

# Graph Machine Learning

**AI-guided Protein Science**

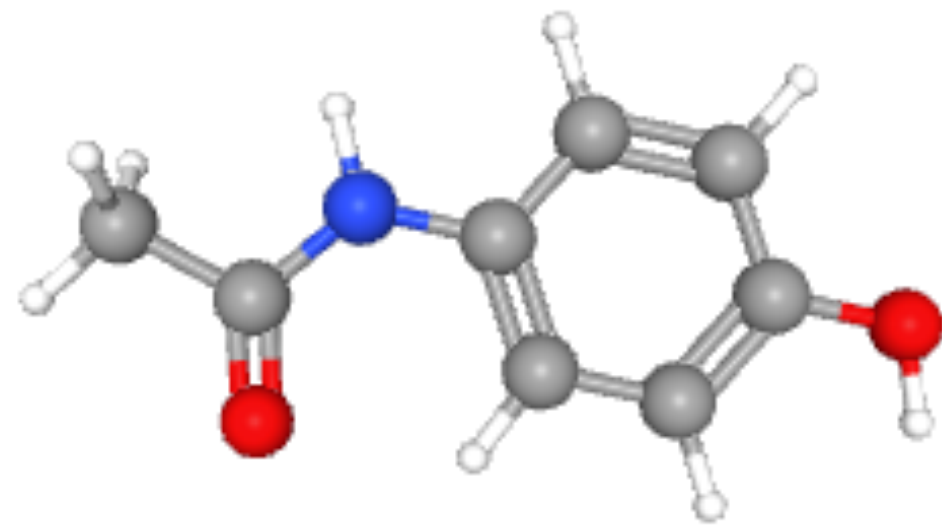
**Alberto Santos — Multi-omics Network Analytics (MoNA)**



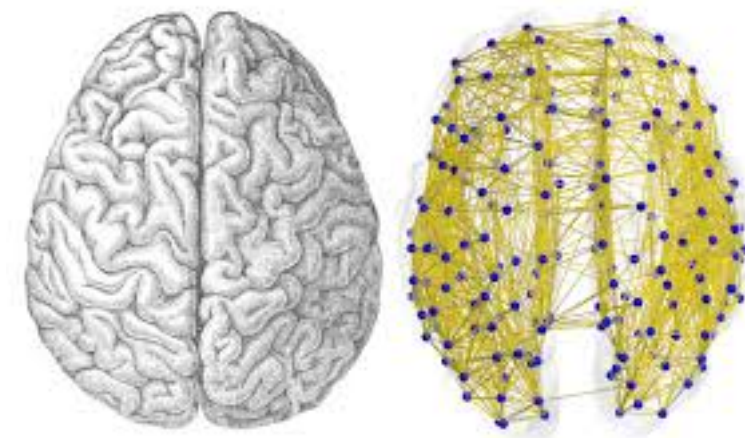
# Limitations of Deep Learning

- Standard DL (CNNs, RNNs, Transformers) is limited to work with data that is **structured** in regular formats, such as **images**, **sequences**, and **grids**.
- What about **different structures**?

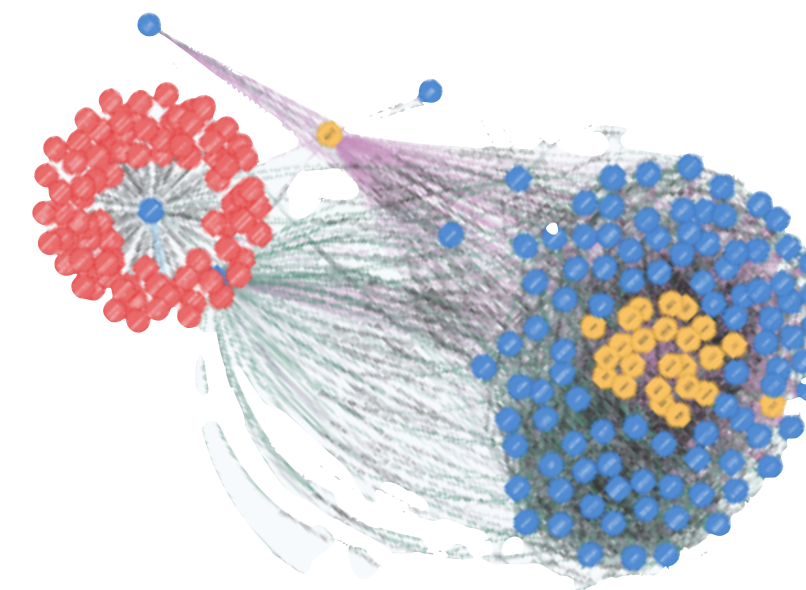
Graphs are everywhere and help describe complex systems



Molecules



Connectivity



Knowledge graphs



PPIs

# Machine Learning on Graphs

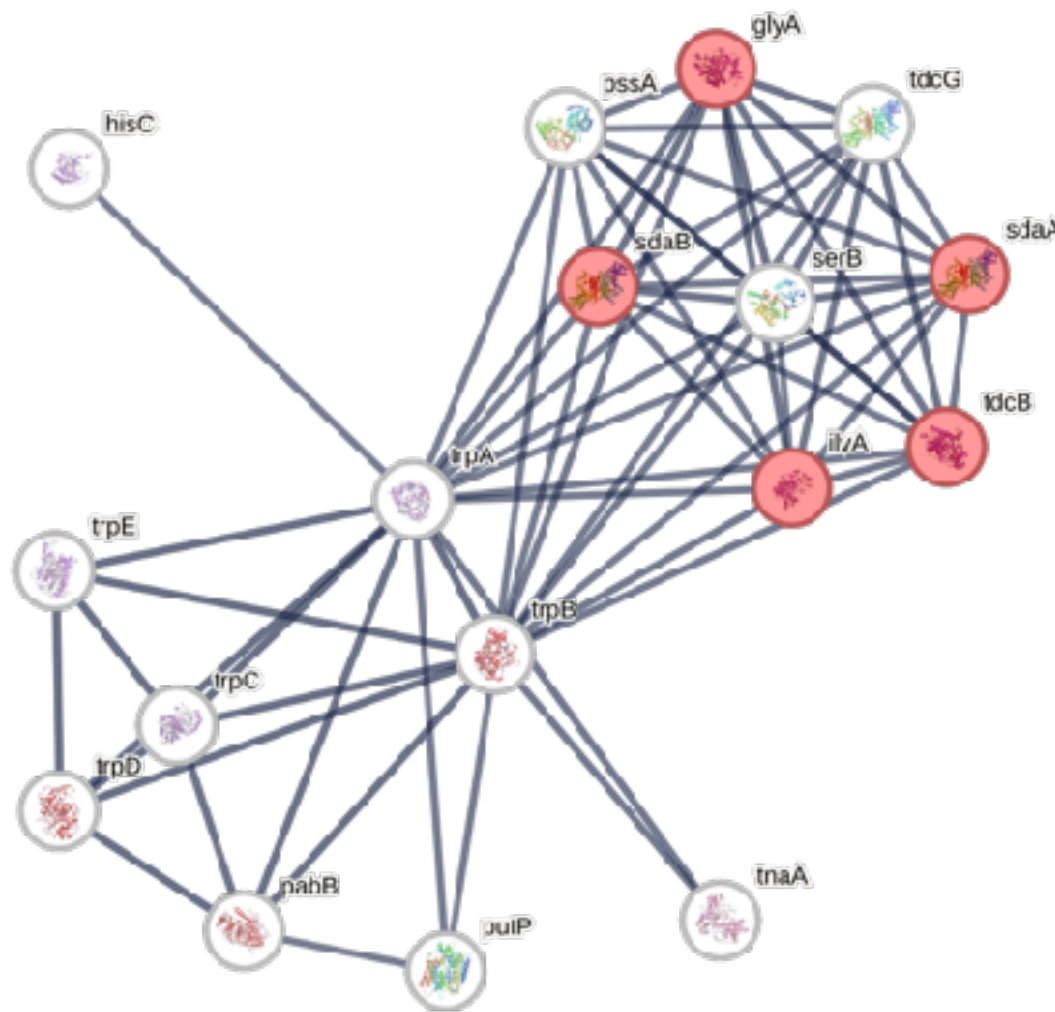
- Three types of prediction tasks:
  - **Node-level**: predict the identity, role or features of nodes within a graph.
  - **Edge-level**: predict relationships between nodes or features of these relationships.
  - **Graph-level**: predict the property of an entire graph.
- Graphs contain different information that we can use to make predictions: nodes, edges, global-context and connectivity.



