

## RESEARCH

# Predicting Comprehensive Drug - Drug Interaction via Similarity Network Fusion and Convolutional Neural Networks

Mohammad.Amin Khodamoradi<sup>1,2</sup>, Bahareh Levian<sup>1,2</sup> and Changiz Eslahchi<sup>1,2\*</sup>

\*Correspondence:

[eslahchi.ch@gmail.com](mailto:eslahchi.ch@gmail.com)

<sup>1</sup>Department of Computer Science, Faculty of Mathematical Science, Shahid Beheshti University, Tehran, Iran  
Full list of author information is available at the end of the article

## Abstract

**Background:** Drug-drug interactions (DDIs) always cause unexpected and even adverse drug reactions. It is important to identify DDIs before drugs are used in the market. However, preclinical identification of DDIs requires much money and time. Computational approaches have exhibited their abilities to predict potential DDIs on a large scale by utilizing premarket drug properties. Nevertheless, most of them only predict whether or not one drug interacts with another, but neglect their enhancive (positive) and depressive (negative) changes of pharmacological effects. Moreover, these comprehensive DDIs do not occur at random, and derived from the structural features of the graph of DDIs. Revealing such a relationship is very important, because it is able to help understand how DDIs occur. Both the prediction of comprehensive DDIs and the discovery of structural relationship among them play an important guidance when making a co-prescription.

**Results:** In this work, treating a set of comprehensive DDIs as a signed network, we design a novel model (SNF-CNN) for the prediction of enhancive and depressive DDIs based on similarity network fusion and convolutional neural networks. SNF-CNN achieves the depressive DDI prediction ( $AUC = 0.9747 \pm 0.0033$  and  $AUPR = 0.9666 \pm 0.0045$ ), enhancive DDI prediction ( $AUC = 0.9686 \pm 0.0028$  and  $AUPR = 0.8221 \pm 0.0184$ ) and the Unknown DDI prediction ( $AUC = 0.9714 \pm 0.0040$  and  $AUPR = 0.9480 \pm 0.0083$ ). Compared with three state-of-the-art approaches, SNF-CNN shows its superiority.

**Conclusions:** This new approach is not only able to predict comprehensive DDI, but also predicts non-DDI.

**Keywords:** Drug-Drug Interaction; Drug Similarity; Drug Similarity Integration; Feature Selection; Recommender System

## Introduction

When two or more drugs are taken together, drugs' effects or behaviors are unexpectedly influenced by each other [1]. This kind of influence is termed as Drug-Drug interaction (DDI), which would reduce drug efficacy, increase unexpected toxicity, or induce other adverse drug reactions between the co-prescribed drugs. As the number of approved drugs increases, the number of drug-unidentified DDIs is rapidly increasing, such that among approved small molecular drugs in Drug Bank, on average, 15 out of every 100 drug pairs have DDIs [2]. The DDIs would put patients who are treated with multiple drugs in an unsafe situation [3, 4, 5, 6]. Understanding DDI is the first step in drug combinations, which becomes one of the most promising

solutions for the treatment of multifactorial complex diseases [7]. Therefore, there is an urgent need for screening and analysis of DDIs before clinical co-medications are administered. However, traditional DDI identification approaches (e.g., testing Cytochrome P450 [8] or transporter-associated interactions [9]) face challenges, such as high costs, long duration, animal welfare considerations [10], the very limited number of participants in the trial, and the great number of drug combinations under screening in clinical trials. As a result, only a few DDIs have been identified during drug development production (usually in the clinical trial phase). Some of them have been reported after drugs approved, and many have been found in post-marketing surveillance.

