

# Drug Target Interaction Prediction with Missing not at Random Labels

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## ABSTRACT

We introduce a novel probabilistic model, Factorization with Missing Not at Random Labels (FMNRL), for Drug-Target Interaction (DTI) prediction. DTI prediction is usually modeled as a binary classification problem. Unlike previous studies which label unknown DTIs as negative samples, we treat the unknown DTIs as missing not at random labels. The proposed model, FMNRL assumes the binary DTI labels are probabilistically generated from feature vectors of both drugs and targets, and a hidden matrix mapping from the drug features to target features. By associating the possibility of a missing label to the sign of the label, FMNRL can learn the hidden feature space mapping better and thus provide more accurate DTI predictions. Experimental results show that FMNRL outperforms state-of-the-art methods.

## KEYWORDS

Missing Not At Random, Drug Target Interaction Prediction, Probabilistic Factor Models

## ACM Reference Format:

Anonymous Author(s). 2018. Drug Target Interaction Prediction with Missing not at Random Labels. In *Proceedings of ACM Conference (Conference'17)*. ACM, New York, NY, USA, 5 pages. <https://doi.org/10.1145/nnnnnnnn.nnnnnnn>

## 1 INTRODUCTION

Drug-Target Interaction (DTI) is fundamental to drug discovery and design. As biochemical experimental methods for DTI identification are extremely costly and time-consuming, computational DTI prediction methods have received a growing popularity in literature. The majority of existing computational methods treat DTI prediction as a binary classification task, where known DTIs are labeled as positive and unknown DTIs are labeled as negative [1]. To address the imbalanced problem arisen from the binary classification scheme, many research has attempted to extract a subset of reliable negative samples, e.g. by random sampling [4] or by Positive Unlabel Learning (PU Learning) [2].

Instead of labeling the unknown DTIs as negative, we argue that it is more natural to consider the unknown DTIs, i.e. DTIs that are neither identified in vivo to be positive nor experimentally validated to be negative (non-interacting drug-target pairs), as missing labels. Furthermore, our assumption in this work is that labels are not missing at random. This is an intuitive and reasonable assumption, because researchers will use their domain expertise to filter DTIs with a high possibility to be positive and prioritize validations for these DTIs in vivo. For example, researchers find the efficacy target of a drug based on principles of biochemistry, biophysics, genetics and chemical biology. If ample evidences exist to support pharmacokinetic interactions with the target, then the possibility of

a positive DTI is high, and the researchers are likely to conduct in vivo experiments. On the contrary, drug target interactions that are less likely to be positive are more likely to be ignored by researchers and their labels are likely to be missing.

### 1.1 Contribution

Our chief contribution in this work is a novel Factorization with Missing Not at Random Labels model (FMNRL). To the best of our knowledge, this is the first time missing not at random theory is applied in DTI identification. The inputs of FMNRL are feature vectors of drugs and targets, the partially observed labels, and the fully observed responses (i.e. labels are given or missing). The feature vectors are learnt and integrated from heterogeneous data sources. The labels and responses are binary variables. The FMNRL model mimics the probabilistic procedures to generate labels from feature vectors and responses from labels. Specifically, the labels are related to feature vectors of both drugs and targets, and a hidden matrix mapping from the drug features to target features. The possibility of giving a response is associated to the sign of the label.

We conduct experiments on a large-scale DPI database. Area Under Receiver Operating Characteristic curve (AUROC) and Area Under P Recall are the most commonly adopted metrics to evaluate DPI prediction performance. Our model achieves significantly better AUPR results and comparable AUROC results to the best of related works [4] on both full dataset and sample sets with balanced number of positive and negative labels. In the biomedical field, AUROC is considered to be a more robust and better assessment than AUROC [4]. Thus our improvement in AUPR is promising.

### 1.2 Related Work

One component of our work (i.e labels are generated by feature vectors learnt and fused from heterogeneous information networks) is inspired by a recent work DTINet [4]. However, there are three key differences between our work and DTINet. (1) DTINet is based on deterministic matrix factorization, our work is based on probabilistic factor models. For example, the hidden feature space mapping matrix, labels, and responses are all random variables. This setting enables the FMNRL model to regulate the parameters (i.e. hidden feature space mapping matrix) by introducing appropriate priors and improves performance on sparse data set. (2) DTINet is based on randomly missing responses, i.e. it samples uniformly a set of unknown DTIs as negative sample, while FMNRL is based on missing not at random theories. Statistical theory in [3] shows that applying a model based on missing at random assumptions can lead to biased parameter estimation on data sets with missing not at random entries. (3) DTINet adopts only a subset of unknown DTIs to preserve a balanced number of positive and negative samples, while our model uses all information in the data set.