# Node Classification

- Predict the label (type, category or attribute) associated with all the nodes in the graph

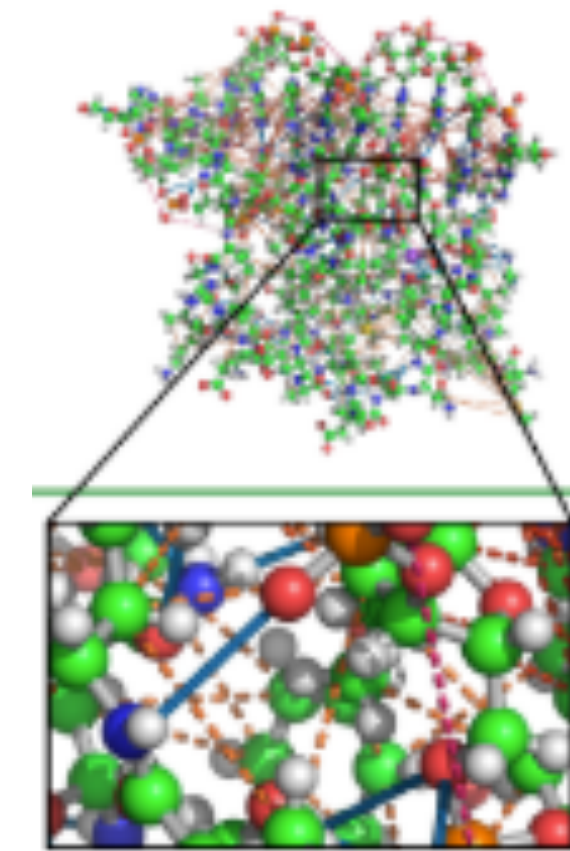
## Examples



Classifying the function of proteins



Classifying cell types

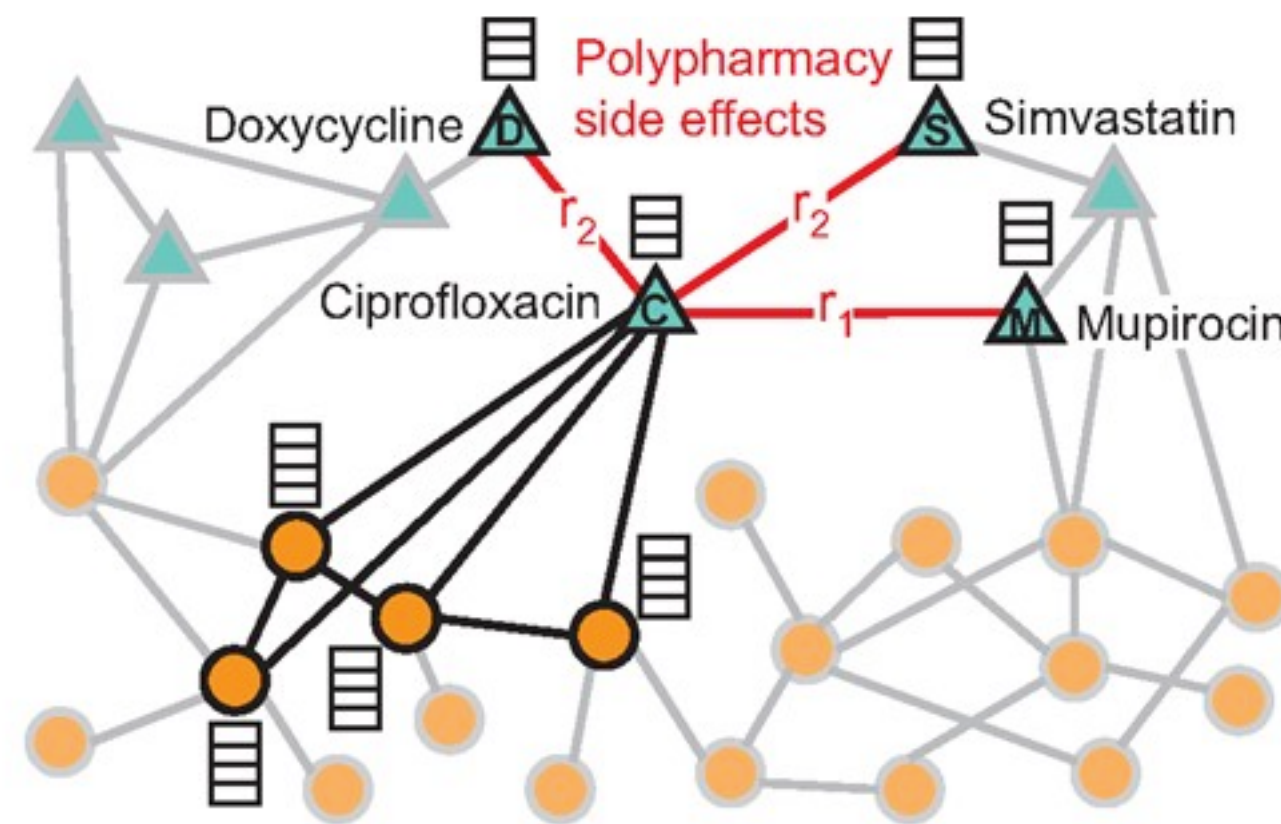


Classifying amino acids

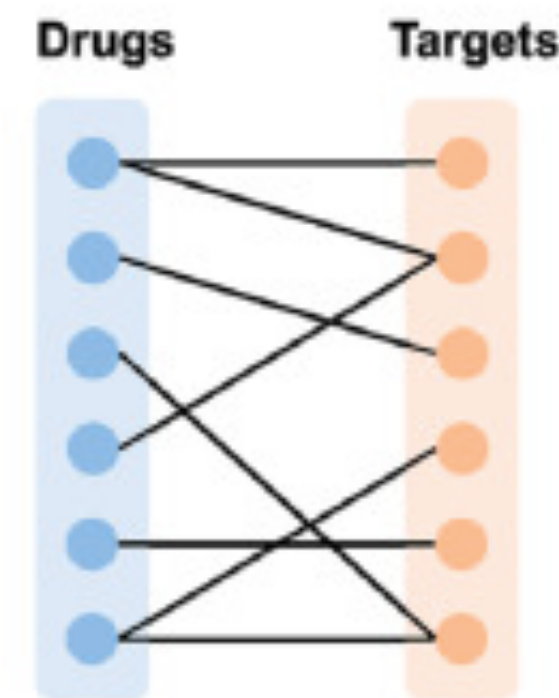
# Relation Prediction

- Given a set of nodes and an incomplete set of edges between these nodes, we want to infer the missing edges using the structure of the graph