Computational approaches are a promising alternative to discovering potential DDIs on a large scale, and they have gained attention from academy and industry recently [11, 12]. Data mining-based computational approaches have been developed to detect DDIs from various sources [10], such as scientific literature [13, 14], electronic medical records [15], and the Adverse Event Reporting System of FDA (<http://www.fda.gov>). These approaches rely on post-market clinical evidence. So, they cannot provide alerts of potential DDIs before clinical medications are administered. In contrast, machine learning-based computational approaches (e.g. Naïve Similarity-Based Approach [16], Network Recommendation-Based [10], Classification-Based [17]) can provide such alerts by utilizing pre-marketed or post-marketed drug attributes, such as drug features or similarities [18]. These methods use different drug features to predict DDIs, such as chemical structures [16], targets [19], hierarchical classification codes [17], side effects, and off-label side effects [10, 20].

Most of these existing machine learning approaches are designed to predict the typical two-class problem, which only indicates how likely a pair of drugs is a DDI. However, two interacting drugs may change their own pharmacological behaviors or effects (e.g., increasing or decreasing serum concentration) *in vivo*. For example, the serum concentration of Flunisolide (DrugBank Id: DB00180) decreases when it is taken with Mitotane (DrugBank Id: DB00648), whereas its serum concentration increases when taken with Roxithromycin (DrugBank Id: DB00778). For short, the first case is degressive DDI, and the second case is enhancive DDI, which contains drug changes in terms of pharmacological effects. It is more important to know exactly whether the interaction increases or decreases the drug's pharmaceutical behaviors, especially when making optimal patient care, establishing drug dosage, designing prophylactic drug therapy, or finding the resistance to therapy with a drug [21].

On the other hand, the occurrence of both enhancive and degressive DDIs is not random, but most current approaches have not yet exploited this structural property and have been developed only for conventional two-classes DDIs. Furthermore, revealing such a structural relationship is very important because it can help us understand how DDIs occur. It is one of the most important steps for treating complex diseases and guides physicians in preparing safer prescriptions to high-order drug interaction. The proposed algorithms for predicting three-classes DDIs are introduced in the following. And how they work are briefly described. All three introduced algorithms use matrix factorization methods, which is a network recommender-based

approach. The matrix factorization approach, with slightly modifying, is a suitable solution for the subject of predicting DDI that has received much attention from researchers.

In this paper, we firstly introduce data and features. Then, a novel algorithm (SNF-CNN) based on the integration of drug similarities and deep learning recommendation systems for predicting DDI is presented in a comprehensive three-class model. This algorithm is called Predicting Comprehensive Drug-Drug Interaction via Similarity Network Fusion and Convolutional Neural Networks.

The paper is organized as follows. In the first section, the data preparation process is explained. The recommendation system is then designed and trained on enhancive and degressive, which detects pairs of non-interacting drugs with high probability. Next, the previous recommender system, based on a convolutional neural network, is trained on incremental and decremental interaction data without interaction (detected in the previous step). In section Results and Discussions, we investigate the results of SNF-CNN in the 10-fold cross-validation process (10-fold CV).

It should be noted that the proposed method of this research is a recommender-based on deep neural networks and has no structural similarities with matrix factorization methods. The only reason for mentioning these methods is the limited number of articles that have used three-class data in their work.

## Methods

### Dataset and features

In this study, we use the data set presented in paper of [22]. This set contains 568 approved small molecule drugs, each of them has at least one interaction with the other drugs in the set. In total, the interactions between these 568 drugs contain 21,351 DDIs, including 16,757 enhancive DDIs and 4,594 degressive DDIs. In addition, each drug represented as an 881-dimensional feature vector  $F_{str}$  based on PubChem chemical structure descriptor and also a 9149-dimensional feature vector  $F_{se}$  according to the off-label side effects provided by OFFSIDES.

### Problem formulation

Without loss of generality, let  $D = \{d_i\}$ ,  $i = 1, 2, \dots, m$  be a set of  $m$  approved drugs. Their interactions can be accordingly represented as an  $m \times m$  symmetric interaction matrix  $A_{m \times m} = \{a_{ij}\}$ . For the conventional DDIs,  $a_{ij} = 1$  if  $d_i$  interacts with  $d_j$ , and  $a_{ij} = 0$  otherwise. For the comprehensive DDIs,  $a_{ij} \in \{1, 0, +1\}$ . Again, if  $d_i$  and  $d_j$  do not interact with each other,  $a_{ij} = 0$ . When there is an enhancive DDI or a degressive DDI between  $d_i$  and  $d_j$ ,  $a_{ij} = +1$  or  $a_{ij} = -1$  respectively.

