Constructing Knowledge Graphs and Their Biomedical Applications

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Abstract

1. Give high level description of review as it pertains to knowledge graphs (creation and application)

Introduction

Knowledge graphs are a practical resource for many real world applications. They have been used in social medial mining to classify nodes [1] or to create a recommendation system [2]. Knowledge graphs have also been used to understand natural language via interpreting simple questions and using relational information to provide answers [3,4]. In a biomedical setting these graphs have been used to prioritize genes relevant to disease [5,6,7,8], perform drug repurposing [9] and identify drug-target interactions [10].

Despite their utility, precisely defining a knowledge graph is a difficult task because there are multiple conflicting definitions [11]. For this review, we define a knowledge graph as the following: a resource that integrates single or multiple sources of information into the form of a graph. This graph allows for the capacity to make semantic interpretation, continuously incorporate new information and uncover novel hidden knowledge through computational techniques and algorithms. Based on this definition resources like Hetionet [9] would be considered a knowledge graph. Hetionet integrates multiple sources of information into the form of a graph (example shown in Figure 1) and was used to derive novel information concerning unique drug treatments [9]. We do not consider databases like DISEASES [12] and DrugBank [13] to be knowledge graphs. These resources contain essential information, but do not represent their data in graph form.

Knowledge graphs are often constructed from manually curated databases [9,14,15,16]. These sources provide previously established information that can be incorporated into a graph. For example, a graph using DISEASES [12] as a resource would have genes and diseases as nodes, while edges would be added between nodes that have an association. This example shows a single type of relationship; however, there are graphs that use databases with multiple relationships. Other approaches have used natural language processing techniques to build knowledge graphs [17,18]. One example used a text mining system to extract sentences that indicated a protein interacting with another protein [19]. Once these sentences have been identified, they are incorporated as evidence for establishing edges in a knowledge graph.

In this review we describe various approaches for constructing and applying knowledge graphs in a biomedical setting. We discuss the pros and cons of constructing a knowledge graph via manually curated databases and via text mining systems. We also compare assorted approaches for applying knowledge graphs to solve biomedical problems. Lastly, we conclude on the practicality of knowledge graphs and point out future applications that have yet to be explored.
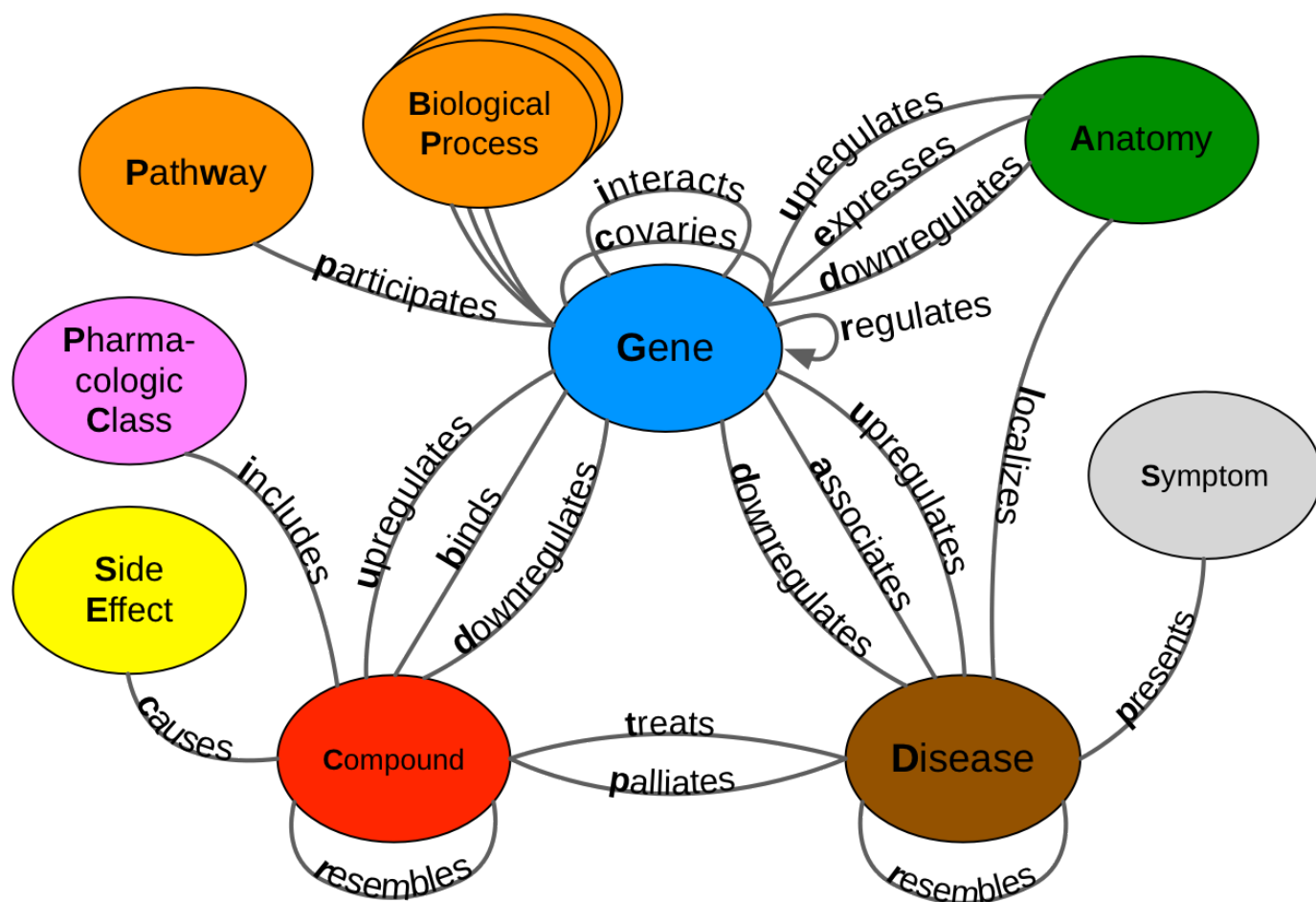
Figure 1: A metagraph (schema) of the heterogeneous network used in the Rephetio project [9]. This undirected network depicts pharmacological and biomedical information. The nodes (circles) represent entities and edges (lines) depict relational information between two entities.

