A Machine Learning Approach to Predict Healthcare Cost of Breast Cancer Patients

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Abstract. This paper presents a novel machine learning approach to perform an early prediction of the healthcare cost of breast cancer patients. The learning phase of our prediction method considers the following two steps: i) in the first step, the patients are clustered taking into account the sequences of actions undergoing similar clinical activities and ensuring similar healthcare costs, and ii) a Markov chain is then learned for each group to describe the action-sequences of the patients in the cluster. A two step procedure is undertaken in the prediction phase: i) first, the healthcare cost of a new patient’s treatment is estimated based on the average healthcare cost of its \( k \neq 1 \) nearest neighbors in each group, and ii) finally, an aggregate measure of the healthcare cost estimated by each group is used as the final predicted cost. Experiments undertaken reveal a mean absolute percentage error as small as 6\%, even when half of the clinical records of a patient is available, substantiating the early prediction capability of the proposed method. Comparative analysis substantiates the superiority of the proposed algorithm over the state-of-the-art techniques.

Keywords: Healthcare Cost, Clustering, Markov Chain, k Nearest Neighbor.

1 Introduction

An electronic health record (EHR) is an electronic version of a patient’s clinical history over time. It comprises all administrative clinical data of a patient in a healthcare organization, including his/her demographics, diagnosis, medications, laboratory data, and associated costs, and so on. The plethora of longitudinal patients’ data of an EHR can be utilized for developing patient-centered personalized healthcare solutions, including cost. It is however worth mentioning that the healthcare costs, ranging from clinician’s fees to the cost of hospital stays and medicines, are escalating at a rapid rate around the world [1] [2]. It has motivated the researchers to take keen interest in controlling this upsurge
in the healthcare costs. The crucial step to control the healthcare cost is to enable the healthcare organizations to predict the possible future cost of individual patients. It in turn helps to identify the individuals at the highest risk of enduring the significant costs in future. It thus helps to prioritize the allocation of scarce resources among the patients in a healthcare organization for efficient care management.

Moreover, a report from The Commonwealth Fund (2012) emphasizes the need to identify high-cost patients as the first step towards achieving “rapid improvements in the value of services provided” [22]. A proactive approach to address this problem is to identify patients who are at risk of becoming high-cost patients accurately before substantial unnecessary costs have been incurred and health condition has deteriorated further. Eventually, this calls for prediction of possible total healthcare cost of a patient as early as possible when a limited volume of clinical records of the given patient is provided. In other words, another important aspect in the context of healthcare cost prediction is to devise a model using a training set of complete clinical records of some patients to predict the total healthcare cost of a new patient as accurately and also as early as possible, preferably before the availability of the patient’s full-length clinical record. Such early prediction of future healthcare cost can be used to judiciously identify high-risk high-cost patients and prevent crises in healthcare organizations. It is obvious that the earliness of the prediction may affect the accuracy. It has motivated the researchers to build a model to predict healthcare cost as early as possible while maintaining an appropriate level of accuracy.

Nevertheless, healthcare cost prediction based on individual patient’s characteristics is a challenging issue from the data mining perspective due to the non-Gaussian skewed distribution of the cost data of the patients [5]. Studies in [6], [7] reveal dubious efficacy of the statistical methods to predict the healthcare cost. Furthermore, the traces of linear regression and rule-based approaches are also found in literature [2], [7] for the cost prediction. But the requirement of a lot of domain knowledge has restricted their applications for most of the real world economic data of the patients [8]. Now-a-days, machine learning algorithms, including clustering and classification techniques, have emerged as an alternative effective tool for this purpose [9], [10].

This paper proposes a machine learning based novel approach for healthcare cost prediction of individual patient’s treatments based on their clinical actions, jointly including the clinical activities and the respective cost over time. The activity here represents diagnosis, medication, pharmacy and the like. A two-step procedure is employed in the learning phase: i) in the first step, the ordered sequences of clinical actions of the patients’ treatments are clustered using the hierarchical DBSCAN [15] with an aim to identify the group of patients undertaking similar clinical activities and incurring similar healthcare costs, and ii) each group is then modelled by means of a Markov chain [11] delineating the probability distributions of transitions between different clinical actions. A new
distance measure is also proposed to measure the similarity of the treatment
patterns of the patients during clustering.

