------------------------------|
| Time - \( t_i \)   | The timestamp that each clinical event registers in the EMR.                 |
| Temporal Event role - \( y_i \) | The following temporal roles were taken into consideration in extracted disease in EMR: |

1 Logical Observation Identifiers Names and Codes

2 [https://www.nlm.nih.gov/research/umls/rxnorm/index.html](https://www.nlm.nih.gov/research/umls/rxnorm/index.html)
Retrospective data (a): This role is assigned to the concepts extracted by processing medical history texts.

New detected finding with a long-lasting effect (b): every disease that registers in current visit. We hypothesized that disease has more lasting effects than other medical events.

Real-time data with a short-term effect (c): The parameter used to model medical events other than a disease, such as laboratory results and prescribed drugs. These items are updated more frequently than disease events. Thus, they are only used to create subtrees (time windows) in which they are recorded.

Event - $e_t$ The extractable medical event type (disease, sign, symptom, drug, lab, procedure.)
Value - $v_t$ The extractable medical event value

3.1.2. Create tree structure and relabeling

Creating a tree includes two phases: creating a tree and relabeling non-leaf nodes with the Weisfeiler-Lehman graph kernels.

Creating the tree: Fig. 2 shows the pseudo-code for tree construction. There is a tree created for each patient, the root of which is the patient identifier. A root node for each subtree is created according to the number of nonempty time windows with information. Each subtree’s branch is created for each data type, and the extracted values are added to the branch as nodes. Following the previous steps, the type of clinical event is added to the tree nodes as a feature and used in the next step of relabeling. Please see Appendix 3 in the supplementary file for pseudo-code.

![Figure 2 An example of creating a tree and relabeling](image-url)
Relabeling: Relabeling non-leaf nodes in the tree allows us to capture the relationship between different medical events. Fig. 3 shows an example. This step is done using the Weisfeiler-Lehman kernel designed for graphs and consists of four steps: multiset-label determination, sorting, label comparison, and relabeling. Only the leaf nodes have labels in the tree created in the previous step, and these leaf nodes can only be accessed through their parent nodes. As a result of two rounds of relabeling, the tree’s root becomes a combination of medical events that occur within a specified time window. Fig. 4 shows the mechanisms for relabeling non-leaf nodes. In this figure, we focus on Part 2-b of Fig. 1. Each subtree corresponds to a time window determined by the field (Time) in quadruple. In the relabeling step, three approaches are used to change the labels of non-leaf nodes based on leaf nodes’ labels. In the following sections, we will apply these three methods the temporal tree [48], UTTree (proposed model), and UTTree-H (enhanced proposed model that is described in the next section). In the temporal tree approach, only real-time nodes (yellow ones) are used for relabeling. In the UTTree approach, we also use nodes related to newly detected findings (red ones) and real-time data.

3.1.3. Traverse Tree
By traversing the nodes of the tree, we can generate sequences of terms. The order in which terms are viewed is vital in the traversal. In this study, we use the breadth-first search (BFS) traversal method. Fig. 3 shows sequences created after tree traversing.

| Seq1 | Disease, Diabetes mellitus type 2, Female 4, Glucose, High, Main Drug, Insulin, Disease, Diabetes mellitus type 2, Female 4, Disease, Diabetic nephropathy, Glucose, High, Main Drug, Insulin, Disease, Diabetes mellitus type 2, Female 4, Disease, Diabetic nephropathy, Symptom, Fatigue, Glucose, Normal |
| Seq2 | Disease Diabetes mellitus type 2, Female 4, Glucose High, Main Drug Insulin, Disease Diabetes mellitus type 2, Female 4, Disease Diabetic nephropathy, Glucose High, Main Drug Insulin, Disease Diabetes mellitus type 2, Female 4, Disease Diabetic nephropathy, Symptom, Fatigue, Glucose, Normal |
| Seq3 | Disease Diabetes mellitus type 2, Female 4, Glucose High, Main Drug Insulin, Disease Diabetes mellitus type 2, Female 4, Disease Diabetic nephropathy, Glucose High, Main Drug Insulin, Disease Diabetes mellitus type 2, Female 4, Disease Diabetic nephropathy, Symptom, Fatigue, Glucose, Normal |
| Seq4 | Disease Diabetes mellitus type 2, Female 4, Glucose High, Main Drug Insulin, Disease Diabetes mellitus type 2, Female 4, Disease Diabetic nephropathy, Glucose High, Main Drug Insulin, Disease Diabetes mellitus type 2, Female 4, Disease Diabetic nephropathy, Symptom, Fatigue, Glucose, Normal |

