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Introduction to Graph Neural Networks

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Outline

- Graph terminology
- Graph neural networks

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Introduction to graphs

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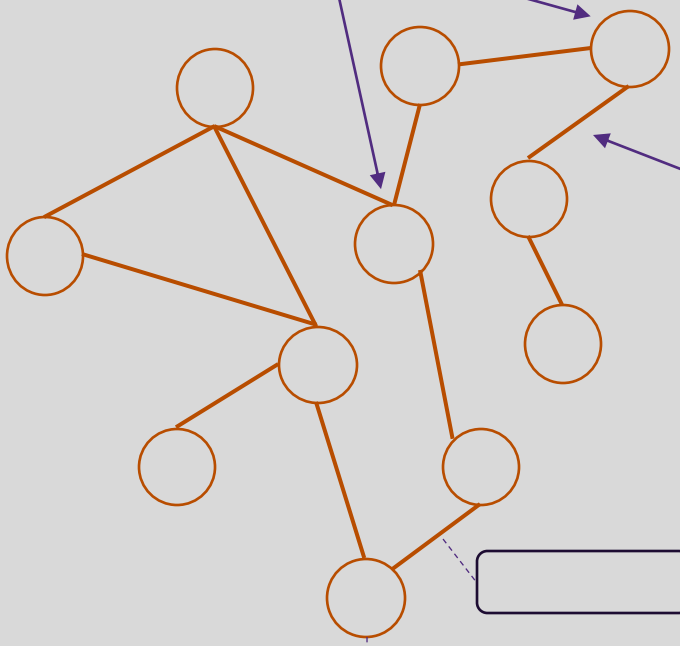
Terminology

Neighbors – two nodes connected by an edge
Neighborhood – all neighbors of a node



Vertices (nodes) usually represent entities (e.g., a patient, symptom, disease, cell type, atom/molecule, gene)

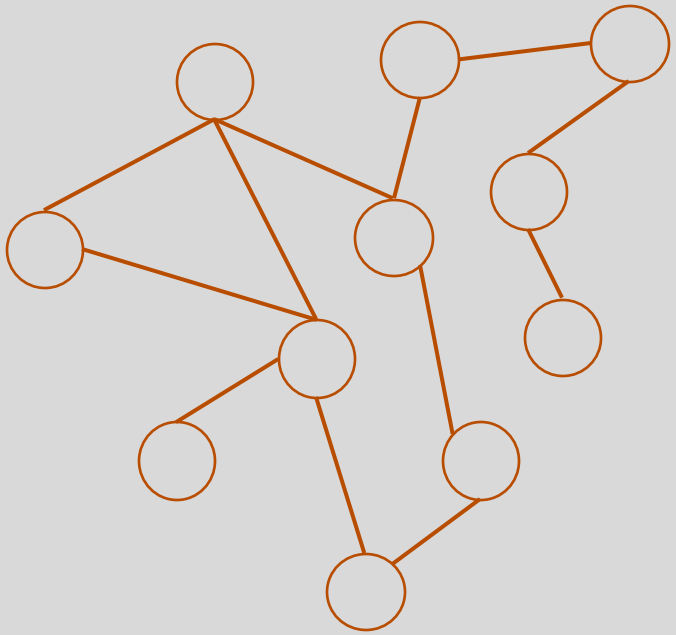
Edges usually represent relationships between nodes (e.g., “has symptom”, “causes disease”, “bonds with”, “regulates expression of”).

Graph representations may also include *attributes* (vertex / edge properties, e.g., text description).
Why not just represent these as additional vertices?

