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Social Media Based Deep Auto-Encoder Model for Clinical Recommendation

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Abstract—One of the most actively studied topics in modern medicine is the use of deep learning and patient clinical data to make medication and ADR recommendations. However, the clinical community still has some work to do in order to build a model that hybridises the recommendation system. As a social media learning based deep auto-encoder model for clinical recommendation, this research proposes a hybrid model that combines deep self-decoder with Top n similar co-patient information to produce a joint optimisation function (SAeCR). Implicit clinical information can be extracted using the network representation learning technique. Three experiments were conducted on two real-world social network data sets to assess the efficacy of the SAeCR model. As demonstrated by the experiments, the suggested model outperforms the other classification method on a larger and sparser data set. In addition, social network data can help doctors determine the nature of a patient's relationship with a co-patient. The SAeCR model is more effective since it incorporates insights from network representation learning and social theory.

Keywords- Adverse Drug Reaction, Collaborative filtering, Deep Learning, Drug recommendation, Clinical Recommendation System, Recommendation System, Social Media

I. INTRODUCTION

Social networks such as We-Chat, Weibo, Instagram, Face book and Twitter have all been widely used worldwide. Under the background of this era, how to implement fast and practical recommendations for users and form decision-making opinions has become one of the issues of widespread concern in the academic community [1].

Academia often defines the social network recommendation model as an active information filtering tool. Its purpose is to provide users with the most targeted and accurate recommendation information. The real-time personalized information is discovered in the dynamic search space of the social network. Recently social media platforms are also being used to share clinical con- tent, which helps healthcare sectors and pharma companies with pharma co-vigilance, drug repositioning and advice reaction detection (ADR) recommendations. In order to recommend the most relevant therapies, paramedical researchers gather reliable health information from social media sites and link it with user profiles. Social media posts with personal and medical information about patients keep them up to date on the latest drug revolution. Centralized social media-based pharma co-vigilance activities must create a virtual podium that identifies the drug and its associated adverse drug reactions (ADRs) in order to anticipate computational medical services. To more effectively offer informative and emotional support, develop a homogeneous e-patient information community on the online platform.

Some of the filtering methods used by social network recommendation include collaborative filtering (CF), content-based filtering (CB), demographic systems (DG), knowledge-based systems (KB), utility-based systems (UB), and hybrid systems [2, 3]. However, the above-mentioned existing filtering models generally have problems such as data sparsity, cold start, synonyms, trust attacks, data privacy, limited content analysis, and excessive specialisation [4]. At present, the collaborative filtering system is caused by problems. On the other hand, its versatility, cross-domain applicability, and the support of large user spaces have been widely used. Therefore, this article attempts to use collaborative filtering technology to establish a social network user information recommendation system for score prediction.

To make decisions faster and more accurately, the development of deep learning technology in recent years has received significant attention from the academic community. Nowadays, the cutting-edge technology of deep learning technology used by academia and industry is mainly concentrated in Computer Vision [5], Natural Language Processing (NLP) [6] and other intelligent system construction fields.

The rapid advancement of deep learning technology in recent years has resulted in its increased use in social network recommendation systems with the aim of bettering the user experience. Wang et al. [7] present collaborative filtering, nonlinear feature extraction, and model stacking, a deep learning joint recommendation sys- tem to collect better nonlinear and complex interactive feature sets between users and target information, and it is confirmed that this system can be concise and high. As a result of the quality, its performance is currently the most advanced and better than traditional models. This paper uses a deep learning architecture with collaborative filtering features for model construction. In addition, with the continuous development of social networks and the continuous increase in user us- age, the trust that users give to others and themselves in social interactions plays an increasingly important role in the personalised processing of social network recommendation models. For example, a research hotspot in recent years is to incorporate the trust link relationship between users in social networks to improve the recommendation model. This research direction can optimise the sparsity and cold start problems of traditional recommendations.

Therefore, this paper extracts the patients social relationship and based on this, the recommendation results are personalised. Nguyen and Nam et al. [8] discussed the advantages of explicit and publicly available user relationship data in improving the accuracy of recommendations. The experimental results show that the real data set is explicit Social information is often sparse and difficult to locate. Chai et al. [9] believe that users' social relationships are often implicit, sparse, complex, and dynamic in terms of recommendation systems. The experimental results show that users' feedback (such as user ratings, reviews, and purchase records) extracting implicit and reliable social network information can increase the personalisation of recommendations, thereby improving the recommendation model.

The latest trend in the academic world in exploring potential social relation- ships is to use the concept of Network Representation Learning (NRL), in which network nodes are embedded in low-dimensional vector space [10]. Network representation learning technology transforms nodes into continuous vectors; its generation method is to close the nodes with structural proximity. On this basis, the network representation learning technology can identify social roles and classic network analysis problems that share similar

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attributes. Therefore, this paper uses the network representation learning technology to identify the patients social relationship.The development of generalized network embedding technologies, such as intensive computing Matrix factorization (Computationally Intensive Matrix Factorization, CIMF) to deep learning technology in recent years [11], has been facilitated by the large number of documents [12] that use dimensionality reduction methods to create new network embedding technologies with good performance in practical applications.

