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THE DRUG COST DEBATE AT A GLANCE



The amount
Americans spent
on prescription
drugs in 2015,
up by about 8
percent over the
previous year

200/0
The rise in prices for the most popular brandname drugs from 2008 to 2016

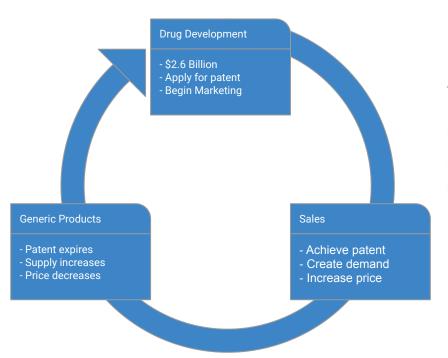
\$14.5 MILLION

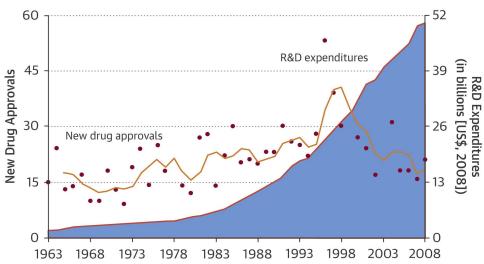
Median salary of a pharmaceutical firm CEO in 2015, more than any other industry \$6.4 BILLION

Amount drug companies spend advertising directly to consumers in the U.S. annually **\$24** Billion

Amount drug companies spend per year marketing to doctors

Motivation





Data

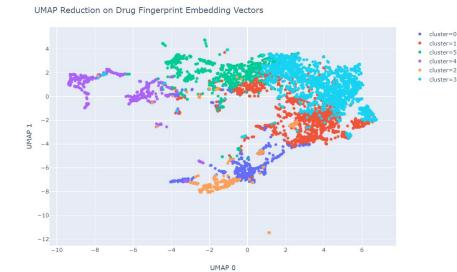
- DrugBank: Drug-target interaction data
 - 6,835 drugs and 4,217 targets
- PubChem: retrieve SMILES (molecular structure in machine readable strings)



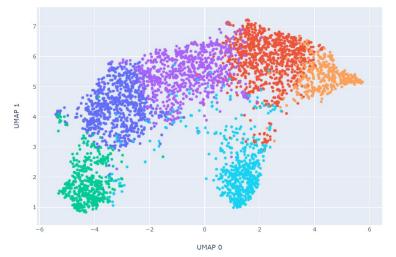
Embeddings for Model Inputs

- Word2Vec for drug fingerprints
- Fasttext for target gene sequences

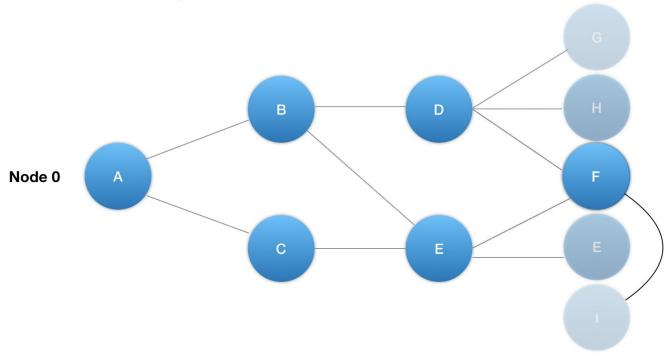




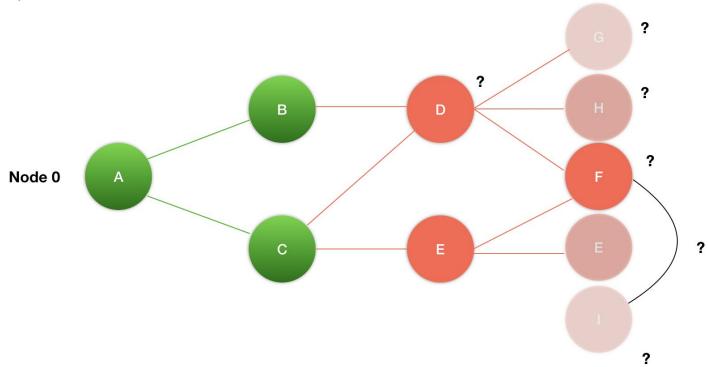




Negative Samples

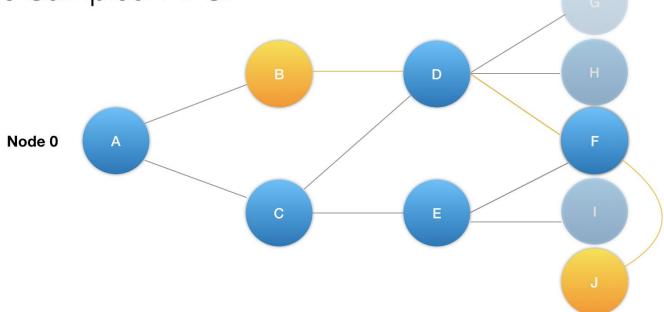


Negative Samples: Problem Statement

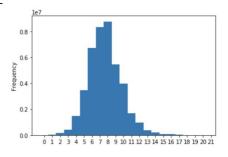


- If we consider all edges, not directly connected, to be negative, we risk overfitting the model
- Hypothesis is that we haven't yet discovered all edges (Drug target interactions)
- Therefore, negative samples must only be edges that we are absolutely certain aren't connected.