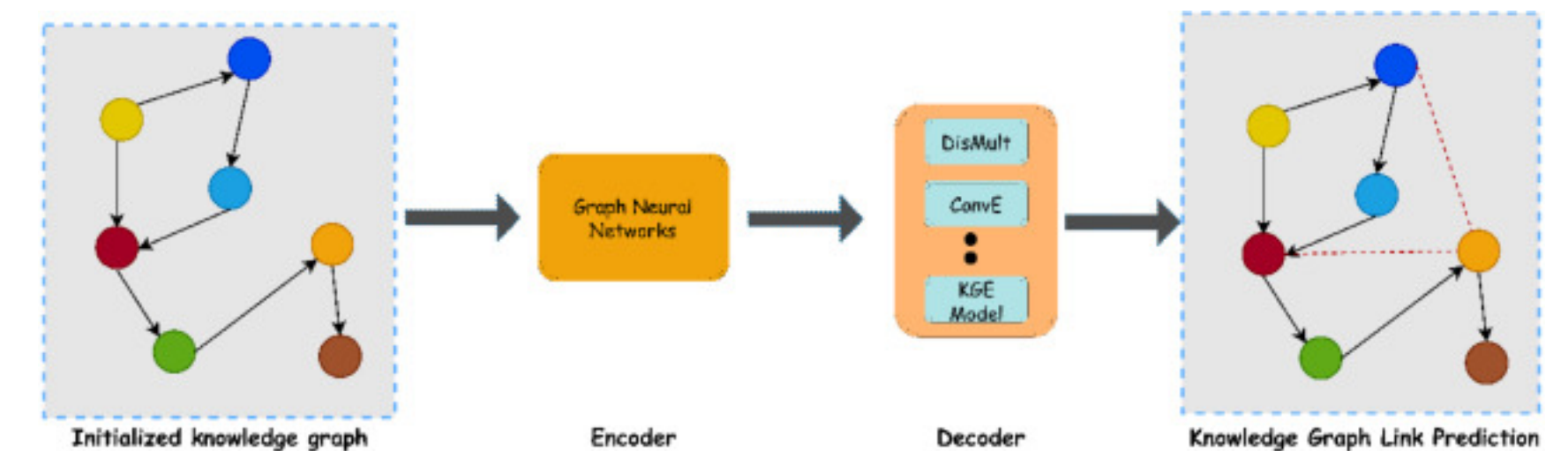
# Examples



# Drug-Side effect prediction



# Drug-Target prediction



# Knowledge Graph completion

Modeling polypharmacy side effects with graph convolutional networks. 2018. Marinka Zitnik, Monica Agrawal, Jure Leskovec

Graph neural network approaches for drug-target interactions. 2022. Zehong Zhang, Lifan Chen , Feisheng Zhong, Dingyan Wang, Jiaxin Jiang, Sulin Zhang, Hualiang Jiang, Mingyue Zheng, Xutong Li