Figure 3. Temporal sequences by the BFS order

3.1.4. Patient representation
We use the document representation technique to represent sequences created in the previous step. In document representation, the semantics of a document is encapsulated in real-valued vectors, and these vectors can be manipulated in downstream tasks. The Doc2Vec is based on Word2vec and uses an unsupervised learning approach to learn the document representation. The input text (in our case, medical events) per document (in our case, temporal tree) can be varied, while the output is fixed-length vectors. The Doc2Vec includes two sub-methods. The Distributed Memory Model of Paragraph Vectors (PV-DM)[49] that we used in our model is similar to the continuous bag-of-words approach in Word2vec. Another Doc2Vec sub-method is the Distributed Bag-of-Words version of Paragraph Vector (PV-DBOW)[50], similar to the Skip-gram approach in Word2vec. The PV-DM model computes the probability of a target word in a lexical context based on the surrounding words. The document and is mathematically expressed as below:

$$\sum_{t \in T_w} \log p(w_t | C_t, d_t)$$

Where $w_t$ is the target word and $T_w$ is the set of training words, $C_t = \{w_{t-L}, \ldots, w_{t-1}, w_{t+1}, \ldots, w_{t+L}\}$ are context words that occur within a window size of L words around $w_t$, and $d_t$ denotes the document corresponding to the $t_{th}$ training instance. The probability is computed using a Softmax function. For optimization, the hierarchical Softmax is used.

3.1.5. Downstream Tasks
In this study, the main objective is to evaluate patient similarity. In this task, the similarity score with other patients is calculated and sorted in descending order for each query patient in the dataset. Following that, the top K patients on the sorted list are returned as output to the algorithm. Moreover, the generated vectors have been used to predict mortality, a supervised classification task. This study uses a set of tools and Python libraries mentioned in Appendix 1.
3.2. **UTTree-H**
All three types of data are used in method UTTree-H to label non-leaf nodes.

Figure 4: The Temporal Tree: relabeling non-leaf nodes in the middle level of the tree only uses the label of real-time node (Real-time data with a short-term effect (c)). The UTTree: relabeling non-leaf nodes in the middle level of the tree by using the label of real-time data (Real-time data with a short-term effect (c)), and New detected finding with a long-lasting effect (b). The UTTree-H: relabeling non-leaf nodes in the middle level of a tree only use all kind of Temporal Event role.
3.3 Gold standard

An example is provided in Fig. 5 to illustrate the importance of using concepts extracted from clinical notes to construct compounds. In the first part, the patient’s pregnancy is used to construct component Cl3. In the second part, in addition to laboratory tests and prescriptions, the patient’s thalassemia history has been extracted from the clinical notes in Cl5 construction. Having more information makes a difference between compounds. Cl3 is not equal to Cl5, and this distinction is critical in assessing patients’ similarities. Unlike iron deficiency anemia, identifying patients with thalassemia is vital for avoiding unnecessary iron replacement therapy. Iron overload can lead to several complications in patients with thalassemia [51], impair the immune system, and place patients at risk of infection and illness [52].

\[
SimIndex(A, B) = \frac{\sum_{i=1}^{n} min(a_{w_i(p)}, b_{w_i(p)})}{\text{avg}(\sum_{i=1}^{n} a_{w_i(p)}, \sum_{i=1}^{n} b_{w_i(p)})}
\]

Fig. 5 The effect of paying attention to the concepts extracted from the clinical notes

An example is provided in Fig. 5 to illustrate the importance of using concepts extracted from clinical notes to construct compounds. In the first part, the patient’s pregnancy is used to construct component Cl3. In the second part, in addition to laboratory tests and prescriptions, the patient’s thalassemia history has been extracted from the clinical notes in Cl5 construction. Having more information makes a difference between compounds. Cl3 is not equal to Cl5, and this distinction is critical in assessing patients’ similarities. Unlike iron deficiency anemia, identifying patients with thalassemia is vital for avoiding unnecessary iron replacement therapy. Iron overload can lead to several complications in patients with thalassemia [51], impair the immune system, and place patients at risk of infection and illness [52].

\[
SimIndex(A, B) = \frac{\sum_{i=1}^{n} min(a_{w_i(p)}, b_{w_i(p)})}{\text{avg}(\sum_{i=1}^{n} a_{w_i(p)}, \sum_{i=1}^{n} b_{w_i(p)})}
\]
where $a_{w_i(p)}$ and $b_{w_i(p)}$ are the weights of diagnosis $i$ with priority $p$ expressed as an ICD9 disease code for patients $A$ and $B$, respectively.