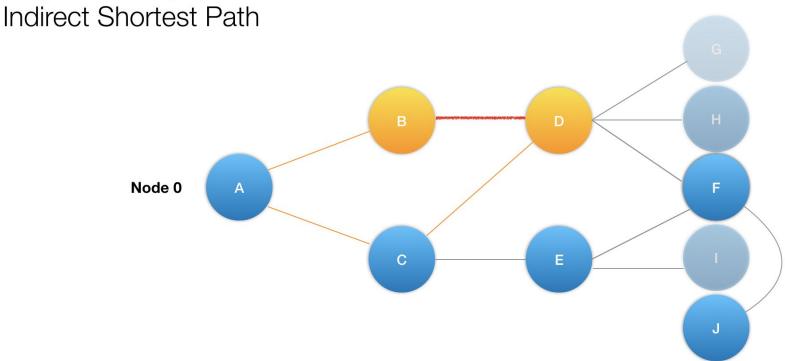




Edge	Shortest Path
A - E	2
B - J	3

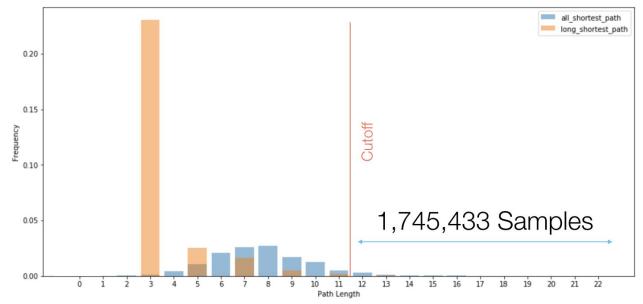


Negative Samples:



- Deleting edge B E, increased its distance to 3
- This is an indication of what the path length of a undiscovered edge might look like

Negative Samples: Comparing Distributions & Takeaways



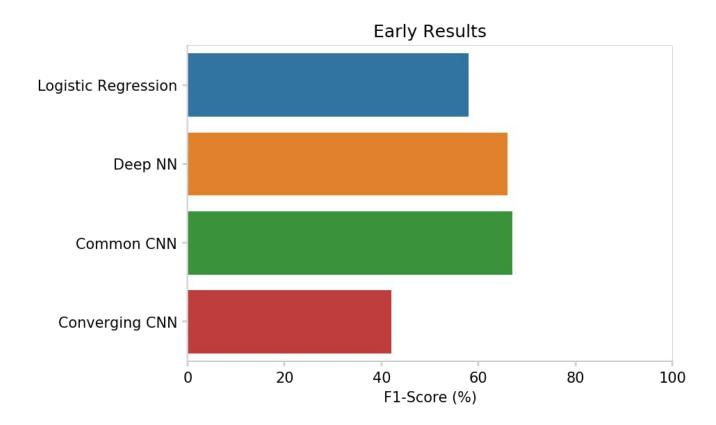
- Most shortest path have a distance of 3
- Most indirect shortest paths have a distance of 8
- There are no indirect shortest paths longer than 11

Therefore, our assumption: Beyond a distance of 12, there is no evidence of an actual interaction

Early Model Results

- Deep Neural Networks: 3 Models that we want to try inspired from WideDTA deep learning model. (https://arxiv.org/abs/1902.04166)
 - Deep Learning Model.
 - Convoluting Drug and Target Together before giving it to Dense Network.
 - Convoluting Drug and Target separate before giving it to Dense Network.

Early Model Results



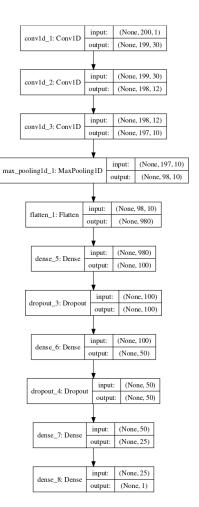
Dense Model Structure

(None, 200) input: dense_1: Dense (None, 100) output: (None, 100) input: dropout_1: Dropout (None, 100) output: (None, 100) input: dense_2: Dense (None, 50) output: (None, 50) input: dropout_2: Dropout (None, 50) output: (None, 50) input: dense_3: Dense (None, 25) output: (None, 25) input: dense_4: Dense

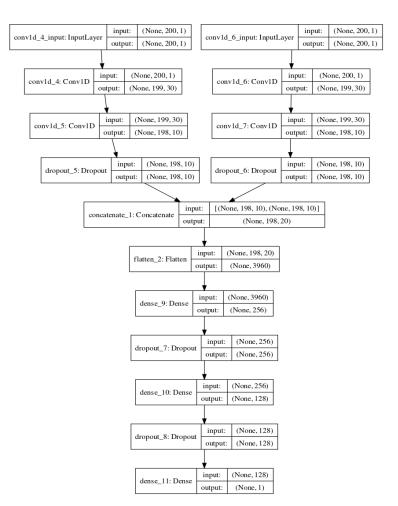
(None, 1)

output:

