A Hybrid Recommendation Model for Drug Selection

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Abstract: Medical errors associated with medication pose significant threats to patients' safety, primarily due to the abundance of drug information available on various online healthcare platforms, leading to challenges in identifying relevant drugs. To address this issue, drug recommendation systems have been developed to assist in selecting appropriate medications for specific medical conditions. Collaborative filtering approaches have been widely used to generate personalized recommendations for various applications. They are easy to implement, debug, and provide justifiable reasoning for recommended items, which is not readily accessible in several other recommendation approaches. Regardless of their success, they still need further enhancements to address challenges related to insufficient rating data, such as data sparsity and new item problems. This paper proposes a drug recommendation model that effectively employs drug taxonomy and multi-criteria collaborative filtering to tackle these challenges. Drug taxonomy enhances recommendation quality by offering a more organized and granular representation of drugs, while multi-criteria rating captures the patients' preferences more accurately, enabling accurate recommendations that better match the patient's specific preferences. Experiments conducted on a real-world drug multi-criteria rating dataset demonstrate that the proposed model outperforms baseline recommendation approaches in addressing these challenges and improving prediction accuracy and coverage, making it a valuable tool to assist patients in selecting relevant drugs for their specific medical conditions.

Keywords: Drug selection, Drug taxonomy, Multi-criteria collaborative filtering, Sparsity, New item problem.

1. Introduction

Throughout the evolution of the Internet, forums and online health platforms have played a significant role in sharing information and creating interactive communities. These platforms are valuable resources and serve as the initial stage in the adoption of e-Health services. As a growing number of individuals become increasingly concerned about their well-being, there has been a surge in the usage of the Internet as a diagnostic tool (Marin et al., 2019). The findings from a health survey conducted in September 2012 by Pew Research Center's Internet & American Life Project (Fox & Duggan, 2013), which aimed to examine the use of the Internet and digital technology for healthcare-related purposes among U.S. adults, indicate that 81% of U.S. adults utilize the Internet, and 59% of them have searched for health information online. Moreover, 35% of U.S. adults were categorized as "online diagnosers", indicating that they have specifically utilized the Internet to diagnose their own or someone else's medical condition online.

For example, healthcare platforms such as WebMD (WebMD, n. d.), offer instructive information for managing patients health, including medicine searches based on their specific conditions. To conduct a medication search on WebMD, patients must enter their condition, which generates a huge list of commonly used medications to treat or lighten the symptoms of that particular condition. Each medicine listed on the website contains a link that leads to additional information, including common uses, side effects, dosage information, and user reviews. However, with the growing number of medicines available daily, patients often face difficulty and time-consuming sorting through all available medicines to determine which ones are best suited for their condition, resulting in incorrect selection.

Modern technology allows for the collection of information from such platforms, which can be exploited to provide personalized healthcare, a trend that is nowadays growing and expected to be a significant disrupting force in healthcare in the coming years. A recommender system for medical use could be implemented to fill this void and assist with treatment decision-making. The recommender system would suggest medicines based on a patient's current conditions, symptoms, and preferences, based on the success obtained in the case of patients with similar health conditions. Such a system would enable patients to make better-informed decisions regarding the medications that are optimal for their condition (Stark et al., 2019).

Recommender systems aim to reduce information overload by providing personalized services to users. These systems recommend the most suitable items to individual users, based on their preferences and past behavior (Shambour et al., 2020). Collaborative filtering (CF) techniques are extensively used in recommender systems to exploit ratings provided by many users, to recommend various items and services, by using a wide range of similarity measures. The benefit of CF-based techniques is that they are extremely adaptable and may be used in any domain. There are two types of techniques that are used in CF: user-based CF and item-based CF approaches.

User-based CF approach exploits ratings of users and similarity metrics to build a user-user similarity matrix, which is used to identify the active user's nearest neighbors to generate recommendations. Item-based CF approach exploits ratings of items and similarity metrics to build an item-item similarity matrix, which is used to identify the target item's nearest neighbors to generate recommendations. Although the item-based CF technique has demonstrated greater accuracy in predicting recommendations than the user-based CF technique, it still has some drawbacks. The item-based collaborative filtering approach may not be effective and could produce inaccurate recommendations for users because of two significant obstacles: the sparsity issue and the new item problem. The sparsity problem arises when the available ratings for recommendations are inadequate, making it challenging to predict users' preferences accurately, while the new item problem arises when there are no adequate ratings available to provide accurate recommendations for a new item introduced into the system (Aggarwal, 2016b; Ko et al., 2022).