The prediction model's effectiveness and the accessibility of pertinent user data should be factors in the social network recommendation model's increased performance. Therefore, the recommendation system is often modelled based on the deep learning method, and the patients implicit social relationship is used to give users to improve the experimental results. However, integrating deep learning methods and user trust information to enhance the social network user information recommendation model is still a challenge facing the academic community. Therefore, this paper proposes social media learning based deep auto-encoder model for clinical recommendation (SAeCR). This hybrid recommendation model expands deep auto-encoders and social information by learning joint optimisations. Specifically, first of all, this paper uses single-modal mapping to form patient and clinical information. Then, the interaction network between patients- patient is constructed in the network's bisection network. Next, the characteristics of the interactive network nodes between patients are extracted by combining the network representation learning technology. Then, the co-patient community of each patient user is dynamically identified. Finally, Then is merged In the collaborative filtering auto-encoder that learns sparse patient rating vectors and in- formation rating vectors, the SAeCRalgorithm proposed in this paper learns two levels of patient disease-drug preferences (clinical rating behaviour and patients Top- k co-patient clinical preferences). Score prediction and extend the model to deal with implicit patient clinical preferences. The main contributions of this article are summarised as follows:

- Proposes the SAeCRmodel, which learns joint optimization functions to incorporate Top n similar clinical information and deep auto-encoders;
- The auto-encoder and Top n similar clinical entity are expanded to propose an SAeCRmodel that can be used for non-observation score prediction;
- The SAeCRmodel is constructed and used to deal with the explicit and implicit clinical preferences of patient.
- Real data sets to run numerous tests and assess how well the SAeCR model and associated models function in order to comprehend and forecast the model's efficacy.

The rest of the article organized as follows: Section 2 covers Literature Survey over different domains of healthcare recommendation system. Section 3 illustrates possible research findings , section 4 present a Proposed framework for ADR classifier, section 5 cover evaluation of result finally, Sect. 6 concludes the recent research, finding and potential gap for upcoming research.

II. Types of Recommender Systems

Since the 1990s, to reduce the difficulty of filtering the most relevant data from a large amount of complex information, the information recommendation model in social networks has been widely used. It is decision-making strategies that can help users find required information according to their preferences. The application of this type of system in the fields of e-book recommendation [13], personalized e-government services [14], intelligent decision support system applications [15], high-quality e-commerce service recommendation [16] and other fields has become increasingly prominent. In recent years, Collaborative filtering systems have received widespread attention. Its principle is to recommend relevant information that users are interested in based on similar users' preferences. Tewari [17] believe that collaborative filtering methods can be based on users' explicit and implicit information in a real social network environment. For example, feedback is calculated based on ratings or rankings.

In the score-based method, collaborative filtering uses different algorithms, which can be based on similarity/proximity calculations (such as KG nearest neighbour method, clustering method, latent hash retrieval method, etc.) [18], Personality Diagnosis (PD) algorithm [19], Bayesian Networks (such as belief net- works, etc. [20], Matrix Factorisation (MF) and other technologies to judge the value of the score matrix. Among them, the matrix factorisation technology is due to the sparseness of the score matrix. It has an excellent role in the performance and the ability to maintain global information, so it is widely used. The scoring matrix in this article can be decomposed into potential user factors and potential information factors. Then, the approximate value of the inner product of the two can be obtained to obtain the predicted score. , That is, the model is expressed as an optimisation problem according to the objective function. Nocera et al. [20] proposed the most commonly used optimisation technology algorithm today-Stochastic Gradient Descent (SGD), which can find out about the patients potential. The gradient of the objective function of the factors and information potential factors, and use the update rules to iteratively modify these factors to minimise the error between the actual score and the predicted score. In addition, many methods can be used to calculate the value of the approximate score matrix, such as the singular values Decomposition method (Singular Value Decomposition, SVD) [21] etc. Computer vision, NLP (natural language processing), and SNA (Social Network Analysis) are just a few examples of the many areas that can benefit from deep learning technology [22]. Deep Learning is a type of machine learning algorithms that attempts to simulate the way a human brain processes information by using a hierarchical structure. For data preparation and feature generation, it employs multi-layer nonlinear transformations. Commonly employed in academic settings are three distinct varieties of deep learning architectures: In order to determine the generating architecture of data relevance, Harshvardhan et al. [23] propose using unsupervised pre-training (2) Radecka and Indurkhya [24] proposed a discriminative architecture for distinguishing data classification; (3) as Liu et al. [25] proposed A hybrid model to achieve synergy. Sharma et al. [26] divided deep learning recommendation methods into two categories based on the side information and the interaction between the user and the target information: integrated model and neural network model. Lee et al. [27] proposed a hybrid model that combines sparse scoring features and side information extracted by Stacked De-noising Auto-encoder (SDAE) into a collaborative filtering framework. The side information includes user personal information (such as age, gender, Occupation, etc.), product characteristics (such as release year, type, and style), interaction data (such as ratings and reviews).

In addition, the performance of the user recommendation model of social networks depends not only on predictions but also on user preferences. An exciting form of data that can identify additional preferences of users is explicit/implicit social information. The objective function extends the Singular Value Decomposition (SVD) method with explicit trust data.

This paper proposes the SAeCR method that can solve sparsity and cold start based on the above research review. It uses a deep auto encoder with collaborative filtering characteristics and incorporates user credit information into the deep learning model to improve the proposed method. Furthermore, the personalised recommendation level of the model and this article uses network representation learning technology to locate reliable and potential social relationships between patients. Finally, based on the existing model, this article designs a method for processing explicit/implicit clinical data and using various data sets for experiments and algorithm comparisons. In short, the fundamental idea of the SAeCR algorithm is to integrate network representation learning technology to build a social network patient information recommendation system based on deep auto-encoders to

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solve the patient clinical information score prediction problem and use social information trains the model to achieve better prediction results.

III. Preprocessing Of Clinical Tweets

It's important to keep in mind that user-generated content on social media platforms sometimes include slang, symbols, and misspelt words related to the topic at hand. In order to make better decisions, pre-processing social media content is crucial. Selecting the right preprocessing methods can increase the precision of drug ADR interactions in disease. In order to further define the feature space, this paper studied the peculiarities of slag language and experimented with user and topic replacement, Word normalisation, and Slag replacement, as shown in figure 1.

