Design and application of a knowledge network for automatic prioritization of drug mechanisms

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Abstract

Motivation: Drug repositioning is an attractive alternative to de novo drug discovery due to reduced time and costs to bring drugs to market. Computational repositioning methods, particularly non-black-box methods that can account for and predict a drug's mechanism, may provide great benefit for directing future development. By tuning both data and algorithm to utilize relationships important to drug mechanisms, a computational repositioning algorithm can be trained to both predict and explain mechanistically novel indications.

Results: In this work, we examine the 123 curated drug mechanism paths found in the drug mechanism database (DrugMechDB) and after identifying the most important relationships, we integrate 18 data sources to produce a knowledge graph, MechRepoNet capable of capturing the information in these paths. Applying the Rephetio repurposing algorithm to MechRepoNet, using only a subset of relationships known to be mechanistic in nature, we find adequate predictive ability on an evaluation set with AUROC value of 0.83. The resulting repurposing model allows us to prioritize paths in our knowledge graph to produce a predicted treatment mechanism. We find that DrugMechDB paths, when present in the network are rated highly among potential mechanisms. We then demonstrate MechRepoNet's ability to use mechanistic insight to identify a drug's mechanistic target, with a mean reciprocal rank of .525 on a test set of known drug-target interactions. Finally, we walk through a repurposing example of the anti-cancer drug imantinib for use in the treatment of asthma, to demonstrate this method's utility in providing mechanistic insight into repurposing predictions it provides.

Availability and implementation: The Python code to reproduce the entirety of this analysis is available at: https://github.com/mmayers12/metapaths

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Supplementary information: Supplemental information is available at Bioinformatics online.

Introduction

Compound repositioning, the discovery and development of new indications for previously developed drugs, promises a quicker, less-costly alternative to traditional *de novo* drug discovery (Ashburn and Thor, 2004). Historically, the majority of repositioning candidates have been identified through clinical observations. Computational repositioning leverages statistical modeling to analyze drug-disease combinations very quickly in the hopes of streamlining this candidate identification process. Unfortunately, most candidates identified through this method fail to progress beyond *in vitro* studies (Oprea and Overington, 2015). Several approaches for overcoming this shortcoming have specifically addressed increasing predictive performance on a known gold standard through either updated algorithms (Luo *et al.*) or improving quality and quantity of validated examples for training (Brown and Patel, 2016; Shameer *et al.*, 2018). Other methods focus on improving interpretability of predictions, aiming to uncover new experimental avenues through testable hypotheses that may improve understanding of a drug's effect on a disease (Malas *et al.*, 2019). Integrating both computational and experimental approaches, so that the results of each and inform the other, is considered the best option for progressing the field of repositioning as a whole (Pushpakom *et al.*, 2019).

Methods for computational repurposing models frequently rely on drug-drug and or disease-disease similarity to produce predictions (Li *et al.*, 2016; Li and Lu, 2012; Luo *et al.*). While this information is both important and predictive, a semantic network can describe complex and contextual relationships between a drug and a disease through connecting several individual statements into an expressive chain of reasoning, or path. *In silico* predictive models built from such knowledge graphs have the potential to inform experimental work through providing interpretable mechanistic explanations. However, these models heavily weight the relatedness of two drugs, through targets or pharmacology, as well as the relatedness of diseases, both carrying significant predictive power (Himmelstein *et al.*, 2017; Emig *et al.*, 2013; Mayers *et al.*, 2019). In cases where there are no known treatments for a disease, or no diseases known to be similar, which

is often the case with rare diseases, these patterns lose their utility. Uncovering connections between a drug and a disease that are less immediate may provide additional evidence for drug repositioning. By taking the few mechanistic details that may be available about a rare disease and identifying how a drug might interact with them could provide better insight.

In this work, we created a heterogeneous network with an emphasis on expressing relationships describing a drug's mechanism of action. This mechanistic repositioning network (MechRepoNet) was then used as the data source to construct a predictive model for drug repositioning, using a modified version of the Rephetio algorithm (Himmelstein *et al.*, 2017). Paths representing drug-drug or disease-disease similarity were excluded from the model, enriching for paths with mechanistic meaning. The resulting model was then used to produce weights to rank the potential mechanisms for a drug-disease pair. We then used these path weights to rank drug targets in a given drug-disease pair. These prioritized candidates were then compared with a set of known drug-target-disease triples to assess the model's ability to also identify a drug's mechanistic target. Finally, we assessed our model's ability to determine the mechanism of action in drug-disease pairs not contained within the training set.

Methods

Integration of data sources to build a mechanistic network MechRepoNet

Selection of data sources

We created DrugMechDB, a database that describes drug mechanisms as paths through a knowledge graph (Mayers *et al.*, 2020). We examined the concept and relationship types contained within the paths of the Drug Mechanism Database (DrugMechDB) to prioritize relationships important to expressing drug mechanisms. Data sources were evaluated based on their ability to express the semantic relationships found in DrugMechDB in order to construct a heterogeneous network capable of capturing these paths. Wikidata and Reactome were selected as primary data sources to serve as the knowledge graph's foundation due to their high level of breadth, high data

quality, and open reuse policies. From this foundation, data sources that contained information on relationships present in DrugMechDB and not abundant in Wikidata or Reactome, were prioritized. In all, eighteen data sources were selected for integration: Wikidata (Vrandečić, 2012), Reactome (Fabregat *et al.*, 2018), InterPro (Mitchell *et al.*, 2019), Ensembl (Cunningham *et al.*, 2019), miRTarBase (Chou *et al.*, 2018), ComplexPortal, Gene Ontology (Ashburner *et al.*, 2000), Uber-anatomy Ontology (Mungall *et al.*, 2012), Cell Ontology (Diehl *et al.*, 2016), Protein Ontology (Natale *et al.*, 2017), Disease Ontology (Schriml et al., 2019), Human Phenotype Ontology (Köhler *et al.*, 2019), NCATS Inxight Drugs, DrugBank (Wishart *et al.*, 2018), DrugCentral (Ursu *et al.*, 2017), Comparative Toxicogenomics Database (CTD) (Davis *et al.*, 2019), RheaDB (Morgat *et al.*, 2017), and GAUSS (Dutta *et al.*, 2020). Although data licensing restrictions prevent the direct redistribution of MechRepoNet, the complete code to assemble the graph is available at https://github.com/mmayers12/metapaths.