Building Biomedical Knowledge Graphs

Knowledge graphs can be constructed in many ways using resources such as text or pre-existing databases. Usually, knowledge graphs are constructed using pre-existing databases. These databases are constructed by domain experts using approaches ranging from manual curation to automated techniques, such as text mining systems. Manual curation is a process that involves extensive use of domain experts to read papers and detect sentences that assert a relationship. Automated approaches involve the use of machine learning or natural language processing techniques to rapidly detect sentences of interest. We categorize these automated approaches into the following groups: rule-based extraction, unsupervised machine learning, and supervised machine learning. We discuss examples of each type of approach and synthesize the strengths and weaknesses of each.

Constructing Databases and Manual Curation

Database construction can date back all the way to 1956 where the first database contained a protein sequence of the insulin molecule [20]. This process involves gathering relevant text such as journal articles, abstracts, or web-based text. At this point curators can read gathered text and detect relationship asserting sentences (i.e. relationship extraction). An alternative to use a text mining system to filter out extraneous sentences, then incorporate curators to perfect the system's findings. This semi-automatic approach is way to augment curators throughout the curation process. We discuss the pros and cons of using manual curation for relationship extraction and mention databases that use this method to populate their fields.

Notable databases have been constructed via manual curation (Table {[**???**]}). For example, COSMIC [21] was constructed via a group of domain experts scanning the literature for key cancer related genes. This database has reached close to 35M entries in 2016 [21] and grew to a total of 45M entries in 2019 [22]. Studies have shown that these databases contain relatively precise data, but in low quantities [23,24,25,26,27,28,29]. This happens because the high publication rate is too much for curators to keep up [30]. This findings highlight a critical need for future approaches to be fast enough to compete with an increasing publication rate.

