Bioinformatics
doi.10.1093/bioinformatics/xxxxxx
Advance Access Publication Date: Day Month Year
Manuscript Category
OXFORD

Subject Section

Voodoo : Combining Bottom-up and top-down approaches through graph learning over interaction networks for drug-target-interaction prediction

Tilman Hinnerichs [1,*] and Robert Hoehndorf [2]

[1] Department, Institution, City, Post Code, Country and
[2] Department, Institution, City, Post Code, Country.

* To whom correspondence should be addressed.

Associate Editor: XXXXXXX

Received on XXXXX; revised on XXXXX; accepted on XXXXX

Abstract

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Contact: tilman.hinnerichs@kaust.edu.sa
Supplementary information:10264703 Supplementary data are available at *Bioinformatics* online.

1 Introduction

(Wang and Kurgan, 2018)
In history, traditional remedies, that were known for their medicinal properties lead to drugs by extraction of the functional ingredients. Alternatively, characteristics and features of potential drugs were detected by accident like in the case of penicillin. More recently, biological drug targets can be found *in silico* through discovery of suitable computational predictors.

The challenge of accurately predicting drug-target-interactions (DTI) has shown its importance in the fields of drug repurposing and repositioning, and in the exploration of novel drugs and their interaction partners. Knowledge about those links between compounds and their target proteins help in an array of medical and pharmaceutical studies. Additionally, those associations can be utilized to identify disease specific targets, leading to desirable therapeutic effects.

With the rapidly growing field of machine learning approaches and their application to bioscientifical problems in the realm of bioinformatics, different kinds of data, such as long DNA sequences could be utilized for feature generation, while rapid advances were made. Almost all state of the art models for drug-target-interaction prediction were based on the usage of neural networks with increasing size.

Only recently, the technique of graph learning was introduced by Kipf and Welling (2016) through graph convolution algorithms, and improved and altered under usage of different kernels (Defferrard *et al.*, 2016; Bianchi *et al.*, 2019), attention mechanisms (Veličković *et al.*, 2017), random walks (Klicpera *et al.*, 2018), and mixtures of both (Hamilton *et al.*, 2017). While based on diverse systems, they can be relevant for testing distinct hypothesis for given graphs. While convolutional filters are suitable for finding patterns among the the given graph, attention mechanisms are more relevant for discovery of important regions within. Lately, graph learning approaches found application for computing compound representations for DTI prediction.

Needs ref, or reformulate

Approaches on this rather sophisticated problem can divided into top-down or network approaches (**CITATION**), and bottom-up or molecular approaches (**CITATION**). Top-down approaches take advantage of other data such as diseases (CITATION), side effects, knowledge graphs or ontologies, in order to learn representations for both compound and protein.

Try to avoid

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We call these approaches "top-down" because they start with the observable characteristics induced by a drug and infer the targets based on the likely molecular mechanisms that result in these phenotypes.

On the other hand, bottom-up approaches attempt to learn from chemical properties of proteins or drugs to infer candidate drug–target interactions. For drugs, molecular structure (CITATION GraphDTA), molecular fingerprints, similarity to other drugs (See Bioinf Survey), and other molecular features may be used. On the protein side, secondary structure prediction (CITATION), contact prediction (CITATION), or simply convolution over the amino acid sequences can be used to obtain a feature representation for a given proteins. However, both bottom-up and top-down approaches to drug–target interaction prediction

Don't use "simply".

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that are not solvable within themselves.

Following is not sufficiently precise; here, you need to clearly state the challenges faced by both approaches, ideally with references.

Thus, bottom-up approaches share the lack of ability to generalize, which we will show in later sections, and usually focus on engineering sophisticated features for the drugs, while neglecting to formulate meaningful features on the protein side. Top-down approaches lack the ability to spot small differences to cope with small differences within the drug structure and rely heavily on given data for the considered drug-target pair. The latter is not suitable for predictions on novel or unseen compounds, as e.g., data on side effects or its impact on diseases is seldom given for novel drugs.

In order to design such a feature for proteins and drugs, respectively, we make use of the interaction networks for both proteins and compounds. Drug-drug interaction networks were introduced and standardized by Ayvaz *et al.* (2015) and have been used for clinical decision support (Scheife *et al.*, 2015). Drug-drug interaction networks may give a hint on common targeted pathways. As an additional compound feature we will use semantic side effect similarity, which we will discuss later on.