Modern recommender systems have addressed these issues by incorporating additional information. By leveraging this supplementary information, recommendation approaches can compensate for insufficient user ratings and produce more precise recommendations. Illustrations of such supplementary information include semantic relationships among items or users (Gohari & Tarokh, 2015; Shambour et al., 2021), as well as multi-criteria ratings that capture more complex user preferences (Shambour, 2016; Shambour, 2021). Semantic information can be

represented using taxonomies. Taxonomies are hierarchical structures that organize information into categories, based on their properties and attributes. In a taxonomy-based recommender system, items are grouped based on their similarity, and the system recommends items from the same group as the user's preferences. Taxonomy-based recommender systems can be useful when the user has limited interactions with the system, making it challenging to generate accurate recommendations. By grouping items based on their attributes and properties, the system can identify relevant items and recommend them to the user. Additionally, taxonomy-based recommender systems can handle new item cold-start problems, by utilizing the existing taxonomy to categorize new items and recommend them to users with similar preferences (Gohari & Tarokh, 2015; Shambour et al., 2021).

In addition, a multi-criteria recommender system is a type of recommender system that takes into account multiple criteria or attributes when generating recommendations. These additional criteria can be used to provide more personalized recommendations that align with the user's preferences and needs (Shambour, 2016; Shambour et al., 2016). For example, WebMD is an example of a platform where patients can rate drugs based on several criteria, including effectiveness, ease of use, and satisfaction, as shown in Figure 1. Developing MC-based recommender systems that utilize additional rating data is essential for accurately understanding user preferences and providing effective recommendations. By considering the crucial factors that impact a user's selection of an item during the recommendation process, multi-criteria-based collaborative filtering can enhance the accuracy of recommendations (Shambour, 2016; Shambour et al., 2016).

Figure 1. An illustration of a multi-criteria rating for a drug (WebMD, n. d.)

The utilization of multiple recommendation techniques in hybrid recommender systems yields recommendations that are more diverse and accurate. According to several studies (Shambour et al., 2022; Shambour, 2012), combining the strengths of different recommendation approaches significantly improves the overall performance of the system. Therefore, it is imperative to develop a hybrid recommender system that can provide patients with personalized medication recommendations based on their specific conditions. By doing so, patients can efficiently select the necessary medications within large healthcare platforms that contain numerous medication options.

The challenges previously discussed have driven the development of the Hybrid Taxonomy-based Multi-Criteria CF (HTMCCF) model. This model aims to assist patients in efficiently and precisely identifying the medication that aligns with their specific conditions. By incorporating Taxonomy-based filtering and multi-criteria CF techniques, the HTMCCF model enhances the quality of recommendations, while mitigating the negative effects of data sparsity and new item problems. It is important to emphasize that the primary objective of the HTMCCF model is to supplement the process of identifying relevant drugs for patients' specific medical conditions. The model serves as a valuable tool for providing suggestions based on the patients' condition, enabling them to explore potential options and gather information about various drugs. However, it is crucial to note that the final decision regarding drug prescriptions should always rest with qualified doctors, who possess the necessary expertise and comprehensive knowledge of the patient's medical history and individual needs.

The proposed model is evaluated through experiments conducted using a real-world drug MC rating dataset, and the results demonstrate that it is superior to other baseline recommendation approaches with respect to prediction accuracy and coverage. The structure of this paper is organized as follows: Section 2 presents a concise overview of the existing related literature on drug recommendations; Section 3 describes the design of the proposed model; and Section 4 depicts the experimental setting and results. Section 5 concludes the study.

2. Literature Review

The swift progress of technology in recent years has led to an increasing need for creativity in all sectors. In the healthcare sector, studies such as those conducted by Etemadi et al. (2022) and Tran et al. (2021) have explored the use of recommender systems. However, despite various works published on the application of recommender systems in the healthcare field, there has been a notable lack of research on drug recommendation systems in this domain.

