

COMPUTATIONAL DRUG REPOSITIONING USING KNOWLEDGE GRAPH AND AI

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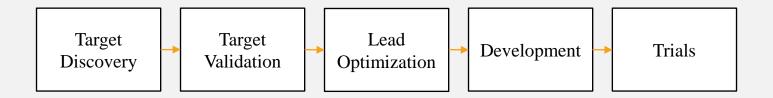
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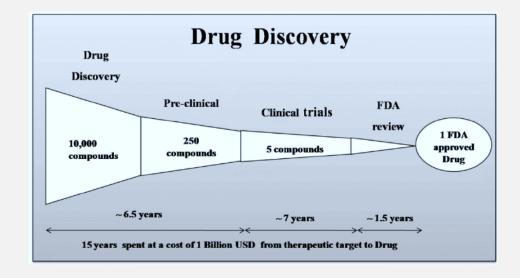


- What is Drug Discovery?
 - O Drug discovery is the process by which new medications are identified and developed.
- What are stages of drug discovery?
 - Identification of a target
 - Lead compound development
 - O Preclinical and clinical testing





- Limitations of Drug discovery
 - Costly and lengthy process.
 - Four to five main stages.



This is where "Drug Repurposing" is helping



- Areas where Computer Science can contribute?
 - Suggesting candidate drugs.
 - Risk Assessment done by FDA.
 - O Dose-Response Analysis can be helped through data science.

• The research paper aims to contribute by identifying existing drugs that could potentially be repurposed for the treatment of other diseases.



- Which tools can be used in perform the above task?
 - Clustering and Classification Algorithms
 - Meticulous analysis and pattern recognition by grouping similar compounds and predicting their efficacy efficiently identify potential drug candidates
 - Undergone extensive research and has reached a saturation point.
 - Regression Analysis
 - Modeling relationships between variables aid in predicting drug effectiveness but not efficient in suggesting candidate drugs.
 - Cornerstone in the realm of drug discovery
 - Deep Learning
 - Forefront of drug discovery research offering immense promise.
 - Our base paper also focuses here.

MOTIVATION

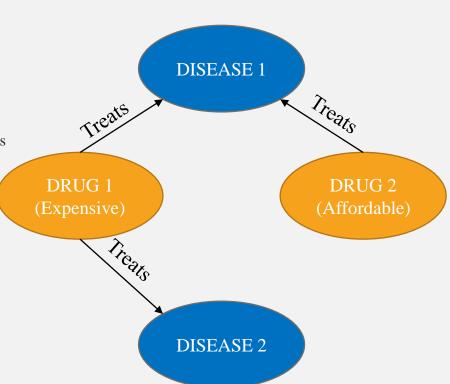






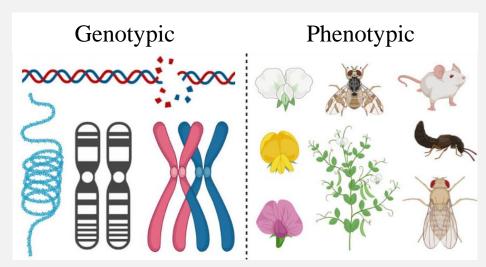
- Knowledge Graph
 - Represents a network of real-world entities
 - Also known as a semantic network
 - Typically made up of datasets from various sources

Our base paper leverages Knowledge Graph technology to facilitate the process of drug repositioning.





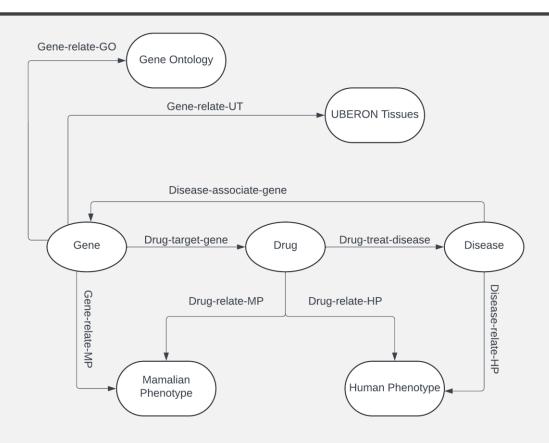
- What is Genotypic and Phenotypic?
 - Genotypic genes are responsible for unique traits or characteristics.
 - O Phenotypic genes are responsible for physical appearance or characteristic of an organism.





- Knowledge Graph Construction
 - O 61,146 nodes with 7 node types
 - o 1,246,726 edges
 - Categorized into 9 semantic relationships
 - 2 from genome-level knowledge databases
 - 1 from text-mined knowledge bases
 - 6 from phenome-level knowledge databases





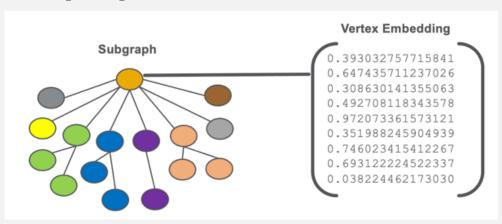


• Traditional machine learning or deep learning algorithms typically operate on fixed-size vectors or matrices.