The prediction phase, concerned with prediction of the healthcare cost of the
sequence of clinical actions of a new patient’s treatment, also encompasses two
steps: i) first, for each group, we compute a tentative cost of the new sequence
by averaging the cost of its $k$-nearest neighbor [12] sequences in the group, ii)
the final cost is obtained as a weighted sum of the cost estimated by each of the
groups. The weights for each group are the likelihood of the new sequence to
the respective group as assigned by the corresponding Markov chain.

The performance of the proposed healthcare cost prediction algorithm is eval-
uated with the economic information together with information of the clinical
activities of the breast cancer patients obtained from the health administrative
department of the public health care system of the Basque Country, Spain. A 10-
fold cross validation is employed with the training dataset resulting the optimal
value of $k$ of $k$-NN as three in the present application with respect to the mean
absolute percentage error (MAPE) [2]. Moreover, the proposed method results
in an MAPE measure of less than 6% when half of the clinical records of a new
patient is available, irrespective of the value of $k$. It substantiates the capability
of the proposed stratagem for early prediction of healthcare cost. Experiments
undertaken also reveal that the proposed algorithm outperforms its state-of-the-
art contenders with respect to MAPE metric. The comparative analyses verify
the significance of jointly considering the clinical activity and the associated cost
data to effectively capture the clinical records of patients for accurate healthcare
cost prediction as early as possible.

The paper is divided into following sections. Section 2 delineates the proposed
method of healthcare cost prediction. Experiments undertaken and the results
are reported in Section 3. Section 4 concludes the paper.

2 Method

2.1 Data Transformation

This section refers to transforming the database of individual patient’s treat-
ments into a series of actions, sorted by time. Here, we provide some definitions
which will be used throughout the paper to develop a solution to the healthcare
cost prediction problem.

Definition-1: Action. Let $X$ be the set of all clinical activities, including
diagnosis, procedure, medicine and the like, $Y \in \mathbb{R}$ be the set of all possible
incurred healthcare cost as recorded in the database and $T$ be the set of visiting
times of the patients to the hospital. An action, say \( a \), is then expressed as a three-tuple, given by

\[
a = \{(x, y, t) \mid \forall x \in X, \forall y \in Y, \forall t \in T\}.
\]

**Definition-2: Patient’s treatment.** A patient’s treatment is defined by a sequence of its corresponding actions, sorted by the visiting time. Symbolically, a patient’s treatment \( P \) is represented by

\[
P = (a_1, a_2, ..., a_n)
\]

where \( a_i = (x_i, y_i, t_i) \) represents the action encompassing the clinical activity \( x_i \in X \) and its respective healthcare cost \( y_i \in Y \) incurred during visiting time \( t_i \in T \) of the specific patient. For sake of simplicity of readers, we drop the notion of visiting time and hence \( a_i \) now can be simplified as

\[
a_i = \{(x_i, y_i) \mid x \in X, y \in Y\}.
\]

The clinical actions of \( P \) in (2) are chronologically ordered. Evidently, if \( i < j \), \( a_i \) occurs before \( a_j \). A sequence of actions of a patient’s treatment is used to jointly track the progression of its activity-outcome and the corresponding healthcare cost over time. The length of the sequence varies across patients because of the diversity in their treatments over time.

**Definition-3: Modified cost.** Intuitively, the number of possible actions for all patients in the database is huge due to infinite number of healthcare cost elements in \( Y \). For the sake of simplicity, \( Y \) is reduced to a finite set in a two step procedure described below.

1) **Discretization:** First, the entire range of \( Y \) is discretized into \( n_s \) segments defined by the \( n_s \)-quantiles of \( Y \). In other words, we set the lower and the upper limit of the \( i \)-th segment respectively to the \((i - 1)\)-th quantile and the \( i \)-th quantile of the healthcare cost elements for all possible clinical activities, recorded in the database.

2) **Quantization:** Then a real healthcare cost element, lying in the \( i \)-th segment is replaced by the mean value of all cost elements of the \( i \)-th segment.

The strategy is pictorially demonstrated in Fig. 1 for the healthcare cost information of two patients only with \( n_s = 8 \). The setting of \( n_s = 8 \) and the cost values used here are illustrative examples only. The healthcare cost, referred henceforth, denotes the modified cost.
It is noteworthy that patients undergoing various clinical activities reveal considerable diversity of their corresponding cost information. Hence, prior to predict cost of a new action-sequence, we cluster the action-sequences of the existing patients into groups. We then consult the cost information of the specific group of patients providing the maximum similarity with the action-sequence of the new patient to predict the respective possible future cost.