In addition, each drug  $d_i$  in the  $D$  is represented as a  $p$ -dimension feature vector  $f_i = [f_1, f_2, \dots, f_k, \dots, f_p]$ , which  $f_k = 1$  indicates the  $k$ -th specific chemical structure fragment or occurs an off-label side effect, and  $f_k = 0$  otherwise. Because each drug has two chemical structure feature vectors and off-label side effects, there are two feature matrices of  $F$  with dimensions of  $m \times p$  (amount of  $p$  depends on kind of feature). Matrices of  $F_{str}$  and  $F_{se}$  are, respectively, the feature matrix of the chemical structure and the feature matrix of off-label side effects.

### Data preparing

Since the new drugs are isolated nodes in the interaction network, we cannot infer their possible interaction from topological information alone. Therefore, additional information (such as chemical structure or off-label side effects) is needed, which is called a drug feature in terms of machine learning. First, we prepare the features based on our model, and then we teach a deep learning model of interaction prediction.

### Similarity matrix calculation

A common method of calculating similarity called Cosine Similarity is used in machine learning articles such as Articles [23, 24]. If we name feature vectors of the drug of  $d_i$  and  $d_j$  as  $x_i$  and  $x_j$ , Cosine Similarity between  $x_i$  and  $x_j$  is defined as follows:

$$S_{Cos}(x_i, x_j) = \frac{x_i \cdot x_j}{\|x_i\|_2 \|x_j\|_2} \quad (1)$$

Where  $\|\cdot\|_2$  is the Euclidean Norm and  $x_i \cdot x_j$  is inner product of two vectors.

It was observed that the values of the feature matrices are discrete, and also the dimensions of the matrices are large. The chemical structure and the off-label side effect have 881 and 9149 dimensions, respectively. On the other hand, machine learning algorithms do not work properly with high-dimensional data and discrete data. As a result, they do not get good results on these kinds of data. Therefore, by exploiting the cosine similarity, that was described above, drug similarity matrices based on chemical structure and off-label side effects are calculated. These matrices are  $S_{str}$  and  $S_{se}$ , respectively. The dimensions of these two matrices are  $m \times m$ , where  $s_{i,j}$  is an element of similarity matrices that shows similarity value between drugs of  $d_i$  and  $d_j$ . Each element of  $S$  has a continuous value between zero and one.

### Integration drug similarity matrices

Similarity Network Fusion (SNF)[25] is a new computational method for data integration. Briefly, SNF combines many different types of features (such as chemical structure and off-label side effect, and more - clinical data, questionnaires, image data, etc.) for a given set of samples (e.g., drugs). SNF first constructs a sample similarity network for each of the data types and then iteratively integrates these networks using a novel network fusion method. Working in the sample network space allows SNF to avoid dealing with different scales, collection bias, and noise in different data types. Integrating data in a non-linear fashion allows SNF to take advantage of the common and complementary information in different data types. Figure 1 is a good visualization of SNF processes that has been used in our method structure.

SNF.pdf

**Figure 1** SNF processes [25]

*Sub-sub heading for section*

Text for this sub-sub-heading...

*Sub-sub-sub heading for section*

$$E[Z_1(vT_x)] = \int_0^{v \wedge 1} Z_0(uT_x) \exp(\lambda_1) du.$$

If we assume that sensitive cells follow a deterministic decay  $Z_0(t) = xe^{\lambda_0 t}$  and approximate their extinction time as  $T_x \approx -\frac{1}{\lambda_0} \log x$ , then we can heuristically estimate the expected value as

$$\begin{aligned} E[Z_1(vT_x)] \\ = \frac{\mu}{r} \log x \int_0^{v \wedge 1} x^{1-u} x^{(\lambda_1/r)(v-u)} du. \end{aligned} \quad (2)$$

## Appendix

Text for this section...