CNN Model Structure

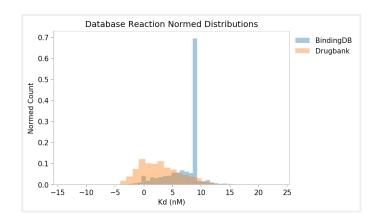


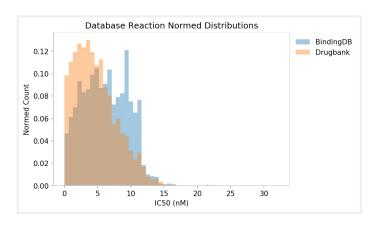
Drug-Target CNN Model Structure

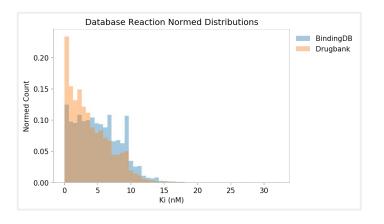


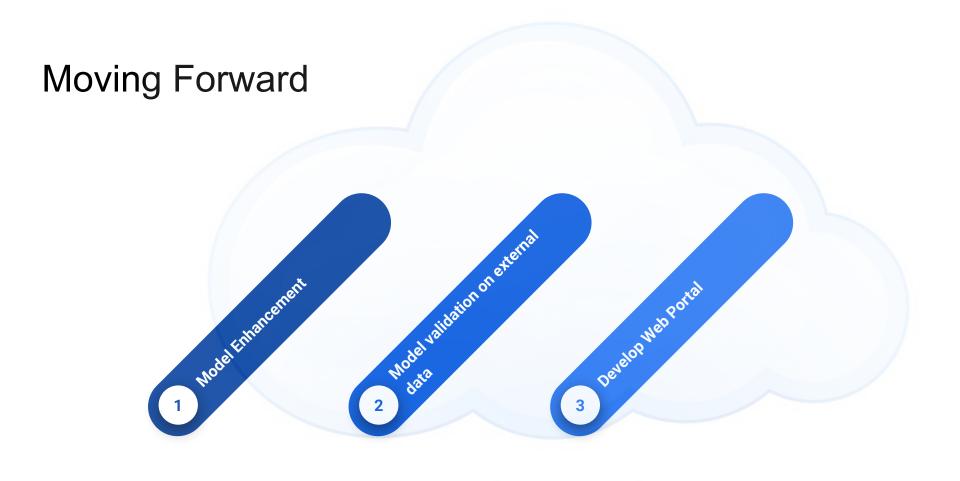
Validation Data

- Different distributions between Drugbank drugs and other chemicals
- 13,336 / 65,472 positive samples if threshold set to 5 log Kd (nM)











Citations

https://www.aarp.org/health/drugs-supplements/info-2017/rx-prescription-drug-pricing.html





			Ab	
			Abarelix DECOTORS CCC(C)CCC(C)-CO)NC(CCCCNC(C)C(C)-C)NC(C)-C)N(NC(C)-C)N(NC(C)-C)N(NC(C)-C)N(NC(C)-C)C(C)-C)C(C)C(C)C(C)C(C)C(C)C(C)C(
	Probability	Result	Abequose DB02890	
	0.7511017918586731	1	CCIC(CC(0)10)0)O	
	0.7453667521476746	1	Abiraterone DB05812	
	0.7343770861625671	1	CC12CCC(CC1+CCC3C2CCC4(C3CC+C4C5+CN+CC+C5)C)O	
	0.719296395778656	1	Abexinostat	
	0.7029346823692322	1	DB12565 CN(C)CC1=C(0C2=CC=CC21)C(=0)NCCCC3=CC=C(C=C3)C(=0)NO	
	0.6986517310142517	1	N. C.	
	0.6979426741600037	1	Abaloparatide DB05084	
	0.6967849135398865	1	CCCC(C)C(2=0)NC(C=0)NC(C=0)NC(C=0)NC(C=0)NC(CC(C)C)C(=0)NC(CCCNC(=N)NC(C=0)NC(CCCNC(=N)NC(=0)NC(CCCNC(=N)NC(=0)NC(CCCNC(=N)NC(C=0)NC(CCC)C)C(=0)NC(CCC)C(C)C(=0)NC(CCC)C(C)C(=0)NC(CCC)C(C)C(C)C(C)C(C)C(C)C(C)C(C)C(C)	
	0.696169376373291	1	Abelson tyrosine-protein kinase 2 BE0000435	
	0.6901637315750122	1	>icil 85E00021263 Abelson tyrosine-protein kinase 2 (ABL2) ATGGTCCTTGGGACAGTTCTCCTTCACCTTATAGTTATGGCAGAGATCAGGACACTTCA CTTTGCTGCCTGTGCACTGAGGCCTCAGAATCTGCTCTCACCGACTTAACAGATCACTTT GCCAGCTGTGTGGAGGATGGATTTGAGGGAG	