Data model determination and data integration

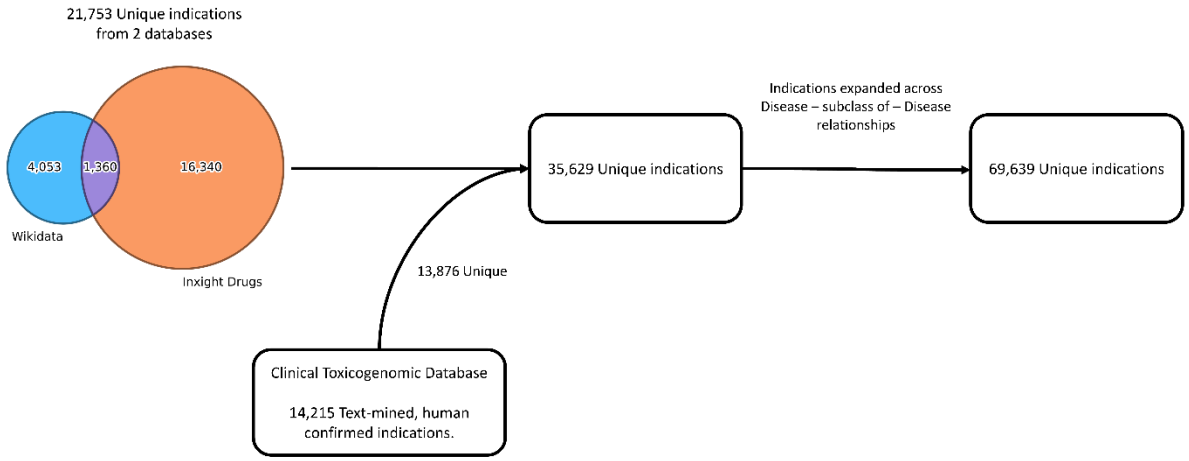
To standardize the data in MechRepoNet, concepts in the graph were normalized to the biolink data model (Mungall *et al.*, 2020). To reduce the number of potential features input into the model, relationships were standardized into one of five general relationships: a positive influence (activates, positively regulates), a negative influence (inhibits, negatively regulates), an influence without direction (affects, regulates), membership (involved in, part of), and a general association (associated with). Finally, to ensure that directed positive and negative influence edges are more specific cases of the undirected case (a proper subset), all directed influence edges were duplicated with their undirected equivalent.

Additional data model normalization was performed to adjust the level of granularity of Wikidata concepts, exact details are provided within the code repository. Wikidata and mygene.info (Xin *et al.*, 2016) were used as primary sources to normalize concepts between resources, augmented by limited string matching for chemical substances.

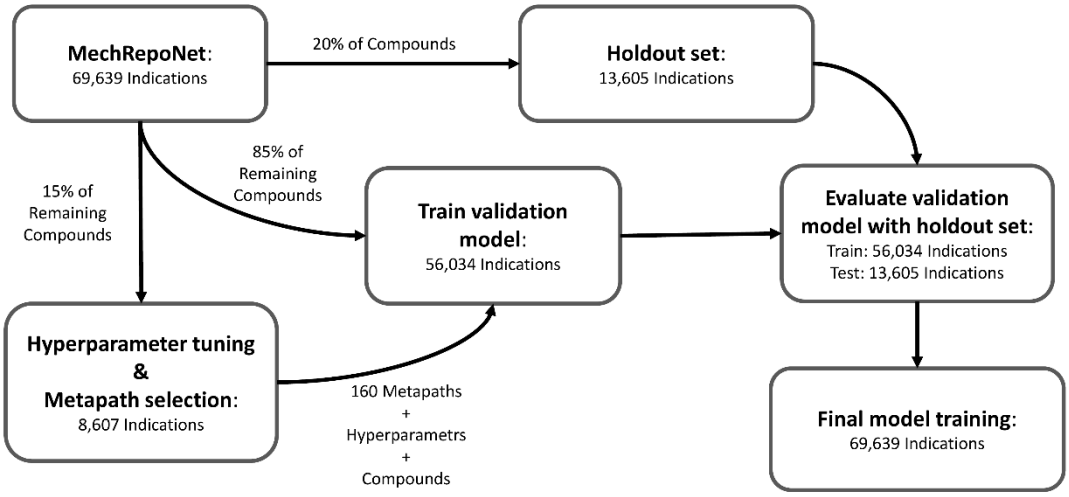
Training a learning model to find mechanistic treatment paths

Learning model

A modified version of the Rephetio algorithm (Himmelstein *et al.*, 2017) was used to train a learning model to predict ChemicalSubstance-treats-Disease relationships. Rephetio uses features based on metapaths that join ChemicalSubstantces and Diseases in a knowledge graph. We deviated from the published Rephetio algorithm in several key ways. First, whereas Rephetio used both degree weighted path counts (DWPC) of each metapath and node degrees of the compound and disease nodes as features in the model, we only used DWPC features. Second, Rephetio used a permutation analysis for feature selection, and we replaced that with a streamlined approach based on feature elimination by weak learners. Finally and most notably, we removed all metapaths that were primarily based on compound-compound and disease-disease similarity, enriching for metpaths which represent a drug's mechanism (https://github.com/mmayers12/metapaths/blob/main/1_code/13b_Model_Prep_Metapath_Membership_Analysis.ipynb).



(a) Data sources for indications



(b) Schematic of model training paradigm

Figure 1: **Indication sources and schematic of model training paradigm** a) Indications were initially sourced from two data sources, Wikidata and NCATS Inxight Drugs. Inxight Drugs is a data aggregator that compiles data from several sources including DrugBank and DrugCentral producing a large number of indications. The Clinical Toxicogenomic Database (CTD) contains over 14,000 indications, all originating from text-mining, with human confirmation of the result. Path contraction along the Compound - treats - Disease - inverse subclass of - Disease path to produce a total of 69,639 indications. b) Initially, 20% of compounds with known indications were removed and placed in a holdout set. A subset of 15% of the remaining compounds with known indications were used for hyperparameter tuning and metapath selection. The 160 metapaths selected were used to train a model on all indications not within the holdout set for validation of the model. Finally all indications were used to produce a final model for mechanistic evaluation.

Training data

A logistic regression was trained on the examples of ChemicalSubstance-treats-Disease triples found within the knowledge graph. There were 69,639 relationships of this type, coming from multiple data sources including Wikidata, NCATS Inxight Drugs, and CTD (Figure 1a). This large number is attributable to the differing chemical and disease vocabulary used by the data sources as well as the use of computational methods for producing network edges including NLP and subclass path contraction. Negative samples were randomly selected from the set of non-positive ChemicalSubstance-Disease pairs. Negative examples were sampled at a rate of 100 times

the positive examples to preserve the known imbalance between positive and negative treats relationships between drugs and diseases. In all instances of model training, pairs were only utilized if at least one path existed between the compound and the disease.

Figure 2: **Data sources for indications**

Before any model tuning or training was performed, a subset of 20% of the 11,303 ChemicalSubstances with at least one known indication were selected, and their 13,605 corresponding "treats" edges were removed from the network to be used as a validation set (Figure 1b).