A web-based decision support system to assist doctors in selecting first-line drugs based on the level of risk of an infection was proposed by Shimada et al. (2005). The system can be operated by doctors using the following steps: (1) input the details regarding a patient's risk factors into the system; (2) confirm a calculated risk level; and (3) choose a bacterium. The system then ranks potential drugs by their level of importance. The system is highly efficient and user-friendly for doctors. Based on patient ontology knowledge and a multiple criteria decision making (MCDM) method, Chen et al. (2011) develop a recommendation system to assist doctors in choosing diabetic medications more appropriately. First, importance weights for diabetic medications are computed using entropy. Then, the system computes entropy to determine the benefits and risks of the final weights. Finally, the recommended medications are sorted and the medical ontology knowledge is integrated to determine the recommended medications. Initial experiments demonstrate the utility of the proposed system. Chen et al. (2012) introduced a domain ontology-based diabetes medication recommendation system that uses a knowledge base. The proposed system first constructs ontology knowledge about the nature elements, form of dispensing, and side effects of drugs, through analysis, then determines the ontology knowledge about the patients' diagnoses. The Java Expert System Shell (JESS) and Semantic Web Rule Language (SWRL) are then used to generate prospective drugs for the patients. The system can analyze diabetes symptoms and choose the most suitable drug from a list of related drugs.

IRS-T2D, a recommendation system for personalized treatment of type 2 diabetes, based on ontology and Semantic Web Rule Language

(SWRL), was proposed by Mahmoud and Elbeh (2016). The official documents for type 2 diabetes management were used as criteria and applied to create ontologies. First, the authors created OWL-based ontologies for patients' profiles and anti-diabetics drugs. Second, SWRL rules for medication constraints were developed. Finally, ontologies and SWRL rules were made available to the JESS inference engine, which reasoned over the data in the developed system and recommended anti-diabetic drugs with appropriate doses for each patient. Bankhele et al. (2017) developed a diabetic healthcare recommendation system that recommends personalized medication, diet, and exercise to assist patients in managing their diabetes effectively. This system examines the input parameters given by the current user and delivers customized services through recommendations on diet, medication, and exercise. A user-based collaborative filtering algorithm is used to make these recommendations. The system prompts the current user to input specific parameters, which are matched with the parameters of other patients stored in the database. This database comprises past cases of diagnosed and treated diabetic patients. Once a match is found, the recommended diet, medication, and exercise plan for the matched patient are presented to the current user. Marin et al. (2019) introduced an online self-diagnosis and drug recommendation tool based on the user's healthcare keyword descriptions of symptoms. Each of the over 2,200 medicines stored in the database is accompanied by a set of usage-specific keywords. Consequently, the tool facilitates the search procedure and provides the user with the most related data, thereby avoiding the need for manual data interpretation. In the end, the fuzzy search algorithm is used to generate a confidence score to rank the results.

Drug-drug interactions, co-occurring diseases, and existing symptoms were all taken into account by the drug recommendation system for the elderly, which was proposed by Montalvo and Villanueva (2020). In the proposed system, a model of the geriatric patient was developed using a Bayesian network that permits inferences to be drawn with limited data about patient. A genetic algorithm is also employed within the system to find the optimal drug combination for a given patient. A specialist confirms the system's consistency in simulated environments.

Garg (2021) introduced a drug recommender system that leverages patients' reviews to anticipate sentiment through multiple vectorization methods such as TF-IDF, Bow, Manual Feature Analysis, and Word2Vec. The system aims to suggest the most effective medication for a particular ailment. The results showed that LinearSVC, a classifier that employs TF-IDF vectorization, performs superiorly to all other models, achieving an accuracy rate of 93%.

To ensure that all patients receive the most appropriate care for infectious diseases, Bhimavarapu et al. (2022) proposed a drug recommender system based on a stacked artificial neural network (ANN) model. Drugs are recommended taking into account the patient's health history, current lifestyle, and habits, in order to lessen the likelihood of side effects. The proposed system achieved an accuracy of 97.5%. The authors argue that a system like this could be helpful in suggesting safe medicine to patients, particularly in health emergencies.

3. The Design of the Proposed Model

The proposed Hybrid Taxonomy-based Multi-Criteria CF (HTMCCF) model is illustrated in Figure 2.
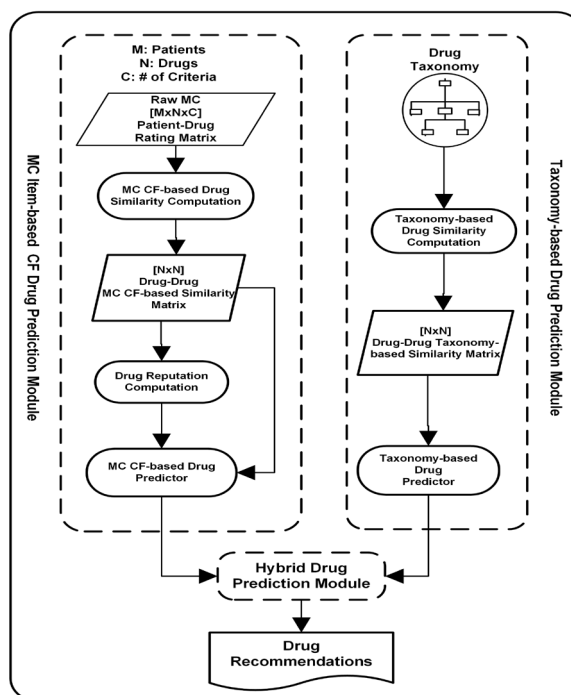