Generally, try to avoid pointers to "later".

Protein-protein interaction networks have shown great results in . . . ((Vazquez *et al.*, 2003), (Ackerman *et al.*, 2019)) in granting context for molecular system biology. However, these contexts were never applied to the problem of drug-target-interaction prediction. Thus we formalized our hypotheses over these interaction graphs and will test them in the following chapters.

2 Methods

2.1 Problem Description

The issue of predicting drug-target interactions can be described quite briefly: For a given drug and a given protein we want to determine whether those interact or not. We do not differentiate between types of interaction such as activation and inhibition, and do not predict the strength of the interaction. If we additionally make the closed world assumption, i.e., assume that our knowledge is complete and all drug–protein pairs without a known interaction do not interact, we can formulate the problem as a binary classification task.

2.2 Datasets

The data for the different parts of this model were obtained from various sources. Starting with the protein-protein interactions, we fetched $\approx$ 11000 human proteins with over 170.000 links from STRING (Szklarczyk *et al.*, 2014). For the drug-target interactions themselves, we fetched 137.000 links from STITCH database (Szklarczyk *et al.*, 2015). As both STRING and STITCH provide probability scores for each association, we filtered them as advised by a threshold of 700, thus only obtaining likely interactions.

precise number

For the ontology segment we utilized PhenomeNET (Hoehndorf *et al.*, 2011), a collection of various ontologies such as Human Phenotype Ontology (Köhler *et al.*, 2018), Gene Ontology (Ashburner *et al.* (2000) and Seth Carbon *et al.* (2020)), Mammalian Phenotype Ontology (Smith and Eppig, 2009) and numerous others. Side effects and their links to drugs were obtained Side Effect Resource (SIDER)(Kuhn *et al.*, 2015) and structured according MedDRA database (Mozzicato, 2009). They were mapped to PhenomeNET with aid of *Phenomebrowser.net*, which provides a SPARQL query endpoint for the mentioned resources.

which ontologies to cite

For comparative evaluation we used the gold standard dataset introduced by **?**, which includes both drug-target interaction pairs and side effects.

Eventually, we only considered proteins that had at least one link in either STITCH or STRING, and drugs with at least one side effect and one existing target. Thus, the intersection between these resources yielded 1160 drugs and 6680 human proteins for the training phase. We provide links to and methods for the necessary data in the provided Github repository.

2.3 Evaluation and metrics

To assess each model, we compute a variety of common metrics for binary classification. As the datasets are highly imbalanced, we chose the *area under receiver operating characteristic*-score (AUROC) on training, validation and testing split. Therefor, we calculated the true positive rate (TPR), false positive rate (FPR) and precision score. We will further compute true positives (TP), false positives (FP), false negatives (FN) and finally true negatives (TN). We calculate the ROC by plotting the TPR against the FPR for various threshold settings for the model predictions. We eventually calculate the area under ROC curve utilizing trapezoidal approximations. We will refer to this measure as $MacroAUC$.

In contrast we also calculate the $MicroAUC$ score. For given lists D, P of drugs and proteins, respectively, and a set of known interactions $Int := \{(d_i, p_i)\}$, *MicroAUC* is calculated as the average per entity (macro) *AUROC* score. With respect to proteins, this can be formalized for given labels and prediction $l, y : D \times P \to \{0, 1\}$ as

$$MicroAUC_p := \underset{p \in P}{mean} \left(\{\text{AUROC}(\{(l(d_i, p), y(d_i, p))|d_i \in D\})\}\right)$$

Note that drugs and proteins can be interchanged in this formulation, which we will denote with $MicroAUC_p$ and $MicroAUC_d$, respectively.

2.4 Model

Before introducing the models core components, we will clarify the previously mentioned notions of top-down and bottom-up. We will refer to features and methods, starting from the observable characteristics of either drug or protein inferring the likely molecular mechanisms as top-down. On the other hand, bottom-up refers to approaches deducing from even finer molecular properties, such as single functional groups or amino acid sequences for drugs and proteins, respectively.