Semi-automatic methods are a way to augment curators during the curation process [27,31,32,33,34,35,36]. First step in this context is to use an automatic system to initally extract sentences from text. This process filters out irrelevant sentences, which means less text for curators to sift through. After the pre-filtering step curators can approve or remove the identified sentences. This semi-automatic process was found to speed up the curation process compared to manual approach [31,37]. Curators in [37] saved an average of 2.8 hours of overall time while curators in [31] saved about the same amount of time (2 hours). Despite the speed up, this process is prone to produce bias results. As automated systems excel in identifying sentences for commonly occurring relationships, they miss out on lessor known relationships [31]. Plus, these systems have a hard time parsing ambiguous sentences that naturally occur in text. This complication results in curators have a difficult time correcting these systems [31]. Given these caveats, a future direction would be using or creating approaches that can mitigate the relationship bias. Furthermore, future approaches should look into using techniques that simplify sentences to solve the ambiguity issue [38,39].

Despite the negatives of manual curation, it is still an essential process for relationship extraction approaches. This process can be used to generate gold standard datasets that automated systems use for validation [40,41]. Furthermore, manual curation can be used during the training process of automated systems (i.e. active learning) [42]. It is important to remember that manual curation alone is precise, but results in low recall rates [29]. Future databases should consider initially relying on automated methods to obtain sentences at an acceptable recall level, then incorporate manual curation as a way to fix or remove irrelevant results.

Database [Reference]	Short Description	Number of Entries	Entity Types	Relationship Types	Method of Population
Entrez-Gene [43]	NCBI's Gene annotation database that contains information pertaining to genes, gene's organism source, phenotypes etc.	7,883,114	Genes, Species and Phenotypes	Gene-Phenotypes and Genes-Species mappings	Semi-automated curation
UniProt [44]	A protein protein interaction database that contains proteomic information.	560,823	Proteins, Protein sequences	Protein-Protein interactions	Manual and Automated Curation
PharmGKB [45]	A database that contains genetic, phenotypic, and clinical information related to pharmacogenomic studies.	43,112	Drugs, Genes, Phenotypes, Variants, Pathways	Gene-Phenotypes, Pathway-Drugs, Gene-Variants, Gene-Pathways	Manual Curation and Automated Methods

Database [Reference]	Short Description	Number of Entries	Entity Types	Relationship Types	Method of Population
COSMIC [21]	A database that contains high resolution human cancer genetic information.	35,946,704	Genes, Variants, Tumor Types	Gene-Variant Mappings	Manual Curation
BioGrid [46]	A database for major model organisms. It contains genetic and proteomic information.	572,084	Genes, Proteins	Protein-Protein interactions	Semi-automatic methods
Comparative Toxicogenomics Database [47]	A database that contains manually curated chemical-gene-disease interactions and relationships.	2,429,689	Chemicals (Drugs), Genes, Diseases	Drug-Genes, Drug-Disease, Disease-Gene mappings	Manual curation and Automated systems
Comprehensive Antibiotic Resistance Database [48]	Manually curated database that contains information about the molecular basis of antimicrobial resistance.	174,443	Drugs, Genes, Variants	Drug-Gene, Drug-Variant mappings	Manual curation
OMIM [49]	A database that contains phenotype and genotype information	25,153	Genes, Phenotypes	Gene-Phenotype mappings	Manual Curation

Table. A table of databases that used a form of manual curation to populate entries. Reported number of entities and relationships are relative to time of publication. {#tbl:manual-curated-databases}

Text Mining for Relationship Extraction

Rule-Based Relationship Extraction

Rule-based extraction consists of identifying sentences that contain important keywords or grammatical patterns that allude to relationships of interest. Keywords are established via expert knowledge or though the use of pre-existing ontologies. Grammatical patterns are constructed via experts curating parse trees, which are tree data structures that depict a sentence's grammatical structure. Parse trees come into two forms a constituency parse tree and a dependency parse trees. Both trees use part of speech tags, labels that dictate the grammatical role of a word such as noun, verb, adjective, etc, for construction. A constituency parse trees breaks a sentence down into a subphrases (Figure 3) while dependency path trees analyzes the grammatical structure of a sentence (Figure 2). Many text mining approaches [50,51,52] use such trees to generate features for machine learning algorithms. These approaches are discussed in later sections. For this section we focus on approaches that mainly use rule based extraction to detect sentences that assert a relationship.