• How to convert this complex graph into a simpler representation while

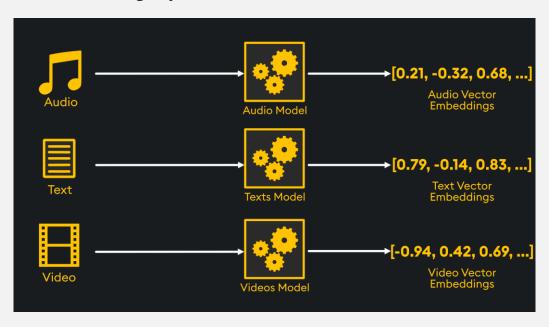
preserving important information?

Graph Embedding - Embeddings encode objects or concepts in a continuous vector space.





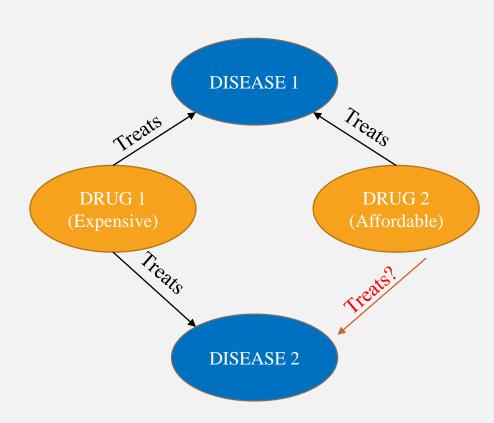
• What do these Numbers Signify?



KNOWLEDGE GRAPH COMPLETION



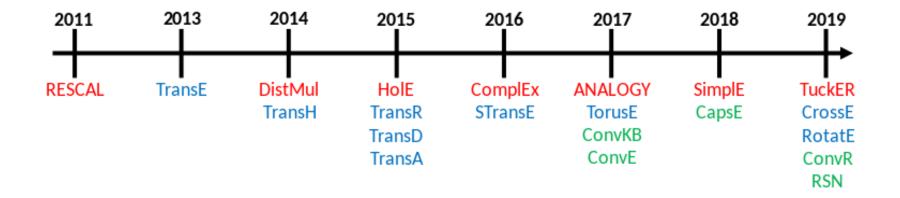
- Given an enormous KG, can we complete the KG?
 - For a given (head, relation), we predict missing tails.
- The graph should contain multiple types of relationships otherwise, you can use the standard link prediction techniques.
- This graph could also include the origin of drugs and the relationship between them.



KG REPRESENTATION



- Edges in KG are represented as triples (h, r, t)
 - \circ head (h) has relation (r) with tail (t)
- Associate entities and relations with shallow embeddings
- Given a triple (h, r, t) the goal is that the embedding of (h, r) should be close to the embedding of t.
 - How to embed (h, r)?
 - How to define score $f_r(h, t)$?
 - \circ Score f_r is high if (h, r, t) exists, else f_r is low



KG EMBEDDING MODELS



- We started looking into pre-existing state of arts model involving different embeddings.
 - o TransE
 - Given by- A. Bordes, N. Usunier, A. Garcia-Duran, J. Weston and O. Yakhnenko.
 - RotatE
 - Given by- Z. Sun, Z.H. Deng, J.Y. Nie and J. Tang.
 - o DistMult
 - Given by- B. Yang, W.T. Yih, X. He, J. Gao and L. Deng

FOUR RELATION PATTERNS



- Symmetric (Antisymmetric) Relations:
 - \circ $r(h,t) \Rightarrow r(t,h)$ and $r(h,t) \Rightarrow \neg r(t,h) \ \forall h,t$
 - Example:
 - Symmetric Family, Roommate
 - Antisymmetric Hypernym (colour and red)
- Inverse Relations:
 - \circ $r_1(h,t) \Rightarrow r_2(t,h)$
 - Example: Advisor and Advisee

FOUR RELATION PATTERNS



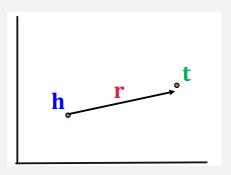
- Composition (Transitive) Relations:
 - $\circ r_1(x,y) \& r_2(y,z) \Rightarrow r_3(x,z) \forall x,y,z$
 - Example: My mother's husband is my father.
- 1-to-N Relations:
 - \circ $r(h, t_1)$, $r(h, t_2)$, ..., $r(h, t_n)$ are all true.
 - Example: *r* is the '*student_of*'