In order to build a method that incorporates both top-down and bottom-up features, we first created a model for each individually. Hence, we assemble rich molecular structure based features for drugs from *SmilesTransformer* (Honda *et al.*, 2019) and proteins from *DeepGO-Plus* (Kulmanov and Hoehndorf, 2019). *SmilesTransformer* introduces an autoencoder, learning over the SMILES strings and thus the molecular organization of each drug in an unsupervised manner. On the other hand,

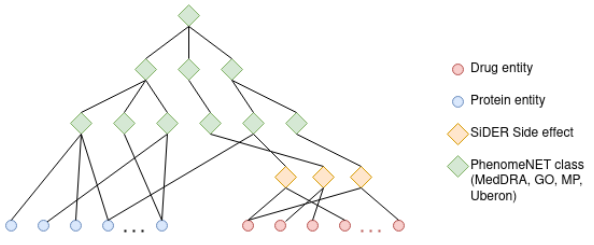

Figure 1. Drugs and proteins with annotations to SiDER and PhenomeNET

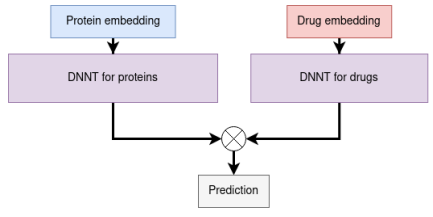

Figure 2. Siamese network applied to molecular and DL2vec features, utilizing deep learnable feature transformations (LFT). The similarity function $\otimes$ yields the similarity between both transformed embeddings e.g. by computing the cosine similarity.

we take advantage of the pretrained models of *DeepGOPlus*, obtaining features from the proteins amino acid sequence, showing significant performance in the field of protein function prediction. Thus, both embeddings seem to suitably supplement the following ontology based representations.

In the top-down section, we used *DL2vec* (Chen *et al.*, 2020) to obtain ontology based representations. DL2vec constructs a graph by introducing vertices and edges for each ontology class and axiom, respectively, followed by random walks starting from each entity. These walks are eventually learned on using a Word2vec (Mikolov *et al.*, 2013) model. Thus, we pick up rich, neighbourhood focused representations for each entity, which has shown great results for representing protein function and phenotypes. The overall structure of the ontology can be seen in Figure 1.

2.4.1 Siamese neural networks and modular learnable feature transformation

As we want to learn from the similarity of drug side effects and protein phenotypes we opted for a deep siamese network approach, hence learning a high-dimensional embedding emphasizing this identity by forcing a similarity between these embeddings. On the other hand we built a deep neural network for the molecular structure based features, also benefiting from the siamese network architecture. Computing the similarity between two representations, allows for a variety of different methods. However, we decided for the cosine similarity measure being invariant to scaling.

Therefore, the precomputed embeddings are run through a regular, neural learnable feature transformation (LFT) network, which also reduces the eventual representation size for drugs and proteins separately. An example structure for both types of features can be found in Figure 2.

While a regular deep neural network, denoted by LFT, for feature space reduction is not particularly novel, we emphasize the versatility of this approach, as both ontology and molecular feature for both drugs and proteins are reduced to similar dimensionality. This allows for a high amount of modularity and different experimental setups by plugging different kinds of features into the model. Additionally, these pretrained features can be used for a variety of other tasks. Additionally, the ontology LFT can be reused for a variety of DL2vec based features with respect to other ontologies and hypotheses. We hereby followed the results of *DL2vec*, indicating that utilizing the activation function $\sigma := \mathrm{LeakyReLU}$ leads to performance increase.

2.4.2 Graph convolutional layers

These molecular and ontology based sub-models were added to a larger graph convolutional model, based on the protein-protein interaction (PPI) graph. The PPI dataset is represented by a graph $G = (V, E)$, where each protein is represented by a vertex $v \in V$, and each edge $e \in E \subseteq V \times V$ symbolizes an interaction between two proteins. Additionally, we introduce mapping $x : V \to \mathbb{R}^d$ projecting each vertex v to its node feature $x_v = x(v)$, where d denotes the dimensionality of the node features.