Two significant issues to categorize the patients based on their action sequences include: i) design of an appropriate distance measure to capture the similarity between action-sequences of varying length, and ii) selection of an efficient clustering algorithm to ensure that action-sequences within a group are
similar to each other than those in other groups.

**Design of distance measure:** There exists plethora of literature on using edit distance [13] to measure the dissimilarity of two strings of characters (or words). Given two strings $S_1$ and $S_2$ over a finite alphabet, an edit distance $ED(S_1, S_2)$ between $S_1$ and $S_2$ can be defined as the minimum cost of transforming $S_1$ to $S_2$ through a sequence of weighted edit operations. These operations primarily include insertion, deletion, and substitution of one symbol by another. Usually, the edit operations are assigned with equal weights of unity. Nevertheless, the string in this paper denotes the action-sequences.

However, there is a major limitation of using the conventional $ED$ directly in the present context. The conventional $ED$ compares two strings of characters (or words) only. In the present work, the components of the string (or action-sequence) is not only representing character (symbolizing a clinical activity) but an activity-cost pair. Hence, application of the conventional $ED$ in the present scenario captures the difference between two action-sequences based on their respective clinical activities only, ignoring the corresponding healthcare cost information. It thus loses the cost information and the temporal relationship of the activity-cost pairs over time.

Consequently, the clusters of patients based on the conventional $ED$ measures identify patients ensuring similar clinical activities only. Evidently, the accuracy of the healthcare cost prediction based on the clusters, thus formed, is reduced to great extent. It has motivated us to design an appropriate distance measure to jointly capture the dissimilarity of two clinical activities (of two different action sequences) and their respective healthcare costs.

The proposed distance measure, referred to as *treatment pattern difference* (TPD) is an extended version of the conventional $ED$. In case of the conventional $ED$, all possible edit operations are associated with equal cost of unity. In TPD, the edit costs are modified as follows to consider the healthcare cost components of two action-sequences.

Let $P_1$ and $P_2$ be two different action-sequences. The cost of insertion of a clinical activity $x_i$ (or a character) to convert $P_2$ to $P_1$ is given by

$$C_1 = y_i$$

where $y_i$ denotes the healthcare cost of the clinical activity $x_i$ at the visiting time $t_i$ in the action-sequence $P_1$. Similarly, the cost of deleting an action $x_j$ from $P_1$ to covert it to $P_2$ is given by

$$C_2 = y_j$$
where the symbols carry their usual meanings. If the clinical activity $x_i$ of $P_1$ is substituted with a different clinical activity $x_j$ of $P_2$, the corresponding edit cost is given by

$$C_3 = |y_i - y_j + \epsilon|.$$  \hspace{1cm} (6)

Here $\epsilon$ is a small positive constant. It is used to ensure that even when $y_i = y_j$ for $x_i \neq x_j$, at least $C_3 = \epsilon$ is used as the edit cost for substitution of $x_i$ by $x_j$.

It is noteworthy that if $x_i = x_j$, the conventional $ED$ gives a zero penalty. However, there are instances of different healthcare costs for the same clinical activity of two different patients. To capture this, $TPD$ uses an additional edit cost, given by

$$C_4 = |y_i - y_j|.$$ \hspace{1cm} (7)

Hence, the total edit cost to convert an action-sequence $P_1$ to another action-sequence $P_2$ is given by

$$TPD(P_1, P_2) = w_1 \times (\sum_{\text{ins.}} C_1 + \sum_{\text{del.}} C_2 + \sum_{\text{sub.}} C_3) + w_2 \times \sum_{\text{match}} C_4.$$ \hspace{1cm} (8)

Here, $w_1$ and $w_2$ denote the weight for the edit operations respectively for different and similar activities. Intuitively, $w_2 < w_1$ as it corresponds to the penalty corresponding to similar activities with different healthcare cost. After a wide experimentation, we set $w_1 = 0.7$ and $w_2 = 0.3$. An example of evaluating the dissimilarity of two action-sequences based on the $TPD$ measure is presented in Fig. 2.
Selection of clustering algorithm: The TPD measures of each pair of patients’ treatments in the given record are used to cluster the similar sequences in the same subgroups. The hierarchical density-based spatial clustering of applications with noise (hierarchical DBSCAN) algorithm [15] is employed to identify the groups of patients’ treatments. The selection of DBSCAN in the present context is justified because of its merit of clustering similar data points (here, the action-sequences of patients) into same groups based on the density (number of nearby neighbors) without prior setting of the number of clusters. Moreover, unlike the traditional partitioning algorithms, DBSCAN can be applied for clusters of arbitrary shape, even when the data may be contaminated with noise [16].

