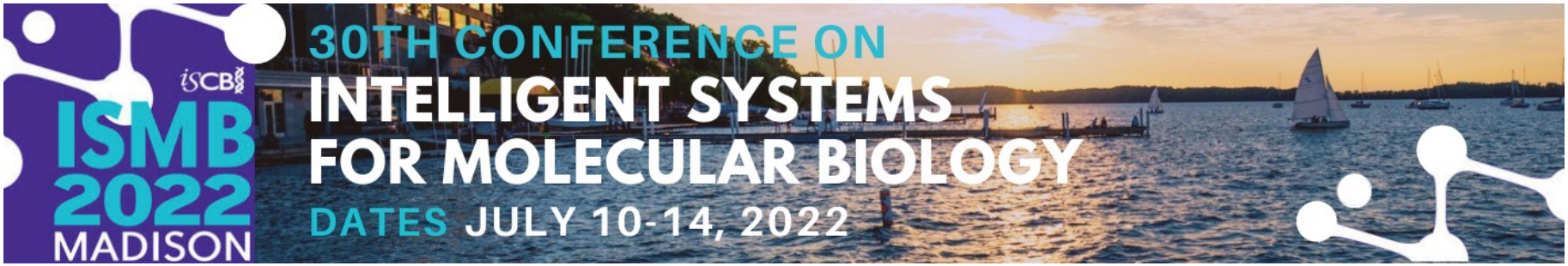
Towards Precision Medicine with Graph Representation Learning

Michelle M. Li & Marinka Zitnik

Department of Biomedical Informatics
Broad Institute of Harvard and MIT
Harvard Data Science

