GNN-based Biomedical Knowledge Graph Mining in Drug Development

Maria Wyrzykowska Seminar: Data Mining - Clustering and Classification

Chapter 24 GNN-based Biomedical Knowledge Graph Mining in Drug Development

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Agenda

1. Data

- Characteristics & challenges
- Biomedical Knowledge Graphs

2. Inference on Knowledge Graphs

- Conventional inference techniques
- GNN-based inference techniques

3. Real-life applications

- Drug repurposing
- Limitations & future directions

Data

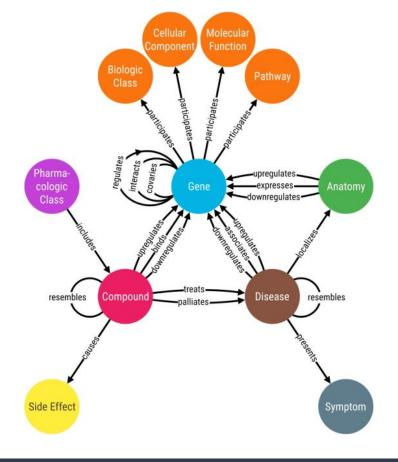
Biomedical data

- a lot of it...
- ...but is usually buried in the literature
- **heterogenous**: genes, diseases, drugs, interactions
- relational



knowledge retrieval & organization is difficult

Solution: using graphs!



- set of <head, relation, tail> tuples
- created by extraction and integration of data from other sources
- examples: Hetionet, Drug Repurposing Knowledge Graphs and many others
- usage: prior knowledge to different models, generation of hypotheses

Inference on Knowledge Graphs

Inference on Knowledge Graphs

Important attributes to take into consideration:

- local and global structure properties
- heterogeneity of entities and relations

Standard pipeline:

- 1. Learning embeddings
- 2. Performing downstream tasks e.g. link prediction

Approaches:

- 1. Conventional: semantic matching, distance models, meta-path-based, CNN
- GNN-based: GCN, GAT

Common notation

Entity	Symbol
Entities (diseases, drugs, genes)	E
Entity i (disease, drug, gene)	e_i
Relation k ("cures", "causes")	r_k
Embedding of entity i	$h_i \in \mathcal{R}^n$
Embedding of relation \boldsymbol{k}	$g_k \in \mathcal{R}^n$

Conventional KG inference: semantic matching models

Based on idea that entities are similar if connected to similar entities via similar relations.

Example: **RESCAL**

$$f(e_i, r_k, e_j) = \mathbf{h}_i^{\mathsf{T}} M_k \mathbf{h}_j$$

where:

 M_k - embedding matrix, $M_k \in \mathcal{R}^{n imes n}$

Loss used for training is standard RMSE + regularization.

Conventional KG inference: translational distance model

Based on idea that relation can be considered as a translation from head entity to tail entity in the embedding space.

Example: TransE

$$f(e_i, r_k, e_j) = ||\mathbf{h_i} + \mathbf{g_k} - \mathbf{h_j}||$$

where:

 $\| \|_{2}$ - Euclidean norm

TransE: training

Loss function:

$$L = \sum_{(e_i, r_k, e_j) \in S} \sum_{(e_i', r_k, e_j') \in S'} [\gamma + d(h_i + g_k, h_j) - d(h_i' + g_k, h_j')]_+$$

where:

S' - corrupted triplets

$$S' = \{(e_i', r_k, e_j) | e_i' \in E\} \cup \{(e_i, r_k, e_j') | e_j' \in E\}$$

 γ - margin

d - dissimilarity measure (e.g. L1 or L2 norm)

TransE: modifications

TransE does well for 1-to-1 relations, but does not manage to model N-to-1, 1-to-N and N-to-N relations. Many modifications try to alleviate this problem:

- TransH
- TransR
- TransD
- TranSparse
- TransF
- ..

Most are based on idea to project the low-dimensional embeddings to hyperplanes, different for each relation.

Conventional KG inference: meta-path-based approaches

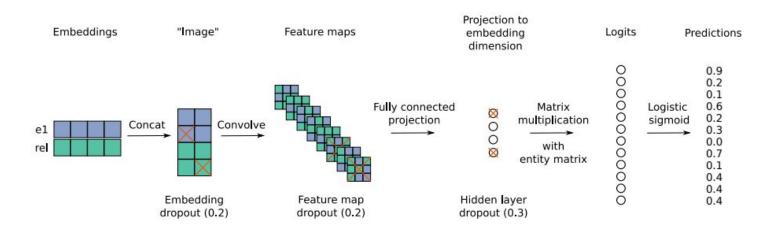
Issue of semantic & distance models is that they focus on one-hop neighbourhoods. The meta-path based models aim at capturing both local and global structure properties.