It is however worth mentioning that the huge economic database includes clusters of records of patients characterized at different density levels. The traditional DBSCAN algorithm with a single global density threshold often fails to effectively identify such clusters. This impasse is overcome here by using the hierarchical DBSCAN, proposed in [15], which discovers all DBSCAN-identified clusters for an infinite range of density thresholds. Finally, it identifies a simplified hierarchical structure of significant clusters only.
2.3 Markov Chain Representation of a Cluster

This step is concerned with representing each cluster of patients’ action-sequences by a Markov chain [11]. The crux of such representation is founded on the underlying premise that the medical practitioners take their decision based on the previous clinical activities. Again, our cost prediction algorithm greatly relies on the recorded action-sequence of a patient.

A first order Markov chain exhibits memoryless property where the current state only depends on the previous state. Let $N$ be the possible number of actions (activity-cost pairs) in the database. The Markov chain model of a group of patients, say $G_l$, is then demonstrated by a state-transition probability distribution, which is denoted as:

$$M_l = [m_{i,j,l}] \text{ for } i,j = 1, 2, \ldots, N$$ (9)

where

$$m_{i,j,l} = p_l(x_{t+1} = s_j | x_t = s_i) = \frac{q_{i,j,l}}{\sum_{k=1}^{N} q_{i,k,l}}.$$ (10)

Here $q_{i,j,l}$ and $p_l(x_{t+1} = a_j | x_t = a_i)$ respectively denote the number of cases and the probability of transition from the current action $x_t = a_i$ to the immediate next action $x_{t+1} = a_j$ in the specific group $G_l$ of action-sequences. Evidently, it satisfies

$$m_{i,j,l} \geq 0 \text{ and } \sum_{j=1}^{N} m_{i,k,l} = 1.$$ (11)

In addition to $M_l$, we also evaluate the initial probability $p_l(a_i)$ of action $a_i$ considering all the action-sequences in the group $G_l$ for $i = 1, 2, \ldots, N$ as follows.

$$p_l(a_i) = \frac{s_{i,l}}{\sum_{k=1}^{N} s_{k,l}}.$$ (12)

Here $s_{i,l}$ denotes the number of action-sequences initiated with the action $a_i$ in $G_l$ for $i = 1, 2, \ldots, N$. This entire process is repeated for all groups identified by the hierarchical DBSCAN.
2.4 Cost Prediction of a Patient’s Treatment from Action Sequence

The aim of this step is to predict the possible total cost of a patient from the respective action-sequence. The action-sequence of the patient is formed following the principle given in Section 2.1. Let the ordered sequence of actions of the new patient’s treatment be denoted by \( P = (a_1, a_2, \ldots, a_n) \) where the action \( a_i \) represents the activity-cost pair at the visiting time instant \( t_i \). The prediction of future cost based on \( P \) is undertaken in three phases.

**Phase-1: Cost estimation of \( P \) based on a specific group.** We employ \( k \)-nearest neighbor (\( k \)-NN) to identify \( k \) action-sequences from a group, say \( G_l \), that offer maximum similarity with \( P \) based on TPD measure as given in (8). First, we compute the TPD values between \( P \) and each member sequence of the group \( G_l \). The member sequences are then sorted in ascending order of their TPD measures thus evaluated. The first \( k \) members are selected as the \( k \) nearest neighbors of \( P \). Next, each of the \( k \) members is assigned a weight \( w_{j,l} \), inversely proportional to its TPD measure from \( P \) for \( j = 1, 2, \ldots, k \). Consequently, the total cost \( \hat{c}_l(P) \) of the new action-sequence \( P \) estimated by the group \( G_l \) is given by

\[
\hat{c}_l(P) = \frac{\sum_{j=1}^{k} w_{j,l} \times c_{j,l}}{\sum_{j=1}^{k} w_{j,l}}.
\]  

(13)

Here \( c_{j,l} \) denotes the total cost incurred by the \( j \)-th nearest neighbor of \( P \) in \( G_l \) for \( j = 1, 2, \ldots, k \). \( \hat{c}_l(P) \) is computed for all clusters of patients identified by the hierarchical DBSCAN.