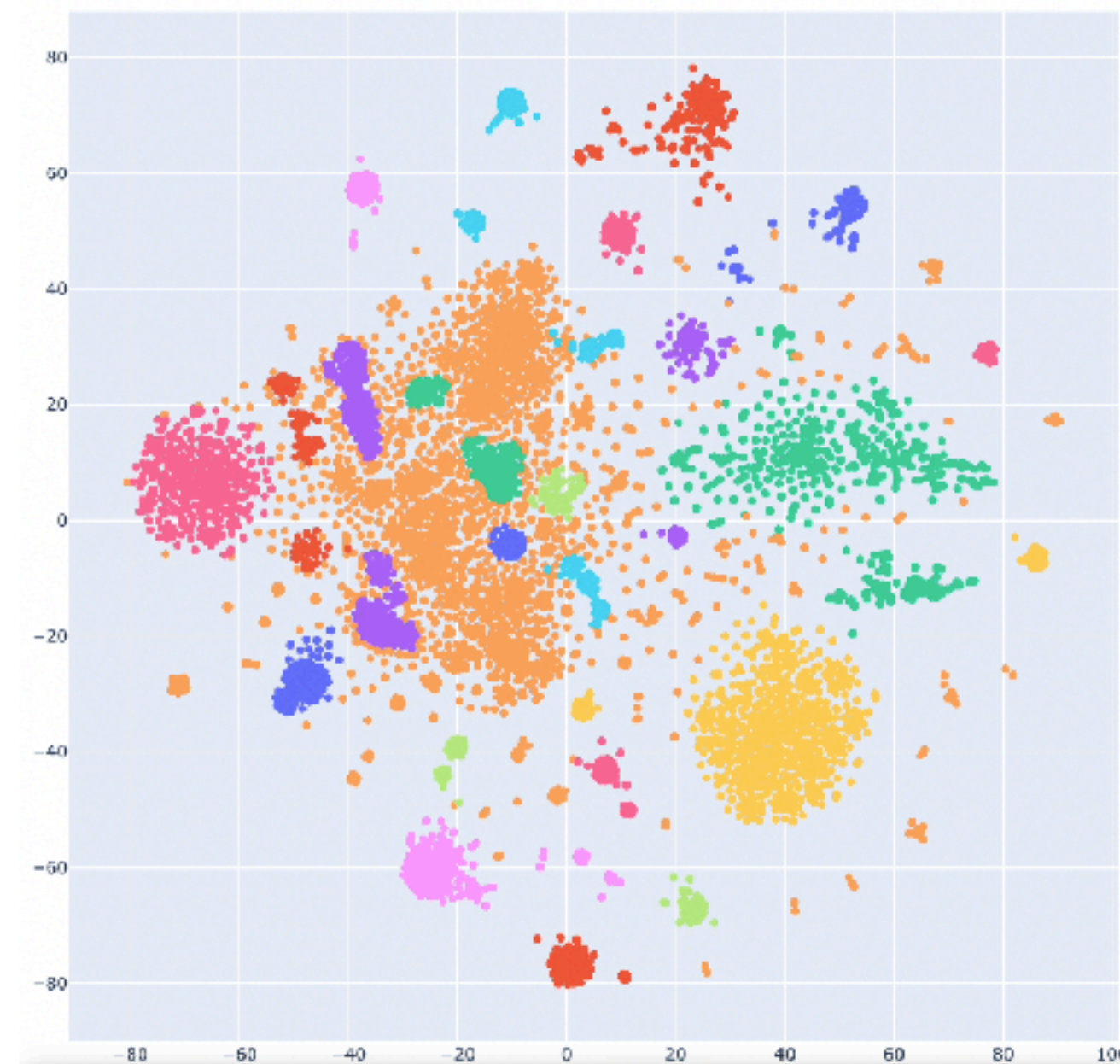
A knowledge graph completion model based on contrastive learning and relation enhancement method.2022. LinYu Li, Xuan Zhang, YuBin Ma, Chen Gao, Jishu Wang, Yong Yu, Zihao Yuan, Qiuying Ma



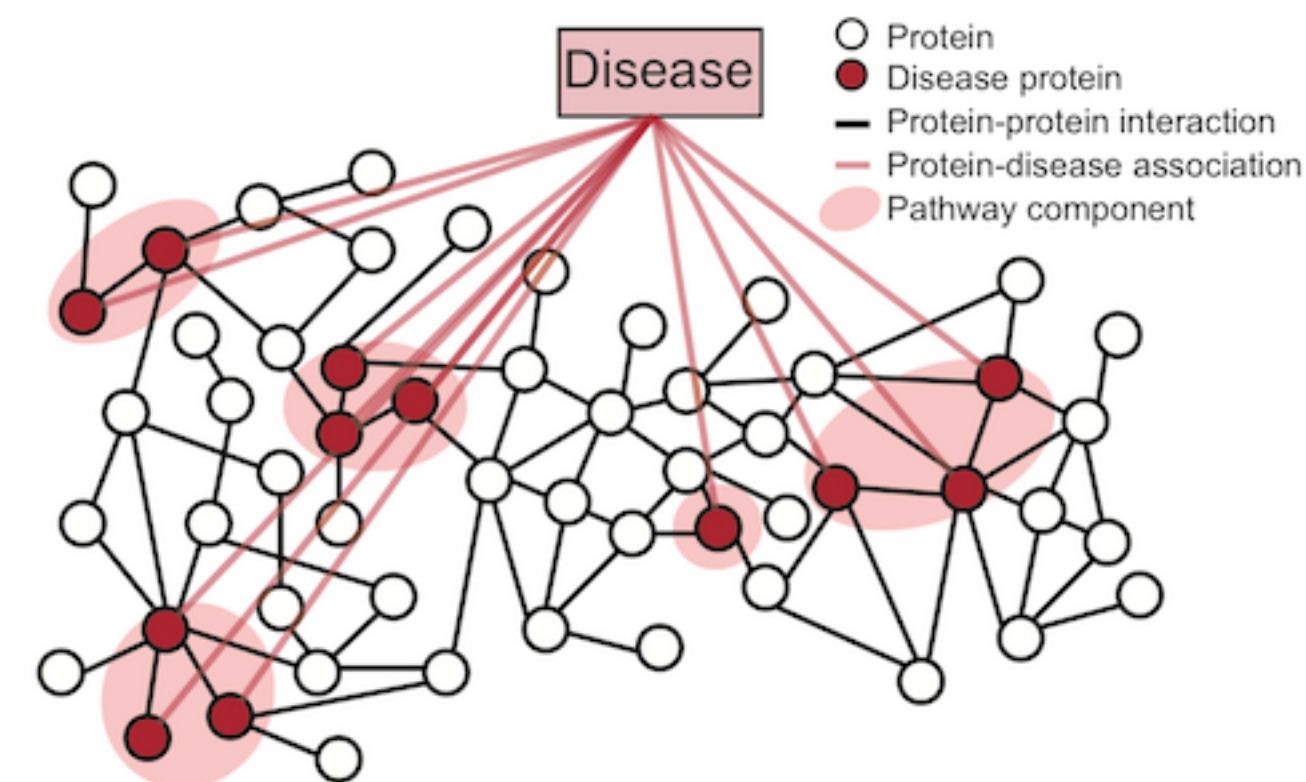
# Community Detection

- Identify clusters where nodes are more likely to form edges

## Examples



Detecting microbial communities



Disease pathways

Large-scale analysis of disease pathways in the human interactome. 2018. Monica Agrawal, Marinka Zitnik, Jure Leskovec.