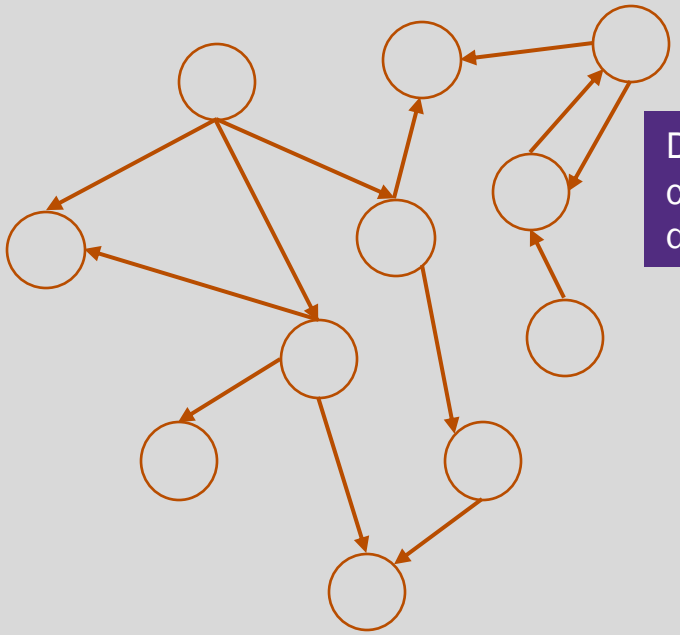
- Tends to lead to very dense networks for properties that are common to most nodes.
- Such properties usually don’t describe relations between nodes
- Computational efficiency

Terminology

Undirected Graph – edges have no direction and define relations that are inherently bidirectional.

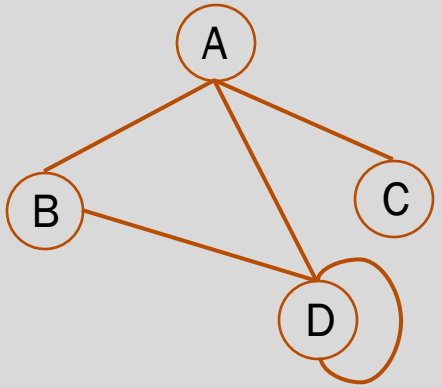


Directed Graph – edges have a specified direction and define relations that are inherently unidirectional.

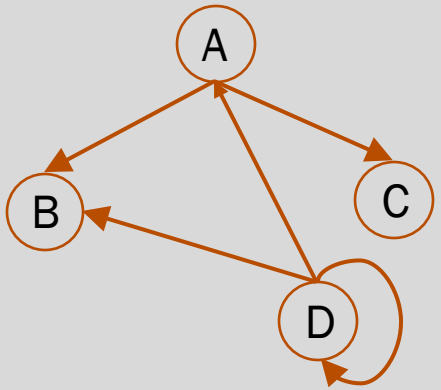


Directed graphs may contain edges in both directions between nodes.