**Phase-2: Evaluation of the likelihood of \( P \) to patients’ groups.** This step is concerned with evaluating the likelihood of \( P \) to each subgroup of patients based on the respective Markov chain model. The likelihood of the ordered sequence of actions \( P = (a_1, a_2, \ldots, a_n) \) to a specific group \( G_l \) is given by

\[
\lambda_l(P) = p_l(a_1) \times \prod_{i=1}^{n-1} p_l(a_{i+1}|a_i).
\]  

(14)

Here \( a_1 \) denotes the initial action of \( P \) and \( a_i \) represents the action of \( P \) occurred at visiting time \( t_i \) for \( i = 1, 2, \ldots, n \). Evidently, \( p_l(a_1) \) and \( p_l(a_{i+1}|a_i) \) respectively symbolize the initial probability of action \( a_1 \) and the probability of transition from the current action \( a_i \) to the immediate next action \( a_{i+1} \) of \( P \) as described by the group \( G_l \). Expression (14) is evaluated using the Markov chain model \( M_l \) representing the group \( G_l \).
After evaluating $\lambda_l(P)$ for all groups, the normalized likelihood of $P$ to each subgroup is computed using

$$\hat{\lambda}_l(P) = \frac{\lambda_l(P)}{\sum_{l' \in \mathcal{L}} \lambda_{l'}(P)}.$$  \hfill (15)

**Phase-3: Cost prediction based on all groups.** After evaluating the estimated cost and the normalized likelihood of $P$ to all groups, the total cost of $P$ is finally predicted following

$$\bar{c}(P) = \sum_{l' \in \mathcal{L}} \hat{\lambda}_l(P) \times \hat{c}_{l'}(P).$$  \hfill (16)

### 3 Results

#### 3.1 Database

The study is performed on the economic data, along with the clinical activities of the patients obtained from the health administrative department of the public health care system (OSAKIDETZA) of the Basque Country, Spain. The database includes medical history of 579,798 patients treated in different levels of healthcare organizations (including 1 hospital, 11 outpatient clinics and emergency care) from January 1, 2017 to December 31, 2019. The clinical data of the patients primarily consists of their clinical assistance and the respective healthcare cost information.

To validate the proposed method of cost prediction, the present work considers the pool of breast cancer patients only. The selection of breast cancer patients from the database conforms the International Statistical Classification of Diseases and Related Health Problems (10-th revision) [17], stating that every code starting by C50 corresponds to breast cancer diagnosis. A few filtering steps are then carried out following [21] to judiciously select the pool of patients of interest. The filtering process affirms that the selected patients have their complete treatment in the above-mentioned time period of two years. Following the medical guideline, a final set of 972 patients is identified. 70% of the entire database is ultimately used as the training dataset, while the remaining as the test data. A 10-fold cross validation is employed on the training dataset for judicious selection of the value of $k$ for $k$-NN.
3.2 Identification and Representation of Patients’ Action- Sequences

The final record of the 464 patients consists of 23 unique clinical activities as described in Table 1. The healthcare cost is next discretized into $n_s$ segments. In Fig. 3, we present a plot of normalized quantization error values for different settings of the number of quantiles $n_s$, varied from 2 to 12 to check a significant improvement in performance. The normalized quantization error ($NQE$) is given by (17).

$$NQE = \frac{1}{N_c} \sum_{i=1}^{N_c} |c(i) - c_m(i)| \max_{i=1}^{N_c} c(i) - \min_{i=1}^{N_c} c(i)$$  \hspace{1cm} (17)

Here $c(i)$ and $c_m(i)$ respectively denote the true and the modified $i$-th healthcare cost (after discretization) of the database with $N_c$ cost elements for $i = 1, 2, ..., N_c$. Fig. 3 reveals that the quantization error is reduced with an increase in the number of segments $n_s$. However, it is also observed that there is no significant change in the error for $n_s \geq 8$. We have thus fixed $n_s = 8$. It is worth mentioning that the setting of $n_s$ here is biased to the healthcare cost values of the present database. The quantization of the healthcare cost range of the present database using 8-quantiles ensures a balanced number of healthcare cost elements in each of the eight cost-segments.

![Figure 3: Normalized quantization error for different values of $n_s$](image)

Next, the healthcare cost of all clinical activities of 464 patients is discretized in eight segments based on 8-quantiles of the healthcare cost range, as demonstrated in Fig. 1. Let the segments (sorted in ascending order) be denoted as very-very-low (VVL), very-low (VL), low (L), medium-low (ML), medium-high (MH), high (H), very-high (VH) and very-very-high (VVH). Eventually, there exist $22 \times 8 = 176$ actions to jointly represent a pair of clinical activity and the
corresponding healthcare cost. However, a close scrutiny of the final record reveals only 63 possible pairs from the recorded medical history of the 464 patients, as reported in Table 2.