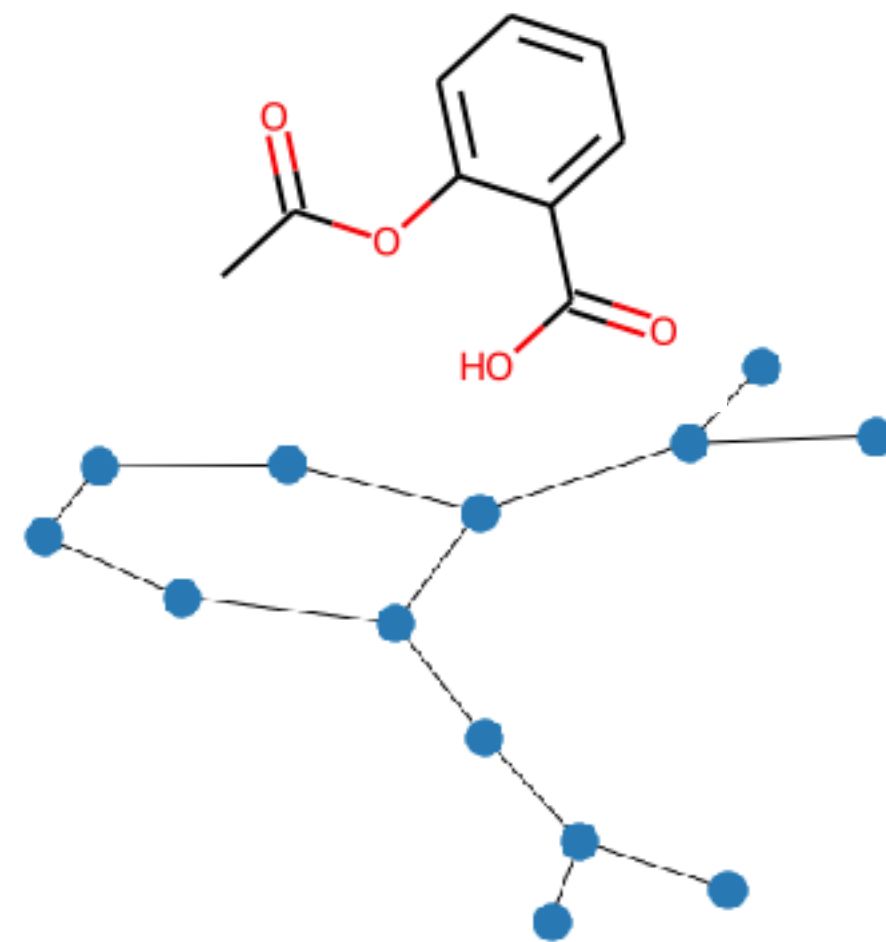
[https://micw2graph.streamlit.app/Microbial\\_association\\_networks](https://micw2graph.streamlit.app/Microbial_association_networks)

[https://github.com/benedekrozemberczki/awesome-community-detection/blob/master/chapters/deep\\_learning.md](https://github.com/benedekrozemberczki/awesome-community-detection/blob/master/chapters/deep_learning.md)

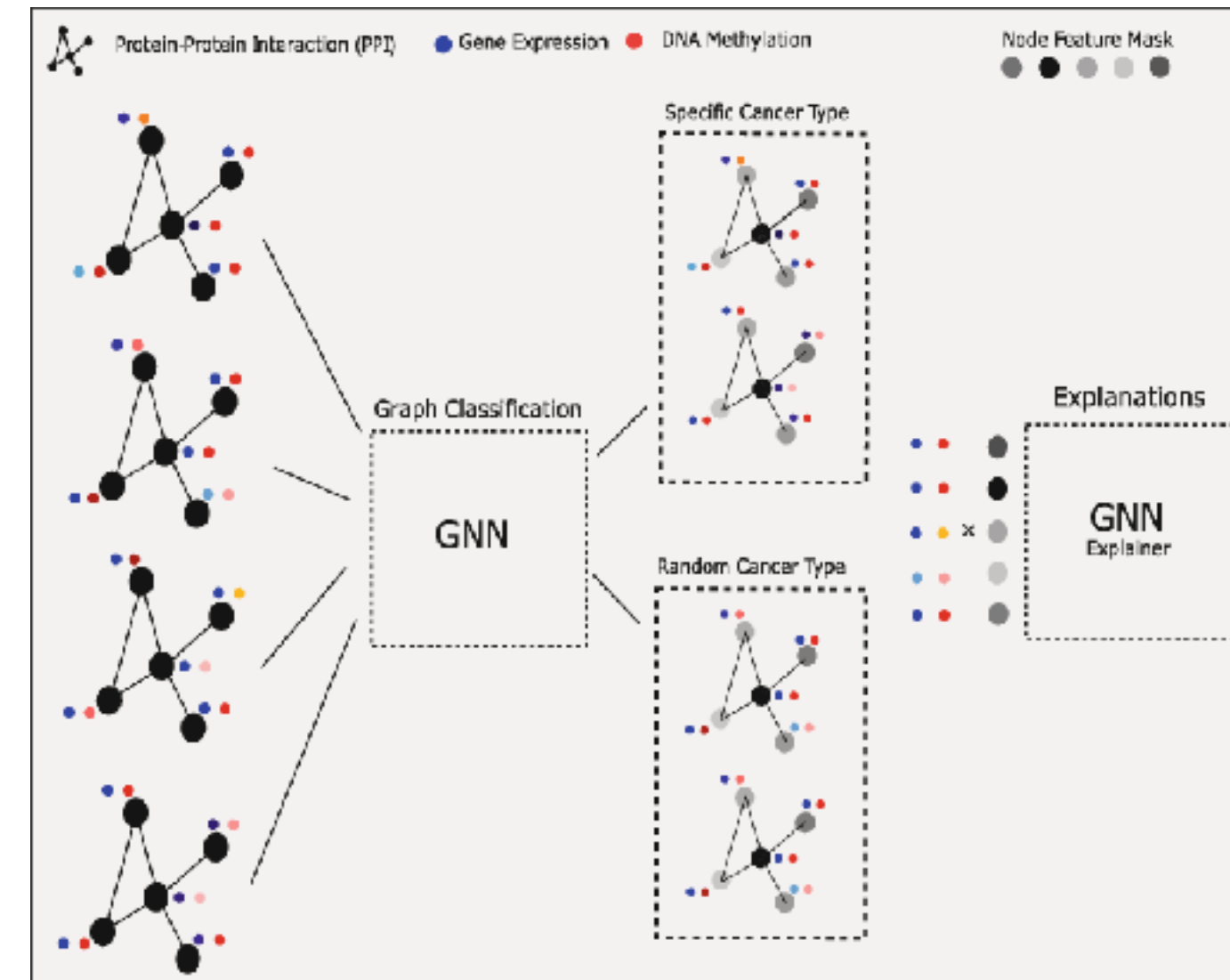
# Graph Classification/Regression

- Learn over graph data and make independent predictions for each graph

## Examples



Predicting molecular properties



Patient stratification

# Important Concepts

- **Independence** — points are not independent and identically distributed (interconnected nodes)
- **Homophily** — tendency of nodes to share attributes with their neighbours
- **Structural equivalence** — Nodes with similar local structures will share similar labels