Figure 2. The design of the Hybrid Taxonomy-based Multi-Criteria CF (HTMCCF) model

This model has two inputs: a raw drug MC rating matrix that consists of M patients rating N drugs upon specific C criteria, and a drug taxonomy that is structured as a tree hierarchy with two levels of nodes. The first level is composed of main medical conditions that each drug can associated with, while the second level consists of the drugs names as leaf nodes. Each drug may be associated with one or more medical conditions. The subsequent three main modules provide a detailed description of the recommendation process involved in the HTMCCF model.

An illustration of a drug taxonomy is presented in Figure 3. The tree structure starts with a "Medical condition" node which is linked to various medical condition branches (such as Joint pain, Backache, Nerve pain, Psoriasis of scalp, and Skin condition) through an "Associated with a drug" relationship type. This relationship type is used to connect drugs with the relevant medical conditions. It is important to note that a drug may be used to treat multiple conditions and, as a result, may be associated with multiple condition branches. In summary, if two drugs are linked to the same medical condition in the drug taxonomy, it suggests that they are related or similar to each other. Consequently, taxonomy-based similarity utilizes the categorical representations of a set of drugs to recommend a new set of related drugs that the patient has not yet explored.
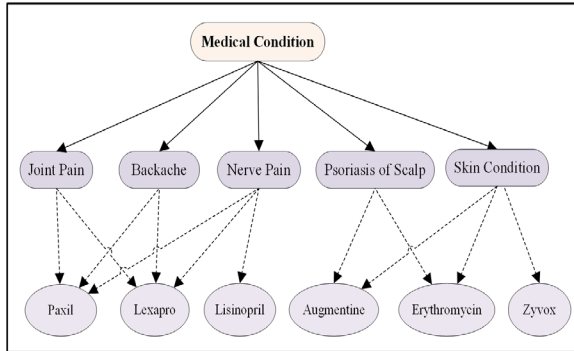

Figure 3. Example of a drug taxonomy

3.1 Taxonomy-based Drug Similarity Computation

In order to compute the taxonomy-based similarity between drugs based on their associated medical conditions, a binary vector is assigned to each drug, as below:

$$\overline{D}_i = (d_{i,1}, d_{i,2}, \ldots, d_{i,x}) \qquad (1)$$

Here, $d_{i,x}$ is defined as a binary variable, as follows:

$$d_{i,x} = \begin{cases} 1 & \text{If } drug \ i \text{ associates with } condition \ x \\ 0 & \text{If } drug \ i \text{ does not associate with } condition \ x \end{cases} \qquad (2)$$

After assigning the binary vector to each drug, the taxonomy-based similarity between any two drugs is calculated using the standard vector-based cosine similarity (Sarwar et al., 2001), as demonstrated in equation (3).

$$drugSim_{i,j}^{Taxonomy} = \frac{\langle \overline{D}_i, \overline{D}_j \rangle}{\|\overline{D}_i\| \times \|\overline{D}_j\|} \qquad (3)$$

3.2 Taxonomy-based Drug Predictor

The mean-based prediction metric (Herlocker et al., 2002) is used as shown below to generate taxonomy-based drug predicted rating of patient p on drug i.

$$Pred_{p,i}^{Taxonomy} = \overline{r}_i + \frac{\sum_{j \in NN} drugSim_{i,j}^{Taxonomy} \times (r_{p,j} - \overline{r}_j)}{\sum_{j \in NN} drugSim_{i,j}^{Taxonomy}} \qquad (4)$$

where $drugSim_{i,j}^{Taxonomy}$ refers to taxonomy-based similarity between drugs i and j; NN is the group of nearest neighbors for drug i based on the drug-drug taxonomy-based similarity matrix; $r_{p,j}$ is the total rating of patient p on drug j, and $\overline{r}_j$ is the average rating of drug j made by all the patients.