Hyperparameter tuning

A subset of 15% of the ChemicalSubstances with known "treats" Disease relationships were selected for hyperparameter tuning, amounting to 1,404 ChemicalSubstances with 8,607 positive training examples (Figure 1b). For each positive indication, 100 negative samples were randomly selected from the set of ChemicalSubstances and Diseases. Negative samples were only selected if at least one path existed between the ChemicalSubstance and its Disease. These examples were used for feature selection (see Feature selection below) and selected features were used to tune the DWPC damping exponent (w), the elastic net regularization strength (λ), and the ratio of L_1 and L_2 penalties (α) (Zou and Hastie, 2005). Hyperparameters were tuned using 50 iterations of the Bayesian hyperparameter optimization method described by Bergstra *et al.* (2013). Optimization was performed to maximize a linear combination of the area under the receiver operator characteristic and precision recall curves, while minimizing the variance in these values across folds.

Feature selection

The fifty-six metapaths that were found in DrugMechDB were all included as features in our model. In addition, a voting strategy was employed between six different feature selection methods, each tasked with selecting 500 metapaths. Each feature selection method obeyed one of the following rules: Features with the largest magnitude of correlation coefficient with respect to

the target, top features after a χ^2 test between features and targets, a recursive feature elimination of the smallest 10% of features in a weak regression classifier with L_2 regularization, the features with largest magnitude of coefficient from a weak regression classifier with L_1 regularization, the largest feature importance values from a weak random forest classifier, and the largest feature importance values from a weak gradient boosted decision tree. Each selected feature from the 6 methods were considered a vote and features with 4 or more votes were kept for the training model. Code describing this full feature selection process is available on github (https://github.com/mmayers12/metapaths/blob/main/1_code/11c_Model_Prep_Hyperparam_tuning.ipynb). This process resulted in fewer than 200 of the 8,284 mechanistic metapaths being selected as features for training.

Performance evaluation

A model was trained on all the "treats" relationships in the network, less the holdout set as described in the training data section (Figure 1b). This holdout set, along with a sampling of non-positive relationships, was used to validate the learning model built from the data within the network.

Results

Analysing DrugMechDB for relevant relationships

Our first task was to build a heterogeneous network capable of expressing drug mechanisms. To help direct the creation of our network, we created DrugMechDB, a manually-curated database of drug mechanisms. DrugMechDB consisted of 123 mechanistic paths for 109 unique indications between 105 drugs and 84 diseases. This dataset spanned a diverse cross-section of drug classes and disease areas (Supplemental Figure 1). The most common edge type in DrugMechDB joins Drug entities with Protein entities, with 94 of the 123 paths containing a relationship of this form (Table 2). Other common edge types join Biological Processes with Disease, and Proteins with Biological Processes.

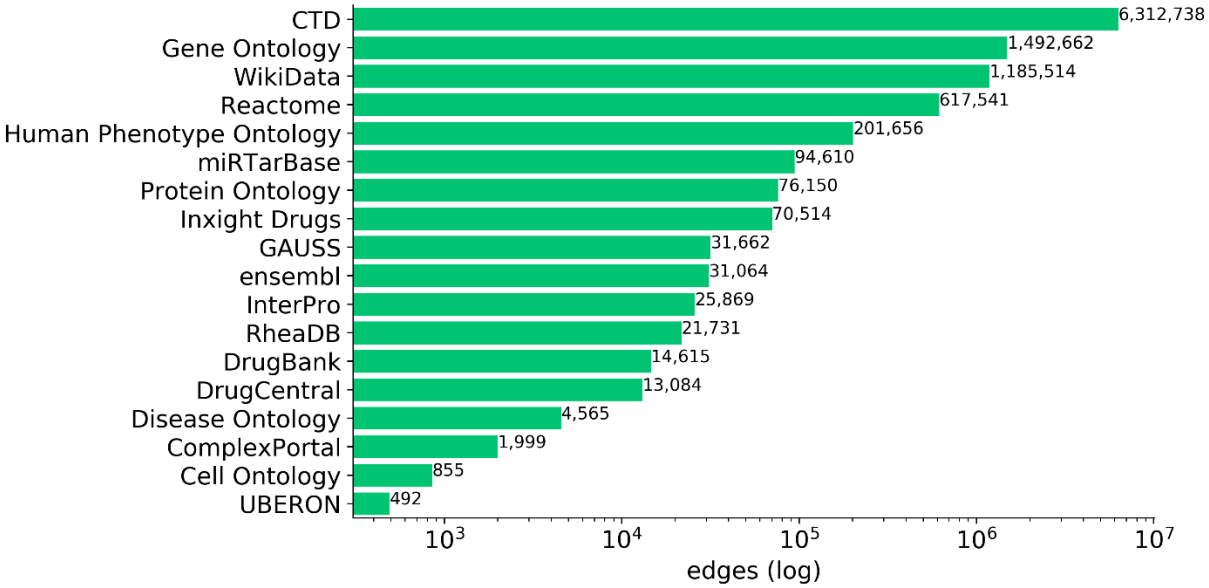
Table 2: **Counts of top relationship types in DrugMechDB.** The most common pairings of concepts found in DrugMechDB and the different relationships that connect them. Whether or not these concepts are expressed in MechReopNet is noted, with "Similar" meaning either different semantics are used with similar meaning (e.g. "Down Regulates" instead of "Inhibits"), or that relationship exists, but something about it is fundamentally different (e.g. Protein Regulates Protein relationships without specific up or down directionality). MRN = MechRepoNet.

Concepts	Relationship	Count	Total	In MRN	Count in MRN
Drug - Protein	INHIBITS	67	94	Yes	416,972
	ACTIVATES	24		Yes	472,948
	INCREASES EXPRESSION	2		Similar	-
	DECREASES EXPRESSION	1		Similar	-
Biological Process - Disease	CAUSES	29	63	No	-
	DISRUPTED IN	11		No	-
	ELEVATED IN	11		No	-
	ASSOCIATED WITH	7		Yes	2,052,856
	REDUCES	5		No	
Protein - Biological Process	INVOLVED IN	38	61	Yes	529,389
	UP REGULATES	14		Yes	22,259
	DOWN REGULATES	7		Yes	16,290
	ACTIVATED BY	1		No	-
	REGULATES	1		Yes	57,329
Taxon - Disease	CAUSES	26	26	Yes	69,058
Biological Process - Taxon	REQUIRED FOR	24	25	Similar	635,544
	REDUCES	1		No	-
Protein - Protein	DOWN REGULATES	9	16	Yes	8,706
	UP REGULATES	7		Yes	4,270
Compound - Biological Process	PART OF	8	12	Yes	48,991
	DOWN REGULATES	3		Yes	39,706
	UP REGULATES	1		Yes	38,936
Protein - Compound Class	PRODUCES	9	9	No	-
Protein - Compound	PRODUCES	5	9	Similar	1,080
	REDUCES	3		Similar	506
	ACTIVATED BY	1		Yes	472,948