Adjacency matrix



	A	B	C	D
A	0	1	1	1
B	1	0	0	1
C	1	0	0	0
D	1	1	0	1

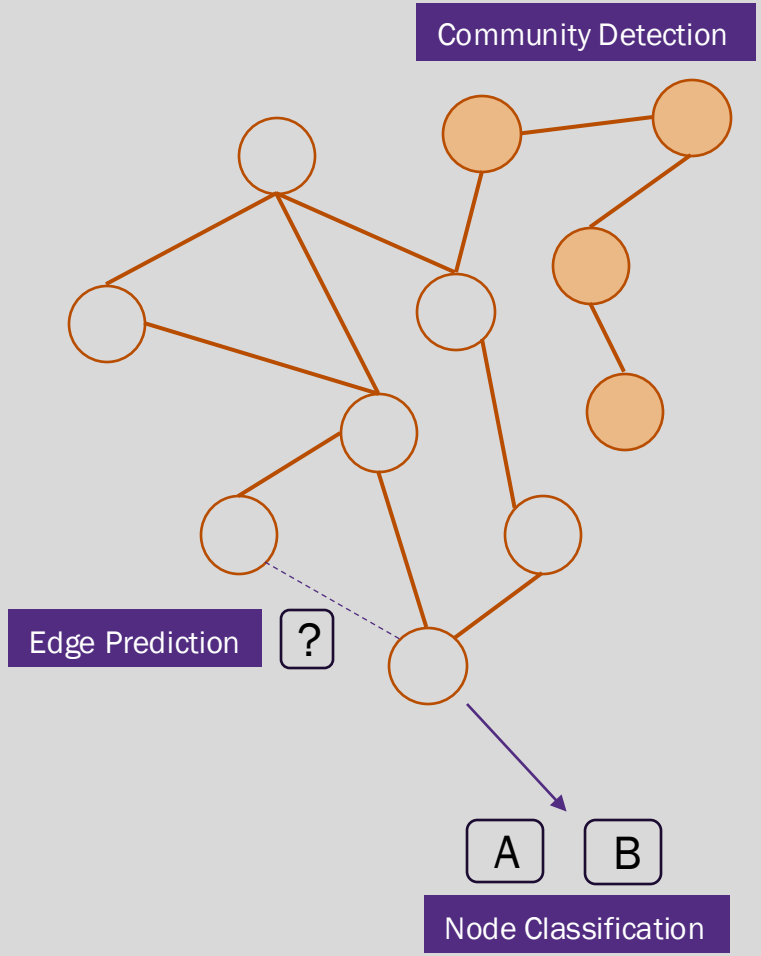


	A	B	C	D
A	0	1	1	0
B	0	0	0	0
C	0	0	0	0
D	1	1	0	1

- Adjacency matrix, A, summarizes the edges in a graph where the element $a_{i,j} \in A$ is the weight of the edge $e_{i,j} \in E$. For unconnected vertices, v_i, v_j, $a_{i,j} = 0$
- Adjacency matrix is symmetric for undirected graphs and usually asymmetric for directed graphs
- For graphs without self loops, $a_{i,i} = 0$, i.e., the diagonal elements are all 0

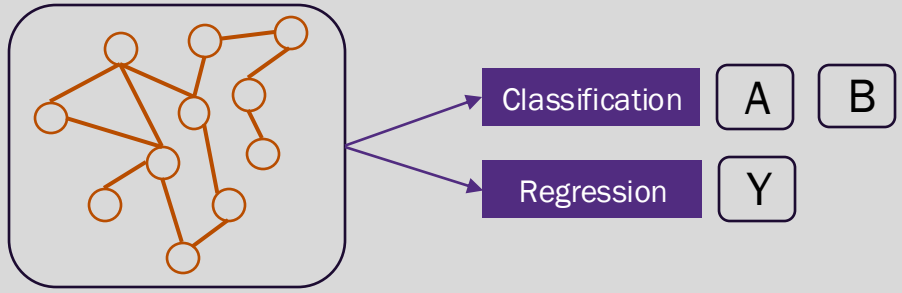
Intra-graph machine learning tasks

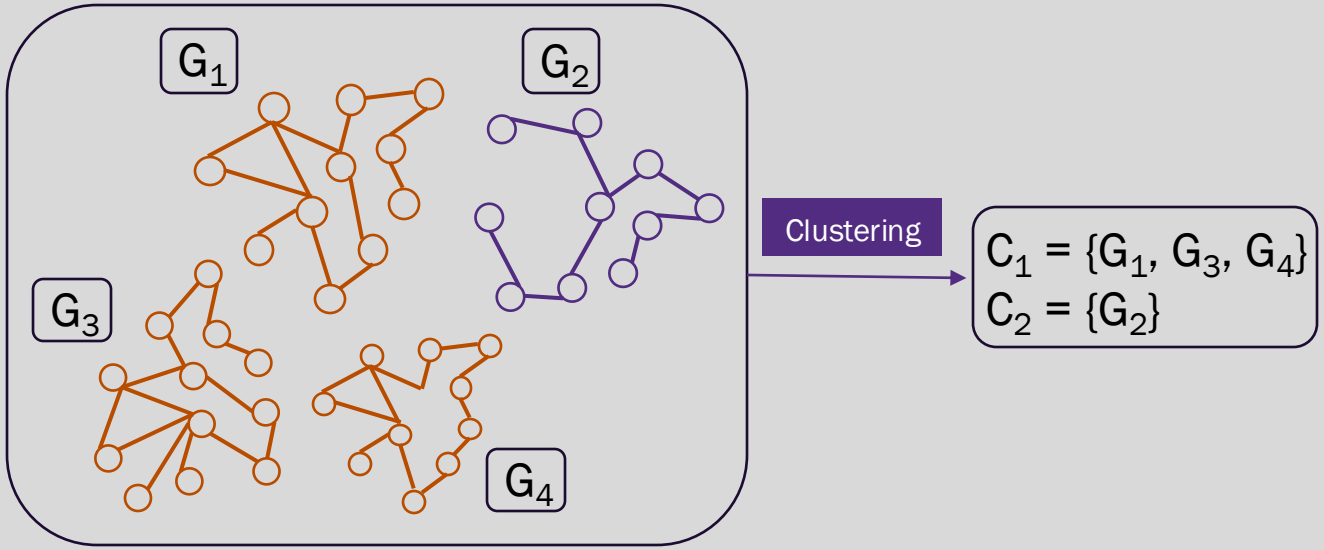
- Node classification – given information about the node (may include neighbors, relationships, attributes), infer class membership (usually an attribute)
- Edge prediction – given information about two nodes, determine if a given relation exists between them
- Community detection (node clustering) – detection of “meaningful” node groups