$$a_1 \stackrel{b_1}{\rightarrow} a_2 \stackrel{b_2}{\rightarrow} \dots \stackrel{b_{l-1}}{\rightarrow} a_l$$

- Heterogeneous Information Network Embedding (HINE) minimizing the difference between meta-path-based proximity and expected proximity in the embedding space
- **metapath2vec** random walks in the graph are treated as sentences and SkipGram with negative sampling is used to learn embeddings

Conventional KG inference: CNN models

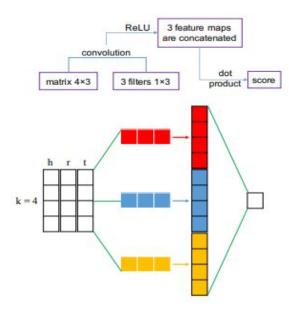
ConvE



Convolutional 2D Knowledge Graph Embeddings

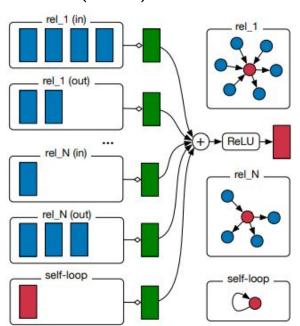
Conventional KG inference: CNN models

ConvKB

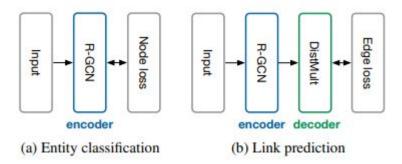


A Novel Embedding Model for Knowledge Base Completion Based on Convolutional Neural Network

Relational GCN (R-GCN)



$$\mathbf{h}_{i}^{(l+1)} = \sigma \left(\sum_{r_k \in \mathbb{R}} \sum_{j \in \mathcal{N}_i^k} \frac{1}{c_{i,k}} W_k^{(l)} \mathbf{h}_j^{(l)} + W_0^{(l)} \mathbf{h}_i^{(l)} \right)$$



Modeling Relational Data with Graph Convolutional Networks

TransGCN combines GCN & translational distance models (e.g. TransE) to learn both entities and relations embeddings.

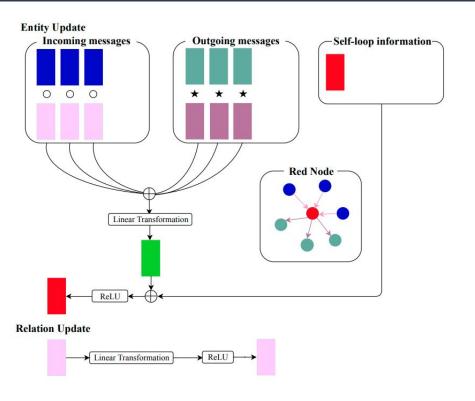
At layer I:

1. Message propagation:

$$m_i^{(l+1)} = rac{1}{c_i} W_0^{(l)} (\sum_{(e_j, r_k, e_i) \in T_{in}(e_i)} (h_j^{(l)} \circ g_k^{(l)}) + \sum_{(e_i, r_k, e_j) \in T_{out}(e_i)} (h_j^{(l)} \star g_k^{(l)}))$$

2. Embedding update:

$$h_i^{(l+1)} = \sigma(m_i^{(l+1)} + h_i^{(l)})$$
 $g_k^{(l+1)} = \sigma(W_1^{(l)}g_k^{(l)})$



$$m_i^{(l+1)} = rac{1}{c_i} W_0^{(l)} (\sum_{(e_j, r_k, e_i) \in T_{in}(e_i)} (h_j^{(l)} \circ g_k^{(l)}) + \sum_{(e_i, r_k, e_j) \in T_{out}(e_i)} (h_j^{(l)} \star g_k^{(l)}))$$

We want the "dot" and "star" operators to translate the entities to $h_i^{(l)}$. Easiest assumption, TransE inspired - "dot" is plus, "star" is minus:

$$h_i^{(l)} = \left\{ egin{aligned} h_j^{(l)} + g_k^{(l)}, (e_j, r_k, e_i) \in T_{in}(e_i) \ h_j^{(l)} - g_k^{(l)}, (e_i, r_k, e_j) \in T_{out}(e_i) \end{aligned}
ight.$$

Loss function is also analogous to TransE:

$$L = \sum_{(e_i, r_k, e_j) \in S} \sum_{(e_i', r_k, e_j') \in S'} [\gamma + f_{g_k}(h_i, h_j) - f_{g_k}(h_i', h_j')]_+$$

Graph attention-based embedding in KG (GATE-KG):

$$\mathbf{c}_{ijk}^{(l)} = W_1^{(l)}[\mathbf{h}_i^{(l)}||\mathbf{h}_j^{(l)}||\mathbf{g}_k^{(l)}]$$