As described before, graph convolution has shown significant performance increase in a variety of tasks. While there are various methods out there we will only introduce the most basic one here. A graph convolutional layer Kipf and Welling (2016) consists of a learnable weight matrix followed by an aggregation step, formalized by

$$\mathbf{X}' = \hat{\mathbf{D}}^{-1/2}\hat{\mathbf{A}}\hat{\mathbf{D}}^{-1/2}\mathbf{X}\mathbf{\Theta} \tag{1}$$

where for a given graph $G = (V, E)$, $\hat{A} = A + I$ denotes the adjacency matrix with added self-loops for each vertex, D is described by $\hat{D}_{ii} = \sum_{j=0} \hat{A}_{ij}$, a diagonal matrix displaying the degree of each node, and Θ denotes the learnable weight matrix. Added self-loops enforce that each node representation is directly dependent on its own preceding one. Notably, the number of graph convolutional layers stacked equals the radius of relevant nodes for each vertex within the graph.

The update rule for each individual node is

$$\mathbf{x}'_i = \mathbf{\Theta} \sum_j^N \frac{1}{\sqrt{\hat{d}_j \hat{d}_i}} \mathbf{x}_j \tag{2}$$

where both $\hat{d}_i, \hat{d}_j$ are dependent on the edge weights e_{ij} of the graph. With simple, single-valued edge weights such as $e_{ij} = 1 \; \forall (i, j) \in E$, all $\hat{d}_i$ reduce to d_i, i.e., the degree of each vertex i. We denote this type of graph convolutional neural layers with GCNConv.

While in this initial formulation the node-wise update step is defined by the sum over all neighbouring node representations, we are able to alter this formulation to another message passing scheme. We are able to rearrange the order of activation function σ, aggregation AGG and linear neural layer MLP with this formulation as proposed by Li *et al.* (2020a):

$$\mathbf{x}'_i = \mathrm{MLP}\left(\mathbf{x}_i + \mathrm{AGG}\left(\left\{\sigma\left(\mathbf{x}_j + \mathbf{e_{ji}}\right) + \epsilon : j \in \mathcal{N}(i)\right\}\right)\right) \tag{3}$$

where we will generally only consider $\sigma \in \{\mathrm{ReLU}, \mathrm{LeakyReLU}\}$. We will denote this generalized layer type as GENConv, following the notation of Fey and Lenssen (2019). While the reordering is mainly import for numerical stability, this alteration also addresses the vanishing gradient problem for deeper convolutional networks (Li *et al.*, 2020a). Additionally, we can also generalize the aggregation function to allow different weighting functions such as learnable $\mathrm{SoftMax}$ or Power for the incoming signals for each vertex, substituting the averaging step in GCNConv. Hence, while GCNConv suffers from both vanishing gradients and signal fading for large scale, highly connected graphs, each propagation step in GENConv emphasizes signals with values close to 0 and 1. The same convolutional filter and weight matrix are applied to and learned for all nodes simultaneously, and the resulting information hold no information on their own connectivity.

Which information? Specify

We employ another mechanism to avoid redundancy and fading signals in stacked graph convolutional networks, which was introduced by Li *et al.*

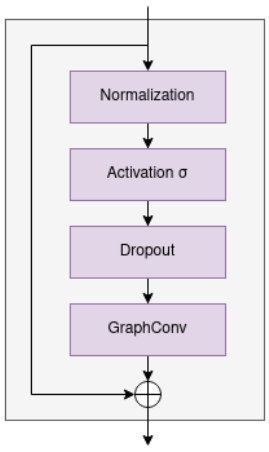

Figure 3. Residual architecture built by Li et al. (2019) and Li et al. (2020b) enabling deeper graph convolutional models

(2019) and refined in Li *et al.* (2020b). The authors propose a residual network architecture and normalization scheme. This structure is depicted in Figure 3 resulting in reusable residual blocks, which can be stacked multiple times, thereby not losing focus of each node neighbourhood.

2.4.3 Hyperparameter tuning

As the number of drug-targets are sparsely given with respect to the number of both drugs and proteins considered, the resulting training, validation and testing datasets are highly imbalanced. As there are only 22.336 links in the considered subset the ratio

$$\frac{\#drugs \cdot \#proteins}{\#dti\_links} \approx 360,$$

consequently needing compensation in the computed loss function and appropriate metrics for the evaluation.