# Traditional Approaches

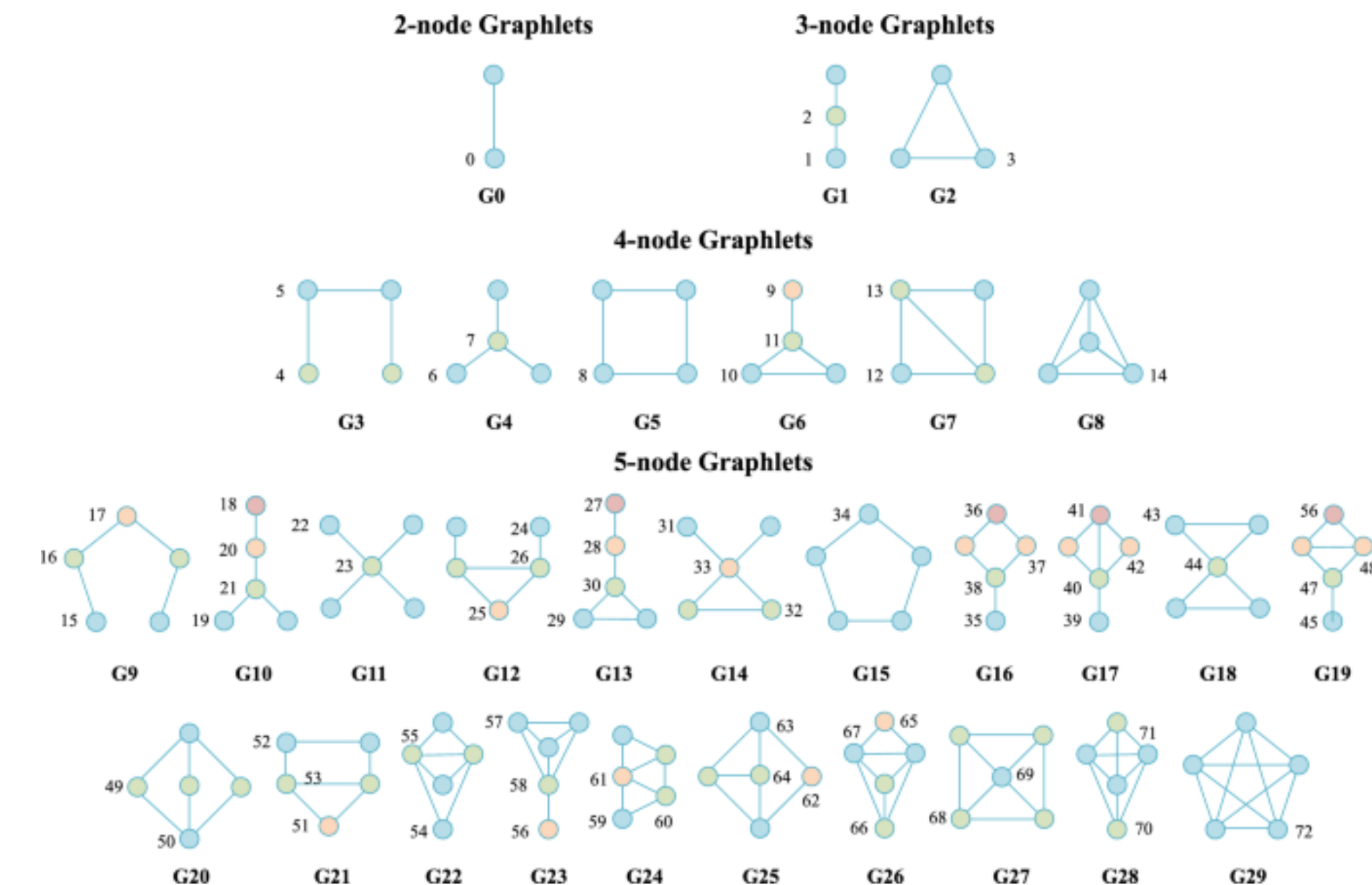
## Node-level statistics

- Extracting some **statistics or features** from the graph and sing these features as input to an standard machine learning classifier
- **Node-level:**
  - Node degree - Node centrality - Clustering coefficient - Motifs or graphlets
- **Edge-level:**
  - Local overlap: Number of common neighbours two nodes share (e.g., Jaccard overlap)
  - Global overlap:
    - *Katz Index*: number of paths of all lengths between two nodes
    - *Leicht, Holme, and Newman* Similarity: ratio between the number of observed paths and the number of expected paths between two nodes.
    - *Random walk methods*: considering random walks instead of exact counts of paths (e.g., Personalised Page Rank, probability that a random walk starting at one node visits another).

# Traditional Approaches

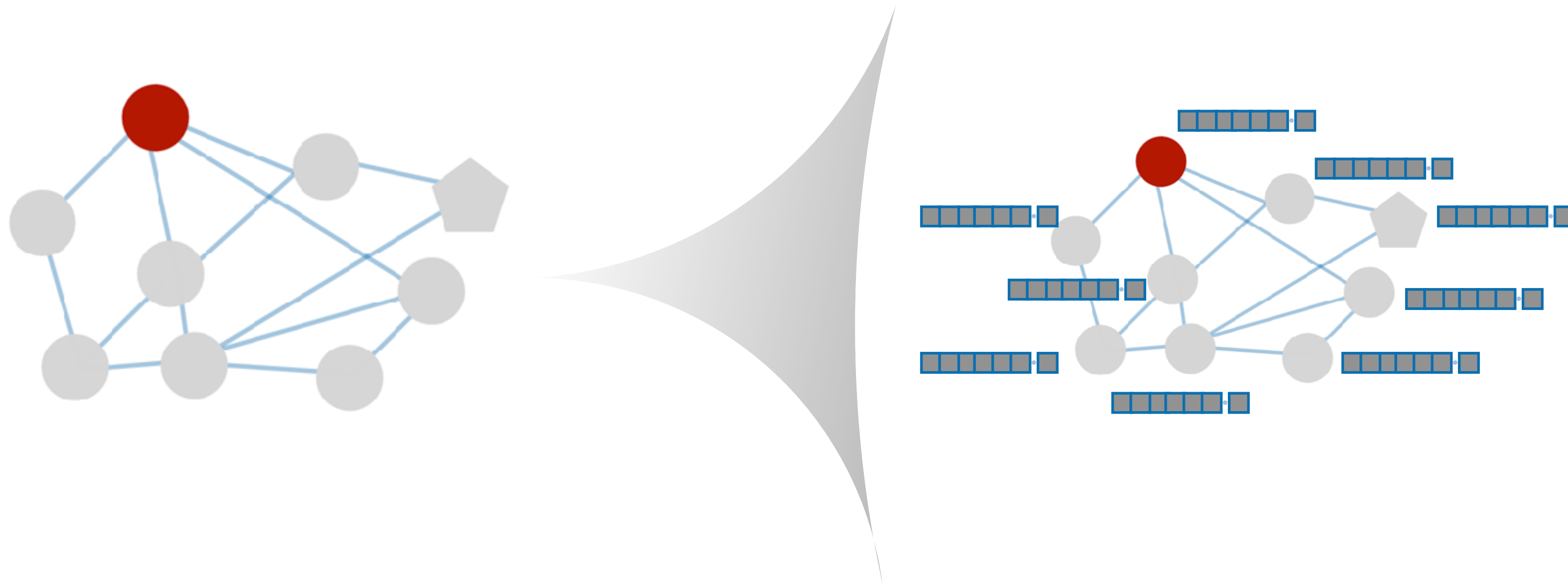
## Graph-level statistics

- **Bag of nodes:** aggregating node-level statistics (summary statistics based on node stats)
- **Iterative Neighbour Aggregation:** extract node-level features that contain rich information about their neighbours and aggregate it at the graph-level — e.g., The Weisfieler-Lehman Kernel
- **Graphlets:** count the occurrence of different small subgraph structures (graphlets)
- **Path-based methods:** evaluates the different kinds of paths that occur in the graph (e.g., random walks/ shortest paths counting occurrence of sequences of node labels (degree) )