We use three evaluation metrics in this study.

4 RESULTS AND EVALUATION

The experimental setting is described in section 4.1, and the utilized dataset is reviewed in section 4.2.

The quality of patient representation vectors is affected by two factors: the performance of the text representation algorithm and the relabeling method used (please see Appendix 2 in the supplementary file for the hyperparameter selection). Since both factors contribute to the production of patient representations, both effects will be studied in the following experiments:

- In section 4.3, we analyze the use of textual data in the construction of the UTTree model. The resulting embedding vectors generated by this model are examined in the patient similarity task.
- In section 4.4, we examine under which circumstances the use of the past medical history records data in constructing the UTTree-H can be beneficial. The generated vectors are evaluated in a patient similarity task.
- In the last experiment, reported in section 4.5, we examine the utility of generated embedding vectors in a supervised prediction problem.

4.1 Experimental Setting

The effectiveness of the proposed representation method is evaluated in two types of downstream tasks: (i) similar patients’ retrieval and (ii) prediction model. Each task has its evaluation criteria.

4.1.1 Evaluation metrics in patient similarity

We evaluate the proposed method on similar patients’ retrieval using the following evaluation measures:

Mean Square Error (MSE@K): The prediction error is the difference between the actual and predicted values [54]. The Top@k query returns $k$ patients most similar to a given patient, based on the cosine similarity measure of the embedding vectors. The query result of the proposed method is compared with other scenarios. The predicted value for each patient is the highest similarity value compared to the actual value of the most similar record based on the gold standard.

Normalized Discounted Cumulative Gain (nDCG@K):

This measure is used for determining the ranking quality. According to the idea, products that the user likes should be ranked first on the recommendation list, rather than at the back, so as to significantly improve the user experience. In DCG (Discounted Cumulative Gain) normalization, $rel_i$ is a sorted list, $i$ is the current result’s position number, and IDCG is the largest DCG in the ideal state.

$$DCG = \sum_{i}^{p} \frac{rel_i}{\log_2(i + 1)}$$
NDCG normalizes DCG by the Ideal DCG, which is simply the DCG measure of the best-ranking result. Thus, the NDCG measure is always a number in [0, 1][55]. The nDCG measure is computed for the Top@k patient rankings retrieved in answer to a query patient. The ideal Top@k ranking based on the gold standard is computed for a query patient. We use the SimIndex function for calculating the scores. We use an ordinary function \( d_i = \log_2(i + 1) \) for calculating the discount. For a query patient, the calculated SimIndex scores for both ideal and actual rankings are considered to be the gains \( g_i \), which are discounted by a function of the rank position.

**Precision@K**: Set a rank threshold \( K \). Compute % relevant in top \( K \), ignores documents ranked lower than \( K \). If a retrieved patient contains any of the top two query diagnoses, the patient is considered relevant[28].

### 4.2. Dataset
We use a subset of The Medical Information Mart for Intensive Care III (MIMIC-III) dataset [56]. MIMIC III is a large, de-identified, and publicly-available clinical database containing data from approximately 40,000 de-identified patients. These data come from patients admitted to a medical center in Boston, Massachusetts, from 2001 to 2012. Each record in the dataset includes ICD-9 codes, which identify diagnoses and procedures performed. The dataset consists of 112,000 clinical reports records (average length 709.3 tokens). This study selected a subset of patients whose final diagnosis is one of the top-10 most frequent first diagnoses in the whole dataset. Records with no laboratory tests or prescriptions are excluded. This collection includes over 7300 admissions. The average number of words in medical notes is about 7800, and the average number of visits per patient is 1.29.