### Acknowledgements

Text for this section...

### Funding

Text for this section...

### Abbreviations

Text for this section...

### Availability of data and materials

the code and data is available at GitHub page of [SNF-CNN code and data](#)

### Ethics approval and consent to participate

Text for this section...

### Competing interests

The authors declare that they have no competing interests.

### Consent for publication

Text for this section...

### Authors' contributions

Text for this section ...

### Authors' information

Text for this section...

### Author details

<sup>1</sup>Department of Computer Science, Faculty of Mathematical Science, Shahid Beheshti University, Tehran, Iran.

<sup>2</sup>School of Bioinformatics, IPM - Institute for Research in Fundamental Sciences, Tehran, Iran.

### References

- Wienkers, L.C., Heath, T.G.: Predicting in vivo drug interactions from in vitro drug discovery data. *Nature reviews Drug discovery* **4**(10), 825–833 (2005)
- Law, V., Knox, C., Djoumbou, Y., Jewison, T., Guo, A.C., Liu, Y., Maciejewski, A., Arndt, D., Wilson, M., Neveu, V., et al.: Drugbank 4.0: shedding new light on drug metabolism. *Nucleic acids research* **42**(D1), 1091–1097 (2014)
- Leape, L.L., Bates, D.W., Cullen, D.J., Cooper, J., Demonaco, H.J., Gallivan, T., Hallisey, R., Ives, J., Laird, N., Laffel, G., et al.: Systems analysis of adverse drug events. *Jama* **274**(1), 35–43 (1995)
- Businaro, R.: Why we need an efficient and careful pharmacovigilance? *Journal of pharmacovigilance* (2013)
- Karbownik, A., Szatek, E., Sobańska, K., Grabowski, T., Wolc, A., Grześkowiak, E.: Pharmacokinetic drug-drug interaction between erlotinib and paracetamol: a potential risk for clinical practice. *European Journal of Pharmaceutical Sciences* **102**, 55–62 (2017)
- Mulroy, E., Highton, J., Jordan, S.: Giant cell arteritis treatment failure resulting from probable steroid/antiepileptic drug-drug interaction. *The New Zealand Medical Journal (Online)* **130**(1450), 102 (2017)