3.3 MC Item-based CF Drug Prediction Module

3.3.1 MC CF-based Drug Similarity Computation

A drug-drug similarity metric based on MC CF that takes into account both distance and structural similarities has been proposed to boost the accuracy and coverage of drug predictions. The similarity of a drug is gauged by its ability, as a prior recommender, to accurately predict another drug. For instance, if drug j has made accurate recommendations to drug i, it will obtain a high similarity score with drug i. The following rating prediction formulation is used to anticipate the rating of drug i for patient p, with only a single neighboring drug j being considered:

$$Pred_{p,i} = \overline{r}_i + (U_{p,i} - \overline{r}_j) \qquad (5)$$

where $\overline{r}_i$ and $\overline{r}_j$ are the mean ratings of drugs i and j, respectively, and $U_{p,i}$ represents the overall

utility of patient p for drug i. The total utility is obtained utilizing an aggregate function (Dyer, 2005) as follows:

$$U_{p,i} = \sum_{k=1}^{c} w_{p,k} \times r_{p,i,k} \, ,$$

$$where \sum_{k=1}^{c} w_{p,k} = 1, \quad w_{p,k} > 0 \tag{6}$$

where $r_{p,i,k}$ denotes the rating of patient p on drug i with regard to criterion k, and $w_{p,k}$ is a weighting factor representing the importance of criterion k for patient p.

Afterward, an adjusted form of the Manhattan similarity measure (Jain et al., 2020) is utilized to compute the preliminary similarity between drugs i and j. This modified version incorporates the inverse item frequency measure originally proposed by Breese et al. (1998). This is based on the prediction errors of their co-rated patients and the significance of these patients in the similarity computation. Hence, $ManSim_{i,j}$ is used to quantify the similarity between drugs based on the differences in their ratings across patients. It plays a significant role in recommending drugs to patients based on their similarity to drugs they have already rated or shown interest in.

$$ManSim_{i,j} = \frac{1}{1 + \sum_{p \in P_{i,j}} |Pred_{p,i} - U_{p,i}|} \times Log \left(\frac{|D|}{|D_p|} \right)^2 \tag{7}$$

where p is a patient from the set $P_{i,j}$, which consists of patients who have rated both drugs i and j; $Pred_{p,i}$ denotes the predicted rating of drug i made by patient p, with only a single neighboring drug j being considered; $|D|$ corresponds to the cardinality of the complete set of drugs within the rating matrix, and $|Dp|$ denotes the cardinality of the set of drugs that have been rated by patient p.

Nonetheless, the aforementioned metric is susceptible to a fundamental shortcoming in that it exclusively depends on the prediction errors of co-rated ratings. To overcome this, the Salton's cosine index (Verma & Aggarwal, 2020) is incorporated as a structural similarity metric to take into account the quantity of patients who have rated both drugs. The level of similarity between drugs is directly proportional to the count of patients who have rated both drugs.

$$SalSim_{i,j} = \frac{|P_i \cap P_j|}{\sqrt{|P_i| \times |P_j|}} \tag{8}$$

where $|P_i \; P_j|$ corresponds to the total count of patients who assigned ratings for both drugs i and j. Additionally, $|P_i|$ and $|P_j|$ represent the total count of patients who rated drugs i and j, respectively. Ultimately, the final drug-drug MC CF-based similarity metric between any given pair of drugs is formulated as follows:

$$drugSim_{i,j}^{MCCF} = ManSim_{i,j} \times SalSim_{i,j} \tag{9}$$

3.3.2 Drug Reputation Computation

To improve the ability of the module to predict unobserved drugs, a drug reputation score has been incorporated. This is due to the sparsity challenge caused by a limited number of trustworthy nearest neighbors. Several aspects are considered to determine the reputation of a drug, such as the difference in ratings between the drug and patients' mean ratings and the associations of the drug with other drugs in the drug-drug similarity matrix, as demonstrated below:

$$drugRep_i = \exp \left(- \frac{\sum_{p \in P_i} |U_{p,i} - \overline{r}_p|}{|P_i|} \right) \times \sqrt{\frac{|D_i|}{|D|}} \tag{10}$$

where $\overline{r}_p$ denotes the mean rating given by patient p, while P_i refers to the set of patients who provided ratings for drug i. D_i represents the set of drugs that share similarity connections with drug i, and D refers to the set of all drugs present in the dataset.