Whole graph and inter-graph machine learning tasks

- Whole graph classification and regression – given one entire graph, infer class membership or estimate (regress) a related numerical property
- Inter graph tasks – given multiple graphs estimate the similarity between graphs and/or identify clusters





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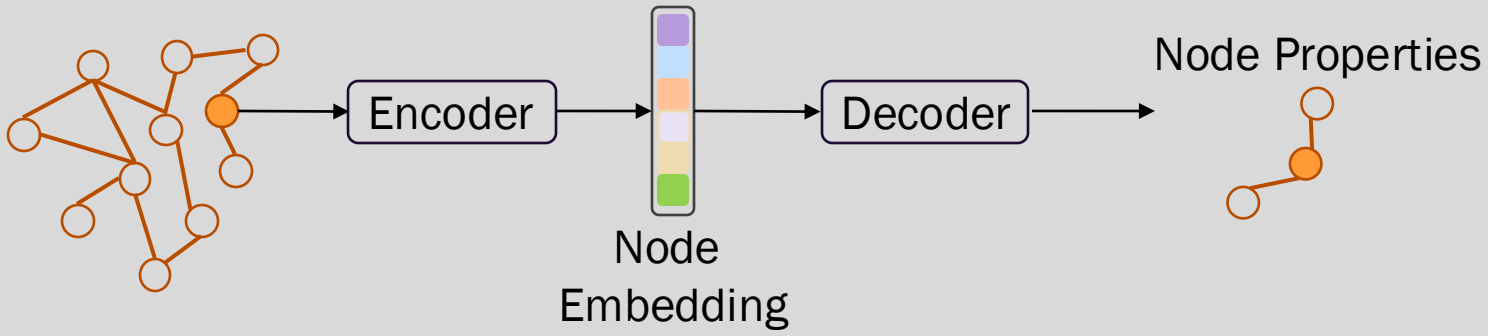
Graph neural networks

Graph representation for machine learning

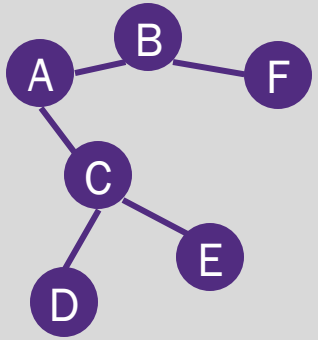
- Traditional approaches utilize engineered features (e.g., node degree, adjacency matrix eigenvalues) to represent nodes, edges, and graphs for analysis
- Graph neural network (GNN) approaches adopt an *encoder – decoder* perspective
  - *encoder* transforms the graph elements (nodes, edges, entire graph) into a latent space
  - *decoder* estimates values of interest (class membership, node attributes, relationships) from the encoded representation



