Control Matching via Discharge Code Sequences

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Abstract

In this paper, we consider the patient similarity matching problem over a cancer cohort of more than 220,000 patients. Our approach first leverages on Word2Vec framework to embed ICD codes into vector-valued representation. We then propose a sequential algorithm for case-control matching on this representation space of diagnosis codes. The novel practice of applying the sequential matching on the vector representation lifted the matching accuracy measured through multiple clinical outcomes. We reported the results on a large-scale dataset to demonstrate the effectiveness of our method. For such a large dataset where most clinical information has been codified, the new method is particularly relevant.

1 Introduction

Recently, using ICD codes encoded in Electronic Medical Records (EMR) for patient similarity matching has attracted a lot of attention. The basic idea is that a patient (called a case) is typically paired with a clinically similar patient (called a control) with respect to ICD code sequence. To determine the similarity of two ICD code sequences, one can compare their primary diagnosis (i.e., their first ICD code) or compute their Hamming distance. A major difficulty in comparing ICD code sequences is the variation in encoding, i.e., different ICD codes can be used to record the same disease. For example, both ICD codes I20.0 and R57.0 are related to “heart issue”. Another difficulty is the sequential importance in the code sequences. Most existing approaches miss to leverage either the clinical relation among syntactically different ICD codes or the relative position of ICD codes within a sequence.

To incorporate these two sets of important information in patient similarity matching, we here introduce WVM, a method that matches sequences of ICD codes within the embedded vector space. The method embeds ICD codes using Word2Vec to capture semantic similarity among syntactically different codes. It also has a new sequential matching technique that leverages the domain coding convention to capture similarity among patients with complex syndromes and comorbidities. Our proposed method not only addresses the unavoidable coding variation problem but also considers the important sequential structure in ICD code sequences. We evaluate the performance of our model based on the similarity of the matched patients on two sets of outcomes: 28-day readmission and death due to cancer. A good matching should produce patient pairs similar in these two outcomes.

Our cohort consists of more than 220,000 patients whose data were collected from a state-wide cancer registry in Australia—The study constitutes the first step for a set of comparative observational studies. While sharing a similarity with medical concept embedding as in Code sum based matching (CSM), our framework with the proposed sequential matching yields better matching result. In comparison with recent non-embedding approaches such as Primary code based matching (PCM) and Hamming distance based matching (HDM), we also achieve a better performance.

2 Word2Vec based matching (WVM)

The proposed WVM method for patient similarity matching has two phases.
2.1 Phase 1: Learning ICD code vectors

WVM uses Word2Vec (Skip-gram model \([7]\)) to learn ICD code vectors that can capture the latent relations among ICD codes. This idea was also used in \([3,2]\). The local context is defined to be ICD codes that appear in the same episode (admission) with a window size of 5. Those ICD code vectors are then used in a sequential matching algorithm in phase 2.

2.2 Phase 2: Building a matching algorithm

The inputs of the sequential matching (SM) algorithm are a group of cases (case group) and a group of controls (control group). We will describe how we select case group and control group in Section \(3.2\). SM has three main steps. **Step 1:** For a given case \(tc(i)\) it finds a validation group that consists of the controls that have the same gender and age group with \(tc(i)\). Matching on factors such as gender and age is commonly used in case-control studies \([8]\). **Step 2:** It generates two sets \(S\) and matched to store the controls that match \(t\) ICD codes in \(tc(i)\) \((t \in [0,n])\), where \(n\) is the number of ICD codes in \(tc(i)\). **Step 3:** It matches \(tc(i)\) with a control based on \(S\) and matched.

In steps 2 and 3, to find a matching control for \(tc(i)\), there are three scenarios to consider.

**Scenario 1:** We can find the controls that match all ICD codes in \(tc(i)\). SM selects randomly a control in \(S\) for it to be the matching control \(mc\).

**Scenario 2:** We cannot find any control that matches all ICD codes in \(tc(i)\) but we are still able to find the controls that match at least one ICD code in \(tc(i)\). Thus, \(S\) is empty but matched is not. Assume that matched contains the controls that match \((k-1)\) ICD codes in \(tc(i)\). Since we cannot find any control that matches the \(k\)th ICD code in \(tc(i)\) (called \(tc_k^{(i)}\)), SM tries to search for a control \(vc(j)\) whose the \(k\)th ICD code (called \(vc_k^{(j)}\)) is similar to \(tc_k^{(i)}\). SM first obtains the ICD code vector \(v_i\) of \(tc_k^{(i)}\). For each \(vc(j)\) in matched, it obtains the ICD code vector \(v_j\) of \(vc_k^{(j)}\). It then computes the cosine distance between \(v_i\) and \(v_j\). The matching control for \(tc(i)\) is the one with the smallest distance.

**Scenario 3:** We cannot find any control that matches the first ICD code in \(tc(i)\). Thus, both \(S\) and matched are empty. SM attempts to match \(tc(i)\) with a control in validation group whose the first ICD code is similar to the first ICD code in \(tc(i)\) by computing the distance between them.

We provide three examples as shown in Figures 1 to demonstrate the three scenarios processed by steps 2 and 3.