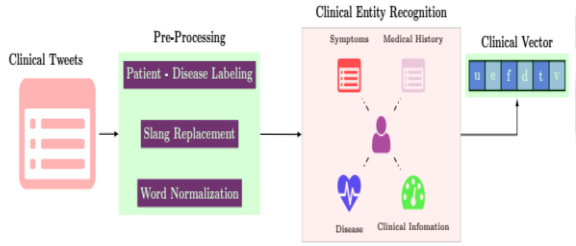

Figure 1. Proposed Pre-processing Framework for Clinical Vector Space Extraction

User and Topic Labeling: Neither the user nor the subject name may be rated. The tweet's "@" mentions of specific individuals are changed to "Medical expert," and the tweet's "#" references to specific topics are changed to "Disease, Drug, and ADR" to ensure high-quality data collection.

1. Word Normalization (WN): Clinical tokens are compared to Roget's Thesaurus terms at this point. If there is no match, the word is broken down into its component parts until a match is discovered (for example, "Higheeeeer BP" would be broken down into "Higheeer BP," "Higher BP," and "Higher BP").

2. Slang Replacement (SR): By matching terms from a corpus of commonly used clinical semantic and token entities, slag replacement can effectively replace the slang term.

When the tokens "Sugar " in the unprocessed comment C1 are compared to the entries in the slang meta data, the processed comment C1 with the token "Diabetes" is returned.

Unprocessed Comment (C1): My father suffers from high Sugar.
Processed Comment (C1): My father suffers from high Diabetes.

A. *Clinical Entity Recognition*

After preprocessing social media based clinical post, Clinical entity recognition (CER) is used to identify medical token in processed post. Basically CER is used to labeled drug, disease and symptoms over the clinical post. Whereas, this phase simultaneously identify owner of post as petitioner, publisher and medical expert as medical consumer.

IV. Proposed Work

The SAeCR model's key feature is to predict user non-observation ratings to in- corporate objective functions that can learn patient clinical condition ratings and the co-patient clinical preferences of each patient. Specifically, the model used the effectiveness of the auto-encoder to make high- quality predictions and extended it with clinical social information. To obtain implicit and reliable social clinical information, SAeCR extracts the network structure of the patient interaction from the interaction between the patient and the target information and recognises the proximity of the system captured by the network representation learning technology. Find out the top and similar patient of each social network patient. Finally, the model is optimised to refine the scoring characteristics of patients and their social co-patient.

A. *SAeCR*

The SAeCR model defined in this paper contains the following three objective functions: Loss Function f (l); Regular function f (r); Social regular function f (s). Therefore, the model can be defined as:

$$f(obj) = \frac{1}{2}f(l) + f(r) + \frac{\gamma}{2}f(s) \quad (1)$$

Among them, f(s), is a crucial part of the model. Through f, the SAeCR model incorporates social data into the scoring prediction model (s). The regular social term known as "parameter" controls how much the patients social data is used. The goal of the function f (s) is to reduce the ratings gap between users and their top n similar co-patients. Thus, the function of f (s) is dependent upon the list S(i) of the top n similarly affected patients of user i. The difference between the actual score and the anticipated score is calculated using the loss function f(l). In order to address the over-fitting of the model, the SAeCR model is regularised in this study using the function f (r). By creating an objective function, it is possible to reduce the discrepancy between the actual score and the predicted score when each patients top n similar patient scores are taken into account.

B. *Patient Clinical Information Extraction*

This paper introduces the implicit social network patient information extraction method used in the *SAeCR*model. The framework follows the network representation learning technology and builds an interaction network between patients from the existing score data between the patients disease, disease-disease, disease-drug related desired clinical information; The specific process is shown in Figure 2, 3 and 4.

Figures 1, p_1, p_1, and p_n represent social network patients, and q_1, q_1, and q_n convey social network information. In the interaction network between users $G = (P, C)$, P is the patient set, $C \in (p, c)$ is at least one or more information scoring edges between patient u and v. This paper patient network representation learning technology SDNE to find similar nodes in social networks and use them as trusted links between patients. For a given Network $G = (P, C)$, this paper finds the mapping function through the network as mentioned above representation learning technology, as shown in equation (2):

$$\phi: p \in P \to \alpha^{|p|*D}(D << |p|) \quad (2)$$

Based on equation (2), the linear projection operator is used to make each node $p \in P$ be mapped to a D-dimensional space and combined with the mixed probability model for modeling. Space retains the node's Structural proximity. According to the latent feature representation, this paper uses the cosine similarity of the node representation (see equation (3)) to find top similar nodes.

$$\text{CosSim}\,(p_1, p_2) = \frac{p_1 * p_2}{|p_1||p_2|} \quad (3)$$

Among them, $p_1 \in \alpha v$ and $p_2 \in \alpha v$ are the clinical vectors of nodes p_1 and p_2. This paper uses the similarity function to fill the Top n similar co-patient of patient node *pi* into the list S(i). In recent years, many scholars have proposed an algorithm that can be used to find the corresponding mapping function of the low-dimensional vector representation of the network node. This paper uses two types of network representation learning techniques based on a random walk and deep learning. Finally, the results obtained are analysed.