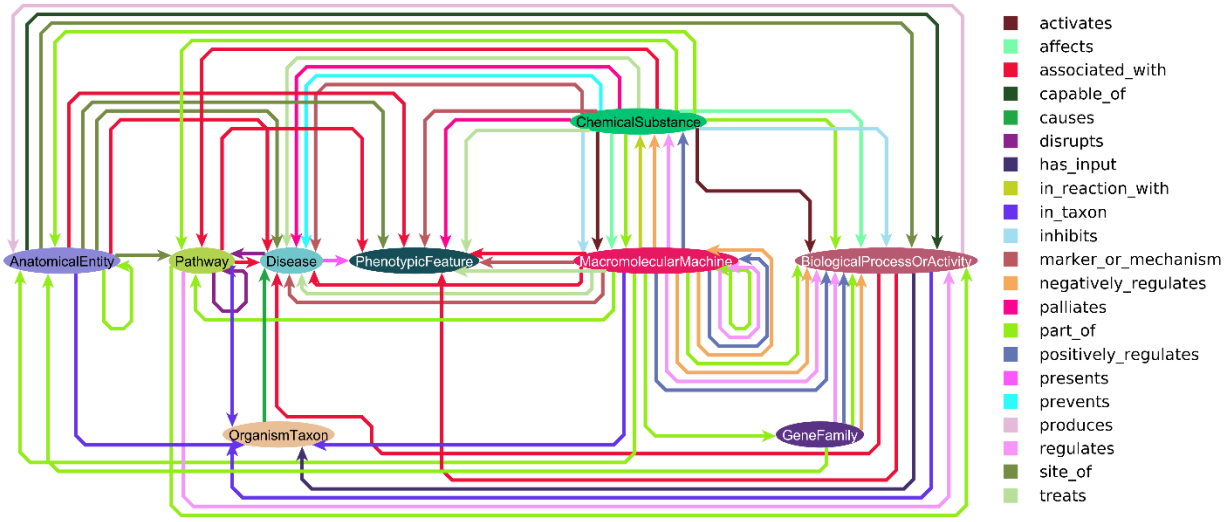
Building a network to express drug mechanisms: MechRepoNet

Based on the analysis of mechanistic paths in DrugMechDB, we integrated 18 publicly available data sources to produce a new mechanistic repositioning heterogeneous network (MechRepoNet) (Figure 2a). MechRepoNet contains 250,035 concepts of 9 different semantic types, and 9,652,116 unique edges of 68 semantic types (Figure 2b). The majority of concepts in MechRepoNet are classified as MacromolecularMachine, which includes Genes, Proteins, RNA Products, and Complexes (Table 3). The most common edge type connects a BiologicalProcessOrActivity to a Disease through a general association, with 2,052,856 examples, representing 21.3% of the edges in MechRepoNet (Table 2).

While MechRepoNet contains many of the concept types found in DrugMechDB, there are a few differences (Table 3). Most notably, we normalized concept types to the biolink data model, a standardized hierarchy of biomedical entity classes, to increase interoperability between data sources (Mungall *et al.*, 2020). Relationships in MechRepoNet were mapped to a flat list of interaction types (Table 4). In general, the relationships in DrugMechDB are more specific than those in MechRepoNet, primarily because data sources use imprecise semantics when describing relationships.



(a) Edges by data source in MechRepoNet



(b) MechRepoNet data model

Figure 2: **Data within MechRepoNet.** (a) The number of edges provided by each data source integrated into MechRepoNet. (b) A graphic representation of the MechRepoNet data model.

Table 3: **Concept types in MechRepoNet**

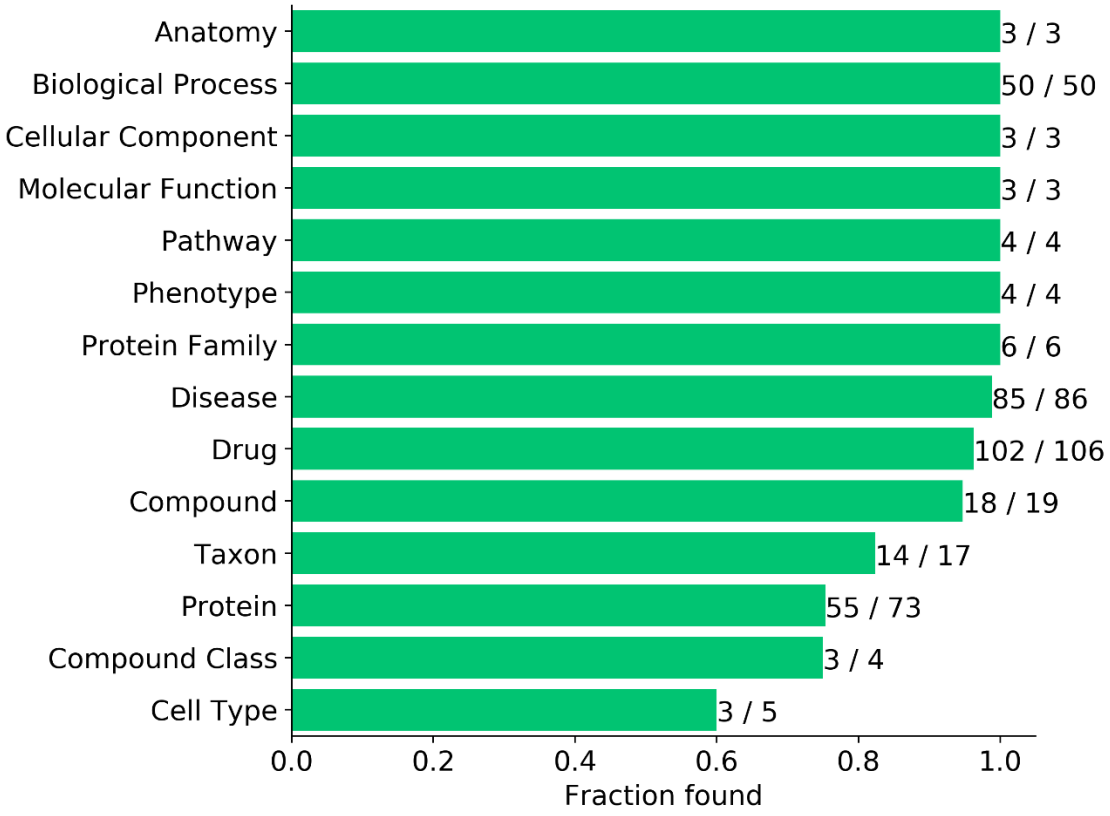
Node type	Abbreviation	Identifier Sources	Count
AnatomicalEntity	A	GO, UBERON, CL	3,580
BiologicalProcessOrActivity	BP	GO	21,065
ChemicalSubstance	C	CHEBI, IKEY, MESH, UNII, PCID, CHEMBL, WD, DB	40,766
Disease	D	DOID, MESH, MONDO, OMIM, WD, UMLS	13,961
GeneFamily	GF	InterPro	10,807
MacromolecularMachine	G	NCBIGene, WD, UniProt, RNAC, REACT, CPX, ENSG, PR	136,991
OrganismTaxon	T	NCBITaxon, WD	12,074
Pathway	PW	REACT, WP, KEGG, WD	5,363
PhenotypicFeature	P	HP, WD, MESH, OMIM	5,428