Grammatical patterns can simplify sentences for easy extraction [39,53]. Jonnalagadda et al. used a set of grammar rules inspired by constituency trees to reshape complex sentences with simpler versions [39]. These simplified versions were manually curated to determine the presence of a relationship. By simplyfing sentences this approach achieved high recall, but had low precision [39]. Other approach used simplification techniques to make extraction easier [54,55,56,57]. Tudor et al., simplified sentences to detect protein phosphorylation events [56]. The sentence simplifier broke complex sentences that contain multiple protein events into smaller sentences that contain only one distinct event. By breaking these sentences down the authors were able to increase their recall. However, sentences that contained ambigious directionality or multiple phosphroylation events were too complex for the simplifier. As a consequence the simplifier produced errors in recall [56]. These errors highlight a crucial need for future algorithms to be generalizable enough to handle various forms of complex sentences.

Pattern matching is a fundamental approach used to detect relationship asserting sentences. In this context patterns can consist of phrases from constituency trees, a set of keywords or some combination of both to detect sentences [27,58,59,60,61,62]. Xu et al. designed a pattern matcher system to detect sentences in PubMed abstracts that indicate drug-disease treatments [61]. This system matched drug-disease pairs from clinicaltrails.gov to drug-disease pairs mentioned in abstracts. This matching process aided the authors in identifying sentences that were used to create simple patterns, such as "Drug in the treatment of Disease" [61], to match sentences in a wide variety of abstracts. The authors hand curated two datasets for evalution and achieved a high precision score of 0.904 and a low recall score of 0.131 [61]. This low recall score was based on constructed patterns being very specific to top occurring drug paris. This flaw resulted in rarely occurring pairs having a high likelihood of being missed. Following approaches using constituency trees, some approaches used dependency trees to construct patterns [50,63]. Depending upon the nature of the algorithm, dependency trees could be more appropiate than constituency trees and vise versa. The performance difference between the two approaches still remains as an open question for future exploration.

Rules based methods provide a basis for many relationship extraction systems. Approaches in this category range from simplifing sentences for easy extraction to identifing sentences based on matched key phrases or grammatical patterns. Both require a significant amount of manual effort and expert knowledge to perform well. A future direction is to develop ways to automatically construct these hand-crafted patterns, which would accelerate the process of creating new rule-based systems.
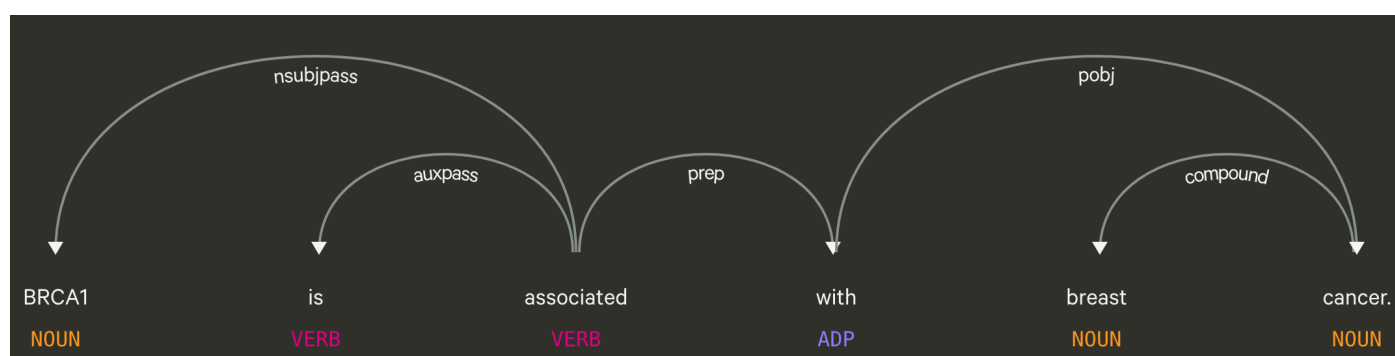