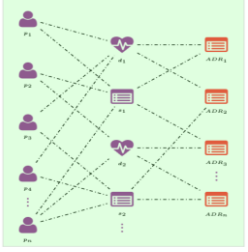

Figure 2. Patient disease ADR interaction network

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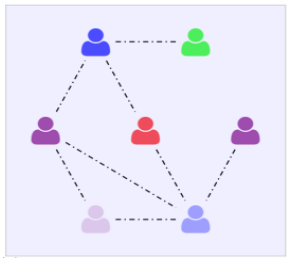

Figure 3. Patient- patient interaction network

Figure 4. Patient clinical information

C. *Collaborative Filtering Deep Auto-encoder*

This paper constructs the collaborative filtering deep auto-encoder architecture used for scoring prediction. The auto-encoder mentioned in this paper is a three- layer neural network that outputs the result vector calculated through a series of functions. The parameters of the three-layer neural network are manually adjusted. As an unsupervised feature machine learning technology, the auto-encoder can generate a deep latent representation of the data. The model in this paper is based on the matrix decomposition feature based on the auto-encoder; the specific model architecture is shown in Figure 5.

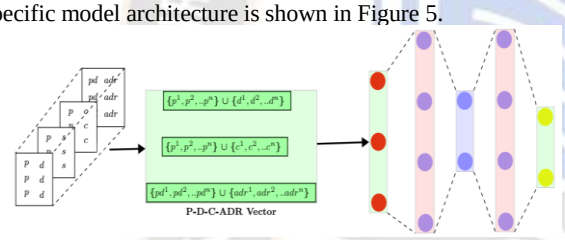

Figure 5. Clinical Auto encoder

$$f(p_i:\beta_1):\alpha^{m\times n}\rightarrow\alpha^{m\times d} \quad (4)$$

$$f(p_j:\beta_2):\alpha^{n\times m}\rightarrow\alpha^{n\times d} \quad (5)$$

$$f(h_{ij}:\beta):(\alpha^{m\times d},\alpha^{n\times d})\rightarrow\alpha^{m\times n} \quad (6)$$

In the architecture shown in figure 5 the auto-encoder is represented by three components:

- The patient's encoder unit that maps the sparse user score to the D-dimensional space, as shown in equation (4);
- The sparse information is scored The information encoder unit mapped to the D-dimensional space can be expressed explicitly as f, as shown in equation (5);

The patient's factor and clinical information factor of the common D-dimensional space are mapped to the clinical decoder unit of the scoring vector αv, The details are shown in equation (6).

The user encoder $f(pi;\beta_1)$ takes the patient's rating vector pi (rows of the clinical rating vector αv), which can be rewritten as latent expression formula shown in equation (7).

$$p=f(p_i:\beta_1)=f(g(p_i\gamma_h+\psi_h)\gamma_d+\psi_d) \quad (7)$$

Among them, $\beta_1=(\gamma h, \psi h, \gamma d, \psi d)$, $\gamma h\in\alpha n\times h$, $\gamma d\in\alpha hd$, $\psi h\in\alpha h$, $\psi d\in\alpha d$ are the symptoms and diseases of the patient's coding layer, and the dimension h is the user hidden layer unit and d is the number of shared layer units. The information encoder $f(qj;\beta_2)$ takes the information score vector qj(column of the score matrix R), as shown in equation (8).

$$q=f(q_j:\beta_2)=f(g(q_i\gamma_h{}'+\psi_h{}')\gamma_d+\psi_d) \quad (8)$$

Among them, $\beta_2=(\gamma h', \psi h', \gamma d, \psi d)$, and $\gamma h'\in\alpha m\times h$ and $\psi h'\in\alpha h$ are the weight and threshold of the hidden layer with the same number of hidden units h. For example, the weight γd and domain the value bd is shared by the patient's and the clinical information coding layer. The learning specific process is shown in equation (9).

$$\hat{r}=h(r_{ij}:\beta)=P^TQ \quad (9)$$

Among them, $\beta=\beta_1\cup\beta_2=(\gamma h, \gamma h', \gamma d, \psi h, \psi h', \psi d)$, so the model target can be defined as equation (10).

$$\underset{\beta}{\operatorname{argmin}}\sum_{i=1}^{m}\sum_{j=1}^{n}\left|r_{ij}-h(r_{ij}:\beta)\right|^2+\mathrm{Reg}(\beta) \quad (10)$$

Reg (β) in equation(10) can be obtained by equation (11).

$$\mathrm{Reg}(\beta)=\frac{\lambda}{2}\left(|Yh|^2+\left|\gamma_{h'}\right|^2+|\gamma_d|^2+|\psi_h|^2+\left|\psi_{h'}\right|^2+|\psi_d|^2\right) \quad (11)$$

The parameter λ in equation (11) controls the overfitting effect of the model through regularisation. In addition, the objective function is optimised by the neural network back propagation algorithm so that the predicted score is closer to the actual score.

D. *Joint Optimization Model Construction*

This paper trains the built model to optimise the objective function $f(obj)$ incorporating. Top similar patient clinical information into the auto-encoder. The components of the objective function $f(obj)$ are shown in equations (12)-(14).

$$f(l)=\sum_{i=1}^{m}\sum_{j=1}^{n}\left|r_{ij}-\mathrm{h}(r_{ij}:\beta)\right|^2 \quad (12)$$

$$f(r)=\mathrm{Reg}(\beta) \quad (13)$$

$$f(s)=\sum_{i=1}^{m}\sum_{s\in s_i}^{n}|f(p_i:\beta_1)-f(p_s:\beta_2)|^{2F} \quad (14)$$

The combined functional is shown in equation (15).

$$f(obj)=\frac{1}{2}\sum_{i=1}^{m}\sum_{j=1}^{n}\left|r_{ij}-\mathrm{h}(r_{ij}:\beta)\right|^2+\mathrm{Reg}(\beta)+\frac{\gamma}{2}\sum_{i=1}^{m}\sum_{s\in s_i}^{n}|f(p_i:\beta_1)-f(p_s:\beta_2)|^{2F} \quad (15)$$

As a result, the function l minimises the variation in the rating characteristics of similar patients while simultaneously reducing the reconstruction error. As a result, optimising the model is identical to minimising the objective function l with respect toβ. This research employs a neural network and back-propagation technique to minimise the objective function and minimise error by determining the number of partial layers of the model's learnable parameters and updating these parameters repeatedly.

