A Short Journey through Graph Embedding Techniques XVI Summer School on Operational Research, Data and Decision Making

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What is a network?

- •A collection of points joined together in pairs by lines
	- Points joined together depend on the context
		- *Points -> Vertices, nodes, actors …*
		- *Lines -> Edges*
- There are many real problems that can be modeled as networks
	- Individual parts linked in some way
		- *Internet*
			- A collection of computers linked together by data connections
		- *Human societies*
			- A collection of people linked by acquaintance or social interaction

Why Networks?

- •Universal language for describing complex data
	- Networks from science, nature, and technology are more similar than one would expect
- •Shared vocabulary between fields
	- Computer Science, Social science, Physics, Economics, Statistics, Biology,…
- •Data availability (+computational challenges)
	- Web/mobile, bio, health, and medical
- •Impact!
	- Social networking, Social media, Drug design

Why networks?

- Both the individual components of a system (e.g., computer machines, people etc.) and the nature of their interaction are important.
- Equally important is the pattern of connections between these components.
	- These patterns significantly affect the performance of the underlying system.
- Patterns in a social network affect the way people obtain information, form opinions etc.
- Patterns in a network of financially connected companies provides the evidence of casual behavior among financial assets.

Social networks

- Network of people
	- Edges can represent friendships, relative relations, co-locations, replies to a given tweet.
- Traditionally social network studies were based on small scale networks
- Online social media have provided network data on previously unreachable scale

The Internet

Studying the Internet structure can help understand and improve the performance

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http://www.jeffkennedyassociates.com:16080/connections/concept/image.html

Node size: # publications per author. Edge size: # pubs shared by pairs of authors

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Networks in Molecular Biology

• **Protein-Protein interactions**

- **Protein-DNA interactions**
- **Genetic interactions**
- **Metabolic reactions**
- **Co-expression interactions**
- **Text mining interactions**
- **Association Networks**

"MATHEMATICS IS THE ART OF GIVING THE SAME NAME TO DIFFERENT THINGS." JULES HENRI POINCARE (1854-1912)

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Networks: definitions

• Formally, a network is (a graph is)…

- $\cdot G = (V, E)$, an ordered tuple of two sets
- $\bullet V = \{v_1, ..., v_n\}$, a set of unique nodes, and

Undirected

Adjacency matrix

- A is $n \times n$ matrix ($n = #$ of nodes)
	- Unweighted graph:
		- $A_{ij} = 1$ if $(i, j) \in E$, and 0 otherwise
	- Weighted graph:
		- A_{ij} = weight of edge (i,j)
	- \cdot A is symmetric for undirected graphs, and asymmetric for directed
- •A can be sparse for real networks (very few non-zero entries)
	- Facebook friendship network:
		- $|V| = n = 2.23e9$
		- $|E| = \#edges = 173e9,$
		- \bullet fraction of non-zero entries ${\sim}7 \approx \ 10e-8$

 $A = \left(\begin{array}{rrrrr} 0 & 1 & 1 & 0 & 0 \\ 1 & 0 & 1 & 0 & 1 \\ 1 & 1 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 1 \\ 0 & 1 & 1 & 1 & 0 \end{array} \right)$

Other network representations

- Edge list: Popular format for storing graphs
- Adjacency list: Fast retrieval of neighbours of node
- Adjacency matrix/list, edge list can be defined for directed graphs

ML tasks on networks

- •Node classification/regression
	- •Predict a type/value of a given node
- •Link prediction
	- •Predict whether two nodes are linked
- •Community detection
	- •Identify densely linked clusters of nodes
- •Network similarity
	- How similar are two (sub)networks

Adapted from Representation Learning on Networks, snap.stanford.edu/proj/embeddings-www

Example: Node Classification

Example: Node Classification

Proteins function classification

Example: Link Prediction

Example: mafia meetings

- Nodes represent the members of the ''Mistretta" and ''Batanesi" family.
- Circled nodes represent the subjects investigated for being association leaders.
- The red and **yellow** circled nodes refer to bosses of other districts.
- The white knots represent the other subjects close to the association or useful for the purposes of the association.
- The width of the edges is proportional to the number of meetings and the size of the nodes to their degree.

•(Supervised) Machine Learning Lifecycle: This feature, that feature. Every single time!

Feature Learning in Graphs

Goal: Efficient task-independent feature learning for machine learning in networks!

Why Is It Hard?

•Modern deep learning toolboxes are designed for simple sequences or grids.