Table 4: **Relationship types in MechRepoNet**

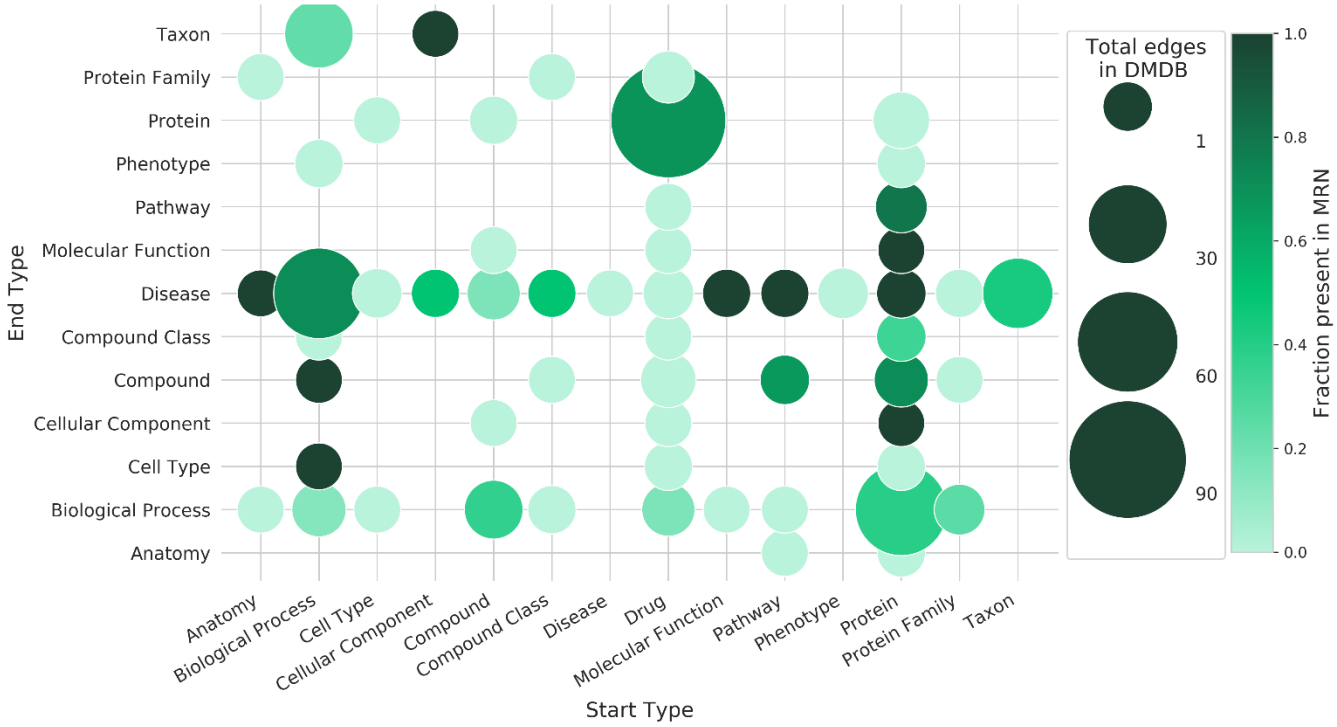
Relationship type	Abbreviation	Count
activates	a	511,884
affects	af	986,843
associated_with	aw	4,488,453
capable_of	co	513
causes	co	69,058
disrupts	d	541
has_input	hi	10,905
in_reaction_with	rx	152,741
in_taxon	it	1,208,845
inhibits	in	456,678
marker_or_mechanism	m	64,300
negatively_regulates	nr	21,439
palliates	pl	2,519
part_of	po	1,252,343
positively_regulates	pr	32,319

presents	ps	66,965
prevents	pv	1,318
produces	p	1,008
regulates	rx	215,855
site_of	so	31,791
treats	t	75,798

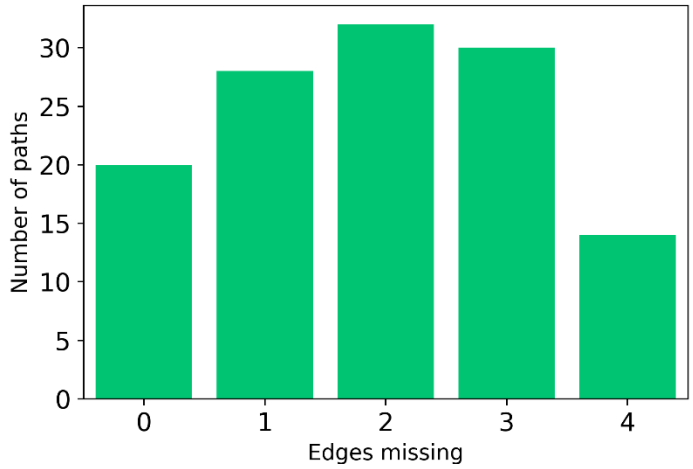
We next examined the degree to which DrugMechDB paths could be found within MechRepoNet. We found that 92.2% of the 383 unique concepts in DrugMechDB are also contained within MechRepoNet (Figure 3a). The majority of the missing concepts belong are either proteins from infectious taxa, or the taxa themselves (Supplemental Table S1). Evaluating relationships as simple edges (ignoring edge predicates), we found that 167, or 45% of the 369 unique node parings found in DrugMechDB are also contained with MechRepoNet (additional details in Figure 3b). Of the 202 missing pairings, 58 are due to one or both concepts not being present, whereas the other 144 have both concepts present, but the connection between them is absent. Finally, when examining full paths from DrugMechDB, we find that 21 are fully expressed in MechRepoNet and another 27 only have one edge missing (Figure 3c), indicating that 37% of the DrugMechDB paths could be analyzed in MechRepoNet with only minor changes to these paths.