3.3.3 MC CF-based Drug Predictor

The mean-based prediction metric is used again, as shown below, to generate MC CF-based drug predicted rating of patient p on drug i:

$$Pred_{p,i}^{MCCF} = \begin{cases} \overline{r}_i + \dfrac{\sum_{j \in NN} drugSim_{i,j}^{MCCF} \times (U_{p,j} - \overline{r}_j)}{\sum_{j \in NN} drugSim_{i,j}^{MCCF}} & ; \text{ if } drugSim_{i,j}^{MCCF} \neq 0 \\[4mm] \overline{r}_i + \dfrac{\sum_{j \in NN} drugRep_j \times (U_{p,j} - \overline{r}_j)}{\sum_{j \in NN} drugRep_j} & ; \text{ if } drugSim_{i,j}^{MCCF} = 0 \end{cases} \tag{11}$$

where $drugSim_{i,j}^{MCCF}$ represents the MC CF-based similarity between drugs i and j, NN denotes the group of MC CF-based nearest neighbors for drug i, based on the drug-drug MC CF-based similarity matrix, and $drugRep_j$ is the drug reputation score for drug j.

3.4 Hybrid Drug Prediction Module

To attain the best rating prediction performance, it has been demonstrated that hybridizing several recommendation approaches is necessary. Therefore, the switching hybridization strategy (Burke, 2007) is implemented, as shown below, to alternate between the illustrated modules based on a specific condition. The selection criterion for determining which module to use is its ability to produce a predicted rating for a potential drug. In situations where both modules can produce predicted ratings, the arithmetic-harmonic mean is employed to merge the predicted scores. The harmonic mean metric is utilized to ensure that a high total predicted rating for a specific drug is obtained only when the predicted ratings from both combined modules are high.

$$P_{p,i}^{Hybrid} = \begin{cases} 0 & ; \text{if } Pred_{p,i}^{Taxonomy} \text{ and } Pred_{p,i}^{MCCF} = 0 \\ Pred_{p,i}^{Taxonomy} & ; \text{if } Pred_{p,i}^{MCCF} = 0 \\ Pred_{p,i}^{MCCF} & ; \text{if } Pred_{p,i}^{Taxonomy} = 0 \\ \dfrac{2 \times Pred_{p,i}^{MCCF} \times Pred_{p,i}^{Taxonomy}}{Pred_{p,i}^{MCCF} + Pred_{p,i}^{Taxonomy}} & ; Otherwise \end{cases} \quad (12)$$

4. Experiments

The effectiveness of the HTMCCF model was evaluated through several experiments using a real-world MC dataset of drugs, and evaluation metrics were utilized to measure its performance. These experiments involved comparing the performance of the HTMCCF model against other baseline recommendation techniques.

4.1 Experimental Setup

4.1.1 Input Datasets

To evaluate the performance of the proposed HTMCCF model, the following inputs were utilized. Firstly, the WebMD MC rating dataset, obtained from the reputable healthcare website (WebMD, n. d.). This dataset serves as a comprehensive source of information on drugs, enabling users to review and rate them based on three criteria: medication effectiveness, ease of use, and satisfaction. Users' ratings are recorded on a scale ranging from 1 to 5. The WebMD MC dataset comprises 32,054 multi-criteria ratings gathered from 2,136 patients, covering a total of 845 unique drugs. This extensive dataset provides a diverse and realistic representation of

user's preferences and experiences with different medications. The input data was structured in the following format: patient, drug, rating of medication effectiveness, rating of ease of use, rating of satisfaction.

Secondly, a drug taxonomy with two levels was incorporated to enhance the organization and categorization of drugs based on medical conditions. The top level of the taxonomy encompasses 915 main categories, representing a wide range of medical conditions, such as joint pain, backache, nerve pain, psoriasis of the scalp, and various skin conditions, among others. The second level of the taxonomy comprises the names of drugs as leaf nodes. This taxonomy structure facilitated a more organized representation of drugs within the model. In terms of input data, a binary vector representation was utilized for each drug, as it has been defined by equation (1). This binary vector representation allowed the relevant medical conditions of each drug to be captured in a concise and informative manner.

The HTMCCF model effectively processed this input data to generate personalized drug recommendations for individual patients. The output of the model was a list of recommended drugs, ranked according to their predicted ratings, calculated using the formulation described in equation (11). These recommendations were tailored to each patient's specific medical conditions and preferences, assisting him/her in selecting suitable medications.

4.1.2 Evaluation Measures

To evaluate the proposed model, its prediction accuracy is gauged using mean absolute error (MAE). Meanwhile, the prediction coverage is assessed using the rating prediction coverage metric. MAE is determined by computing the average absolute difference between the predicted and actual ratings. In MAE, a lower score indicates more accurate predictions. Furthermore, rating prediction coverage measures the percentage of cases in which the recommendation approach can produce a numeric prediction. A high coverage value indicates a broad range of item suggestions for users, while a low coverage value implies limited recommendation capabilities of the recommender system (Aggarwal, 2016a).