To simplify the experimental process, this paper let γP, γQ, ψP, and ψQbe the learnable parameters, where $\gamma P$and γQrepresent the patient encoder weight and the information encoder weight, respectively; similarly, ψP and ψQ represent these two encoders. The threshold of the layer using these symbols is based on the following assumption: the coding layer of this learning model is equivalent to learning two Multilayer Perceptions (MLP) through back propagation. There- fore, γP includes the weights γh and γd, and ψP has the thresholds ψh and ψd of the patient coding layer. The partial derivatives of the above parameters are shown in equation (16).

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$$\frac{\partial f(obj)}{\partial \gamma_p} = \frac{1}{2}\frac{\partial f(l)}{\partial \gamma_p} + \frac{\partial f(r)}{\partial \gamma_p} + \frac{\gamma}{2}\frac{\partial f(s)}{\partial \gamma_p} \quad (16)$$

where , $$\frac{\partial f(l)}{\partial \gamma_p} = \frac{\partial f(l)}{\partial f(r_{ij}:\beta_1)} \quad (17)$$

And $$\frac{\partial f(l)}{\partial f(r_{ij}:\beta_1)} = 2\left(r_{ij} - \mathrm{h}(r_{ij}:\beta)\right) \quad (18)$$

Since *h*(*rij*; *β*) is a function of f() and g() (where f() and g() are linear rectification functions), it is easy to obtain the slope, So the third component of function l can be rewritten as:

$$\frac{\partial f(s)}{\partial \gamma_p} = \frac{\partial f(s)}{\partial f(p_i:\beta_1)} \cdot \frac{\partial f(p_i:\beta_1)}{\partial \gamma_p} \quad (19)$$

And $$\frac{\partial f(s)}{\partial f(p_i:\beta_1)} = 2\big(f(p_i:\beta_1) - f(p_s:\beta_1)\big) \quad (20)$$

Since f(pi; β1) is a function including f() and g(), the slope ∂l∂f(pi:β1) can be obtained, and the partial derivatives ∂l/∂γp and ∂l/∂ψp can be obtained as equations (21) and equation (22).

$$\frac{\partial l}{\partial \gamma_p} = \left(r_{ij} - \mathrm{h}(r_{ij}:\beta)\right) \cdot \frac{\partial \mathrm{h}(r_{ij}:\beta)}{\partial \gamma_p} + \lambda\gamma_p + \lambda\big(f(p_i:\beta_1)\big) - \big(f(p_i:\beta_1)\big) \cdot \frac{\partial f(p_i:\beta_1)}{\partial \gamma_p} \quad (21)$$

and

$$\frac{\partial f(obj)}{\partial \psi_p} = \left(r_{ij} - \mathrm{h}(r_{ij}:\beta)\right) \cdot \frac{\partial \mathrm{h}(r_{ij}:\beta)}{\partial \psi_p} + \lambda b_p + \lambda\big(f(p_i:\beta_1)\big) - \big(f(p_i:\beta_1)\big) \cdot \frac{\partial f(p_i:\beta_1)}{\partial b_p} \quad (22)$$

According to the learn able parameters of the coding layer of the optimized information, the slopes ∂l/∂γ q and ∂l/∂ψ q can be obtained, as shown in equations (23) and (24).

$$\frac{\partial f(obj)}{\partial \gamma_q} = \left(r_{ij} - \mathrm{h}(r_{ij}:\beta)\right) \cdot \frac{\partial \mathrm{h}(r_{ij}:\beta)}{\partial \gamma_q} + \lambda\gamma_q \quad (23)$$

$$\frac{\partial f(obj)}{\partial \psi_q} = \left(r_{ij} - \mathrm{h}(r_{ij}:\beta)\right) \cdot \frac{\partial \mathrm{h}(r_{ij}:\beta)}{\partial \psi_q} + \lambda\psi_q\ ) \quad (24)$$

Although the shared weights of the patient's encoder and the information encoded in the above model are *γd* and the threshold *ψd*, respectively, this paper assumes that these encoders are learned as two independent MLP units, and the decoder unit contains simple learning parameters without any learning parameters. Proposed method describes the operating program of the social recommendation system based on the self-encoder. *γp* and *γq* represent the user encoder weight and the information encoder weight, respectively; similarly, *ψp* and *ψq* represent the thresholds of these two encoder layers. Using these symbols is based on the following assumption: the encoding layer of this learning model is equivalent to passing Back propagation learns two multilayer perceptrons. Therefore, *γp* includes the weights *γh* and *γd*, and *ψp* has the thresholds *ψh* and *ψd* of the patients coding layer.

V. Prediction of Hidden Preferences Based onGeneralized AE-NRL Model

In real social network scenarios, there may not always be explicit user rating information. For example, Google only recommends new information by analyzing the patients"click" event. Therefore, the rating is not necessarily an explicit value given by the user, which can be the interaction between users or between users and target information, such as viewing, purchasing, and commenting on target information. This type of information is also called the patients implicit preferences. The model, as mentioned above, aims to provide detailed ratings. The data provides support, but it is not suitable for the processing of implicit preference information. For this reason, this article generalizes the model as follows, as shown in equation (25).

$$f(obj = \frac{1}{2}\sum_{i=1}^{m}\sum_{j=1}^{n} c_{ij} \parallel -\mathrm{h}\left(r_{ij:\beta} \parallel^2 + f(r) + \frac{\rho}{2}f(s)\right. \quad (25)$$

$$\hat{p}_{ij} = \begin{cases} 1, \text{ if } r_{ij} > 0 \\ 0, \text{ if } r_{ij} = 0 \end{cases} \quad (26)$$

Among them, pij is the user preference indicator function, which can be calculated by equation (26). Also, rij represents the interaction between the user and the target information. In addition, combined with the conclusions of Sun et al. [48], this article believes that if the user does not interact with specific target information, it does not mean that the user is not interested in the target information. , It may just ignore the existence of these target information, so this paper sets different confidence levels in the objective function, as shown in equation (27).

$$c_{ij} = 1 + \varphi r_{ij} \quad (27)$$

The scoring result in formula (27) is determined by the parameter φ. To obtain better results, this paper combines Sainath et al. [49] to set the φ value to 40. Finally, the neural network back-propagation algorithm is used to optimise the parameters of the model.