(a) Nodes found by type



(b) Edges found by type



(c) Edges missing per path

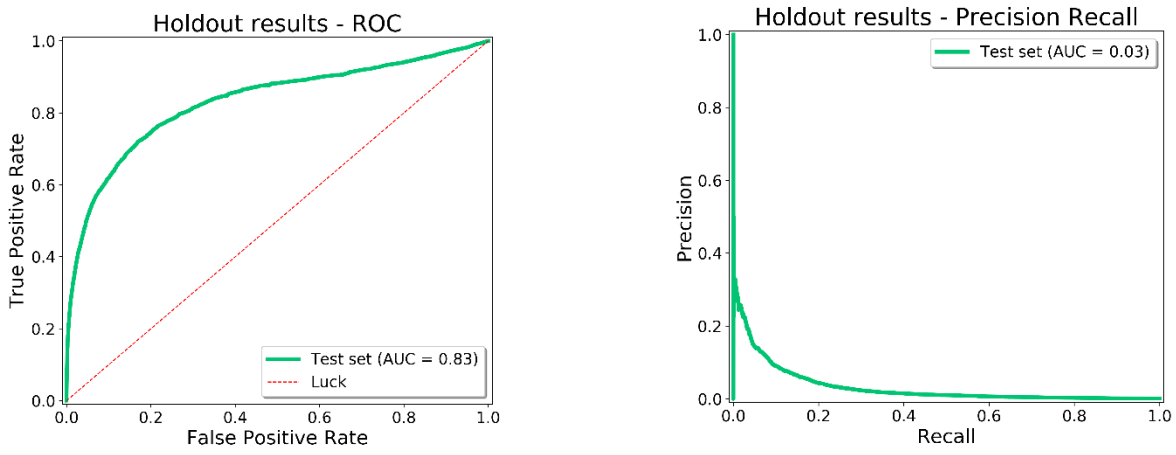
Figure 3: **Comparison of concepts, edges and paths found in DrugMechDB and MechRepoNet.** (a) Number of unique concepts in DrugMechDB, represented in MechRepoNet by type. (b) Analysis of edges in DrugMechDB and comparison to MechRepoNet. Bubble size is proportional to the number of edges in DrugMechDB, and darker bubbles indicate greater percentage overlap between DrugMechDB and MechRepoNet. (c) Number of paths with 0 to 5 edges missing from MechRepoNet for each of the 123 DrugMechDB paths.

Metapaths for feature extraction

MechRepoNet contains 17,277 unique metapaths of length 2, 3, and for between a ChemicalSubstance and a Disease. Removing those that express compound-compound or disease-disease similarity (see Methods) resulted in 8,284 remaining metapaths. Even though these metapaths may exist within the data model of a network, it is not guaranteed that there are paths within the network that follow that metapath structure. Of the 8,284 mechanistic metapaths, 7,012 (84.6%), were found to be present in MechRepoNet. A feature selection voting scheme (see Methods) filtered this list down to 105 metapaths. After adding the 55 metapaths found in DrugMechDB, we ended up with a final set of 160 metapaths to use as features for training our learning model.

Learning model results

The model performed well on the validation set with an ROC AUC of 0.83 (Figure 4a). The precision recall AUC of was much lower at 0.03, which is expected in a complicated task with imbalanced classes (Figure 4b). Of the 160 features used to train the model, 89 were assigned positive coefficient values by the regression model, making their associated metapaths meaningful in the mechanistic descriptions of the prediction. From the 55 DrugMechDB metapaths, 27 were selected by the model with positive coefficients (Table 5). The selected features contained all of the graph's 9 node types, with MacromolecularMachine nodes appearing most frequently after ChemicalSubstance and Disease nodes which are guaranteed to be present in every metapath (Figure 5).



(a) ROC - Holdout sets

(b) Precision recall - Holdout set

Figure 4: **MechRepoNet model validation performance** Model's performance on holdout set of 20% of indications (a) ROC & (b) precision recall. The blue line is the model and the red abscissa denotes a coin flip.

Metapath	Coefficient
CinGpoPWawD	1.449461
CinGpoBPitTcD	1.147065
CinBPawD	1.106648
CinBPitTcD	0.895034
CinGmPpsD	0.806721
CinGrxCmD	0.610118
CinGmD	0.608036
CinGpoBPawD	0.548079
CinGnr>GnrBPawD	0.515218
CaGnr>GprBPawD	0.505722
CaBPawD	0.37717
CaGnr>GrxCmD	0.28347
CaGprBPpAsoD	0.245871
CinGawD	0.220636
CafGitTitBPawD	0.197495

CafGitThiBPawD	0.192309
CinGpoAawD	0.191279
CaGnrBPpoCmD	0.180797
CaGpoBPawD	0.175543
CinGpoBPawPpsD	0.173977
CaGnr>GpoBPawD	0.167894
CinGrxCpoBPawD	0.149697
CinGrxCinGawD	0.109253
CafGpoAcoBPawD	0.10243
CinGpr>GpoAawD	0.086991
CinGawPpsD	0.040159
CinGpoApoGtD	0.000009

Table 5: **Positive model coefficients for DrugMechDB metapaths.** This table contains all of the metapaths that were assigned positive coefficients by the logistic regression as well as the coefficient value. Node abbreviations are in capital letters, annd relationship abbreviations are in lower case. Node abbreviations are capitalized while edge abbreviations are lower case. See Tables 3 and 4 for node and edge abbreviations. For example, the 'CinGpoPWawD' indicates a metapath corresponding to ChemicalSubstance -inhibits- MacromolecularMachine -part of- Pathway -associated with- Disease.

Ranking known mechanistic paths

The 21 full paths from DrugMechDB that were found within MechRepoNet were utilized to evaluate the model's ability to rank mechanistic paths. From these paths, 12 had a metapath structure that had been assigned a positive coefficient by the model and thus could be used to evaluate their rankings compared to other metapaths. After ranking paths according to their model metric, we see that for all examples except one, the mechanistic path ends up in the 90th percentile of all paths (Table 6). In some cases, these rankings may be high enough to quickly support a repurposing prediction, but in others there are still hundreds or thousands of paths ranked above the mechanistic path in DrugMechDB, making the mechanistic path unlikely to be discovered. For this reason, several filtering strategies can be employed to enrich for these paths.

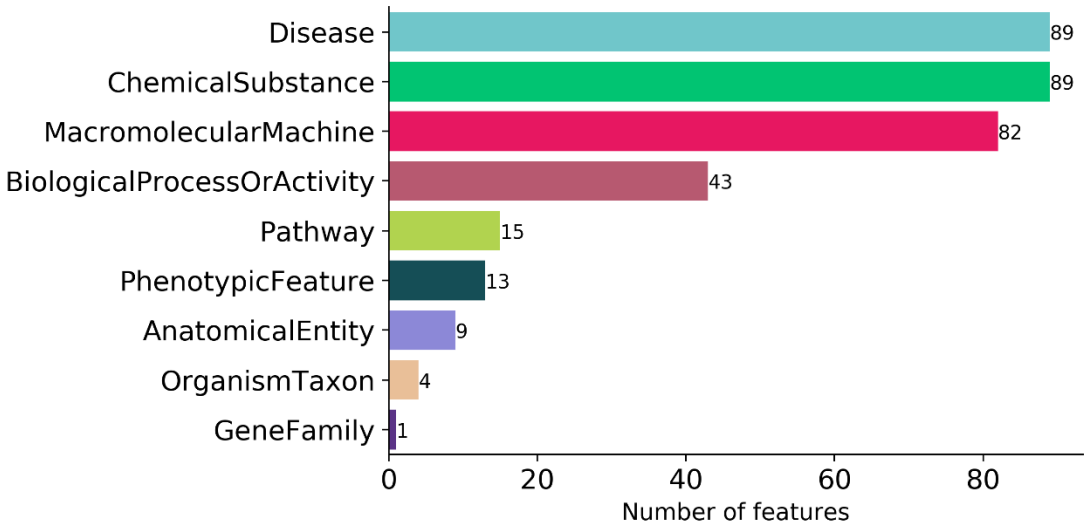


Figure 5: **Feature selected concepts.** Number of selected features passing through each concept type.