4.1.3 Baseline Approaches

To conduct a comparative analysis, the following conventional and state-of-the-art item-based CF recommendation methods have been included in the present study. The outcomes of these baseline approaches will be contrasted with those of the proposed HTMCCF model:

- The Single-Criteria Item-based CF (SC-ICF) recommendation approach (Sarwar et al., 2001);

- The Multi-Criteria Item-based CF (MC-ICF) recommendation approach (Adomavicius & Kwon, 2007), which utilizes multi-criteria ratings among items to enhance prediction accuracy;

- The Multi-Criteria Item-based Semantic-enhanced CF (MC-SeCF) recommendation approach (Shambour et al., 2016), which employs multi-criteria ratings and item semantic relationships to improve prediction accuracy and address data sparsity and cold-start item problems.

4.2 Results and Discussion

Several experiments are carried out to assess the recommendation performance of HTMCCF model over the baseline approaches, particularly in addressing sparsity and new item challenges, by improving prediction accuracy and coverage.

4.2.1 Assessment of Performance with Respect to Various Neighborhood Sizes

Figure 4 compares the prediction accuracy of the HTMCCF model, measured by MAE results, with baseline approaches on the WebMD MC dataset.
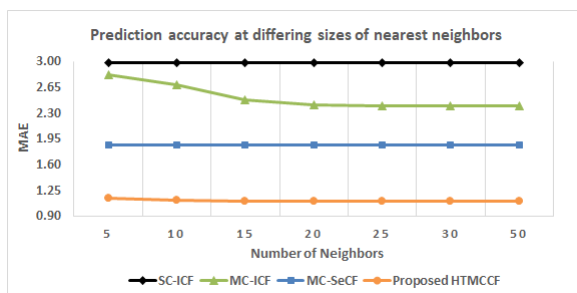

Figure 4. Assessing the MAE of various approaches across varying numbers of nearest neighbors

The comparison includes the baseline approaches, and the proposed HTMCCF model achieves exceptional MAE performance across different

neighboring sizes ranging from 5 to 50. On average, the HTMCCF model outperforms the baseline approaches by approximately 62%, 55%, and 40%, respectively, in terms of MAE results. The analysis and comparison of all baseline approaches against the HTMCCF model confirm that the proposed model significantly enhances prediction accuracy.

4.2.2 Assessment of Performance Across Varying Degrees of Sparsity

To confirm the efficacy of the proposed HTMCCF model in mitigating the problem of data sparsity, a range of experiments were performed. Specifically, six datasets were created with varying degrees of sparsity, ranging from 99.8% to 98%, with the purpose of evaluating the capability of the compared approaches to handle varying levels of sparsity.

Figure 5 displays the average MAE results of the proposed HTMCCF model in comparison to the baseline approaches, which exhibit enhancements of approximately 67%, 61%, and 30%, correspondingly. These results highlight the superior performance of the HTMCCF model in accurately predicting ratings under varying levels of sparsity, when compared to the baseline approaches.
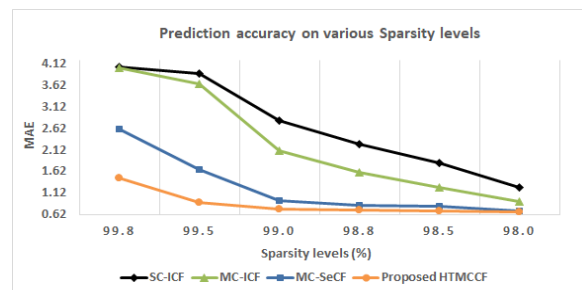

Figure 5. Assessing the MAE of various approaches under varying degrees of data sparsity

Moreover, Figure 6 demonstrates that the proposed model not only significantly improves MAE, but also enhances prediction coverage. When compared to the baseline approaches, the HTMCCF model demonstrates a significant increase in Coverage by 56%, 43%, and 12%, respectively. This indicates that the proposed model surpasses the baseline methods in terms of prediction coverage as well. The observed improvements in both MAE and Coverage results provide strong evidence that the HTMCCF model is more robust than other baseline approaches, especially when dealing with highly sparse datasets.
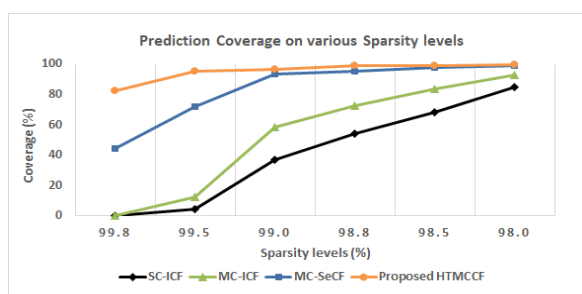
Figure 6. Assessing the prediction Coverage of various approaches under varying degrees of data sparsity