Therefore, we weighted all positive drug-protein pair samples with this ratio by introducing the following loss function with respect to binary cross-entropy:

$$l(x, y) = -w\left[y \cdot \log x + (1 - y) \cdot \log(1 - x)\right] \tag{4}$$

for given prediction x and target y. We average this loss among all drug-protein pairs in the training set, leading to a stable environment for the used optimizing scheme *Adam* (Kingma and Ba, 2014). We implemented a 5-fold cross validation among the proteins as justified in the results section. Furthermore, we used early stopping to detect plateaus in the training process.

To find the best hyperparameter configuration for the proposed model we performed a grid search to find the most expressive and non-redundant representation. We pretrained the bottom-up and the top-down model separately and aimed at best performing models w.r.t. previously described metrics. We optimized embedding sizes, depth of the neural network, optimizer, learning rate and layer types using an extensive, manual grid search.

Specify range of values searched here; even better if you have the intermediate results and can put them here (better: in the supplement).

3 Results

3.1 Voodoo : computational model to identify drugs that target a protein

Within DTI prediction, one can observe basic biases resulting from the underlying datasets (Pahikkala *et al.*, 2014). First, novel drugs are often designed by altering non-functional components of a drug, leading to two and more very similar drugs designed to target the same proteins (Overington *et al.*, 2006). This can lead to a bias when it leads to „hidden duplicates“ that can distribute among the train–test split, resulting in a better (measured) predictive performance than would be expected when the model is applied to genuinely unknown interactions. Second, some proteins (which we will denote as *hub proteins*) have significantly more known interactions with drugs than others. In the STITCH database, 5% of the proteins have 40% of the interactions, and similar distributions are present in the Yamanishi and Drugbank datasets (Wishart *et al.*, 2007, 2017) datasets; preferentially predicting these proteins can often increase predictive performance while again not reflecting the actual performance when applied to a new protein (e.g., a protein for which no interactions are known). This bias in the number of drugs targeting certain proteins may be the result of study bias where more „valuable“ proteins have more drugs designed to target them due to their involvement in more common diseases (or diseases for which drugs can be more profitably marketed).

We developed Voodoo as a computational model to predict drug–target interactions. Specifically, given a protein, Voodoo will identify and rank known drugs that likely target this protein. Voodoo combines two types of features: structural information for drugs and proteins that can be used to determine if they may physically interact, and information about drug effects that may localize on an interaction network. As structural features, Voodoo uses structural representations of drugs from the SMILES transformer (Honda *et al.*, 2019) and representations of protein amino acid sequences from DeepGOPlus (Kulmanov and Hoehndorf, 2019). Voodoo learns representations of drug effects and protein functions using the ontology-based machine learning method DL2Vec (Chen *et al.*, 2020).

We use two Siamese neural networks to combine the molecular and phenotype representations of drugs and proteins, and add these to a protein interaction network as node features. We then train this model in an end-to-end manner. The overall architecture is depicted in Figure 4.

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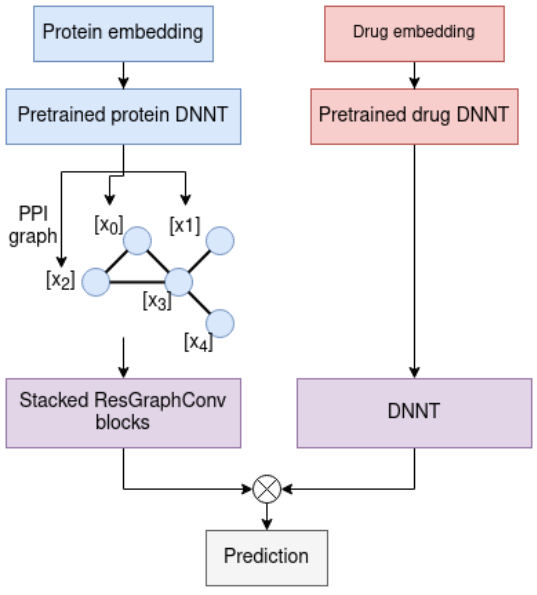

Figure 4. Full DTI prediction model based on the pretrained learnable feature transformations (LFT) for either molecular structure or ontology based features. The transformed protein representations are added to each corresponded protein as node features for the graph convolutional steps.

Note that this approach can be easily generalized, profiting from other protein function and phenotype representation methods.