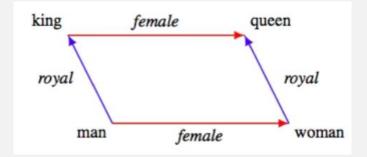
TransE



- Translation:
 - For a triple (h, r, t), let $h, r, t \in \mathbb{R}^d$ be embedding vectors.
 - if the given link exists $h + r \approx t$
 - \blacksquare else $h + r \neq t$

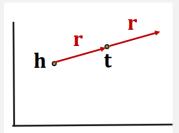
• Entity scoring function: $f_r(h, t) = -||h + r - t||$





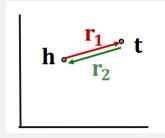
TransE





Antisymmetric: $r(h, t) \Rightarrow \neg r(t, h)$

$$h + r = t but t + r \neq h$$

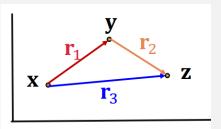


Inverse:

$$r_1(h,t) \Rightarrow r_2(t,h)$$

 $h + r_2 = t$ and we can set

$$r_1 = -r_2$$



Composition:

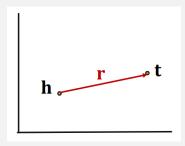
$$r_1(x,y) \& r_2(y,z)$$

 $\Rightarrow r_3(x,z) \quad \forall x,y,z$

$$r_1 + r_2 = r_3$$

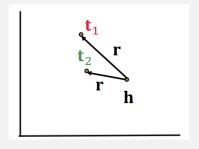
TransE - Limitation





Symmetric: $r(h,t) \Rightarrow r(t,h)$

Only if r = 0 and h = t



I-to-N: $r(h, t_1), r(h, t_2), ..., r(h, t_n)$ are all true.

$$t_1 = h + r = t_2$$

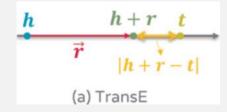
 t_1 and t_2 will map to the same vector although they are different entities.

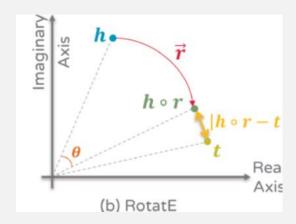
RotatE



• Translation:

- For a triple (h, r, t), let $h, r, t \in \mathbb{R}^d$ be embedding vectors.
 - if the given link exists $h \circ r \approx t$
 - \blacksquare else $h \circ r \neq t$
 - where 'o' is the Hadamard product on the embeddings.
- Entity scoring function: $f_r(h, t) = -||h \circ r t||^2$

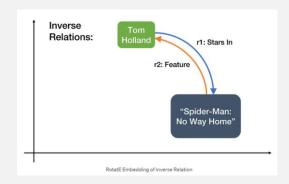


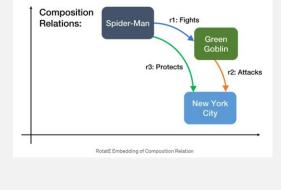


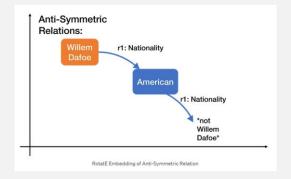
The Hadamard product is a binary operation that takes in two matrices of the same dimensions and returns a matrix of the multiplied corresponding elements.

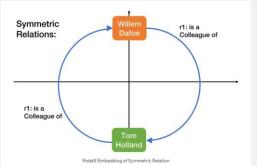
RotatE







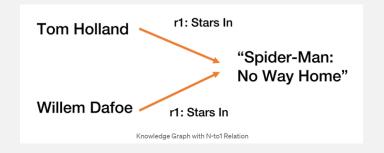


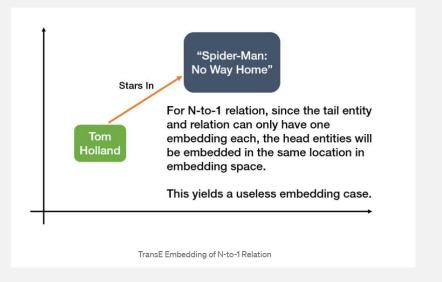


RotatE can model symmetric relations that TransE cannot express! It does so as 180-degree rotations.

RotatE - Limitation







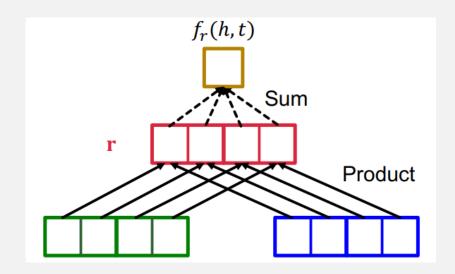
DistMult



• For a triple (h, r, t), let $h, r, t \in \mathbb{R}^d$ be embedding vectors.