4.2.3 Assessment of Performance with Regard to Varying Number of Ratings for New Items

To assess the effect of the new item problem on the recommendation performance of the proposed HTMCCF model and other baseline approaches, a series of comparative experiments focusing on prediction accuracy and coverage was conducted. To this end, six datasets were created, each containing different numbers of ratings for new items, ranging from 2 to 25. The results of these experiments were then compared with the HTMCCF model and the baseline approaches in terms of MAE and Coverage, as depicted in Figures 7-8.
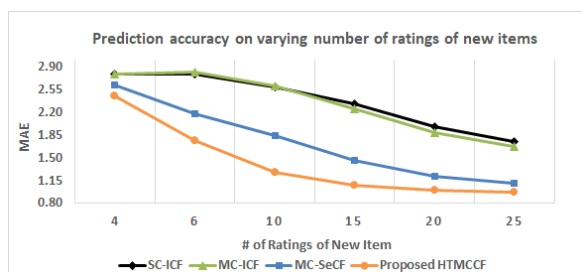

Figure 7. Assessing the MAE of various approaches across different numbers of ratings for new items
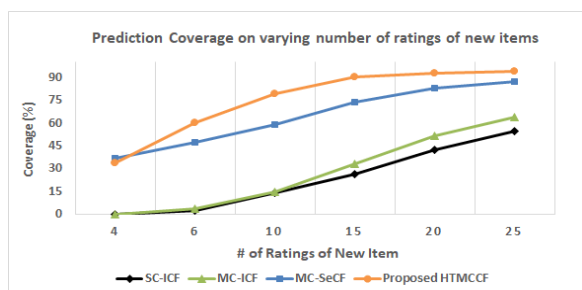

Figure 8. Assessing the prediction Coverage of various approaches across different numbers of ratings for new items

Figure 7 indicates that the proposed HTMCCF model outperforms the baseline approaches by improving the average MAE results by 40%,

39%, and 18%, respectively. This demonstrates that the proposed model is superior to the baseline approaches regarding prediction accuracy for new items across various numbers of ratings. Moreover, as shown in Figure 8, the proposed HTMCCF model achieves significant improvements in prediction coverage, in addition to MAE improvements. In comparison to the baseline approaches, the proposed model exhibits a 68%, 62%, and 14% increase in Coverage, indicating that it outperforms the baseline methods in terms of prediction coverage as well. In conclusion, the proposed model is more dependable and effective in dealing with new items, as evidenced by the noteworthy improvements in both MAE and Coverage results. These improvements can be attributed to the incorporation of the overall reputation and taxonomy of drugs, which compensate for the lack of rating and, thus, mitigate the new item problem.

5. Conclusion

Patients and healthcare providers face challenges when it comes to identifying relevant drugs, due to the abundance of drug information available on various online healthcare platforms. To address this issue, the present study proposes an effective drug recommendation model that assists patients in selecting suitable drugs for their specific medical conditions. The proposed model incorporates a taxonomy-based drug prediction module and a multi-criteria item-based CF drug prediction module to mitigate the effects of data sparsity and new item issues.

The taxonomy-based drug prediction module significantly enhances the recommendation process by providing a structured and detailed representation of drugs. By incorporating domain-specific knowledge, this module offers a more comprehensive understanding of drugs, augmenting the accuracy and relevance of the recommendations. On the other hand, the multi-criteria CF module further advances the capability of the model to capture the patients' complex preferences. It employs a novel similarity metric that considers both distance and structural similarities, while also incorporating a drug reputation score to overcome challenges related to data sparsity and new items. The efficacy of the proposed model is demonstrated through experimental results obtained from a real-world

drug MC rating dataset, where it outperforms traditional and state-of-the-art approaches. The model successfully addresses the identified challenges, leading to enhanced prediction accuracy and broader coverage.

However, it is crucial to clarify that while the proposed HTMCCF model is designed to support and empower patients, it should not be viewed as a replacement for professional medical guidance, diagnosis, or treatment provided by healthcare providers. Patients must consult with their healthcare professionals to make personalized and informed decisions regarding their medication needs. The HTMCCF model should be used responsibly and in conjunction with the expertise of medical professionals, to ensure the best possible healthcare outcomes.

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