### 4.3. Evaluation of UTTree
In the following evaluation, the research question is to what extent the use of textual data can be effective in the result? The UTTree relabeling model will be compared with the temporal tree model [7]. Together with the structured data, The UTTree model uses the disease concepts extracted from the document. We use BFS for traversing tree that leads to sequences. The doc2vec algorithm represents the resulting sequences, and then the embedding vectors are used in the downstream similarity calculation. The distance of embedding vectors is calculated using a cosine metric and compared with the gold standard as described in section 4.3 by mean of MSE, nDCG, and precision for retrieving 1, 5, 10, and 20 similar patients. Table. 4 shows the results. Our comparisons in this section have been with these methods:

- **TFIDF_Structured data**: The TFIDF is used to find non-negative vectors from the documents based on the t frequency, which indicates how frequently the term occurs in the document, and the inverse document frequency, which indicates the frequency of the term across the collection. We use only structured data in constructing the tree structure.
- **TFIDF+ Structured and Unstructured data**: same as the previous baseline, the representation is TFIDF, but we use structured and unstructured related to one visit.
- **The Temporal Tree with [PV-DBOW]**: This baseline is the implementation of [7] that resulted in sequences represented by Doc2vec (PV-DBOW).
- **UTTree with [PV-DBOW]**: this implementation use of UTTree relabeling, and after traversing the tree, the resulting sequences represent by Doc2vec (Distributed Bag-Of-Words (DBOW) Model similar to the skip-gram model of word2vec, which guesses the context words from a target word).
- **The Temporal Tree with [PV-DM]**: This baseline is the implementation of [7] that resulted in sequences represented by Doc2vec (Distributed Memory (DM)-that is similar to Continuous-Bag-of-Words (CBOW) model in word2vec, which attempts to guess the output (target word) from its neighboring words (context words) with the addition of a paragraph ID that in this case is the tree ID).
- **UTTree with [PV-DM]**: this implementation uses UTTree relabeling, resulting in sequences represented by Doc2vec PV-DM.

|                      | MSE@1 | MSE@5 | MSE@10 | MSE@20 |
|----------------------|-------|-------|--------|--------|
| TFIDF_Structured data| 0.320 | 0.129 | 0.080  | 0.052  |
| TFIDF+ Structured and Unstructured data | 0.310 | 0.128 | 0.078  | 0.050  |
| The Temporal Tree with [PV-DBOW] | 0.283 | 0.098 | 0.062  | 0.044  |
| UTTTree with [PV-DBOW] | 0.239 | 0.096 | 0.069  | 0.045  |
| The Temporal Tree with [PV-DM] | 0.280 | 0.095 | 0.058  | 0.041  |
| UTTTree with [PV-DM] | 0.235 | 0.091 | 0.064  | 0.044  |

**Table 3**-The effect of using clinical notes in constructing the model
4.4. Evaluation of UTTree-H

We compared the UTTree model with the UTTree-H model. The UTTree-H model uses extracted concepts from the past medical history section of discharged sheets in relabeling non-leaf nodes. Our comparisons in this section have been with these methods:

- TFIDF with Structured and Unstructured data
- UTTree with [PV-DBOW]
- UTTree-H with [PV-DBOW]
- UTTree with [PV-DM]
- UTTree-H with [PV-DM]

Table 5 shows the comparison. This model is expected to be more effective when the data recorded in the previous section is of higher quality and volume. To investigate this issue, we created a binary target field based on the superiority of the UTTree-H method and an executed decision tree on the new dataset. The results illustrated in Fig. 7 show that UTTree-H results are best when more than eight concepts are detected and extracted from the history section.

Table 4 - Evaluation of UTTree-H relabeling method

|                      | MSE          |               |               |               |
|----------------------|--------------|---------------|---------------|---------------|
|                      | MSE@1        | MSE@5         | MSE@10        | MSE@20        |
| TFIDF+ Structured and Unstructured data | 0.310        | 0.128         | 0.078         | 0.050         |
| UTTree with [PV-DBOW]| 0.239        | 0.096         | 0.069         | 0.045         |
| UTTree-H with [PV-DBOW]| 0.233       | 0.094         | **0.061**     | 0.039         |
| UTTree with [PV-DM]  | 0.235        | **0.091**     | 0.064         | 0.040         |
| UTTree-H with [PV-DM]| **0.232**    | 0.093         | **0.061**     | **0.038**     |