Random walk methods

- Shallow embedding approaches that attempt to encode random walk statistics
- Goal is for the decoder to approximate the probability distribution of visiting a node v on a path of length T starting at node u on graph G

$$P_{G,T}(v|u)$$



Random Walks

- Assume we have transition states, $p(u, v \mid v \epsilon N(u))$ that define the probability of traversing from node u to v
- Random walks are generated by starting at a randomly selected node, u , and probabilistically selecting the next node from $N(u)$ and repeating
- Sample paths from the graph above include
  - ABF
  - ABACE
  - ABADC

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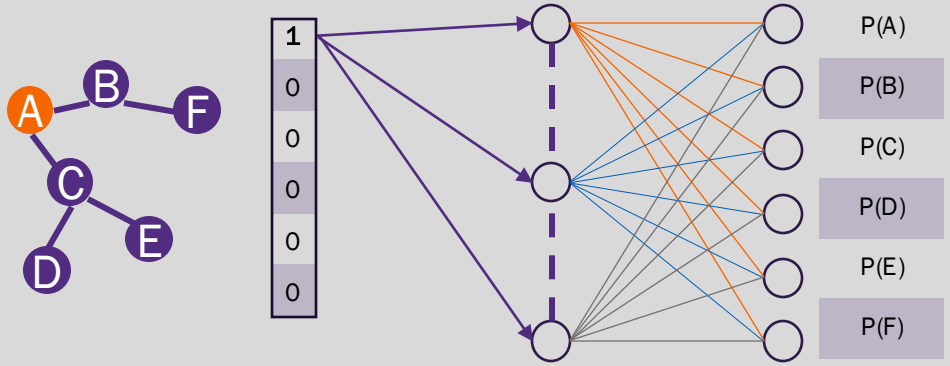
+node2vec



Input Node Represented as a 1-hot encoding

Hidden linear layer. Effectively a look up for the weight row corresponding to the input node.

Softmax output represents probabilities of encountering each node in a random walk

Training with Negative Sampling

- Assume we've sampled many random walks
- From those we can generate sample node pairs *(u,v)*
- Computing normalized probabilities over all nodes is expensive
- Instead, for each sample, the input is *u* and the target output is a 1 hot encoding where the value at the index for node *v* is set to 1 and 0 for indices corresponding to a small number of randomly selected nodes

	T=1	T=2
ABF	AB	AF
	BF	
ABACE	AB	AA
	BA	BC
	AC	AE
	CE	
ABACD	AB	AA
	BA	BC
	AC	AD
	CD	

+Grover, Aditya, and Jure Leskovec. "node2vec: Scalable feature learning for networks." Proceedings of the 22nd ACM SIGKDD international conference on Knowledge discovery and data mining. 2016.

Message passing methods

- Intended to address limitations of shallow embeddings - especially inability to use node feature information and transductive nature (i.e., can only learn embeddings for nodes present during training)
- Methods are motivated by the need to satisfy *permutation invariance,* i.e., the results should not depend on node ordering as there is no natural ordering of nodes in a graph
- Defining characteristic of most recent graph neural networks (GNNs) is the use of *message passing* – vector messages sent between nodes

Convolutional graph neural networks

- Convolutional in the sense that parameters are shared across the graph
- Assume node features are represented by $N \times D$ matrix X (N nodes, D features). For graphs where nodes have no features, set $X = I$
- Every layer, $H^{(l)}$, can be written as

$$H^{(l+1)} = f\left(H^{(l)}, A\right)$$

  where A is the adjacency matrix, $H^{(0)} = X$.
- For *vanilla* convolutional neural network

$$f\left(H^{(l)}, A\right) = \sigma\left(\hat{D}^{-\frac{1}{2}}\hat{A}\hat{D}^{-\frac{1}{2}}H^{(l)}W^{(l)}\right)$$

Diagonal node degree matrix (used to normalize rows of A)

Augmented adjacency matrix (diagonal elements all set to 1)

Weight matrix for layer l. Importantly, the dimension of W is independent of the size of the graph.