•CNNs for fixed-size images/grids….

•RNNs or word2vec for text/sequences…

Why Is It Hard?

Networks are complex

• Complex topographical structure (i.e., no spatial locality like grids)

- No fixed node ordering or reference point (i.e., the isomorphism problem)
- Often dynamic and with multimodal features.

Background and traditional approaches

Graph Statistics and Kernel Methods

- Traditional approaches to ML using graph data follow the standard machine learning paradigm that was popular prior to the advent of deep learning.
- •We begin by extracting some statistics or features—based on heuristic functions or domain knowledge—and then use these features as input to a standard machine learning algorithm (e.g., logistic regression).

Node degree

• The most straightforward node feature is *degree*, which is usually denoted d_u for a node $u \in V$ and simply counts the number of edges incident to a node:

$$
d_u = \sum_{v \in V} \mathbf{A}[u, v]
$$

- In cases of directed and weighted graphs, one can differentiate between different notions of degree.
	- corresponding to outgoing/incoming edges by summing over rows or columns
- In general, the node degree is an essential statistic, and it is often one of the most informative features in traditional ML models for node-level $\textsf{tasks.}$

Node centrality

- More powerful are the node centrality measures, which can form useful features in a wide variety of node classification tasks.
- One popular measure of centrality is the eigenvector centrality, which takes into account the importance of node's neighbors.
- \cdot In particular, we define a node's eigenvector centrality e_{ν} via a recurrence relation in which the node's centrality is proportional to the average centrality of its neighbors:

$$
e_u = \frac{1}{\lambda} \sum_{v \in V} \mathbf{A}[u, v] e_v \,\forall u \in \mathcal{V},
$$

• where λ is a constant.

Node centrality

• Rewriting this equation in vector notation with e as the vector of node centralities, it defines the standard eigenvector equation for the adjacency matrix:

λ e = Ae

- •the centrality measure that satisfies the above equation corresponds to the eigenvector of the adjacency matrix corresponding to the largest eigenvalue.
- One view of eigenvector centrality is that it ranks the likelihood that a node is visited on a random walk of infinite length on the graph.

The clustering coefficient

• The popular local variant of the clustering coefficient is computed as follows:

$$
c_u = \frac{|(v_1, v_2) \in \mathcal{E} : v_1, v_2 \in \mathcal{N}(u)|}{\binom{d_u}{2}}.
$$

- The numerator counts the number of edges between neighbours of node u in $\mathcal{N}(u) = \{v \in \mathcal{V} : (u, v) \in \mathcal{E}\}.$
- The denominator calculates how many pairs of nodes there are in u 's neighborhood.

The clustering coefficient

- The clustering coefficient measures how tightly clustered a node's neighborhood is.
- A clustering coefficient of 1 would imply that all of u 's neighbors are also neighbors of each other.
- •As with centrality, there are numerous variations of the clustering coefficient (e.g., to account for directed graphs).
- •An important property of real-world networks is that they tend to have higher clustering coefficients than one would expect if edges were sampled randomly.

Node embeddings

William L. Hamilton, *Graph Representation Learning*, 2020

Node embeddings

- These methods encode nodes as low-dimensional vectors that summarize their graph position and the structure of their local graph neighborhood.
- In other words, we project nodes into a latent space, where geometric relations in this latent space correspond to relationships (e.g., edges) in the original graph or network.
- Node embeddings can be explained in the framework of encoding and decoding graphs.

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Encoding and decoding graphs

- First, an encoder model maps each node in the graph into a low-dimensional vector or embedding.
- Next, a decoder model takes the low-dimensional node embeddings and uses them to reconstruct information about each node's neighborhood in the original graph.

The encoder

- The encoder maps nodes $v \in V$ to vector embeddings $z_v \in \mathbb{R}^d$, where z_n corresponds to the embedding for node $v \in V$.
- •In the simplest case, the encoder has the following signature: $ENC: V \rightarrow \mathbb{R}^d$
- The encoder often relies on what we call the *shallow embedding* approach, where this encoder is simply an embedding lookup based on the node ID:

$$
ENC(v) = \mathbf{Z}[v]
$$

• where $\mathbf{Z} \in \mathbb{R}^{|V| \times d}$ is a matrix containing the embedding vectors for all nodes and $\mathbf{Z}[v]$ denotes the row of **Z** corresponding to node v .