|                      | nDCG         |               |               |               |
|----------------------|--------------|---------------|---------------|---------------|
|                      | nDCG@1       | nDCG@5        | nDCG@10       | nDCG@20       |
| TFIDF+ Structured and Unstructured data | 0.421        | 0.419         | 0.412         | 0.406         |
| UTTree with [PV-DBOW]| 0.481        | 0.471         | 0.449         | 0.431         |
| UTTree-H with [PV-DBOW]| 0.491       | 0.481         | 0.449         | 0.437         |
| Method                  | Precision @1 | Precision @5 | Precision @10 | Precision @20 |
|------------------------|--------------|--------------|----------------|---------------|
| UTTree with [PV-DM]    | 0.495        | 0.483        | 0.455          | 0.438         |
| UTTree-H with [PV-DM]  | 0.492        | 0.482        | 0.454          | 0.437         |
| TFIDF+ Structured and Unstructured data | 0.561        | 0.560        | 0.543          | 0.546         |
| UTTree with [PV-DBOW]  | 0.609        | 0.601        | 0.589          | 0.579         |
| UTTree-H with [PV-DBOW]| 0.612        | 0.605        | 0.597          | 0.590 *       |
| UTTree with [PV-DM]    | 0.614        | 0.606        | 0.597          | 0.593         |
| UTTree-H with [PV-DM]  | 0.613        | 0.607        | 0.599          | 0.592         |

Figure 7: The effect of the number of words extracted on the error rate

The Wilcoxon test, a non-parametric statistical test (36), was used to evaluate the differences between the UTTree method and other approaches. The result indicates statistical significance with a p-value<0.01 except the one detected by a star. For analysis for selecting hyperparameters, please refer to the supplementary file.

4.5. Evaluation metrics in Mortality Prediction

The effectiveness of embedding vectors tested on supervised mortality prediction task. This task is concerned with predicting whether a patient will pass away in the hospital or after discharge. This problem could be formulated as a binary problem. The algorithm for the proposed model is given below:

1. Utilize the PCA [57] algorithm to reduce the dimensionality of each dataset’s embedding vectors.
2. Create random subsets of each dataset for training and testing. The proportion of the test split is 0.3
3. In step three, the reduced dataset is used to train XGBoost [58], SVM [59], and the Random Forests [60] classifiers.
4. The performance of the model is evaluated considering accuracy based on test data.
5. 10-fold cross-validation is used to evaluate the models
6. To summarize and compare groups of data visually, we use the box plot method to identify hidden patterns. Fig. 8 shows the results:
 According to Fig. 8, it is evident that the XGBoost algorithm outperforms RF and SVM on every three datasets. The medians of the proposed model's boxplots are all at the same level. However, the box plots show different distributions of views. It is observed that the box plot of UTTree+[PV-DM] is comparatively short compared to the boxplot of UTTree-H+[PV-DM] in XGBoost that suggesting the overall results of UTTree+[PV-DM] are close to each other. The box plot of UTTree+[PV-DM] is higher than others.

5 DISCUSSION
This study found that using textual data in the model construction process improved the accuracy of modeling EMR by a tree structure. The results obtained in this regard are consistent with the findings of other studies that have used other methods [10].

The following findings were obtained concerning the analysis of evaluation metrics. As for MSE, it is evident that by increasing K, MSE decreases. The reason is that by retrieving a more extensive set of patients, there is a greater likelihood that at least one is more similar to the query patient, reducing the overall error. Another promising finding of MSE was that the two approaches that used unstructured data yielded a less-than-average MSE. The amount of nDCG decreases for higher values of K. This finding confirms the previous findings [7], which show that as the set of retrieved responses grows, the likelihood of patients who do not look like the query patient will increase. As a result, a more extensive set of retrieved patients is more likely to contain unrelated values. We found that the precision decreases with the increase of K; in other words, the probability of retrieving irrelevant patients is higher with a larger K.

6 CONCLUSION AND FUTURE WORK
This paper proposed a new approach (the UTTree) to use extracted concepts from unstructured clinical notes for EMR representation. The unstructured and structured data (laboratory tests and prescriptions) were integrated to develop new data modeling for the patient similarity assessment.