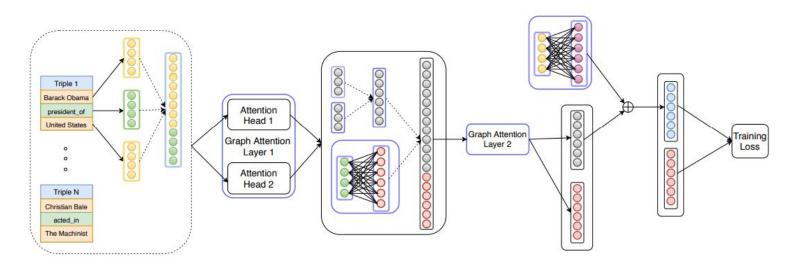
$$\boldsymbol{\beta}_{ijk}^{(l)} = \text{LeakyReLU}\left(W_2^{(l)}\mathbf{c}_{ijk}^{(l)}\right)$$

$$\alpha_{ijk}^{(l)} = \frac{\exp(\beta_{ijk}^{(l)})}{\sum_{j' \in \mathscr{N}_i} \sum_{k' \in \mathscr{R}_{ij'}} \exp(\beta_{ij'k'}^{(l)})}$$

$$\mathbf{h}_i^{(l+1)} = \sigma \left(\sum_{j \in \mathscr{N}_i} \sum_{k \in \mathscr{R}_{ij}} lpha_{ijk}^{(l)} \mathbf{c}_{ijk}^{(l)}
ight)$$

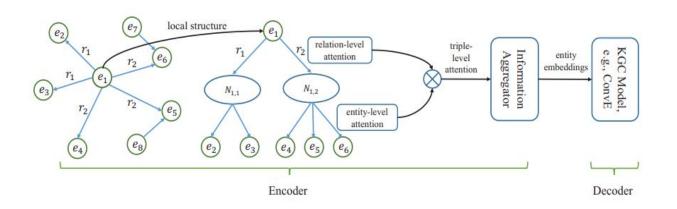
Loss function is also analogous to TransE. For edge prediction, ConvKB is used as a decoder.

Graph attention-based embedding in KG (GATE-KG):



<u>Learning Attention-based Embeddings for Relation Prediction in Knowledge Graphs</u>

Relational Graph neural network with Hierarchical ATtention (RGHAT)



$$\alpha_{ik} = \frac{\exp(\sigma(\mathbf{z}_1 \cdot \mathbf{a}_{ik}))}{\sum_{r_x \in \mathcal{N}_i} \exp(\sigma(\mathbf{z}_1 \cdot \mathbf{a}_{ix}))}$$

$$\mathbf{b}_{ikj} = W_2 \left[\mathbf{a}_{ik} || \mathbf{h}_j\right]$$

$$\beta_{kj} = \frac{\exp(\sigma(\mathbf{z}_2 \cdot \mathbf{b}_{ikj}))}{\sum_{r_y \in \mathcal{N}_{i,k}} \exp(\sigma(\mathbf{z}_1 \cdot \mathbf{b}_{iyj}))}$$

$$\mu_{ikj} = \alpha_{ik} \cdot \beta_{kj}.$$

$$\hat{\mathbf{h}} = \sum_{r \in \mathcal{N}_h} \sum_{t \in \mathcal{N}_{h,r}} \mu_{h,r,t} \mathbf{b}_{h,r,t}.$$

 $\mathbf{a}_{ik} = W_1 \left[\mathbf{h}_i || \mathbf{g}_k \right]$

Real-life applications

Drug repurposing

Drug repurposing process:

- 1. Hypothesis generation
- 2. Assessment
- 3. Validation

KG can be helpful in the hypothesis generation step and has been used to investigate potential drugs for COVID-19:

- <u>Repurpose Open Data to Discover Therapeutics for COVID-19 Using Deep Learning</u>: used RotatE (modification of TransE); identified 41 potential drugs, from which 9 were under clinical trials
- <u>Drug Repurposing for COVID-19 using Graph Neural Network with Genetic, Mechanistic, and Epidemiological Validation</u>: used variational graph autoencoder and transfer learning, identified 22 potential drugs

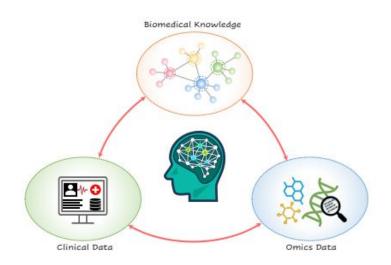
Limitations & future directions

Limitations:

- Data quality:
 - incorrectness
 - incompleteness
- Scalability:
 - KG can include hundreds of millions of relations
 - it can be a challenge for complex GNNs

Future directions:

- Data quality control
- Improving scalability
- Incorporating other data sources:
 - To improve robustness against data quality problems



Thanks for your attention!