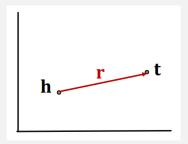
• Score function: $f_r(h, t) = \langle h, r, t \rangle$ = $\sum_i h_i . r_i . t_i$

- Intuition of score function:
 - \circ Cosine similarity between $h \cdot r$ and t



DistMult

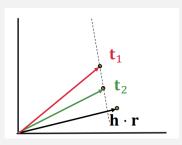




Symmetric:
$$r(h,t) \Rightarrow r(t,h)$$

$$f_r(h,t) = \langle h, r, t \rangle = \sum_i h_i . r_i . t_i$$

= $\langle t, r, h \rangle = f_r(t,h)$



I-to-N: $r(h, t_1), r(h, t_2), ..., r(h, t_n)$ are all true.

$$< h, r, t_1 > = < h, r, t_2 >$$

DistMult - Limitations



Antisymmetric: $r(h, t) \Rightarrow \neg r(t, h)$

$$f_r(h, t) = \langle h, r, t \rangle$$

= $\sum_i h_i . r_i . t_i$
= $\langle t, r, h \rangle = f_r(t, h)$

Inverse:

$$r_1(h,t) \Rightarrow r_2(t,h)$$

$$< h, r_1, t> = < t, r_2, h>$$

 $r_1 = r_2$ solves this

But semantically it does not make sense (advisor is not equal to advisee)

Composition:

$$r_1(x, y) & r_2(y, z)$$

 $\Rightarrow r_3(x, z) \quad \forall x, y, z$

Since dot product is commutative, it can distinguish between head and tail entities

Summary – Embedding Models



Model	Score	Symmet.	Antisym.	Inverse	Compos.	1-to-N
TransE	- h+r-t	×	✓	/	1	×
RotatE	$- h \circ r - t ^2$	√	1	/	1	×
DistMult	< h, r, t >	1	×	×	×	/



- This Led us to our Base Paper "KG-Predict: A knowledge graph computational framework for drug repurposing"
- How well did KG-Predict outperformed the other state of art embedding methods?

Data	Method	Hits@1	Hits@3	Hits@10	MRR
GP-KG	TransE	0.116	0.226	0.399	0.209
	DistMult	0.103	0.207	0.379	0.191
	ConvE	0.126	0.232	0.399	0.216
	RotatE	0.119	0.231	0.403	0.212
	KG-Predict	0.174	0.266	0.447	0.261



- This Led us to our Base Paper "KG-Predict: A knowledge graph computational framework for drug repurposing".
- The authors extended the Composition based multi regional graph Convolutional network (CompGCN).



- Let's take a look at the algorithm what the authors used
 - Input: Feature Vector x_v of node v (e.g. drug, disease) and feature vector S_r of edge r (e.g. Drug-treat-disease).
 - CompGCN Layer: The model Stacked several convolutional layers.
 - Used 2 different functions.
 - $AGGREGATE_n(.)$
 - CONCAT(.)
 - KG-Predict uses learnable transformational matrix W_{rel}^n which project all relations to same embedding space as entities and relations which are to update
 - Output: z_v represent the set of entity embedding and z_r represent the set of relation embedding



Pseudo Code for the explained algorithm

```
Algorithm 1: GP-KG Embedding Algorithm
   Input: G = (V, E, X, R, S), \forall n \in \{1, 2, ..., N\}, aggregator function
            AGGREGATE_n(.), concat function CONCAT(.),
            relation-specific coefficient matrix W_{rol}^n, self-specific
            coefficient matrix W_a^n, learnable transformation matrix
             W_{vol}^n, the set of entity v's neighbors N(v).
   Output: entity embedding Z_V, relation embedding Z_R.
1 h_v^0 \leftarrow X_v, h_r^0 \leftarrow S_r;
2 for n = 1, 2, ..., N do
       for v \in V do
         h_{N(v)}^{n} \leftarrow AGGREGATE_{n}(W_{\lambda}^{n}\psi\left(h_{u}^{n-1},h_{r}^{n-1}\right)), u,r \in N(v);
        h_v^n \leftarrow f(CONCAT(h_{N(v)}^n, W_o^n h_v^{n-1})) ;
       for r \in R do
      h_r^n \leftarrow W_{rel}^n h_r^{n-1} ;
8 Z_V \leftarrow \{h_v^N\}, \forall v \in V;
9 Z_R \leftarrow \{h_r^N\}, \forall r \in R;
```



• How well did KG-Predict outperformed the other state of art embedding methods?

Data	Method	Hits@1	Hits@3	Hits@10	MRR
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OBJECTIVE



- Modify the GP-KG embedding process to construct a unique embedding methodology
- Investigate state-of-the-art embedding and make necessary alteration to them.
- Use Altered embedding to develop new technique and use them to find results on Prediction model.

THANKYOU