Beyond shallow embedding

- The encoder can also be generalized beyond the shallow embedding approach.
- For instance, the encoder can use node features or the local graph structure around each node as input to generate an embedding.
- These generalized encoder architectures are often called graph neural networks (GNNs)

The decoder

- The role of the decoder is to reconstruct some graph statistics from the node embeddings that are generated by the encoder.
- For example, given a node embedding z_u of a node u , the decoder might attempt to predict u's set of neighbors $\mathcal{N}(u)$.
- It is standard to define pairwise decoders, which have the following signature:

$$
\text{DEC}: \mathbb{R}^d \times \mathbb{R}^d \rightarrow \mathbb{R}^+.
$$

•Pairwise decoders can be interpreted as predicting the relationship or similarity between pairs of nodes.

The decoder

- A simple pairwise decoder could predict whether two nodes are neighbors in the graph.
- Applying the pairwise decoder to a pair of embeddings $(\mathbf{z}_u, \mathbf{z}_v)$ results in the reconstruction of the relationship between u and v .
- The goal is optimizing the encoder and decoder to minimize the reconstruction loss, so that:

 $DEC(ENC(u);ENC(v)) = DEC(\mathbf{z}_u, \mathbf{z}_v) \approx S[u; v]$

- Here, we assume that $S[u; v]$ is a graph-based similarity measure between nodes.
- For example, the simple reconstruction objective of predicting whether two nodes are neighbors would correspond to

 $\mathbf{S}[u; v] \triangleq \mathbf{A}[u, v].$

Optimizing an Encoder-Decoder

• The standard practice is to minimize an empirical reconstruction $\cos \mathcal{L}$ over a set of training node pairs \mathcal{D} :

$$
\mathcal{L} = \sum_{(u,v)\in\mathcal{D}} \ell(\text{DEC}(\mathbf{z}_u, \mathbf{z}_v), \mathbf{S}[u; v]),
$$

- where $\ell: \mathbb{R} \times \mathbb{R} \to \mathbb{R}$ is a loss function measuring the discrepancy between the estimated $DEC(\mathbf{z}_u, \mathbf{z}_v)$ and the true values $S[u; v]$.
- Depending on the definition of DEC and S, the loss function ℓ can be a mean-squared error or even a classification loss.
- Most approaches minimize the loss using stochastic gradient descent, but matrix factorization can be also used.

Encoder-Decoder Approaches

Factorization-based approaches

- One way of viewing the encoder-decoder idea is from the perspective of matrix factorization.
- •Indeed, decoding local neighborhood structure from a node's embedding is closely related to reconstructing entries in the graph adjacency matrix.
- •We can view this as a matrix factorization task to learn a lowdimensional approximation of a node-node similarity matrix S, where S generalizes the adjacency matrix and captures some user defined notion of node-node similarity

Laplacian eigenmaps

- One of the earliest factorization-based approaches is the Laplacian eigenmaps (LE) technique, which builds upon the spectral clustering.
- In this approach, the decoder based on the L2-distance between the node embeddings is:

$$
\text{DEC}(\mathbf{z}_u, \mathbf{z}_v) = ||\mathbf{z}_u - \mathbf{z}_v||_2^2.
$$

• The loss function then weighs pairs of nodes according to their similarity in the graph:

$$
\mathcal{L} = \sum_{(u,v)\in\mathcal{D}} \text{DEC}(\mathbf{z}_u, \mathbf{z}_v) \cdot \mathbf{S}[u; v].
$$

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Laplacian eigenmaps

- The intuition behind this approach is that we penalize the model when very similar nodes have embeddings that are far apart.
- If S satisfies the properties of a Laplacian matrix, then the node embeddings that minimize the loss are identical to the solution for spectral clustering.
- If we assume the embeddings z_u are d-dimensional, then the optimal solution is given by the d smallest eigenvectors of the Laplacian (excluding zero eigenvalues and the eigenvector of all ones).

Inner-product methods

- Following on the Laplacian eigenmaps technique, we can use an inner-product based decoder, defined as follows: $DEC(z_u, z_v) = z_u^{\top} z_v$
- Here, we assume that the similarity between two nodes e.g., the overlap between their local neighborhoods – is proportional to the dot product of their embeddings.
- Some examples of this style of node embedding algorithms include the Graph Factorization (GF) approach [*Ahmed et al., 2013*], GraRep [*Cao et al., 2015*], and HOPE [*Ou et al., 2016*].