# Representation Learning

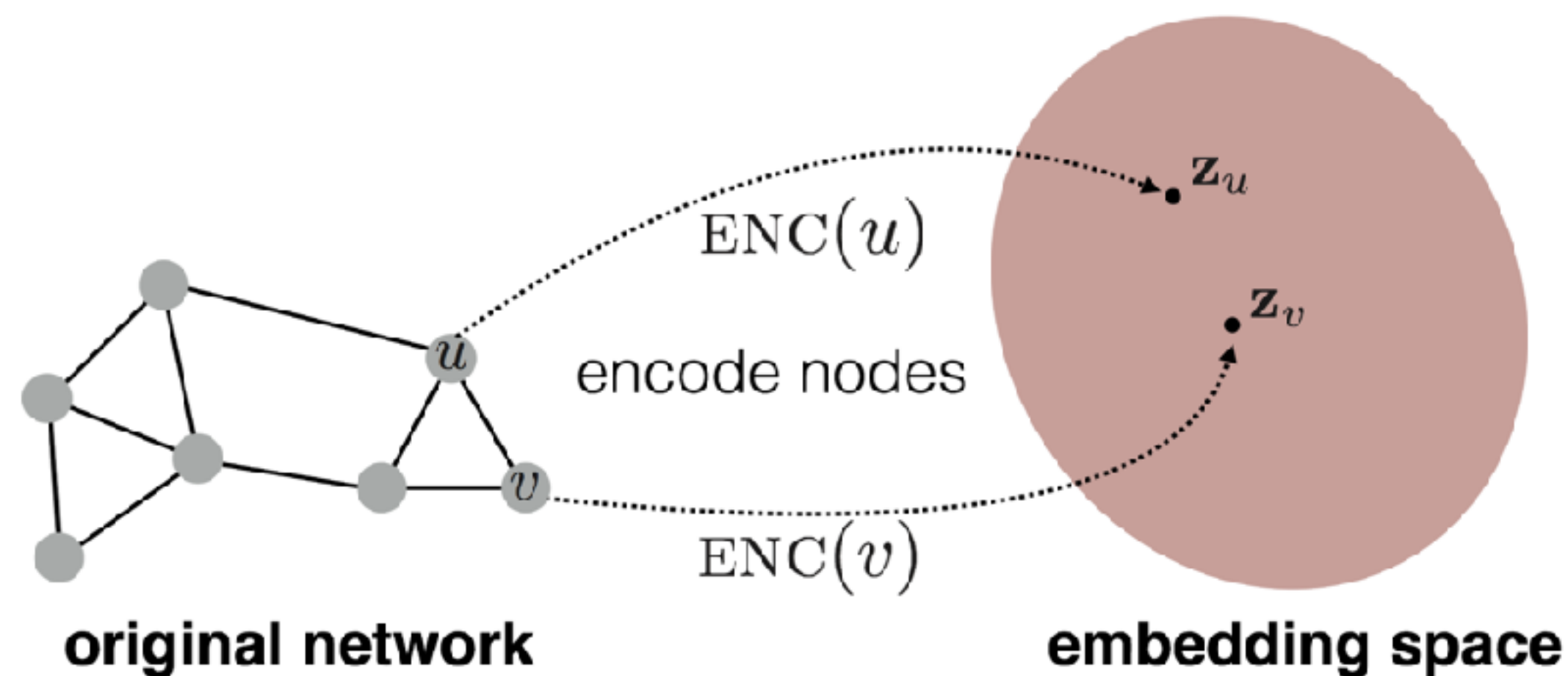
- The node- and graph-level statistics approached are limited
- Graph Representation Learning — learn representations that encode structural information about the graph to use them downstream





# Node Embeddings

- Encode nodes as low-dimensional vectors summarising their position and structure of the local graph neighbourhood
- Similarity in the embedding space (e.g., dot product) approximates similarity in the original graph
- Encoder-decoder methods:



**Encoder (ENC):** goal learn a mapping from nodes to embeddings. We Define a node similarity function and optimise the parameters of the encoder so that similarity

$$S[u, v] \approx \mathbf{z}_u^T \mathbf{z}_v$$

**Decoder (DEC):** reconstruct certain graph statistics from the node embedding (e.g., pairwise decoders predict whether two nodes are neighbours in the graph).

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

# Shallow Embedding Methods

| Type                 | Method              | Decoder  | Similarity measure                     | Loss function                                |
|----------------------|---------------------|--|--|--|
| Matrix Factorisation | Laplacian Eigenmaps | $\ z_u - z_v\ _2^2$  | General                                | $\text{DEC}(z_u, z_v) \cdot S[u, v]$         |
|                      | Graph Factorisation | $z_u^\top z_v$   | $A[u, v]$                              | $\ \text{DEC}(z_u, z_v) \cdot S[u, v]\ _2^2$ |
|                      | GraRep              | $z_u^\top z_v$   | $A[u, v], A^2[u, v], \dots, A^k[u, v]$ | $\ \text{DEC}(z_u, z_v) \cdot S[u, v]\ _2^2$ |
|                      | Hope                | $z_u^\top z_v$   | General                                | $\ \text{DEC}(z_u, z_v) \cdot S[u, v]\ _2^2$ |
| Random walk          | DeepWalk            | $\frac{e^{z_u^\top z_v}}{\sum_{k \in \mathcal{V}} e^{z_u^\top z_k}}$ | $p_{\mathcal{G}}(v \mid u)$            | $-S[u, v] \cdot \log(\text{DEC}(z_u, z_v))$  |
|                      | node2vec            | $\frac{e^{z_u^\top z_v}}{\sum_{k \in \mathcal{V}} e^{z_u^\top z_k}}$ | $p_{\mathcal{G}}(v \mid u)$ (biased)   | $-S[u, v] \cdot \log(\text{DEC}(z_u, z_v))$  |