Figure 2: A visualization of a dependency parse tree using the following sentence as in example: "BRCA1 is associated with breast cancer" [64]. For these type of trees the root begins at the main verb of a sentence. Each arrows depicts the dependency shared between two words. For example, the dependency between BRCA1 and associated is nsubjpass, which stands for passive nominal subject. This means that BRCA1 is the subject of the sentneces and it is being referred to by the word associated.
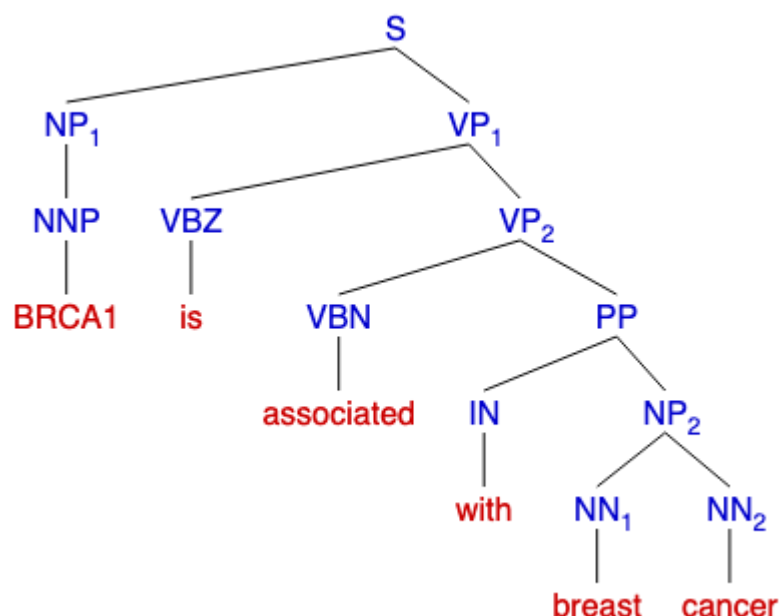
Figure 3: A visualization of a constituency parse tree using the following sentence: "BRCA1 is associated with breast cancer" [65]. This type of tree has the root beginning at the start of the sentence. Each word is grouped into subphrases depending on the part of speech tags of a word. For example, the word "associated" is a past particple verb (VBN) that belongs to the verb phrase (VP) subgroup.

Extracting Relationships Without Labels

Unsupervised methods of extraction involve drawing inferences from data without the use of labels. These methods involve some form of clustering or statistical calculations. In this section we discuss methods that use unsupervised learning to detect relationship asserting sentences from text.

An unsupervised method to extract relationships exploits the fact that two entities can appear together in text. This kind of event is called co-occurrence and studies that use this phenomenon can be found in table 1. Two databases DISEASES [12] and STRING [66] were populated using a co-occurrence scoring method on PubMed abstracts. Both databases used the same scoring method that measured the frequency of co-mention pairs within individual sentences as well as the abstracts themselves. This method assumes independence between each individual occurrence. Under this assumption mention pairs that occur more than expected were presumed to indicate the presence of an association or interaction. This approach was able to identify 543,405 disease gene associations [12] and 792,730 high confidence protein protein interactions [66], but is limited to only using PubMed abstracts.

Full text articles are able to drastically amplify text mining power to detect relationships [67,68]. Westergaard et al. used a co-occurrence approach, similar to DISEASES [12] and STRING [66], to mine full articles for protein-protein interactions and other protein related information [67]. The authors discovered that full text provided better prediction power than using abstracts alone. This improvement suggests that future text mining approaches should consider using full text to increase detection power.

Unsupervised methods have been focused on treating multiple biomedical relationships as multiple isolated problems. These methods repeatedly use the same model for each biomedical relationship type. An alternative to this persepctive is to capture all different relationship types at once. Clustering is an approach that accomplish this concept of simultaneous extraction. Percha et al. used a biclustering algorithm on generated dependency parse trees to group PubMed abstract sentences [69]. Each cluster was manually curated to determine which relationship they represented. This approach captured 4,451,661 dependency paths for 36 different groups [69]. Despite the success, this approach suffered from technical issues such as dependency tree parsing errors. This type of error

resulted in sentences not being grouped by the clustering algorithm [69]. Future clustering approaches should consider simplifying sentences to prevent this type of issue.

Overall unsupervised methods provide a means to rapidly find relationship asserting sentences without the need of annotated text. Approaches in this category range from using co-occurrence scores to clustering sentences. These methods provide a generalizable framework that can be used on large repositories of text. Future methods can improve detection power by considering the use of methods that simplify sentences and use datasets that include full text articles.

Table 1: Table of approaches that mainly use a form of co-occurrence.