We also want to distinguish our work with another line of research. Usually only positive DTIs are deposited in known databases.

Due to the lack of negative samples, recently **Positive Unlabel Learning** (PU Learning) is employed in DTI identification, e.g. to facilitate negative sample extraction [2]. PU learning does not explicitly associate the status of an instance (i.e. being labeled or unlabeled) with the value of its label. We also want to mention here that, although we experiment with datasets where only positive DTIs are deposited, FMNRL is extendable without difficulty to databases where positive and negative DTIs are available. Thus our model is applicable in more scenarios.

## 2 THE PROPOSED METHOD

We start with the problem definitions and notations in Sec. 2.1. We then describe the proposed model FMNRL in Sec. 2.2. Finally we present the influence algorithm in Sec. 2.3.

### 2.1 Preliminaries

DTI identification is often modeled as a binary classification task. Formally, we are given  $P \in \mathcal{R}^{N \times M}$  a set of DTI labels, where  $p_{i,j} = 0$  indicates a negative interaction between drug  $i$  and target  $j$ ,  $p_{i,j} = 1$  indicates a positive DTI, the feature vectors on drug side  $X \in \mathcal{R}^{N \times K}$ , where  $x_{i,k}$  represents drug  $i$ 's weight on drug feature  $k$ , the feature vectors on target side  $Y \in \mathcal{R}^{M \times L}$ , where  $y_{j,l}$  represents target  $j$ 's weight on target feature  $l$ . The problem is to predict for a new drug-target pair  $\langle i', j' \rangle$ , the possibility of a positive DTI  $p(p_{i',j'} = 1)$ .

It is worthy to note that many previous studies have shown that extracting features  $X, Y$  from heterogenous data sources are beneficial. Similar to DTINet [4], we use a compact feature expression learnt from aggregating diffusion probabilities on multiple information networks. For example, on the drug side, we can collect drug side-effect network, drug similarity network and so on. On the target side, we can collect protein disease network, protein protein network and so on. The feature learning phase is beyond the scope of this paper. We refer the readers to [4].

In addition to the features  $X, Y$  and labels  $P$ , we make one essential modification to the problem definition. We assume that the inputs also contain responses  $R \in \mathcal{R}^{N \times M}$ , where  $R_{i,j} = 0$  indicates an unknown DTI,  $R_{i,j} = 1$  indicates a verified DTI (positive or negative). For positive responses  $R_{i,j} = 1$ , the labels  $P_{i,j}$  are observed. For negative responses  $R_{i,j} = 0$ , the labels are hidden and unknown.

### 2.2 FMNRL Model

We use a factor model, depicted in Fig. ?? The features  $X, Y$  are in different dimensions. To associate the drug features with the target features, we introduce a hidden variable  $Z \in \mathcal{R}^{K \times L}$ , where  $Z_{k,l}$  is a projection that maps the drug feature dimension  $k$  to the target feature dimension  $l$ . We assume that  $Z$  is sampled from a Gaussian distribution,

$$\forall k, l, Z_{k,l} \sim \mathcal{N}(0, \sigma^2), \quad (1)$$

where  $\sigma^2$  is the variance. We use zero mean to favor sparse feature mapping, i.e. a drug feature  $k$  is associated with a few target features.

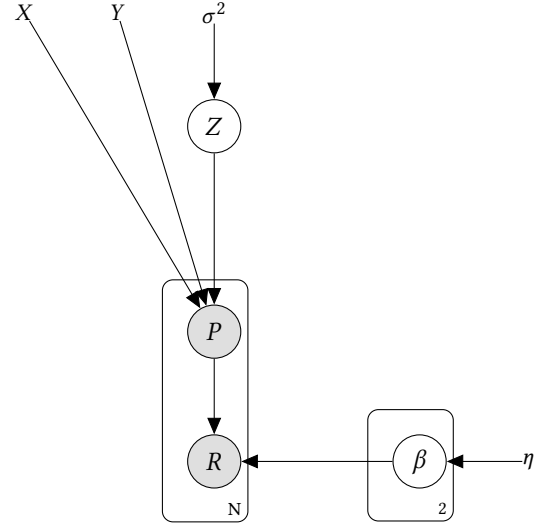


Figure 1: Graphical Representation of the FMNRL model

We then assume that the binary label  $P_{i,j}$  is generated from the following process:

$$\forall i, j, p(P_{i,j} = 1 | X, Y, Z) = \frac{1}{1 + \exp(XZY)_{i,j}}. \quad (2)$$