$p_{\mathcal{G}}(v \mid u)$  Probability of visiting  $v$  on a fixed length random walk starting from  $u$

# Random Walk Methods

- Two nodes have similar embeddings if they cooccur on short random walks

| Type        | Method   | Decoder  | Similarity measure                   | Loss function                               |
|-------------|----------|--|--------------------------------------|---|
| Random walk | DeepWalk | $\frac{e^{z_u^\top z_v}}{\sum_{k \in \mathcal{V}} e^{z_u^\top z_k}}$ | $p_{\mathcal{G}}(v \mid u)$          | $-S[u, v] \cdot \log(\text{DEC}(z_u, z_v))$ |
|             | node2vec | $\frac{e^{z_u^\top z_v}}{\sum_{k \in \mathcal{V}} e^{z_u^\top z_k}}$ | $p_{\mathcal{G}}(v \mid u)$ (biased) | $-S[u, v] \cdot \log(\text{DEC}(z_u, z_v))$ |

- These methods differ on how they overcome the complexity of evaluating the loss function ( $O(|V|)$ ).



# Limitations of Shallow Embeddings

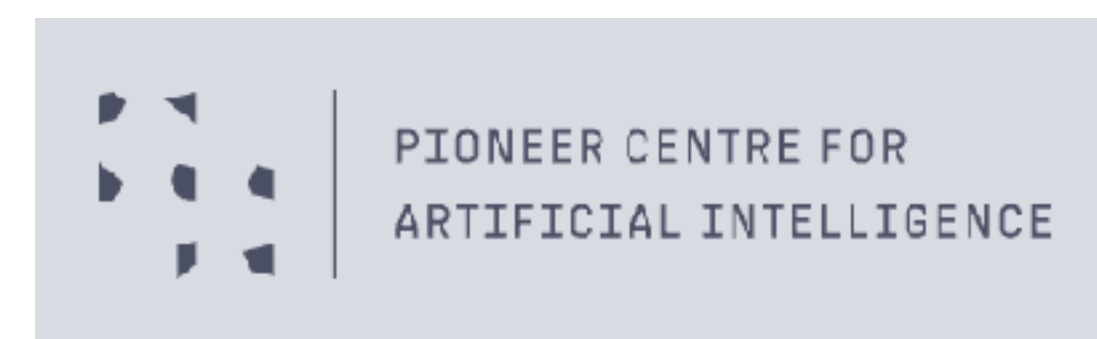
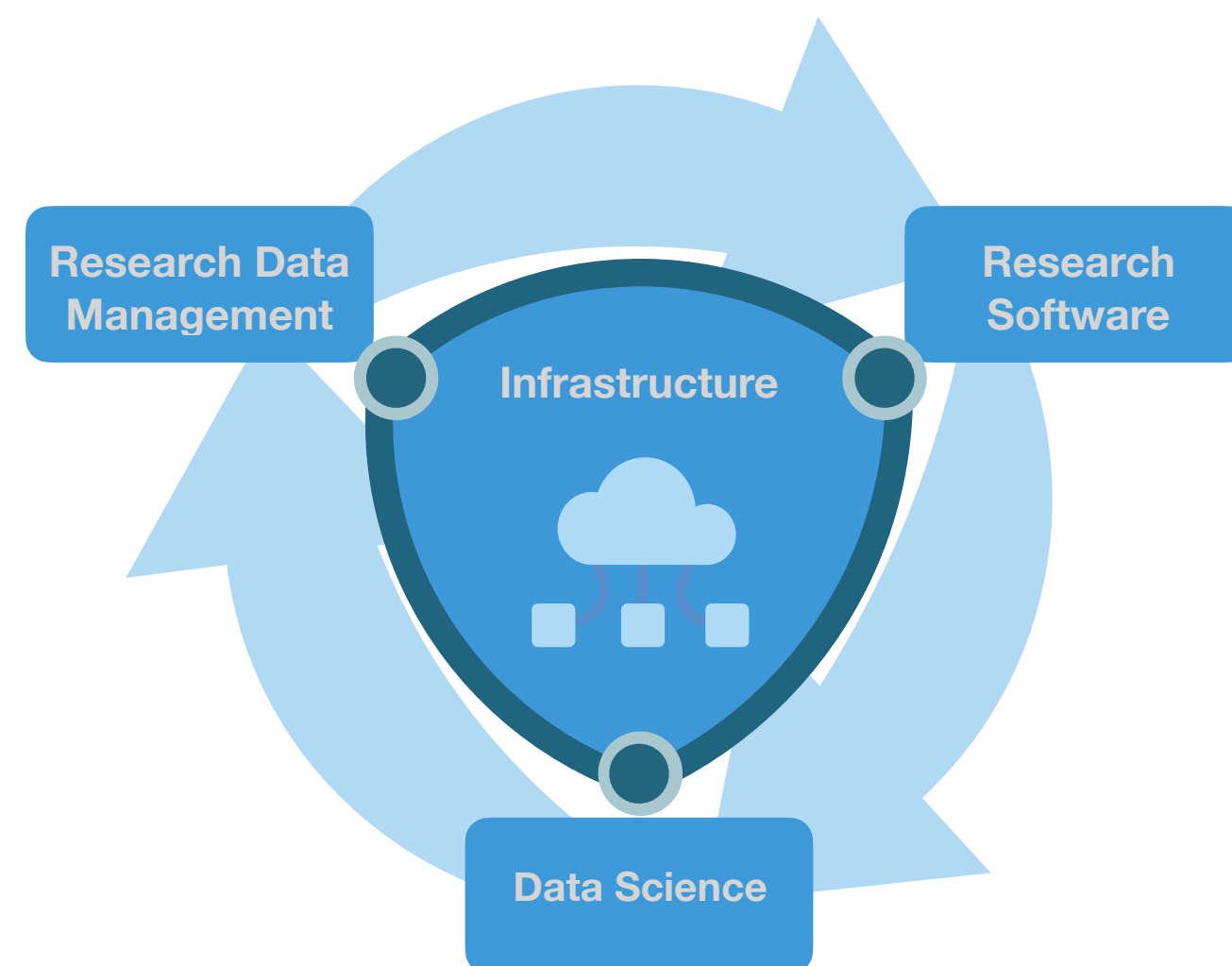
- **Complexity grows** with the number of nodes ( $O(|V|)$ ) — problem with large graphs
- They **do not use node features**
- They are **transductive** — can only generate embeddings for nodes present during the training phase (no generalizable to unseen nodes)

# Thank you

## Multi-omics Network Analytics Research Group



## Informatics Platform



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<https://github.com/Multiomics-Analytics-Group>



<https://multiomics-analytics-group.github.io/>