![Figure 1: We can find the controls that match all ICD codes in \(tc(1)\): \(vc(3)\) is identical to \(tc(1)\). Note that \(tc(1)\) is a case and \(vc(3)\) is a control](image)

3 Experiments

3.1 Data

The dataset is a cancer cohort of more than 220,000 patients (58.2% males, median age 71), collected between 1997 and 2012 from a state-wide cancer registry including 21 hospitals in Australia. The data attributes include patient demographic and diagnoses indicated by ICD-10 codes. There is no information of labs, procedures, and drugs. A subset of data for control matching was selected as follows: 1) we removed the ICD codes occurring less than 30 times; 2) we only kept the admissions
that have at least one ICD code; and 3) we removed the admissions that have discharge date after 2008/12/31. The remaining dataset contains 1,810,967 admissions (216,844 unique patients).

3.2 Construction of case group and control group

First, we selected randomly a combination of a hospital \(H\) and an admission year \(Y\) from the dataset. We then selected the admissions that have the same hospital and admission year as \(H\) and \(Y\). Note that each admission is associated with a different patient. This set is called Hy. Final, we constructed the case group by sampling 200 admissions from Hy. The remaining admissions in Hy were used to construct the control group. The admissions in the control group are associated with the patients who are different from those in the case group.

3.3 Performance evaluation

We ran four methods randomly in 150 times. To have a fair comparison, all baselines were performed after step 1 in SM was done (i.e., after we obtained a validation group). Each time of running, we obtained 200 cases and 200 matching controls and measured the agreement of the two cohorts on the two clinical outcomes.

3.3.1 Readmission matching accuracy

Let \(trial^{(i)} = (y_1,y_2,...,y_{200})\) be a set of readmission statuses of 200 cases at the iteration \(i\) (true values). \(y_r = trial^{(i)}_r\) \((r \in [1,200])\) is one of four readmission statuses: “Missing” (0.01%), “Readmitted within 28 days to another facility” (4.07%), “Readmitted within 28 days to the same facility” (23.03%), and “Not formally readmitted within 28 days” (72.89%). Let \(match^{(i)}\) be a set of readmission statuses of 200 matching controls at the iteration \(i\) (predicted values). The readmission matching accuracy at the iteration \(i\) is computed as follows.

\[
acc^{(i)} = \sum_{r=1}^{200} \omega \left( trial^{(i)}_r, match^{(i)}_r \right) / 200,
\]
where $\omega(trial_i, match_i) = \begin{cases} 0 & \text{if } trial_i \neq match_i \\ 1 & \text{if } trial_i = match_i \end{cases}$.

Table 1 reports the average readmission matching accuracy for 150 running times of each method. Our proposed method (WVM) is better than non-embedding ICD code methods (PCM and HDM). Although both CSM and WVM learn ICD code vectors, CSM\(^1\) however does not consider the importance of the orderliness of ICD codes within a code sequence; its accuracy is thus lower than WVM.

### 3.3.2 Incidence rate (IR) error for cancer mortality

Let $trial_i = ((s_1, t_1), (s_2, t_2), ..., (s_{200}, t_{200}))$ be a set of 2-tuples (discharge date, death date) of 200 cases at the iteration $i$. Each case has a discharge date and a death date that may be null. For example, the first case in the case group has (discharge date, death date) of (2005/07/11, 2008/05/12); the second case has (discharge date, death date) of (2005/10/27, null). The incidence rate of the case group at the iteration $i$ (true value) is computed as follows.

$$IR(trial_i) = \frac{\text{count (number of death cases)}}{200} \sum_{r=1, t_r \neq \text{null}} (t_r - s_r) + \sum_{r=1, t_r = \text{null}} (d_{\text{censor}} - s_r),$$

where \text{count (number of death cases)} is the number of cases that have death date (i.e., their death dates are not null), $t_i$ and $s_i$ are death date and discharge date respectively, and $d_{\text{censor}}$ is the censoring date (i.e., the end date of our study, that is 2008/12/31).

Similarly, we can compute the incidence rate of 200 matching controls at the iteration $i$ (predicted value), called $IR(match_i)$. The incidence rate error (absolute error) at the iteration $i$ is computed as follows.

$$IR_{err}^{(i)} = |IR(trial_i) - IR(match_i)|$$

Table 2 reports the mean incidence rate error of each method in 150 running times. Again, the mean incidence rate error of our proposed method (WVM) has the smallest value.

### 4 Conclusion

We have introduced WVM, a case-control matching method that leverages both representational similarity among ICD-10 codes and the sequential structure of coding in each admission. The evaluation on two similarity measures based on clinical outcomes, namely readmission matching accuracy and incidence rate error for cancer mortality, proves that WVM constitutes an effective solution for patient similarity matching in a large cancer cohort. In practice, it means that WVM can identify a control cohort better matching the case cohort, hence minimizing the potential bias between the two cohorts. This enables more effective experiment or quasi-experiment designs using a large coded dataset that is similar to ours.

\(^1\)For a given case $tc^{(i)}$, CSM sums up the vectors of all ICD codes in $tc^{(i)}$ into a single vector. For each control, it performs the same task. It then determines the similarity between $tc^{(i)}$ and a control by computing the cosine distance between their summed vectors.
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