Through the very nature of the graph convolutional neural network, we build the transformed representation for all proteins in every forwarding step of the model. Note particularly, that the same convolutional filter and weight matrix are applied to and learned for all nodes simultaneously. By construction, for a single drug we can compute and predict all its interactors in a single run of the model, leading to significantly less computing time.

3.2 Voodoo identifies drugs that target a protein

Likely discussion:

The aim of Voodoo is to predict candidate drugs that target a given protein; the challenge is to develop a training and evaluation scheme that does not simply overfit to the inherent biases in training and testing data. In general, when performing cross-validation for DTI prediction, the options are to split over

1. split over drugs,
2. split over drug–target pairs, or
3. split over proteins

where the first and third option concern splitting drugs and proteins, respectively, into train, validation and test sets, and arranging the corresponding drug-target interactions. They ensure that at least parts of the interactions are not seen during training and evaluate either how well targets are predicted for unseen drugs or unseen proteins. Hereby, different training and prediction schemes lead to divergent expressiveness of the resulting model.

Likely discussion:

The most common scheme for DTI prediction is the split over drug-target pairs (Wang and Kurgan, 2018), where likely all drugs and targets of the validation and testing phase have already occurred in the training phase, as part of other drug-target pairs. The second most prevalent arrangement is the split over drugs, while only close to none is aiming on a protein split. However, the first and second splitting scheme are exposed to the first dataset bias and are hence more likely vulnerable to transductive inference by just predicting recently seen structures, rather than implementing inductive inference and generalizing over the drug representations. Second, these two strategies are more susceptible to the second bias, as only in these cases the model may overfit on the number of existing interactions for a single protein, while in the third scheme the number of interactions of the test proteins is entirely unknown during training process.

Assuming a hypothetical, perfectly generalizing model built upon an unbiased dataset, this very model would yield similar performances for all three splitting schemes, not overfitting on the known structures. On the other hand, for a hypothetical entirely overfitting model, trained on a highly biased dataset, this model would show substantial deviations from the original performance over another split.
We emphasize, that all real-world models are prone to some sort of overfitting, and unknown, deviant entities in both validation and testing set will likely lead to some sort of performance gap for relevant metrics. However, a large disparity may hint the biases stated above.

Hence, we will perform a cross-validation over proteins for the training and prediction phase of our model, despite predicting per protein is rather counter-intuitive as there only limited drug-targets (Overington *et al.*, 2006), and thus novel drugs are more likely to arise than novel targets. Yet, we aim to find all interacting drugs for existing targets motivating our split choice even further.

3.3 Experiments

In this section we will present the results of Voodoo

3.4 MicroAUC

Continuing this line, we propose the well known metric *MicroAUC* for a better evaluation for this purpose.

Note further that both are applicable to all three kinds of splitting schemes, but $MicroAUC_p$ and $MicroAUC_d$ are only plausible for protein split and drug split, respectively. As we want to evaluate the models performance to find all suitable drugs for each protein individually, $MicroAUC_p$ seems to be more reasonable in comparison to both $MicroAUC_d$ and $AUROC$ with respect to the previously proposed protein split cross-validation.

3.5 Baseline model

Before introducing the core of our eventual model, we propose a suitable naive baseline model in order to analyze and understand the existing approaches and this novel method for drug target interaction prediction. For given lists D, P of drugs and proteins, respectively, and a set of known interactions $Int := \{(d_i, p_i)\}$, we construct an interaction matrix $M_{int} \in \{0,1\}^{|D|\times|P|}$ with

$$M_{ij} = \begin{cases} 1 & \text{if } (d_i, p_j) \in Int \\ 0 & otherwise \end{cases}$$

describing for all drug–protein whether there is a known interaction or not. We now rank all proteins $p_j \in P$ descending by their number of drug interactors, characterized by

$$f : P \to \mathbb{N} \text{ with } f : p_j \mapsto \sum_{i=0}^{|D|} M_{ij}$$

by summing over the columns of M_{ij} and ranking these sums. We now finish our baseline predictor P_k by predicting all drugs to interact with

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the top k targets, denoted by $TopK(P)$ w.r.t. M_{ij} from the previously introduced ranking, formalized by

$$P_k : D \times P \to \{0,1\} \text{ with } P_k : d_i, p_j \mapsto \begin{cases} 1 & \text{if } p_j \in TopK(P) \\ 0 & otherwise \end{cases}$$

with the only hyperparameter k. Note particularly, that the consequent prediction of P_k is not dependent on the considered drug d_i, and will thus predict all drugs similarly for a given protein p_j. Subsequently, this naive predictor is not yielding any valuable information on the individual interactions with drugs for a given protein. Also note the possibility for a similar predictor by calculating the top k interacting drugs, respectively.