The binary response is sampled from a Bernoulli distribution. The parameters of the Bernoulli distribution are related to the value of each  $P_{i,j}$ . Therefore we define  $\beta_p \in \mathcal{R}^2, p \in \{0, 1\}, \forall p, \beta_{p,0} > 0, \beta_{p,1} > 0, \beta_{p,0} + \beta_{p,1} = 1$ , we have:

$$\forall p \in \{0, 1\}, \beta_p \sim \text{Beta}(\eta), \quad (3)$$

$$\forall i, j, R_{i,j} \sim \text{Bern}(\beta_{P_{i,j},1}), \quad (4)$$

where  $\eta$  is the hyperparameter for the Beta distribution.

### 2.3 Inference

The objective is to maximize the likelihood which consists of two terms. The first term is on partial observations, i.e.  $R_{i,j} = 0$  and  $P_{i,j}$  unknown. The second term is on full observations, i.e.  $R_{i,j} = 1$  and known  $P_{i,j}$ .

$$\mathcal{L} = \sum_{R_{i,j}=0} \sum_{P_{i,j}} \log p(R_{i,j}, P_{i,j} | X, Y, \sigma^2, \eta) + \sum_{R_{i,j}=1} \log p(R_{i,j}, P_{i,j} | X, Y, \sigma^2, \eta) \quad (5)$$

Direct optimization for both terms in Equ. 5 are intractable, as they involve integration over continuous hidden variables. For example,  $p(R | X, Y, \sigma^2, \eta) = \int_{P, Z, \beta} p(R | P, \beta, \eta) p(P | X, Y, Z) p(Z | \sigma^2)$ . We employ variational inference to infer the parameters. That is, we use the mean field assumption to factorize the posterior distribution:

$$q(P, Z, \beta | R, X, Y, \sigma^2, \eta) = q(P | \theta) q(Z | \mu, \nu) q(\beta | \rho), \quad (6)$$

It is convenient if  $q(P | \theta), q(Z | \mu, \nu), q(\beta | \rho)$  are exponential distributions. We approximate the sigmoid function in Equ. 2 by an exponential distribution. We use the property that any sigmoid function  $\sigma(\cdot)$  has a lower bound:

$$Q(P | \theta) = \sigma(\theta) \geq \sigma(\zeta) \exp(\theta - \zeta) / 2 - \lambda(\zeta)(\theta^2 - \zeta^2), \quad (7)$$

where  $\lambda(\zeta) = [\sigma(\zeta) - 1/2]/[2\zeta]$ .

As shown in Alg. 1, in each iteration of the inference we alternatively optimize the variational parameters for  $q(Z)$ ,  $q(\beta)$ ,  $q(P)$  and the parameters for the lowerbound  $\sigma(\cdot)$ . We divide the data objects into two disjoint sets,  $s_1 = \{(i, j) \in \mathcal{R}^{N \times M} | R_{i,j} = 1\}$ , and  $s_2 = \{(i, j) \in \mathcal{R}^{N \times M} | R_{i,j} = 0\}$ . In each iteration, we first obtain the optimal  $\theta$ ,  $\mu$ ,  $v$ ,  $\rho$  and then we update  $\zeta$ . The iteration is repeated until convergence is achieved.

```

input : P, R, X, Y
output:  $\mu, v, \rho, \theta, \zeta$ 
1 initialization;
2 repeat
3   for  $Z_{k,l} \in Z$  do
4      $\mu_{k,l} \leftarrow \frac{\sum_{(i,j) \in s_2} (\theta_{i,j} - \frac{1}{2}) X_{i,k} * Y_{j,l} + \sum_{(i,j) \in s_1} \frac{1}{2} X_{i,k} * Y_{j,l}}{2 * (\sum_{i,j} \lambda(\zeta_{i,j}) X_{i,k}^2 Y_{j,l}^2 + \frac{1}{\sigma^2})}$ ;
5      $v_{k,l} \leftarrow \frac{1}{\sqrt{2 * (\sum_{i,j} \lambda(\zeta_{i,j}) X_{i,k}^2 Y_{j,l}^2 + \frac{1}{\sigma^2})}}$ ;
6   end
7   for  $\beta$  do
8      $\rho_{0,0} \leftarrow \eta_{0,0}$ ;
9      $\rho_{0,1} \leftarrow \sum_{(i,j) \in s_2} (1 - \theta_{i,j}) + \eta_{0,1}$ ;
10     $\rho_{1,0} \leftarrow |s_1| + \eta_{1,0}$ ;
11     $\rho_{1,1} \leftarrow \sum_{(i,j) \in s_2} \theta_{i,j} + \eta_{1,1}$ ;
12  end
13  for  $(i, j) \in s_2$  do
14     $l_1 = \exp(\psi(\rho_{1,1}) - \psi(\rho_{1,0} + \rho_{1,1}) + X_i \mu Y_j^T)$ ;
15     $l_2 = \exp(\psi(\rho_{0,1}) - \psi(\rho_{0,0} + \rho_{0,1}))$ ;
16     $\theta_{i,j} \leftarrow \frac{l_1}{l_1 + l_2}$ ;
17  end
18  for  $(i, j) \in s_1 + s_2$  do
19     $\zeta_{i,j} \leftarrow |X_i \mu Y_j^T|$ ;
20  end
21 until convergence;