The hierarchical DBSCAN algorithm is then employed on the training dataset to cluster the sequences using TPD values. The algorithm results in eight clusters. The clusters thus identified are pictorially represented in Fig. 4. The descriptions of the actions of the sequences, shown in different colors, are tabulated in Table 2. Each cluster is then described by a Markov chain following Section 2.3.

Figure 4: Cluster of sequences of visit records (activity-cost pairs) of patients with $n_p$ as number of patients and $L$ as the length of the sequence.

### 3.3 Performance Evaluation of Proposed Healthcare Cost Prediction Method

**Performance metric:** The performance of the proposed cost prediction algorithm is evaluated with respect to mean absolute percentage error (MAPE) with a lower error indicating a better performance.

$$MAPE = \frac{1}{N_t} \sum_{i=1}^{N_t} \left| \frac{c(P_i) - \bar{c}(P_i)}{\frac{1}{N_t} \sum_{i=1}^{N_t} c(P_i)} \right| \times 100.$$  (18)

Here $c(P_i)$ and $\bar{c}(P_i)$ (evaluated using (16)) respectively represent the true and the predicted cost of the $i$-th patient’s treatment $P_i$ in the test dataset with $N_t$ records for $i = 1, 2, \ldots, N_t$. 

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### Table 1. Description of the clinical activities

| Activity | Abbreviated form | Full form                           |
|----------|------------------|-------------------------------------|
| 1        | ANES             | Aesthesia                           |
| 2        | APAT             | Pathological Anatomy                |
| 3        | CEXT             | External Consultation               |
| 4        | CONS             | Consultation                        |
| 5        | FAMB             | Hospital Pharmacy Services          |
| 6        | FAMR             | Pharmacy                            |
| 7        | HCRI             | Critical Care Hospitalization       |
| 8        | HDIA             | Day Hospital                        |
| 9        | HDOM             | Home Hospitalization                |
| 10       | HOSP             | Hospitalization                     |
| 11       | INCO             | Interconsultation                   |
| 12       | LABO             | Laboratory                          |
| 13       | MNUC             | Nuclear Medicine                    |
| 14       | OSAT             | Osatek (Magnetic Resonance Service) |
| 15       | PFUN             | Functional Testing                  |
| 16       | QUIR             | Surgery Unit                        |
| 17       | RADI             | Radiology                           |
| 18       | REHA             | Rehabilitation                      |
| 19       | RTER             | Radiotherapy                        |
| 20       | UCRI             | Nursing Critical Care Unit          |
| 21       | UCSI             | Surgery without Hospitalization     |
| 22       | UENF             | Nursing Unit                        |
| 23       | URP              | Post Anesthesia Care Unit           |

**Validation of Earliness Prediction and Selection of $k$ of k-NN:** The capability of the proposed algorithm to predict the possible total healthcare cost of patients is verified by varying the length of sequence of the recorded treatments of the patients from 20% to 100%. The appropriate selection of $k$ (of $k$-NN) for the optimal performance is undertaken using 10-fold cross validation on the training dataset. The MAPE values for different settings of $k$ and percentage of length of sequence of the recorded treatments of the patients using 10-fold cross validation are tabulated in Table 3 (for the training data). Table 3 reveals that the longer the length of the sequence, the better is the prediction accuracy with smaller MAPE measures, irrespective of the setting of $k$. The optimal performance of the method is obtained for $k = 3$ with the entire se-
quence information. It is also noted that an MAPE smaller than 6% is obtained even when 50% of a visit sequence is utilized. It proves the effectiveness of the proposed method for an early prediction of the healthcare cost.

Table 2A. Description of the clinical actions (activity-cost pairs)