The experimental results showed that our approach in extracting meaningful information from unstructured data could increase the accuracy of the patient similarity assessment model. We enhanced the model by applying the patient’s past medical history to enrich the model and proposing the UTTree-H model. We showed under what conditions better results are obtained with this method.

The document-representation algorithms used in this study are context-agnostic methods. The research has several directions for further development. For instance, the weight of different clinical events that make compounds is considered the same in this study. In future works, the issue of weighting different types of events will be examined. Also, the knowledge resources for enriching the model structure will be considered. Testing the model using context-aware methods such as transformer-based models will be another future work. Further, we plan to create different methods of generating noise in the input text and determine which method can generate a more robust tree. Another idea is to construct a graph instead of a tree structure and extend the relationships between nodes derived from knowledge sources.

REFERENCES
[1] A. The degree of compliance of the registered codes with the items considered by the physician, J. A. Dubin, J. Lee, A. Sharafoddini, J. A. Dubin, and J. Lee, “Patient similarity in prediction models based on health data: a scoping review,” JMIR Med. informatics, vol. 5, no. 1, p. e7, Mar. 2017, doi: 10.2196/medinform.6730.
A APPENDICES

A.1 Tools and libraries

Table 5: List of tools and libraries

| Processing step                  | Tools/python libraries | Setting                                                                 | Ref     |
|----------------------------------|------------------------|--------------------------------------------------------------------------|---------|
| Section detection                | Medspacy               | nlp.pipe_name : ‘medspacy_sectionizer’                                   | [43]    |
| Negation detection               | Negspacy               |                                                                          | [47]    |
| Concept mention detection, Concept encoding | MetaMap           | the (2018AA) release of UMLS with the following list of options -V USAbase-L 18 -Z 18 -E -AsI+ –XMLf –negex -E. | [44]    |
|                                  | cTAKES                 | the Default Clinical Pipeline of cTAKES and Python library               | [45]    |
|                                  |                        | ctakes-parser 0.1.0                                                      |         |
|                                  | scispaCy4              | a Python library with en_ner_bc5cdr_md model                             | [46]    |
| Creating Tree                    | NetworkX               | Python library5                                                         | [61]    |
| Doc2Vec Embedding                | Gensim                 | vector_size = 200, window_size= 5, sampling_threshold = 1e-5, negative_size = 5, alpha = 0.025, minimum_alpha = 0.0001, min_count =5, training_epochs = 10, DM=0 and1,hs=1(for hierarchical softmax) and negative =1 (for negative sampling) | [62]    |

3 https://pypi.org/project/ctakes-parser
4 http://allenai.github.io/scispaCy
5 https://networkx.org/
A.2 Hyperparameters

We examine the cosine and euclidean metrics to determine the distance between the two patient representation vectors. The result shows that the cosine metric is better than euclidean, so this metric was used in all experiments.

**Cosine distance**: The similarity between two vectors is computed by cosine similarity:

$$\cos \theta = \frac{\mathbf{v} \cdot \mathbf{u}}{||\mathbf{v}|| \cdot ||\mathbf{u}||}$$

Where $\mathbf{v}$ and $\mathbf{u}$ the TFIDF vectors and $\theta$ is the angle between two vectors. As $\theta$ ranges from 0 to 90 degrees, $\cos \theta$ ranges from 1 to 0.

**Euclidean distance**: the similarity between two vectors is computed by the Euclidean similarity:

$$d(\mathbf{v}, \mathbf{u}) = ||\mathbf{v} - \mathbf{u}|| = \sqrt{(v_1 - u_1)^2 + (v_2 - u_2)^2 + \cdots + (v_n - u_n)^2}$$

|                  | TFIDF_S_Cosine | TFIDF_S_Eclidean |
|------------------|----------------|------------------|
| MSE@1            | 0.320          | 0.329            |
| MSE@5            | 0.129          | 0.131            |
| MSE@10           | 0.080          | 0.085            |
| MSE@20           | 0.052          | 0.057            |
| DCG@1            | 0.410          | 0.408            |
| DCG@5            | 0.408          | 0.407            |
| DCG@10           | 0.407          | 0.406            |
| DCG@20           | 0.407          | 0.406            |
| Precision@1      | 0.554          | 0.554            |
| Precision@5      | 0.551          | 0.550            |
| Precision@10     | 0.542          | 0.541            |
| Precision@20     | 0.541          | 0.540            |