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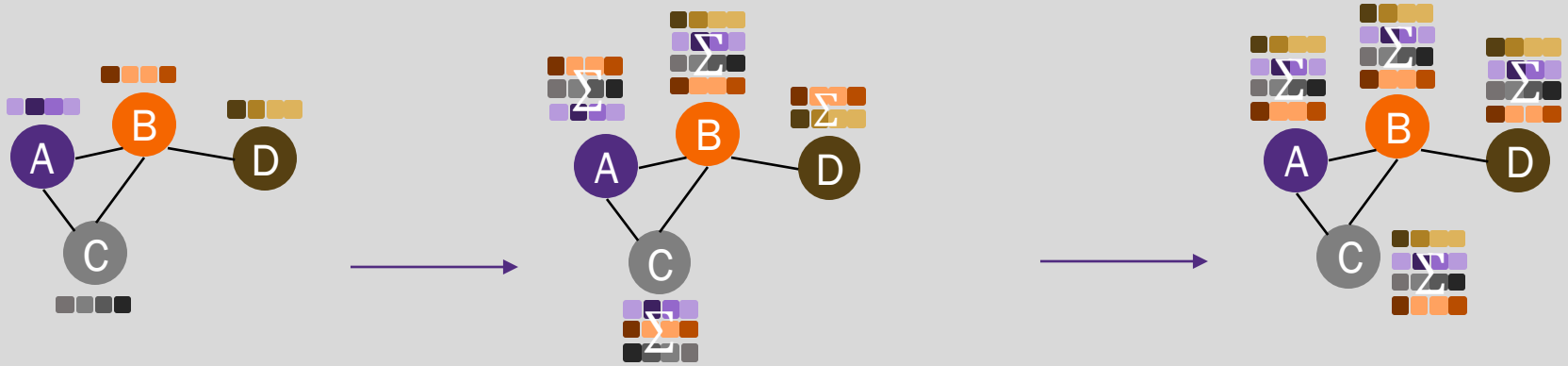
Convolutional graph neural networks

After the first layer, each node representation is now the weighted sum of its input feature representation and its neighbors input features (**the messages**)

After the second layer, each node representation is now the weighted sum of its input feature representation and its 1 and 2 hop neighbors



$$H^{(0)} = X$$

$$H^{(1)} = \sigma\left(\hat{D}^{-\frac{1}{2}}\hat{A}\hat{D}^{-\frac{1}{2}}XW^{(1)}\right)$$

$$H^{(2)} = \sigma\left(\hat{D}^{-\frac{1}{2}}\hat{A}\hat{D}^{-\frac{1}{2}}H^{(1)}W^{(2)}\right)$$

$\hat{A} =$

	A	B	C	D
A	1	1	1	0
B	1	1	1	1
C	1	1	1	0
D	0	1	0	1

Consider $\hat{A}X$. This updates the feature row for each node as the sum of its features and its neighbor's features

Consider $\hat{A}H^1$. This updates the feature row for each node as in the first layer, but now the representation of each node neighbor contains information from their neighbors as well.

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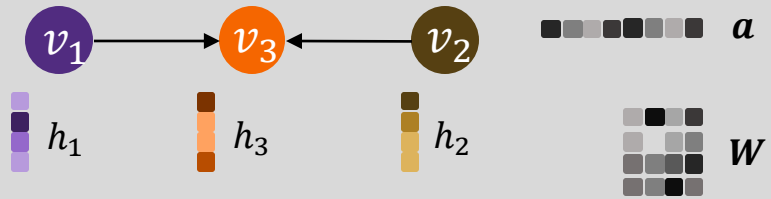
Graph attention

- Similar attention mechanism to transformers. Recall the QKV paradigm.
- The key (K) and value (V) are the transformed message from a neighboring node (e.g., output of an MLP applied to message).
- The receiving node uses the transformed version of its feature representation as the query (Q)



Message transformation MLP weights

GCN weights

$$\alpha_{ij} = \frac{exp\left(\sigma\left(\boldsymbol{a}\left[\boldsymbol{W}h_i || \boldsymbol{W}h_j\right]\right)\right)}{\sum_{k \in N_i} exp\left(\sigma\left(\boldsymbol{a}\left[\boldsymbol{W}h_i || \boldsymbol{W}h_k\right]\right)\right)}$$