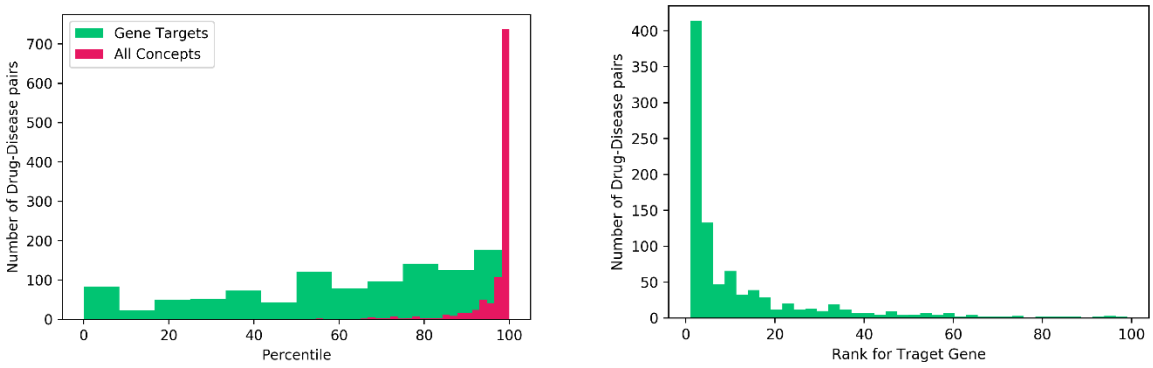
Drug	Disease	Paths	DMDB Path Rank	Path Percentile	Drug's Target	Paths through Target	DMDB Target Path Rank	Target Path Percentile	Metapath
imatinib methanesulfonate	chronic myeloid leukemia	1,236,778	23	99.99%	ABL1	1,165	1	99.91%	CafGmD
Terguride	pulmonary hypertension	16,523	1	99.99%	HTR2B	1,104	1	99.91%	CafGmD
Glutethimide	Insomnia	88,253	197	99.78%	GABRA1	143	10	93.01%	CafGpoBPawD
mosapramine	schizophrenia	4,410	15	99.66%	DRD2	1,792	5	99.72%	CinGpoPWawD
Etizolam	anxiety disorder	42,582	210	99.51%	GABRA1	280	28	90.00%	CafGpoBPawD
Vinpocetine	dementia	291,650	2,612	99.10%	PDE1A	134	21	84.33%	CinGpoAawD
(R)-duloxetine	major depressive disorder	36,692	458	98.75%	SLC6A4	243	39	83.95%	CafGpoBPawD
landiolol	atrial fibrillation	1,218	25	97.95%	ADRB1	1,005	21	97.91%	CafGpoBPawD
metolazone	hypertension	13,044	296	97.73%	SLC12A3	646	74	88.54%	CinGpoBPawD
(R,R)-tramadol	Pain	172,613	6,822	96.05%	OPRM1	951	290	69.51%	CafGpoBPawD
gepirone	major depressive disorder	603	34	94.36%	HTR1A	304	24	92.11%	CafGpoBPawD
Trimethadione	absence epilepsy	409	244	40.34%	CACNA1G	141	83	41.13%	CafGpoBPawD

Table 6: **DrugMechDB paths as ranked by the repurposing model.** DrugMechDB paths found in MechRepoNet and their rankings among all paths between the drug disease pair of an indication. Rankings of subset paths through the drug's known mechanistic target are also examined (DMDB stands for DrugMechDB).

The most basic filtering strategy is to filter by known drug targets. Most drugs have only a small number of known targets, so filtering this way is fairly straightforward. When filtering these paths by the known mechanistic targets, 9 of the 12 examples are in the top 50 paths, with 4 of 12 in the top 10 paths, making them easy for an expert to identify from the total list of paths (Table 6). The high rankings of the mechanistic paths that pass through known drug targets means that a drugs mechanism for an unknown disease could potentially be found if known targets are used as a filtration step. However, when a true mechanistic target for a drug is not known this result could also be used to identify candidate targets.

Concept weighting to identify drug targets

The weightings used to rank paths from a drug to a disease can also be used to determine the importance of any single concept connecting them by summing the weights of all the paths containing a given concept. This method could have utility in prioritizing the target of a drug in the treatment of a disease. To evaluate this method, a set 1,124 of known drug-target-disease triples were curated from DrugCentral and compared to either all concepts or only the subset of gene targets, in the paths that connect the drug-disease pair. Examining the percentile rank of known mechanistic targets against all other concepts, the majority of the known targets ranked in the 90th percentile (Figure 6a). When limiting the comparison to only other gene targets, the percentile rank for the known target was less favorable, producing a distribution that approaches uniform (Figure 6a). However, as some drugs only have a very limited number of potential targets, the absolute ranking of the known target may be informative. Examining the absolute rank of mechanistic targets, when compared to all potential target genes, found 944 of the 1,124 in the top 100, and 637 of those in the top 10 (Figure 6b). The mean reciprocal rank of the known targets, when taking only the highest ranked target for a given drug-disease pair, was found to be 0.525.



(a) Percentile rank of known targets (b) Absolute ranking of known targets

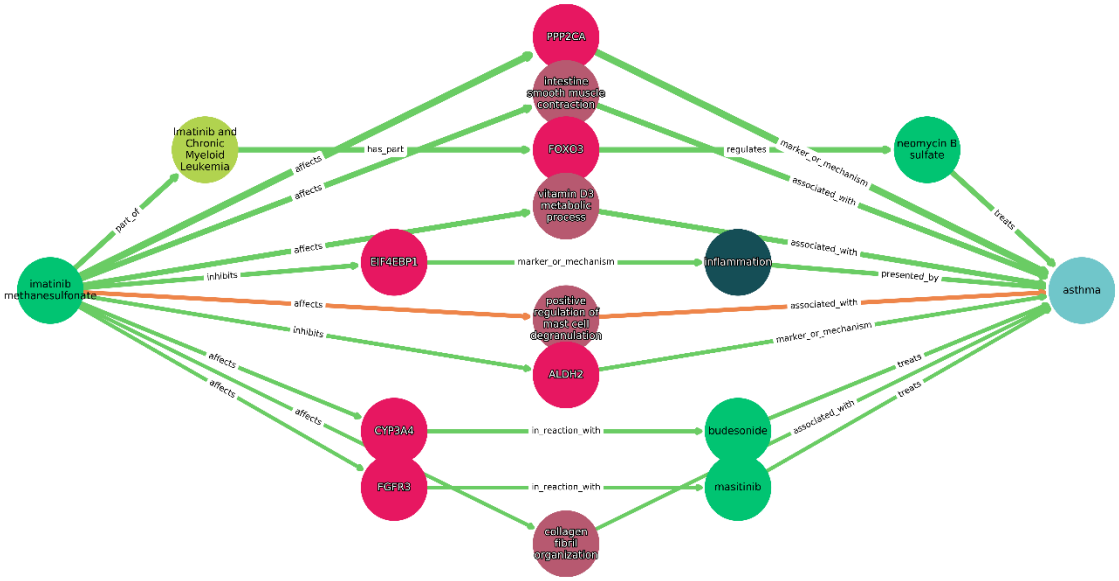
Figure 6: **Known target ranking results** (a) Percentile rank of known mechanistic targets of a drug as compared to either all concepts connecting a drug and disease, or only potential gene targets connecting the two. (b) Absolute rank of known mechanistic targets of a drug when compared to other potential gene targets of the drug.