```

Algorithm 1: FMNRL algorithms

### 3 EXPERIMENT

#### 3.1 Experimental Setup

**Datasets.** We use the same datasets as in [4]: i.e. the drug-target interaction labels are obtained from the latest version of DrugBank (version 3.0); the feature vectors  $X$  are extracted from four heterogeneous networks: the drug-drug interaction network (dd), the drug-disease network (di), the drug-side-effect network (de) and the drug structure similarity network (ds); the feature vectors  $Y$  are extracted from three heterogeneous networks, the protein-disease association network (pd), the protein-protein network (pp) and the protein sequence similarity network (ps). As shown in Tab. 1, in the full data set, only 0.18% of the drug-target interactions are labelled as positive, none is labelled as negative. As in [4] we also construct a sample dataset, where all the positive interactions are reserved and an equal number of unknown interactions are sampled to be negative.

Table 1: Statistics of the dataset

Data	#Drugs	#Targets	#Positive	#Negative	#Unknown
Full	708	1512	1923	0	1068573
Sample	708	1512	1923	1923	1066650

**Evaluation.** Throughout the experiment section, the major evaluation metric is Area Under Precision Recall curve (AUPR), which is commonly adopted in bioinformatic studies. An auxiliary evaluation metric is Area Under ROC curve (AUROC).

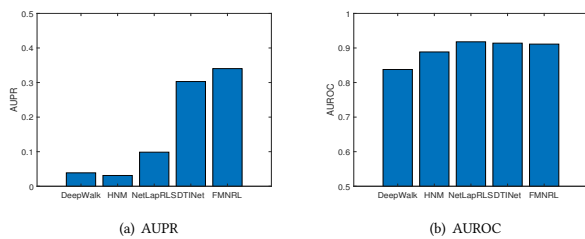
#### 3.2 Results and Analysis

**DTI Prediction Performance.** We first evaluate the accuracy of DTI prediction of the proposed FMNRL model. We compare our FMNRL model with 5 state-of-the-art methods: (1)DeepWalk [7]: a similarity-based drug-target prediction method that enhanced similarity computation by deep learning method within a linked tripartite network. (2)HNM [6]: a network model in which strength between a disease-drug pair is calculated through an iterative algorithm on the heterogeneous graph that also incorporates drug-target information. (3) NetLapRLS [5]: a manifold regularization semi-supervised learning method (4)PUDTI [2]: an SVM-based optimization model that is trained on negative samples extracted based on positive-unlabeled learning. (5)DTINet [4]: a regression model that learns feature space mapping  $Z$  by the loss function  $\min_Z \sum_{i,j} (P_{i,j} - (XZY)_{i,j})^2$ . We do not change the default settings for all the above comparative methods.

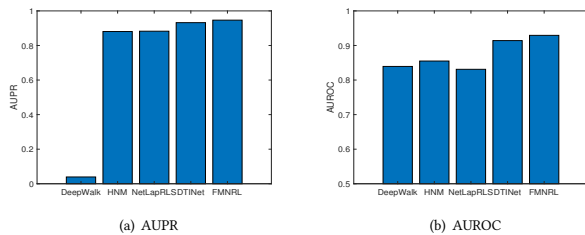
We perform the evaluation on two data sets. The first one is on the full data set, i.e. we randomly segment the whole data set to 10 divisions and conduct 10-fold cross-validation. The second one is on the sample data set, i.e. keeping the ratio of positive and negative samples to 1 : 1, we conduct random sampling for 10 times and the reported results are averaged over the 10-sets.