Attention weight applied to message from node j to node i , where N_i are the neighbors of node i (which includes node i)

$$h'_i = \sigma\left(\sum_{j \in N_i} \alpha_{ij} \boldsymbol{W}h_j\right)$$

Attention based representation of node i

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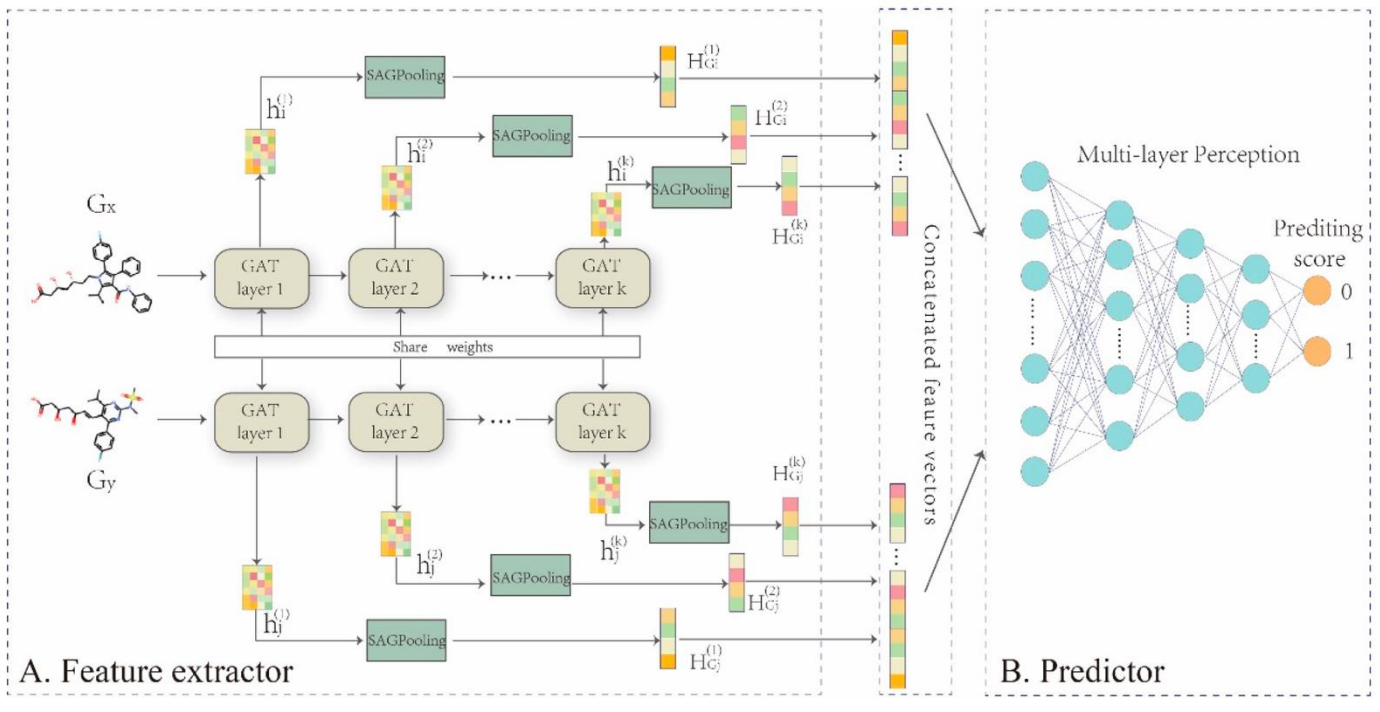
Applications