| Action | Activity | Cost | Action | Activity | Cost | Action | Activity | Cost |
|--------|----------|------|--------|----------|------|--------|----------|------|
| 1      | ANES     | VVL  | 26     | FAMB     | L    | 51      | HDIA     | VVH  |
| 2      | ANES     | VL   | 27     | FAMB     | ML   | 52      | HDOM     | VVL  |
| 3      | ANES     | L    | 28     | FAMB     | H    | 53      | HDOM     | VL   |
| 4      | ANES     | ML   | 29     | FAMB     | VH   | 54      | HDOM     | L    |
| 5      | ANES     | MH   | 30     | FAMB     | VVH  | 55      | HDOM     | ML   |
| 6      | ANES     | H    | 31     | FAMR     | VVL  | 56      | HDOM     | H    |
| 7      | ANES     | VH   | 32     | FAMR     | VL   | 57      | HDOM     | VH   |
| 8      | ANES     | VVH  | 33     | FAMR     | L    | 58      | HDOM     | VVH  |
| 9      | APAT     | VVL  | 34     | FAMR     | ML   | 59      | HOSP     | VVL  |
| 10     | APAT     | L    | 35     | FAMR     | MH   | 60      | HOSP     | VL   |
| 11     | APAT     | VH   | 36     | FAMR     | H    | 61      | HOSP     | L    |
| 12     | APAT     | VVH  | 37     | FAMR     | VH   | 62      | HOSP     | ML   |
| 13     | CEXT     | VL   | 38     | FAMR     | VVH  | 63      | HOSP     | MH   |
| 14     | CEXT     | L    | 39     | HCRI     | VVL  | 64      | HOSP     | H    |
| 15     | CEXT     | ML   | 40     | HCRI     | VL   | 65      | HOSP     | VH   |
| 16     | CEXT     | H    | 41     | HCRI     | L    | 66      | HOSP     | VVH  |
| 17     | CONS     | VVL  | 42     | HCRI     | VH   | 67      | INCO     | L    |
| 18     | CONS     | L    | 43     | HCRI     | VVH  | 68      | INCO     | ML   |
| 19     | CONS     | ML   | 44     | HDIA     | VVL  | 69      | INCO     | MH   |
| 20     | CONS     | MH   | 45     | HDIA     | VL   | 70      | INCO     | VH   |
| 21     | CONS     | H    | 46     | HDIA     | L    | 71      | INCO     | VVH  |
| 22     | CONS     | VH   | 47     | HDIA     | ML   | 72      | LABO     | L    |
| 23     | CONS     | VVH  | 48     | HDIA     | MH   | 73      | LABO     | MH   |
| 24     | FAMB     | VVL  | 49     | HDIA     | H    | 74      | LABO     | VH   |
| 25     | FAMB     | VL   | 50     | HDIA     | VH   | 75      | LABO     | VVH  |
Table 2B. Description of the clinical actions (activity-cost pairs)

| Action | Activity | Cost | Action | Activity | Cost | Action | Activity | Cost |
|--------|----------|------|--------|----------|------|--------|----------|------|
| 76     | MNUC     | L    | 91     | QUIR     | MH   | 106    | REHA     | ML   |
| 77     | MNUC     | ML   | 92     | QUIR     | H    | 107    | REHA     | MH   |
| 78     | MNUC     | H    | 93     | QUIR     | VH   | 108    | RTER     | VVL  |
| 79     | MNUC     | VH   | 94     | QUIR     | VVH  | 109    | RTER     | MH   |
| 80     | MNUC     | VVH  | 95     | RADI     | VVL  | 110    | RTER     | H    |
| 81     | OSAT     | L    | 96     | RADI     | VL   | 111    | RTER     | VH   |
| 82     | OSAT     | H    | 97     | RADI     | L    | 112    | RTER     | VVH  |
| 83     | OSAT     | VH   | 98     | RADI     | ML   | 113    | UCRI     | VVH  |
| 84     | OSAT     | VVH  | 99     | RADI     | MH   | 114    | UENF     | VH   |
| 85     | PFUN     | VVL  | 100    | RADI     | H    | 115    | UENF     | MH   |
| 86     | PFUN     | VL   | 101    | RADI     | VH   | 116    | UENF     | H    |
| 87     | PFUN     | L    | 102    | RADI     | VVH  | 117    | UENF     | VH   |
| 88     | QUIR     | VL   | 103    | REHA     | VVL  | 118    | UENF     | VVH  |
| 89     | QUIR     | L    | 104    | REHA     | VL   | 119    | URP      | ML   |
| 90     | QUIR     | ML   | 105    | REHA     | L    |        |          |      |