Some hyperparameters were tested in these experiments, including Doc2vec mode, improvement method, and vector size. The vector size and distance metric in this experiment are fixed at 200 and cosine, respectively. The figure shows that the generated result by PV-DM with hierarchical softmax leads to lower mean error and higher mean nDCG compared to negative sampling. Our discussion section will cover the possible causes of these changes.
PV-DM performs better than PV-DBOW, but PV-DM takes longer to train. Compared to the negative sampling method, the hierarchical softmax performed better. According to the result, the hierarchical softmax is more efficient in this problem. The generated vectors by the hierarchical softmax are determined by traversing the network layers rather than by evaluating/updating $O(\log(N))$ network units. The weights are essentially expanded to support a large vocabulary - a given the word is related to fewer neurons and vice versa. As with stochastic gradient descent, negative sampling is a method of sampling the training data, but it looks for negative examples. This algorithm trains by sampling places. The algorithm might have expected a word but did not find one, which is faster than training an entire corpus every iteration and makes sense for common words.

To select the size of the embedding vector, we execute Doc2vec to hierarchical softmax. After that, we tested the different vector sizes. The results showed that after 200, the amount of change in the final result is minimal; therefore, we select vector size 200 for all experiments.
A.3 Pseudo-code

ALGORITHM: Create tree

1. \( Q \leftarrow \text{Repository of quadruples} \)
2. // each record in \( Q \) has four fields: Time (t), Event – Type (y), Event (e), and value (v)
3. \( L_p \leftarrow \text{list(PatientID)} \)
4. For i in \( L_p \):
   5. \( T = \text{DiGraph()} \)
   6. // Filter \( Q \) by Patient ID
   7. \( Q_p \leftarrow Q.\text{PatientID} \)
   8. Node PatientID \( \leftarrow \) PatientID
   9. Sort \( (Q_p) \) by Time
10. // Retrospective data (a)
11. \( A \leftarrow \text{Filter } Q_p \text{ by Temporal Event role = Retrospective data (a)} \)
12. // \( W_p \) = Number of Time window for each Patient ID
13. Node\_Ret \( \leftarrow \text{str}(\text{p}p_{id}) + "-" + \text{str}(A_{Event}) + "-" + \text{str}(A_{Value}) \)
14. \( T.\text{addnode}(\text{Node}_{Ret}.\text{label} = \text{str}(A_{Event}) + "-" + \text{str}(A_{Value}) . \text{type} = \text{str}(A_{EventType})) \)
15. For w in \( W_p \):
   16. // Level 0 – root of subtrees
   17. Node\_TimeWindow \( \leftarrow \text{str}(\text{p}id) + "-" + \text{str}(w) \)
   18. \( T.\text{addnode}(\text{Node}_{TimeWindow}.\text{label} = "$") \)
   19. \( T.\text{addedge}(\text{Node}_{PatientID} . \text{Node}_{TimeWindow}) \)
20. For all \( R \in Q_p \)
21. \( \text{EventType} \leftarrow R_{EventType} \)
22. Event \( \leftarrow R_{Event} \)
23. Value \( \leftarrow R_{Value} \)
24. \( \text{Node}_{EventType} \leftarrow \text{str}(\text{p}id) + "-" + \text{str}(R_{Event}) \)
25. \( T.\text{addnode}(\text{Node}_{EventType}.\text{label} = "$") \)
26. \( T.\text{addedge}(\text{Node}_{TimeWindow} . \text{Node}_{EventType}) \)
27. \( \text{Node}_{EventValue} \leftarrow \text{str}(\text{p}id)^* "-" + \text{str}(R_{Event}) + "-" + \text{str}(R_{Value}) \)
28. \( T.\text{addnode}(\text{Node}_{EventType}.\text{label} = \text{str}(R_{Event}) + "-" + \text{str}(R_{Value}) . \text{type} = \text{str}(R_{EventType}) ) \)
29. \( T.\text{addedge}(\text{Node}_{EventType} . \text{Node}_{EventValue}) \)
30. \( T.\text{addedge}(\text{Node}_{Ret} . \text{Node}_{EventValue}) \)
31. End For
32. End For
33. End For