The comparative performances on the full dataset are shown in Fig. ?? . We can see that (1) FMNRL model significantly boost the AUPR by 10% percent, compared with the best of state-of-the-art methods. The best comparative method is DTINet, which achieves 30%. Our FMNRL model obtains a 34% AUPR. As AUPR is well regarded to be a more robust and accurate evaluation metric than AUROC, this observation demonstrates the potential of our model. (2) Most of the state-of-the-art methods have a very low AUPR result on the full dataset. This observation again reveals that obtaining a high RUPR performance is challenging on the full data set. (3) In term of AUROC, the best result is obtained by NetLapRLS. However, the best comparative result is 92%, the result of FMNRL is 90%, which is comparable.

The comparative performances on the sample dataset are shown in Fig. ?? . We can see that (1) FMNRL model achieves better AUPR than all state-of-the-art methods. The best comparative method is DTINet, which achieves 80%. Our FMNRL model obtains a 94% AUPR. (2) Most of the state-of-the-art methods have a higher AUPR result on the sample dataset than the full dataset, due to the balanced ratio of positive and negative samples. (3) Surprisingly DeepWalk has a very low AUPR performance on the sample set. (4) FMNRL model outperforms all state-of-the-art models in AUROC



**Figure 2: On the full dataset, FMNRL model significantly boost AUPR while remaining comparable AUROC.**



**Figure 3: On the sample dataset, FMNRL model outperforms state-of-the-art methods in terms of both AUPR and AUROC.**

performance. The best comparative method is again DTINet, which achieves 90%. Our FMNRL model obtains a 92% AUROC.

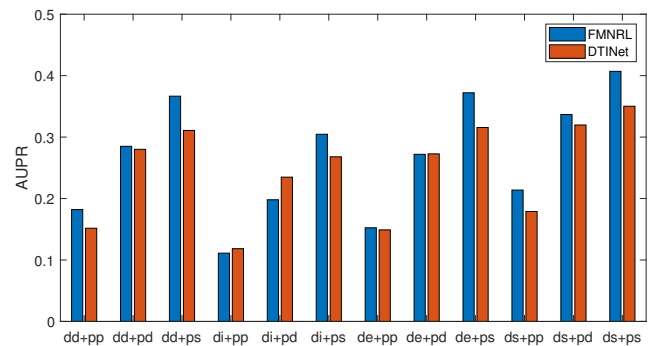
#### Stability.

**Parameter Tunning.** If there's more space, include the effects of parameters  $\sigma^2, \eta$ .

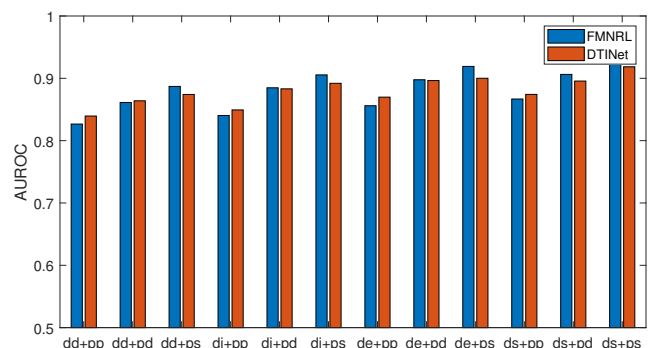
## 4 CONCLUSION

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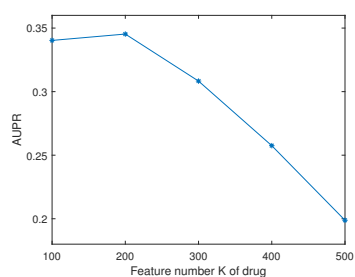


(a) AUPR

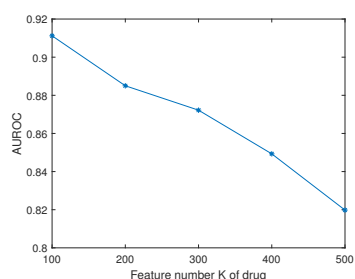


(b) AUROC

**Figure 4: Our model is stable with different feature inputs on the full dataset.**

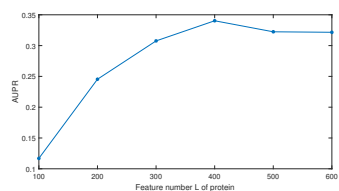


(a) AUPR

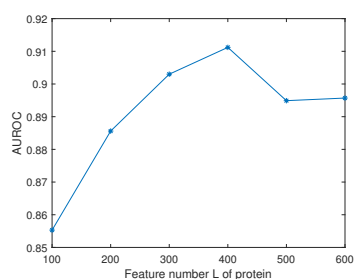


(b) AUROC

**Figure 5: AUPR and AUROC performance of our model with different  $K$  number of drug features.**



(a) AUPR



(b) AUROC

**Figure 6: AUPR and AUROC performance of our model with different  $L$  number of protein features.**