A. Evaluation of Comparative Result

Clinical tweets of 10000 medical users (male and female) ages 20 to 80 are collected by MedHelp (https://www.medhelp.org/). The disease-drug-ADR interaction of clinical tweets is examined using three cross- validation. Evaluating benchmark classifier performance with original clinical posts (OCP), preprocessed clinical posts (PCP), and Clinical vector (CT) derived from the proposed framework using standard model evaluation measures such as precision, recall, F1-Score, and accuracy.

(i) Precision is the ratio of actually labelled (True Positive) disease and medication ADRs to the total number of truly labelled (True Positive, False Positive) cases.

$$\text{Precision } = \frac{tp}{tp+fp} \quad (28)$$

The Precision for ADR classification over SIDER and Pharma-GKD data set for OCP, PCP and CT are respectively shown in table 1. The Precision for ADR classification over SIDER and Pharma-GKD data set for OCP, PCP and CT are respectively shown in table I.

TABLE I. Precision for ADR Classification

Classification Techniques		SIDER		Pharma-GKD	
		CF	CBF	CF	CBF
	SVM	71.83	73.18	65.99	66.64
OCP	Naive Bayes	73.2	75.56	68.9	69.7
	Decision Tree	68.1	69.44	55.66	56.22
	Nearest Neighbor	69.68	71.04	57.9	58.9
	SA$_e$CR	74.52	76.54	69.21	72.56
PCP	SVM	74.88	75.45	67.45	68.9
	Naive Bayes	75.29	76.26	70.96	73.65
	Decision Tree	71.16	72.99	57.52	59.29
	Nearest Neighbor	72.4	73.71	59.91	62.02
	SA$_e$CR	76.78	78.29	72.72	74.21
CT	SVM	79.96	80.75	73.06	75.91
	Naive Bayes	81.99	82.67	75.82	78.26
	Decision Tree	74.41	76.58	60.98	63.15
	Nearest Neighbor	75.34	77.53	61.63	65.54

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	SA$_e$CR	83.2	84.7	76.98	80.28

The Precision is the statistical distributed for Disease Drug-ADR labelling with linguistics diversity of SIDER and Pharma-GKD data set and shown in table 1.

With OCP clinical tweets, the value of precision for clinical recommendation is statistically distributed over the range 65.99 - 73.18, 68.90 - 75.56, 55.66 - 69.44 and 57.90 - 71.04 and 69.21 - 76.54 respectively for SVM, Naive Bayes, Decision Tree, Nearest neighbour and *SAeCR*.

Whereas, PCP clinical tweets, the value of precision for clinical recommendation is statistically distributed over the range 67.45 - 75.45, 70.96 - 76.26, 57.52 - 72.99, 59.91-73.71 and 72.72 - 78.29 respectively for SVM, Naive Bayes, Decision Tree, Nearest neighbour and *SAeCR*. However, with CT clinical tweets, the value of precision for clinical recommendation is statistically distributed over the range 73.06 - 80.75, 75.82 - 82.67, 60.98 - 76.58, 61.63 - 77.53 and 76.98 - 84.70, respectively for SVM, Naive Bayes, Decision Tree, Nearest neighbour and *SAeCR*, as shown in figure 6.

Whereas, after pre-processing, the clinical tweets and Drug-ADR classification has been carried out over Clinical vector space and acquired significant improvement as 10.31% - 13.91%, 9.4% - 12.28%, 3.34% - 5.4%, 9.2%-12.3%, 6.4%-11.2% and 9.6%- 10.66% respectively for SVM, Naive Bayes, Decision Tree, Nearest neighbour and *SAeCR* over precision, as shown in figure 7.

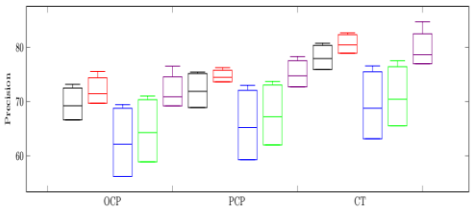

Figure 6. Statistical Distribution of Precision for ADR classification

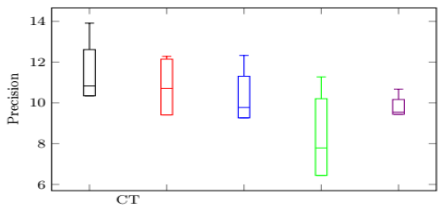

Figure 7. Statistical Distribution of Improvement in Precision with Clinical Vector

(ii) Recall is defined as is the summation of the truly indeed labelled (True Positive) ratio of disease and drug ADR, w.r.t total number of testing size (True Positive, False Negative) as:

$$\text{Recall} = \frac{tp}{tp+fn} \quad (29)$$

The Recall for ADR classification over SIDER and Pharma-GKD data set for OCP, PCP and CT are respectively shown in table II.