7. Zhao, X.-M., Iskar, M., Zeller, G., Kuhn, M., Van Noort, V., Bork, P.: Prediction of drug combinations by integrating molecular and pharmacological data. *PLoS Comput Biol* **7**(12), 1002323 (2011)
8. Veith, H., Southall, N., Huang, R., James, T., Fayne, D., Artemenko, N., Shen, M., Inglese, J., Austin, C.P., Lloyd, D.G., et al.: Comprehensive characterization of cytochrome p450 isozyme selectivity across chemical libraries. *Nature biotechnology* **27**(11), 1050–1055 (2009)
9. Huang, S.-M., Temple, R., Throckmorton, D., Lesko, L.: Drug interaction studies: study design, data analysis, and implications for dosing and labeling. *Clinical Pharmacology & Therapeutics* **81**(2), 298–304 (2007)
10. Zhang, P., Wang, F., Hu, J., Sorrentino, R.: Label propagation prediction of drug-drug interactions based on clinical side effects. *Scientific reports* **5**(1), 1–10 (2015)
11. Wiśniowska, B., Polak, S.: The role of interaction model in simulation of drug interactions and qt prolongation. *Current pharmacology reports* **2**(6), 339–344 (2016)
12. Zhou, D., Bui, K., Sostek, M., Al-Hunuti, N.: Simulation and prediction of the drug-drug interaction potential of naloxegol by physiologically based pharmacokinetic modeling. *CPT: pharmacometrics & systems pharmacology* **5**(5), 250–257 (2016)
13. Bui, Q.-C., Sloot, P.M., Van Mulligen, E.M., Kors, J.A.: A novel feature-based approach to extract drug–drug interactions from biomedical text. *Bioinformatics* **30**(23), 3365–3371 (2014)
14. Zhang, Y., Wu, H.-Y., Xu, J., Wang, J., Soysal, E., Li, L., Xu, H.: Leveraging syntactic and semantic graph kernels to extract pharmacokinetic drug drug interactions from biomedical literature. *BMC systems biology* **10**(3), 67 (2016)
15. Yamanishi, Y., Araki, M., Gutteridge, A., Honda, W., Kanehisa, M.: Prediction of drug–target interaction networks from the integration of chemical and genomic spaces. *Bioinformatics* **24**(13), 232–240 (2008)
16. Vilar, S., Uriarte, E., Santana, L., Lorberbaum, T., Hripcsak, G., Friedman, C., Tatonetti, N.P.: Similarity-based modeling in large-scale prediction of drug-drug interactions. *Nature protocols* **9**(9), 2147 (2014)
17. Cheng, F., Zhao, Z.: Machine learning-based prediction of drug–drug interactions by integrating drug phenotypic, therapeutic, chemical, and genomic properties. *Journal of the American Medical Informatics Association* **21**(e2), 278–286 (2014)
18. Pahikkala, T., Airola, A., Pietilä, S., Shakyawar, S., Szwajda, A., Tang, J., Aittokallio, T.: Toward more realistic drug–target interaction predictions. *Briefings in bioinformatics* **16**(2), 325–337 (2015)
19. Luo, H., Zhang, P., Huang, H., Huang, J., Kao, E., Shi, L., He, L., Yang, L.: Ddi-cpi, a server that predicts drug–drug interactions through implementing the chemical–protein interactome. *Nucleic acids research* **42**(W1), 46–52 (2014)
20. Shi, J.-Y., Huang, H., Li, J.-X., Lei, P., Zhang, Y.-N., Yiu, S.-M.: Predicting comprehensive drug-drug interactions for new drugs via triple matrix factorization. In: *International Conference on Bioinformatics and Biomedical Engineering*, pp. 108–117 (2017). Springer
21. Koch-Weser, J.: Serum drug concentrations in clinical perspective. *Therapeutic drug monitoring* **3**(1), 3–16 (1981)
22. Yu, H., Mao, K.-T., Shi, J.-Y., Huang, H., Chen, Z., Dong, K., Yiu, S.-M.: Predicting and understanding comprehensive drug-drug interactions via semi-nonnegative matrix factorization. *BMC systems biology* **12**(1), 14 (2018)
23. Zhang, W., Chen, Y., Tu, S., Liu, F., Qu, Q.: Drug side effect prediction through linear neighborhoods and multiple data source integration. In: *2016 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, pp. 427–434 (2016). IEEE
24. Zhang, W., Chen, Y., Li, D., Yue, X.: Manifold regularized matrix factorization for drug-drug interaction prediction. *Journal of biomedical informatics* **88**, 90–97 (2018)
25. Wang, B., Mezlini, A.M., Demir, F., Fiume, M., Tu, Z., Brudno, M., Haibe-Kains, B., Goldenberg, A.: Similarity network fusion for aggregating data types on a genomic scale. *Nature methods* **11**(3), 333 (2014)

## Figures

**Figure 2** Sample figure title

**Figure 3** Sample figure title

## Tables

**Table 1** Sample table title. This is where the description of the table should go

	B1	B2	B3
A1	0.1	0.2	0.3
A2	...	..	.
A3	..	.	.

**Additional Files**

Additional file 1 — Sample additional file title

Additional file descriptions text (including details of how to view the file, if it is in a non-standard format or the file extension). This might refer to a multi-page table or a figure.

Additional file 2 — Sample additional file title

Additional file descriptions text.