Study	Relationship of Interest
[70]	Protein-Protein Interactions, Disease-Gene and Tissue-Gene Associations
[71]	Drug Disease Treatments
[72]	Drug, Gene and Disease interactions
[67]	Protein-Protein Interactions
[12]	Disease-Gene associations
[73]	Protein-Protein Interactions
[74]	Genotype-Phenotype Relationships

Supervised Machine Learning

1. Mention the availablility of publically available data
    1. PPI - 5 datasets
        1. 10.1016/j.artmed.2004.07.016
        2. 10.1186/1471-2105-8-50
        3. Learning language in logic - genic interaction extraction challenge
        4. 10.1093/bioinformatics/btl616
        5. http://helix-web.stanford.edu/psb02/ding.pdf
    2. DaG - 3 datasets
        1. 10.1016/j.jbi.2012.04.004
        2. 10.1186/s12859-015-0472-9
        3. 10.1186/1471-2105-14-323
        4. 10.1186/1471-2105-13-161
    3. CiD
    4. 10.1093/database/baw068
    5. CbG
    6. Biocreative VI track 5 - raw citation
    7. more if exists talk about deep learning methods
2. Mention the use of Support Vector Machines and other non deep learning classifiers
    1. Will have to mention that field has moved to deep learning.
    2. 10.1186/s13326-017-0168-3
    3. 10.1371/journal.pcbi.1004630
3. Mention deep learning methods
    1. 1901.06103v1
    2. 10.1016/j.knosys.2018.11.020
    3. 10.1177/0165551516673485
    4. 1706.01556v2
    5. ^^ A few papers here but a lot more will be put into place
    6. Mention caveat which is the need for large annotated datasets

7. Mention a direction the field is moving to which is weak supervision and more that info that will come in time.

Applying Knowledge Graphs to Biomedical Challenges

1. Mention that these graphs can be used for discovery
2. Mention representation learning (aka representing a graph as dense vectors for nodes and/or edges)
3.

Unifying Techniques

Mapping high dimensional data into a low dimensional space has greatly improved modeling performance in fields such as natural language processing [75,76] and image analysis [77]. The success of these approaches provides rationale for projecting knowledge graphs into a low dimensional space as well [78]. Techniques that perform this projection often require information on how nodes are connected with one another [79,80,81,82], while other approaches can work directly with the edges themselves [83]. We group methods for producing low-dimensional representations of knowledge graphs into the following three categories: matrix factorization, translational methods, and deep learning.

Matrix Factorization

1. Mention techniques for these with some papers

Translational Distance Models

Translational distance models treat edges in a knowledge graph as linear transformations. As an example, one such algorithm, TransE [84], treats every node-edge pair as a triplet with head nodes represented as $\mathbf{h}$, edges represented as $\mathbf{r}$, and tail nodes represented as $\mathbf{t}$. These representations are combined into an equation that mimics the iconic word vectors translations ($\mathbf{king} - \mathbf{man} + \mathbf{woman} \approx \mathbf{queen}$) from the Word2vec model [76]. The equation is shown as follows: $\mathbf{h} + \mathbf{r} \approx \mathbf{t}$. Starting at the head node ($\mathbf{h}$), add the edge vector ($\mathbf{r}$) and the result should be the tail node ($\mathbf{t}$). TransE optimizes embeddings for $\mathbf{h}$, $\mathbf{r}$, $\mathbf{t}$, while guaranteeing the global equation ($\mathbf{h} + \mathbf{r} \approx \mathbf{t}$) is satisfied [84]. A caveat to the TransE approach is that it the training steps force relationships to have a one to one mapping, which may not be appropriate for all types of relationships.

Wang et al. [85] attempted to resolve the one to one mapping issue by developing the TransH model. TransH treats relations as hyperplanes rather than a regular vector and projects the head ($\mathbf{h}$) and tail ($\mathbf{t}$) nodes onto the hyperplane. Following this projection, a distance vector ($\mathbf{d}_r$) is calculated between the projected head and tail nodes. Finally, each vector is optimized while preserving the global equation ($\mathbf{h} + \mathbf{d}_r \approx \mathbf{t}$) [85]. Other approaches [86,87] have built off of the TransE and TransH models. In the future, it may be beneficial for these models is to incorporate other types of information such as edge confidence scores, textual information, or edge type information when optimizing these embeddings.