Case Study: Explaining the link from imatinib to asthma

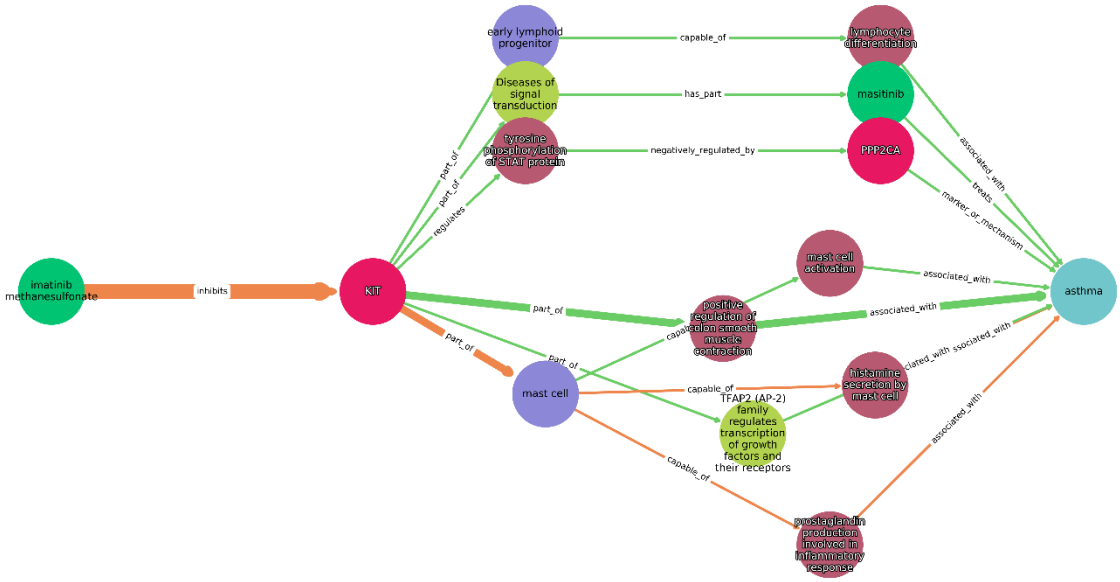
In 2017 Cahill *et al*. reported that imatinib, a tyrosine kinase inhibitor used to treat chronic myelogenous leukemia, could potentially be repositioned to treat asthma, with promising preliminary results (Cahill *et al.*, 2017). We wanted to determine whether the MechRepoNet model was capable of both predicting and explaining this potential repositioning result. The probability of treatment returned by the model for imatinib to asthma was 0.143. However, probability in this sense does not have a lot of meaning, and ranking is much more important. The ranking of the imatinib to asthma indication, compared the over 90 million potential drug-disease combinations, was in the top 250,000 putting it squarely in the 99.7th percentile. In terms of the drug and disease specific percentiles, imatinib was ranked 581 of 14,804 drugs, putting it in the 95th percentile of treatments for asthma, and asthma was ranked 143 of 6,481 diseases, or in the 97th percentile of indications for imatinib.

Simply looking at the model's top 10 paths that connect imatinib and asthma does not immediately reveal why imatinib could treat asthma. However, one path passes through the compound masitinib, and this compound is stated as treating asthma (Figure 7a). Masitinib is also

a tyrosine kinase inhibitor that has been shown to have some effect on reducing asthma symptoms (Humbert *et al.*, 2009). As both imatinib and masitinib are tyrosine kinase inhibitors, examining their common targets yields cKIT, a proto-oncogene that plays a role in acute myeloid leukemia (Gari *et al.*, 1999; Edling and Hallberg, 2007). Filtering on cKIT, we find that in the top 10 paths, three paths that pass the concept mast cell leading to biological processes associated with asthma mast cell activation, histamine secretion by mast cell, and prostaglandin production involved in inflammatory response (Figure 7b). The role of the mast cell in the pathophysiology of asthma is well established and inhibiting activation of these cells could be one plausible mechanism for imatinib's efficacy (Bradding *et al.*, 2006; Amin, 2012). Reexamining the top 10 paths irrespective of target yields a path through "mast cell degranulation" where imatinib purported to affect this process. Combining the results from these two sets of paths (Figures 8a & 8b) yields a more general and equally plausible mechanism, where cKIT inhibition by imatinib, prevents cKIT's function in mast cell activation and degranulation, which in turn promotes asthma. This mechanism found through examining the top weighted paths in MechRepoNet is highly consistent with that proposed by Cahill *et al*. (2017).



(a) Top 10 paths selected by the model



(b) Top 10 paths that go through the target KIT

Figure 7: **Top weighted paths from imatinib to asthma** The paths with the 10 largest weights connecting imatinib and asthma either (a) overall or (b) through cKIT. Paths mentioned in the text have been highlighted in orange.

Discussion

Arguably more important than the percentile of the probability for any individual indications is the reasoning behind a prediction. The reasoning chain provides a human interpretable explanation as to what mechanisms could be at play when producing a repurposing prediction. Guided by a mechanistic prediction, a domain expert would be better able to assess a prediction's evidence than just the model's probability result alone, and even guide further experimental validation of the hypothesis. If our goal were to produce the absolute best classifier for drug repositioning with maximized evaluation metrics, a model that includes the much more predictive similarity metapaths, or possibly a more abstract deep learning model would have been preferable. However, this weaker predictor, being entirely based on paths with mechanistic meaning, provides a level of human interpretability not otherwise present.

Our method outlined in this work is not only able to rank potential repurposing candidates, but provide important biological context to the results. Each path identified through this method consists of relationships from multiple sources, joined together through common concepts. The data sources selected for integration individually have a high level of curation and therefore contain extensive knowledge regarding individual drugs and diseases. However, the large amount of data produces numerous multi-step paths from any single drug to a disease. Through well-engineered features derived from true drug mechanisms, our repurposing model is able to identify the patterns in this data most likely to be important in a treatment context. Our case study identified informative paths that potentially warrant follow-up experimentation and further research. In these paths, every link represents a testable hypothesis that can be verified through experimentation, or some new potential avenue of treatment that can be explored. These predictive models can aid in research by providing new hypotheses about a drug's connections to a disease. Finally, our method is generalizable and could be applied to other applications such as to predict drug-phenotype or drug-physiological process pairs and its mechanistic rationalization for personalized medicine.

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