Inner-product methods

• These three methods combine the inner-product decoder with the following mean-squared error:

$$
\mathcal{L} = \sum_{(u,v)\in\mathcal{D}} ||\text{DEC}(\mathbf{z}_u, \mathbf{z}_v) - \mathbf{S}[u; v]||_2^2.
$$

- They differ primarily in how they define $S[u; v]$, i.e., the notion of node-node similarity or neighborhood overlap that they use.
- •Whereas the GF approach directly uses the adjacency matrix and sets $S \triangleq A$, the GraRep defines S based on powers of the adjacency matrix, while the HOPE uses neighborhood overlap measures.

Random walk embeddings

- The inner-product methods discussed so far all employ deterministic measures of node similarity.
- \cdot They often define S as a polynomial function of the adjacency matrix, and the node embeddings are optimized so that $\mathbf{z}_u^{\mathsf{T}} \mathbf{z}_v \approx$ $\mathbf{S}[u, v]$.
- •Building on these, many methods have adapted the innerproduct approach to use stochastic measures of neighborhood overlap.
- •Key innovation: two nodes have similar embeddings if they tend to co-occur on short random walks over the graph.

- Similar to the matrix factorization approaches described so far, DeepWalk and node2vec use a shallow embedding approach and an inner-product decoder.
- The key distinction in these methods is in how they define the notions of node similarity and neighborhood reconstruction.
- Instead of directly reconstructing the adjacency matrix $A or$ some deterministic function of $A -$ these approaches optimize embeddings to encode the statistics of random walks.

- The goal is to learn embeddings so that the following holds: $DEC(\mathbf{z}_u, \mathbf{z}_v) \equiv$ $e^{\mathbf{z}_u^{\mathsf{T}}\mathbf{z}_v}$ $\overline{\sum_{\substack{\bm{\nu}_k\in V}}\mathbf{z}_{u}^{\top}\mathbf{z}_{\bm{\nu}}}$ $\approx p_{\mathcal{G},T}(u|v)$
- where $p_{G,T}(u|v)$ is the probability of visiting v on a length-T random walk starting at u , with T usually defined to be in the range $T \in \{2, ..., 10\}$.
- •Again, a key difference with the factorization-based approaches is that here the similarity measure is both stochastic and asymmetric.

• To train random walk embeddings, the general strategy is to use the above decoder and minimize the cross-entropy loss:

$$
\mathcal{L} = \sum_{(u,v)\in\mathcal{D}} -\log(\text{DEC}(\mathbf{z}_u, \mathbf{z}_v)).
$$

- Here, we use D to denote the training set of random walks, which is generated by sampling random walks starting from each node.
- \cdot For example, we can assume that N pairs of co-occurring nodes for each node u are sampled from the distribution $(u, v) \sim p_{G,T}(u|v)$.

- Evaluating that loss function can be computationally expensive.
- node2vec employs a *noise contrastive* approach, where the normalizing factor is approximated using negative samples [Grover and Leskovec, 2016]:

$$
\mathcal{L} = \sum_{(u,v)\in\mathcal{D}} -\log(\sigma(\mathbf{z}_{u}^{\top}\mathbf{z}_{v})) - \gamma \mathbb{E}_{v_{n} \sim P_{n}(V)}[\log(-\sigma(\mathbf{z}_{u}^{\top}\mathbf{z}_{v_{n}}))].
$$

• Here, σ denotes the logistic function, $P_n(\mathbf{V})$ to denote a distribution over the set of nodes V, and $y > 0$ is a hyperparameter.

Limits: parameter sharing

- Shallow embedding methods do not share any parameters between nodes in the encoder, since the encoder directly optimizes a unique embedding vector for each node.
- This lack of parameter sharing is both statistically and computationally inefficient.
- From a statistical perspective, parameter sharing can improve the efficiency of learning and also act as a powerful form of regularization.
- From the computational perspective, the number of parameters necessarily grows as $O(|V|)$, which can be intractable in massive graphs. **ORA 2024**

Limits: leveraging

- •A second key issue with shallow embedding approaches is that they do not leverage node features in the encoder.
- Many graph datasets have rich feature information, which could potentially be informative in the encoding process.

Limits: transductivity

- Shallow embedding methods are transductive: they can generate embeddings only for training nodes.
- Generating embeddings for new nodes is sometimes possible with additional optimizations to learn their embeddings.
- This restriction prevents shallow embedding methods from being used on inductive applications, which involve generalizing to unseen nodes after training.