4 Findings

4.1 Deification of our method

- we built protein function and ontology based features based on DL2vec
- Ontology derived protein function focused features are highly predictive for dtis
- We built a versatile template for various features to test localization on the PPI graph
- normal GCNs don't work on PPI graph, as it is highly connected → needs stronger more expressive aggregation function → GENConv in residual blocks for better numerical stability
- protein functions localize on the PPI graph, while molecular features don't
- all AUROC in % AUROC score on STITCH

DNNT model	Without graph model	With graph model
MolPred	69	69
PhenomeNETPred	88	92
MolPred + PhenomeNETPred	89	93

- microAUC for MolPred + PhenomeNETPred on graph is about $93 +-$
- and on yamanishi dataset

DNNT model	Without graph model	With graph model
PhenomeNETPred	83	84
MolPred + PhenomeNETPred	83	84.5

- MicroAUC is about 83

4.2 How to insult other methods

- Only few other methods perform their split over proteins (Wang and Kurgan, 2018), DTI-CDF does it
- Running split over proteins is harder than, drug and drug protein pair split (see below table)
- this applies for both DTI prediction and drug target affinity prediction (and Saras gene-disease association)
- using indications is like cheating, as not applicable for searching new drugs
- drug indications are highly predictive for downstream tasks, but lack capability to differentiate highly related drugs/proteins
- Stratified Cross validation is suitable for training, but **NOT** for validating and testing (Uselessly high AUPRC)
- microAUC is a superior and more intuitive metric for drug repurposing → why for each protein and not for each drug

Approach	Splitting scheme	Original AUROC score	Protein split AUROC	MicroAUC
DTINet	DP pairs	91	84.1	67.2
DTIGEMS+	DP pairs	93	72.2	67.8
DTI-CDF	Proteins	83	83	79

Approach	Splitting scheme	Original AUROC score	Protein split AUROC	MicroAUC
DeepDTI	Drugs	87.6	75.9	70.1
DeepDTA	DP pairs	87.6	76.7	69.4
DeepConv-DTI	DP pairs	88.3	76.6	73.0
MolTrans	DP pairs	89.5	77.0	74.0

- A naive predictor (ranking proteins) and predict each drug similarly achieves cutting edge performance (87.5 AUROC for whole dataset, 85.5 for 5-fold cross validation in drug-split) → No prot focused microAUC possible. → hub proteins
- Yamanishi Dataset is only partially suitable , if everybody just derives a suitable subset (DTIGEMS) — for comparing results
- This also applies to drug target affinity prediction. We were hereby able to roughly reproduce the results from MolTrans (Bioinformatics) on BioSnap

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4.3 Tested hypotheses

In this work we are testing the following hypotheses:

1. Can we build a model that outperforms state of the art approaches, combining top-down and bottom-up approaches?
2. Are interaction networks sufficient to improve the performance of simple molecular predictors?

We will test the first hypothesis by building a model that takes both top-down and bottom-up features into account. Thus, we propose a novel approach to combine those mutual exclusive attempts, through the usage of interaction networks, similarity and molecular features. Additionally, we test the latter by building a simple molecular DTI predictor and enhance it under usage of the interaction networks.

For the bottom-up approach we build a model that only relies on molecular features, which we will discuss in more detail in the following methods chapter. For the combination of both approaches we now attach the predictions to the protein-protein interaction graph as node features for future graph learning steps. In this graph we tried to find both patterns and regions for each drug that could be of interest through application of different graph convolutional layers, which in return represent the feature for each protein. Representing the drug we take the drug-drug interaction graph and the semantic similarity over side effects which we will explain in the following paragraphs.