TABLE II. RECALL FOR ADR CLASSIFICATION

Classification Technique		**SIDER**		**Pharma-GKD**	
		CF	**CBF**	**CF**	**CBF**
OCP	SVM	59.56	62.22	57.23	58.29
	Naive Bayes	65.09	68.21	62.95	63.7
	Decision Tree	57.31	58.62	54.41	55.09
	Nearest	62.22	65.09	59.51	60.3
	SA$_e$CR	66.78	69.72	64.12	65.25
PCP	SVM	66.91	71.28	58.73	60.3
	Naive Bayes	68.21	71.59	64.73	66.61
	Decision Tree	59.4	62.45	55.79	57.23
	Nearest	65.09	71.59	61.11	62.8
	SA$_e$CR	70.2	72.74	66.12	68.72
CT	SVM	77.64	72.04	62.81	68.41
	Naive Bayes	79.33	72.82	71.97	72.33
	Decision Tree	65.54	70.28	62.02	63.74
	Nearest	72.01	77.47	65.88	64.71
	SA$_e$CR	82.12	83.12	72.16	74.21

The Recall is the statistical distributed for DiseaseDrug-ADR labelling with linguistics diversity of SIDER and Pharma-GKD data set and shown in table 2. With OCP clinical tweets, the value of recall for clinical recommendation is statistically distributed over 57.23 - 62.22, 62.95 - 68.21, 54.41- 58.62, 59.51-65.09 and 64.12 - 69.72 respectively for SVM, Naive Bayes, Decision Tree, Nearest neighbour and *SAeCR*.

Whereas, PCP clinical tweets, the value of recall for clinical recommendation is statistically distributed over 58.73-71.28, 64.43-71.59, 55.79-62.45, 61.11-71.59 66.12 - 72.14 respectively for SVM, Naive Bayes, Decision Tree, Nearest neighbour and *SAeCR*. However, with CT clinical tweets, the value of recall for clinical recommendation is statistically distributed over the range 2.81-77.64, 71.97-79.33, 62.02-70.28, 65.88-77.47 and 72.16 - 83.12, respectively for SVM, Naive Bayes, Decision Tree, Nearest neighbour and *SAeCR*, as shown in figure 8.

Whereas, after pre-processing, the clinical tweets and Drug-ADR classification has been carried out over Clinical vector space and acquired significant improvement as 9.7%-30.35%, 6.7%-21.87%, 13.98%- 19.98%, 7.3%-19.01%, and 13.59%- 22.97% respectively for SVM, Naive Bayes, Decision Tree, Nearest neighbour and *SAeCR* over recall, as shown in figure 9.

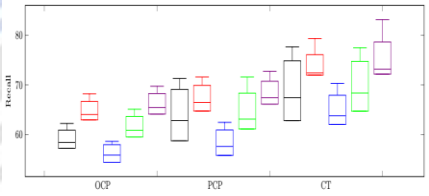

Figure 8. Figure 6. Statistical Distribution of Recall for Clinical Recommendation

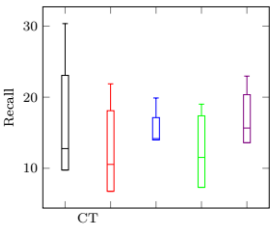

Figure 9. Statistical Distribution of Improvement in Recall with Clinical Vector

(iii) F1-Score is the harmonic mean of the precision and recall values, is represented as follows:

$$F1 - \text{Score} = \frac{2 * \text{Precision} * \text{Recall}}{\text{Precision} + \text{Recall}} \quad (30)$$

The F1-Score for ADR classification over SIDER and Pharma-GKD data set for OCP, PCP and CT are respectively shown in table 3. The F1-score is the statistical distributed for Disease Drug-ADR labelling with linguistics diversity of SIDER and Pharma-GKD data set and shown in table III.

With OCP clinical tweets, the value of F1-score for clinical recommendation is statistically distributed over 61.31-66.42, 65.74-

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70.31, 59.57- 64.01, 63.44- 68.4 and 66.98-71.26 respectively for SVM, Naïve Bayes, Decision Tree, Nearest neighbour and *SAeCR*.

Whereas, PCP clinical tweets, the value of F1-score for clinical recommendation is statistically distributed over 62.81-70.18, 67.65-72.98, 61.16-67.34, 65.23-72.62 and 68.12-73.56 respectively for SVM, Naive Bayes, Decision Tree, Nearest neighbour and *SAeCR*. However, with CT clinical tweets, the value of F1-score for clinical recommendation is statistically distributed over the range 67.6 - 78.31, 73.77 - 81.39, 66.23-_78.15, 68.6 - 77.0 and 74.12 - 82.76, respectively for SVM, Naive Bayes, Decision Tree, Nearest neighbour and *SAeCR*, as shown in figure 10.

Whereas, after pre-processing, the clinical tweets and Drug-ADR classification has been carried out over Clinical vector space and acquired significant improvement as 10.2% - 17.9%, 12.2% - 19.8%, 11.18%-_29.81%, 8.1% - 16.49%, and 10.65%- 20.18%, respectively for SVM, Naive Bayes, Decision Tree, Nearest neighbour and *SAeCR* over F1-Score, as shown in figure 11.