Deep Learning

Deep learning is a paradigm that uses multiple non-linear transformations to map high dimensional data into a low dimensional space. Many techniques that use deep learning for knowledge graphs are based on word2vec [75,76], a set of approaches that are widely used for natural language processing. The goal of word2vec is to project words into a low dimensional space that preserves their semantic

meaning. Strategies for training word2vec models use one of two neural network architectures: skip-gram and continuous bag of words (CBOW). Both models are feed-forward neural networks, but CBOW models are trained to predict a word given it's context while skip-gram models are trained to predict the context given a word [75,76]. Once training has finished, words are now associated with dense vectors that downstream models, such as feed forward networks or recurrent networks, can use for input.

Deepwalk [88] is an early method designed to project a knowledge graph into a low dimensional space. The first step of this method is to perform a random walk along a knowledge graph. During the random walk, every generated sequence of nodes is recorded and treated like a sentence in word2vec [75,76]. After every node has been processed, a skip-gram model is trained to predict the context of each node thereby projecting a knowledge graph into a low dimensional space [88]. A limitation of this method is that the random walk cannot be controlled, so every node has an equal chance to be reached. Grover and Leskovec [89] demonstrated that this limitation can hurt performance when classifying edges between nodes and developed node2vec as a result. Node2vec [89] operates the in the same fashion as deepwalk; however, this algorithm specifies a parameter that lets the random walk be biased when traversing nodes. A caveat to both deepwalk and node2vec is that both algorithms ignore information such as edge type and node type. Various approaches have evolved to fix this limitation by incorporating node, edge and even path types when projecting nodes into a low dimensional space [90,91,92,93]. These approaches primarily capture a network's local structure. An emerging area of work is to develop approaches that capture both the local and global structure of a network when projecting knowledge graphs into a low dimensional space.

Some deep learning approaches use an adjacency matrix as input [75,76] instead of using the word2vec framing. Algorithms such as auto-encoders can also generate network embeddings [94,95,96]. Autoencoders [97,98] are neural networks that map input such as an adjacency matrices into a low dimensional space and then learns how to construct this space by reconstructing the same input. The generated low dimensional space captures the node connectivity structure of the knowledge graph and every node is mapped onto this space [94,95,96]. Despite the high potential of this approach, this method relies on an adjacency matrix for input. If a knowledge graph asymptotically increases in size, these approaches could run into scalability issues as discovered by Khosla et al. [99]. Plus, Khosla et al.[99] discovered that approaches akin to node2vec outperformed algorithms using autoencoders when undergoing link prediction and node classification. Overall, the performance of these models largely depends upon the structure of nodes and edges within a knowledge graph [99]. Future approaches should consider creating hybrid models that use both node2vec and autoencoders to construct complementary low dimensional representations of knowledge graphs.

Unifying Applications

Knowledge graphs have been used in many biomedical applications ranging from identifying protein functions [100] to prioritizing cancer genes [101] to recommending safer drugs to patients [102,103]. In this section we discuss how knowledge graphs are being applied in biomedical settings. We put particular emphasis on an emerging set of techniques: those that project knowledge graphs into a low dimensional space.

Disease and Gene Interactions

1. Mention disease gene prioritization
2. Mention Disease gene associations

Protein Protein Interactions

1. Mention predicting genes interacting genes

Drug Interactions

1. Talk about drug side effects
2. Drug repurposing
3. Drug-Disease Interations

Clinical applications

1. Can mention EHR use and other related applications
2. Mention Tiffany's work on private data embeddings

Conclusion

1. Summarize discussed positives and pitfalls
2. Leave some open ended questions yet to be explored
3. Will come into play as I write this review paper

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7. **Biological Random Walks: Integrating heterogeneous data in disease gene prioritization**
Michele Gentili, Leonardo Martini, Manuela Petti, Lorenzo Farina, Luca Becchetti
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Mona Alshahrani, Robert Hoehndorf
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Daniel Scott Himmelstein, Antoine Lizee, Christine Hessler, Leo Brueggeman, Sabrina L Chen, Dexter Hadley, Ari Green, Pouya Khankhanian, Sergio E Baranzini

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Simon A. Forbes, David Beare, Harry Boutselakis, Sally Bamford, Nidhi Bindal, John Tate, Charlotte G. Cole, Sari Ward, Elisabeth Dawson, Laura Ponting, … Peter J. Campbell
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