5 Methods

5.1 Models

The used model consists of two separate models, that help to fuse together the two methods:

1. The molecular predictor
2. The interaction network based predictor

We build the molecular predictor by using pretrained, molecular fingerprints models for both drugs and proteins. Regarding proteins, we used the pretrained feature generator from *DeepGoPlus* ((Kulmanov and Hoehndorf, 2019)) that was originally designed for protein function prediction and is regarded as state of the art for this purpose. For drugs we used a pretrained fingerprint model from *SMILES transformer* ((Honda *et al.*, 2019)), that provides a simple and fast method to compute fingerprints through autoencoder models. The encodings from these two models were funneled into a simple deep neural network (see Figure **??**) with few fully connected.
The results of that prediction flow into the annotation of the protein-protein interaction (PPI) graph as depicted in (IMAGE). Hereby, the predictions of the molecular predictor are used as node features for the graph, with respect to the given drug. Thus, given a compound-target pair, the nodes of the PPI graph now hold bottom-up features, which can now be processed by the graph learning algorithms.
The PPI graph is processed by different graph convolutional layers, that may underline the importance of either patterns or regions within the graph, to obtain a feature vector for the wanted node. In contrast to learning over whole graphs we perform node classification within the graph. These layers are either graph convolutional layers, that learn a certain kernel over the graph, or attention based. Different layers of both and other types such as were tested.
The drug-drug interaction features are retrieved by choosing the corresponding row in the adjacency matrix of the graph, thus leading to quite simple features.
For the semantic similarity feature, that once again represents a top-down attribute, we artificially link each drug to its corresponding side effects in the MedDRA hierarchy. Concerning this hierarchy, drug-drug similarity is computed by the Resnik similarity ((Resnik, 1995)). For the given compound we take the corresponding row of this symmetric similarity matrix.

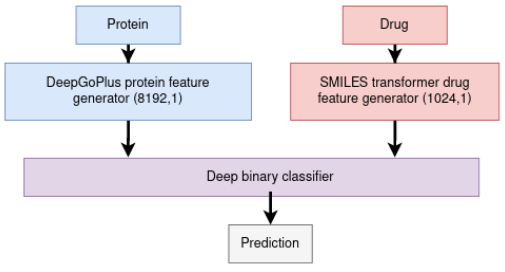

Figure 5. Molecular predictor based on the generated features from DeepGoPlus and SMILES transformer.

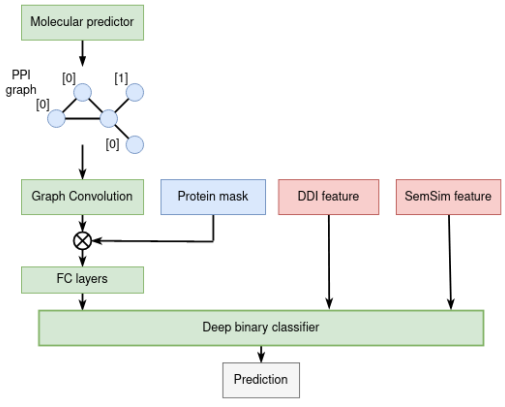

Figure 6. Deep neural network that predicts based on drug-drug interaction features and semantic similarity features over side effects for drugs, and graph convolution over protein-protein interaction networks for proteins. Protein and drug features are represented by blue and red, respectively.

Thereby, we concatenate these three features together and funnel them into another deep neural network as depicted in figure 6. This network finally yields our prediction. We hereby perform splits over both drugs and proteins, in order to test and show the discrepancy and increasing difficulty.
Implementation was done in PyTorch ((Paszke *et al.*, 2019)) and is available on Github under github.com/thinnerichs/KAUST-dti-metabol. Graph learning methods were build with help of PyTorch-Geometric ((Fey and Lenssen, 2019)), a geometric deep learning extension library for PyTorch, that recently got a lot of attention in the machine learning community. This library gives the potential to use many state of the art graph learning mechanisms, such as plain but effective graph convolution (Kipf and Welling (2016)), Chebychev kernels ((Defferrard *et al.*, 2016)), ARMA kernels ((Bianchi *et al.*, 2019)), translation-invariant operators ((Verma *et al.*, 2017)), attention mechanisms ((Veličković *et al.*, 2017)), random walks ((Klicpera *et al.*, 2018)) and mixtures of the latter two ((Hamilton *et al.*, 2017)). The performance of these various layer types were tested for this particular problem, as discussed in the results section.

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6 Discussion

7 Conclusion

Acknowledgements

Funding

This work has been supported by the... Text Text Text Text.

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