TABLE III. F1 SCORE FOR ADR CLASSIFICATION

Classification Techniques		SIDER		Pharma-GKD	
		CF	CBF	CF	CBF
OCP	SVM	64.75	66.42	61.31	62.21
	Naive Bayes	68.47	70.31	65.74	66.53
	Decision Tree	63.12	64.01	59.57	60.2
	Nearest neighbour	66.64	68.4	63.44	64.32
	SAeCR	69.98	71.26	66.98	67.56
PCP	SVM	69.3	70.18	62.81	64.32
	Naive Bayes	70.66	72.98	67.65	69.89
	Decision Tree	65.21	67.34	61.16	62.75
	Nearest neighbour	68.56	72.62	65.23	67.11
	SAeCR	71.28	73.56	68.12	71.12
CT	SVM	76.27	78.31	67.6	71.98
	Naive Bayes	77.61	81.39	73.77	79.72
	Decision Tree	69.26	72.32	66.23	78.15
	Nearest neighbour	72.66	77	68.6	74.93
	SAeCR	78.12	82.76	74.12	81.2

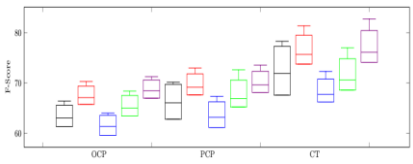

Figure 10. Statistical Distribution of F-Score for Clinical Recommendation

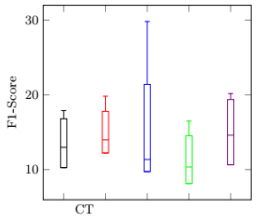

Figure 11. Statistical Distribution of Improvement in F1-Score with Clinical vector

(iv)Accuracy is the ratio of correct ADR prediction and total ADR prediction, as:

$$\text{Accuracy} = \frac{tp+tn}{tp+tn+fp+fn} \quad (31)$$

The accuracy for ADR classification over SIDER and Pharma-GKD data set for OCP, PCP and CT are respectively shown in table IV. The accuracy is the statistical distributed for DiseaseDrug-ADR labelling with linguistics diversity of SIDER and Pharma-GKD data set and shown in table 4. With OCP clinical tweets, the value of accuracy for clinical recommendation is statistically distributed over 59.86-66.09, 65.85-70.97, 57.24- 62.92, 62.86- 68.63 and 67.26 - 72.86 respectively for SVM, Naïve Bayes, Decision Tree, Nearest neighbour and *SAeCR*.

TABLE IV. ACCURACY FOR ADR CLASSIFICATION

Classification Technique		SIDER		Pharma-GKD	
		CF	CBF	CF	CBF
OCP	SVM	63.86	66.09	59.86	61.16
	Naive Bayes	68.74	70.97	65.85	66.84
	Decision Tree	61.6	62.92	57.24	58.19
	Nearest	66.4	68.63	62.86	64.05
	SAeCR	70.26	72.86	67.26	68.12
PCP	SVM	69.74	72.08	61.96	64.05
	Naive Bayes	71.38	74.02	68.25	70.95
	Decision Tree	64.55	67.34	59.61	61.87
	Nearest	68.84	73.62	65.25	67.62
	SAeCR	73.16	76.72	70.26	72.18
CT	SVM	77.57	79.73	68.55	73.65
	Naive Bayes	78.92	82.67	75.39	78.38
	Decision Tree	69.73	73.39	66.81	69.2
	Nearest	73.41	78.19	69.55	76.45
	SAeCR	80.86	84.96	78.12	81.37

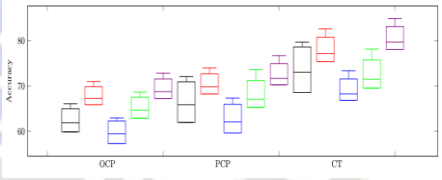

Figure 12. Statistical Distribution of Accuracy for Clinical Recommendation

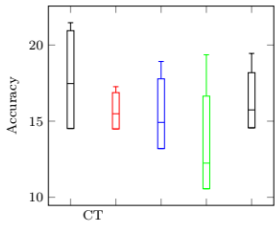

Figure 13. Statistical Distribution of Improvement in Accuracy with Clinical Vector

Whereas, PCP clinical tweets, the value of accuracy for clinical recommendation is statistically distributed over 61.96- 72.08, 68.25-74.02, 59.61-67.34, 65.25-73.62 and 70.26 -76.72 respectively for SVM, Naive Bayes, Decision Tree, Nearest neighbour and *SAeCR*. However, with CT clinical tweets, the value of accuracy for clinical recommendation is statistically distributed over the range 68.55-79.73, 75.39 - 82.67, 66.81- 73.39, 69.55 - 78.19 and 78.12 - 84.96, respectively for SVM, Naive Bayes, Decision Tree, Nearest neighbour and *SAeCR*, as shown in figure 12.

Whereas, after pre-processing, the clinical tweets and Drug-ADR classification has been carried out over Clinical vector space and acquired significant improvement as 14.5% - 21.4%, 14.4% - 17.2%, 13.1% - 18.9%, 10.6% - 19.35%, and 14.56%- 19.45%, respectively for SVM, Naive Bayes, Decision Tree, Nearest neighbour and *SAeCR* over F1-Score, as shown in figure 13.

VI. CONCLUSION

Incorporating deep auto-encoders with network representation learning technologies, this study suggests a social network recommendation model (SAeCR). In the context of the

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recommendation process, this model is employed to address the issues of sparsity and cold start. Through the acquisition of a joint optimisation function, the SAeCR model successfully incorporates the social network. Social data is gathered using network representation learning technology and placed into the deep auto-encoder. Furthermore, the model is expanded by developing an objective function that supports implicit score data, allowing for the prediction of implicit user preferences. Finally, three experiments and a comparison to the state-of-the-art recommendation model and other similar recommendation models based on a real social network data set demonstrate the model's superior performance. Future study can be conducted from the following perspectives because of the limitations of this article. It is possible to further optimise the social network recommendation model through the use of various neural network models and the exploration of heterogeneous dynamic network embedding technologies, and the proposed model can be further verified through the use of both social survey methods and computational experiments, all of which increase the accuracy with which user preferences can be predicted.

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