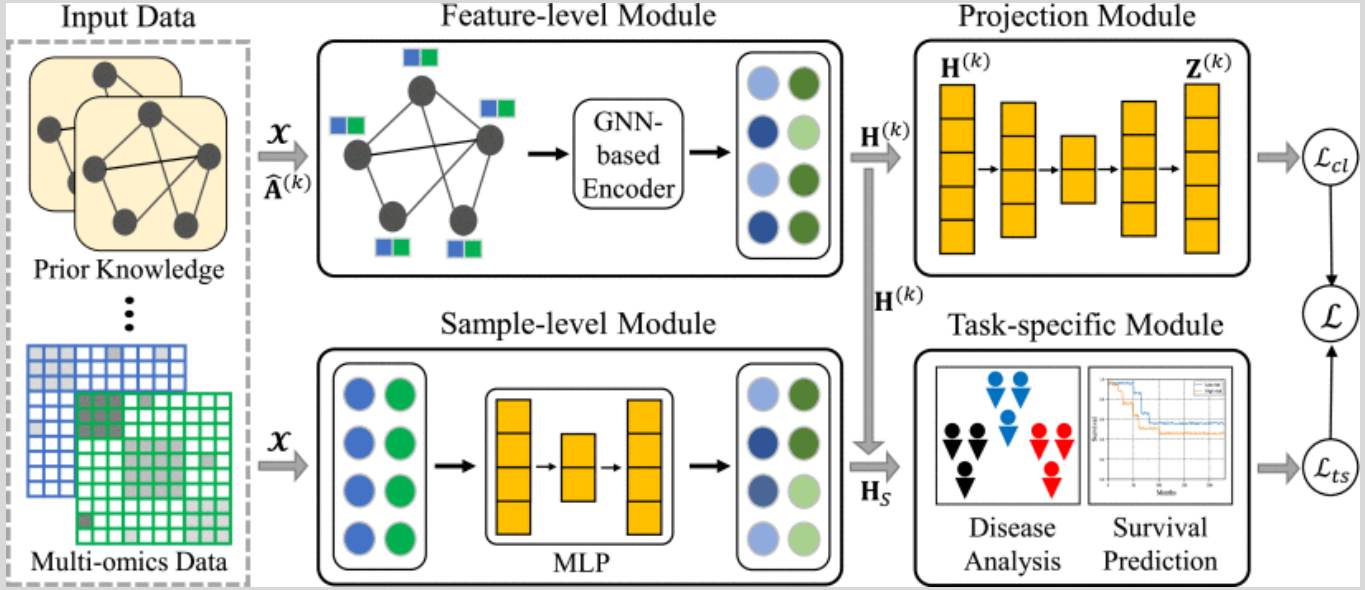
GNN drug-drug interaction prediction



- Each drug is represented by a graph
  - Nodes represent atoms
  - Edges represent bonds
  - Node features (78 dims) include atomic symbol, valence, formal charge, number of free radical electrons, hybridization, number of hydrogen bonds, and aromaticity
- Each drug in a candidate DDI pair is passed through a 5-layer GCN with attention
- Output node representations are down sampled via Self-attention graph (SAG) pooling to form an overall representation of each drug
- Drug representations are concatenated and passed through a FFN for DDI classification

Feng, Y.-H.; Zhang, S.-W. Prediction of Drug-Drug Interaction Using an Attention-Based Graph Neural Network on Drug Molecular Graphs. Molecules 2022, 27, 3004

Integrating prior knowledge for cancer subtype prediction



- Prior knowledge is represented as a graph
  - Nodes represent genes (selected based on omics)
  - Edges represent relationships between genes (bespoke rules based on the knowledge base)
  - Graph representation from GNN encoder
  - Projection model attempts to maximally contrast gene representations from knowledge base
- Patient level omics data processed in MLP
- Output representations of prior knowledge and patient omic data combined and passed to task-specific module

S. Xiao, H. Lin, C. Wang, S. Wang and J. C. Rajapakse, "Graph Neural Networks With Multiple Prior Knowledge for Multi-Omics Data Analysis," in IEEE Journal of Biomedical and Health Informatics, vol. 27, no. 9, pp. 4591-4600, Sept. 2023

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Biology informed AI – improving explainability

Central hypothesis: AI that utilizes abductive reasoning through integration of formal biology knowledge with observational data will demonstrate improved inference performance and explainability in limited data settings.

Our Methodological Research

- Selective attention mechanisms to identify knowledge graph concepts relevant to AI system output
- Pathway analysis methods to trace the paths in the knowledge graph that lead to a particular prediction