Comparative performance analysis: The next experiment aims at comparative performance analysis of our proposed algorithm. Three state-of-the-art techniques are considered in the comparative framework, including gradient boosting (GB) [18], artificial neural net (ANN) [19] and lasso [20]. These existing methods have utilized the healthcare cost data only to predict the future cost [2]. The MAPE measures for these algorithms are tabulated in Table 4. The reported results substantiate that our proposed method overcomes its contenders with GB acquiring the second rank. It in turn validates the efficiency of jointly considering the clinical activity and the associated cost data for the healthcare cost prediction.
Table 3. MAPE values (training error during 10-fold cross validation) for different values of $k$ and length of sequence (in percentage per)

| per k | 20% | 30% | 40% | 50% | 60% | 70% | 80% | 90% | 100% |
|-------|-----|-----|-----|-----|-----|-----|-----|-----|------|
| 1     | 9.25 | 7.43 | 6.01 | 5.85 | 5.53 | 4.68 | 4.15 | 3.76 |
| 2     | 8.83 | 8.08 | 6.95 | 6.54 | 6.04 | 5.80 | 5.15 | 4.10 | 3.65 |
| 3     | 8.87 | 7.74 | 5.89 | 5.39 | 4.98 | 4.62 | 4.38 | 4.07 | 3.49 |
| 4     | 9.36 | 7.82 | 6.04 | 5.47 | 4.86 | 4.65 | 3.94 | 3.77 | 3.63 |
| 5     | 8.90 | 7.14 | 5.69 | 5.13 | 4.84 | 4.49 | 4.24 | 3.77 | 4.03 |
| 6     | 9.01 | 7.35 | 5.76 | 5.32 | 5.17 | 5.15 | 4.51 | 4.26 | 4.33 |
| 7     | 9.29 | 7.58 | 5.77 | 5.27 | 5.58 | 4.97 | 4.62 | 4.46 | 4.35 |
| 8     | 9.13 | 7.39 | 5.72 | 5.64 | 5.18 | 5.28 | 4.46 | 4.13 | 4.21 |
| 9     | 9.57 | 7.66 | 5.92 | 5.42 | 5.57 | 5.14 | 4.64 | 4.11 | 4.08 |
| 10    | 9.68 | 8.51 | 6.27 | 6.26 | 6.11 | 5.93 | 5.22 | 4.60 | 4.41 |

Table 4. MAPE values (with test data) for different competitive methods for different length of sequence (in percentage per)

| per | 20% | 30% | 40% | 50% | 60% | 70% | 80% | 90% | 100% |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Prop. method | 8.89 | 7.84 | 6.27 | 6.05 | 5.94 | 5.53 | 5.29 | 4.17 | 3.59 |
| GB    | 9.70 | 8.63 | 6.41 | 6.37 | 6.57 | 5.91 | 5.55 | 4.94 | 4.43 |
| ANN   | 10.89 | 10.69 | 9.83 | 9.45 | 8.58 | 7.98 | 7.55 | 6.95 | 6.61 |
| LASSO | 12.08 | 11.93 | 11.86 | 10.80 | 9.85 | 9.32 | 8.85 | 8.12 | 7.65 |

4 Conclusion

The paper presents a novel method to predict healthcare cost of breast cancer patients as early and accurately as possible. The early prediction capability of the proposed method is used for identifying patients at risk of becoming high-cost healthcare users, before incurring substantial avoidable costs. The merit of the paper lies in the following counts. First, it considers the clinical activity and the associated healthcare cost data jointly to model the treatment of a patient. Second, it recommends a novel distance measure to capture the dissimilarity of two treatment patterns, encompassing both clinical activities and healthcare cost information. Third, it employs the hierarchical DBSCAN to categorize patients into different clusters with an aim to effectively identify the high-need and/or high-cost patients. Fourth, each cluster of patients is depicted by a Markov chain model to mathematically represent the treatment patterns. Finally, the Markov
chain models of all the clusters are used to predict the possible future (total) cost of a patient’s treatment. The performance of the proposed algorithm is compared for different length of sequence of the recorded treatments of patients. The experimental results reveal that the method achieves an MAPE value, as small as 6% even with half of the clinical records of a patient. Experiments undertaken also substantiate the superiority of the proposed algorithm to three state-of-the-art techniques which utilize only the healthcare cost data of the patients for prediction.

As a continuation of the present work, we first plan to test our method on different databases from different healthcare organizations for patients suffering from different diseases. More experiments on different databases could help to take a deeper dive into the data and explore ways to obtain more solid evidence on the performance of the proposed method, irrespective of databases. Second, we may consider the socio-demographic information of the patients along with the clinical actions with an aim to be utilize their joint explanatory power to understand the root causes of patients’ costs. Third, we have not exploited time feature in the present work. Intuitively, inclusion of time feature may effectively capture the differences of treatment patterns of patients and thus may enhance the prediction performance of the proposed method. Finally, appropriate stratagem needs to be developed to effectively balance the trade-off between the accuracy and earliness of the healthcare cost prediction.

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