A Comparison of Collaborative Filtering Methods for Medication Reconciliation

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Abstract

Maintaining an accurate list of a patient's medications is a very challenging task for which the current solution is a process driven medication reconciliation approach. In this study, we extend our original data driven approach through the use of collaborative filtering algorithms to improve the accuracy of the medication list and test them using medication data from a long-term care clinic. The results are encouraging and suggest several promising directions for the future, including embedding these methods in current medication reconciliation processes and evaluating them in actual clinical settings.

Keywords:

Patient safety, Medication reconciliation, Collaborative filtering

Introduction

Motivated by patient safety considerations, medication reconciliation is defined as a process for creating the most accurate list of all medications that a patient is taking. Given the availability of vast amounts of prescription data in electronic repositories, in this study, we propose several collaborative filtering (CF) algorithms to improve the accuracy of the medication list and test them using medication data from a long-term care clinic.

Methods

Model Formulation and Evaluation

Each patient's medication information can be represented in the form of a drug list, which is the set of all drugs that has ever been recorded for this patient. The complete medication list of all patients is then a sparse binary matrix, $M = \{m_{ij}\}$, for patients $i = 1 \ldots N$, $j = 1 \ldots M$, where

$$m_{ij} = \begin{cases} 1 & \text{if drug } j \text{ occurs in patient } i\text{'s list} \\ 0 & \text{other wise} \end{cases}$$

We make predictions about a missing drug based on what other drugs have been prescribed for this patient as indicated by the medication list available for this patient. Demographic information is used to refine the result in order to make more accurate predictions.

We evaluate several machine learning algorithms such as Naïve Bayes, cGraph, D-Similarity, Co-occurrence, K-Nearest neighbors, and Popular using the standard AllBut1 metric used in the collaborative filtering domain, where we compare our algorithms on how well they predict a patient's missing medication (one that has been removed prior to testing) given the patient's remaining medication list. These drugs are then sorted in decreasing order based on this score and the one with the highest score is assumed to be the most probable missing drug from the partial list. We used medication data from an online pharmacy that provides medications to long-term care clinics in the Eastern United States. The clinic we chose for our experiments is the largest individual clinic in our data set. It contains medication records for 701 patients and 318 different drugs occur in these records.

Results and Conclusions

Table 1-Results for medication-only dataset

Methods	Top 1	Top 5
Co-occurrence	0.3283	**0.4216**
KNN	0.3244	0.3898
Popular	0.3226	**0.4181**
N-Bayes	0.3123	0.4011
cGraph	0.2389	0.3238
D-Similarity	**0.3421**	**0.4231**

Our experimental results suggest that simple CF approaches, such as D-Similarity that use only drug information can do a relatively good job at guessing missing drugs (Table 1). On the other hand, simply introducing additional information about patients, such as demographics does not guarantee improved predictions. An easy and effective multi-stage solution is to predict the therapeutic class in the first stage and use this prior information to refine drug prediction results. This significantly improves the performance, increasing top-1 accuracy to 36.3% and top-5 accuracy to 47.5% for the D-Similarity method. Predicting the theraputic class also produces additional useful information for end users, without introducing too much complexity. Combining these predictions with their potential consequences, adverse or otherwise, can produce more insightful recommendations for physicians at the point of prescribing.