zitniklab.hms.harvard.edu/biomedgraphml



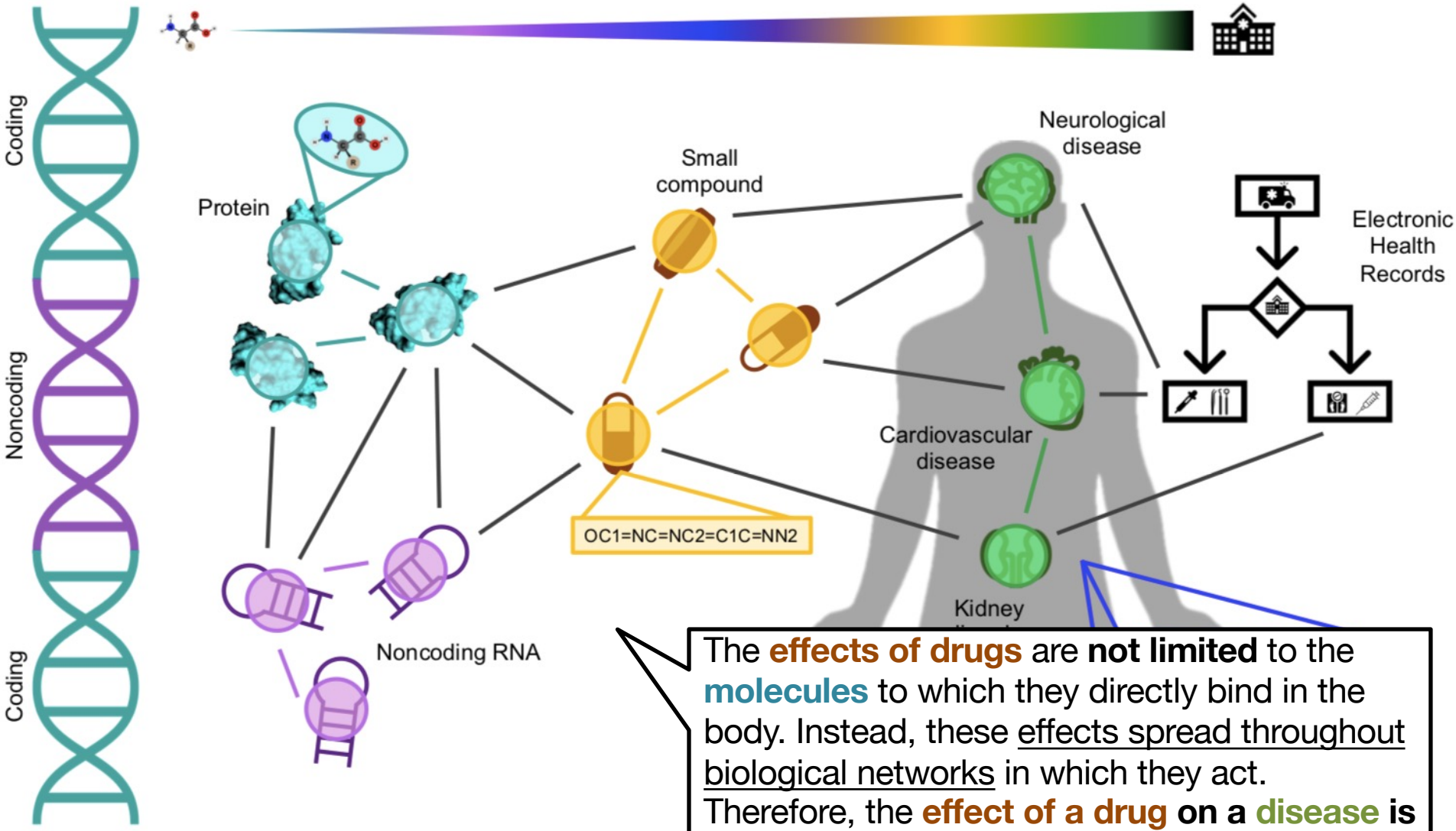
Tutorial VT4

July 7, 2022 at 9am – 1pm CDT

All tutorial materials are available at

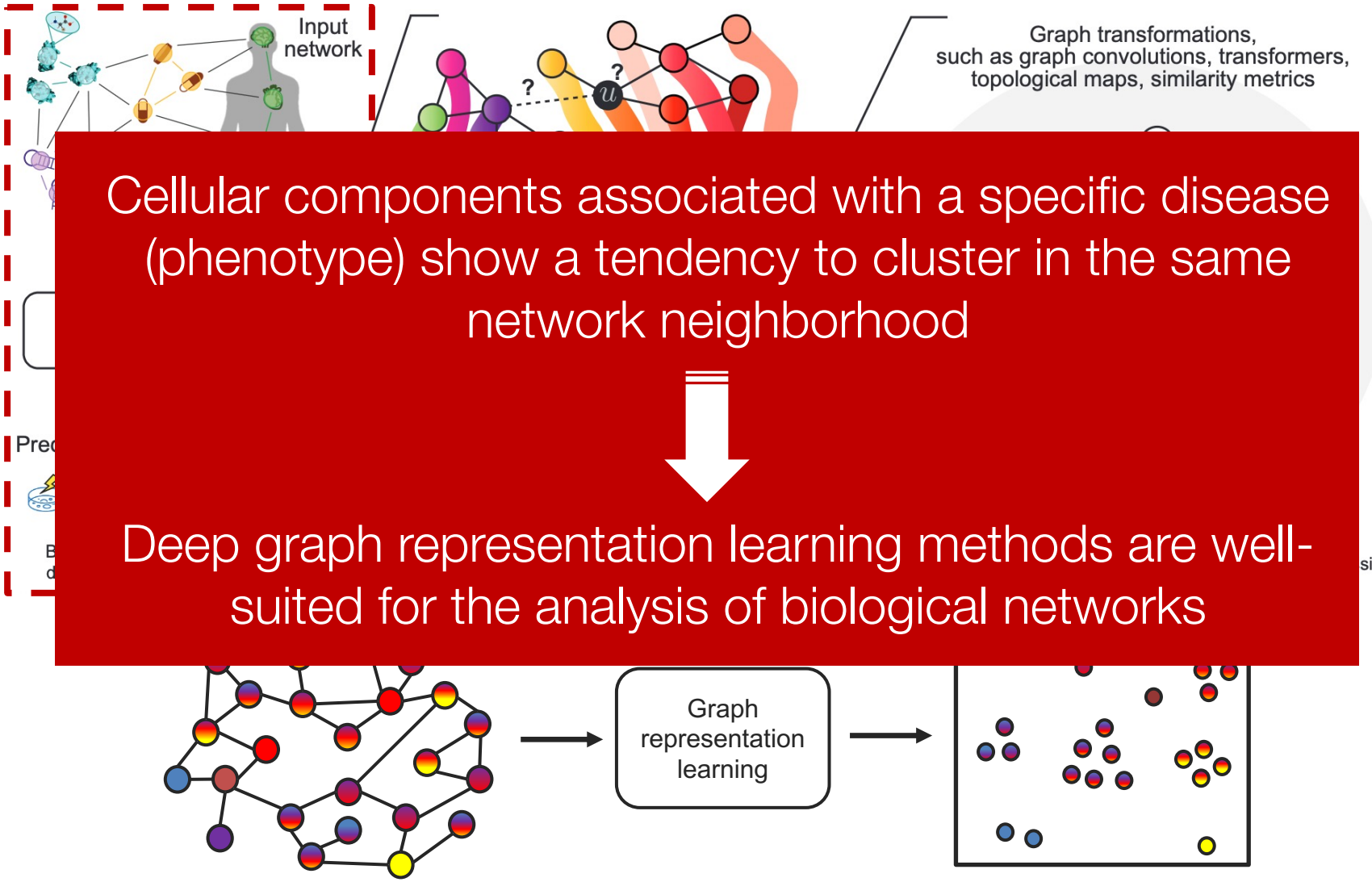
zitniklab.hms.harvard.edu/biomedgraphml

Biology is interconnected



The **effects of drugs** are **not limited** to the **molecules** to which they directly bind in the body. Instead, these effects spread throughout biological networks in which they act. Therefore, the **effect of a drug** **on a disease** **is inherently a network phenomenon**

Graph representation learning realizes key network principles for data-rich biomedicine



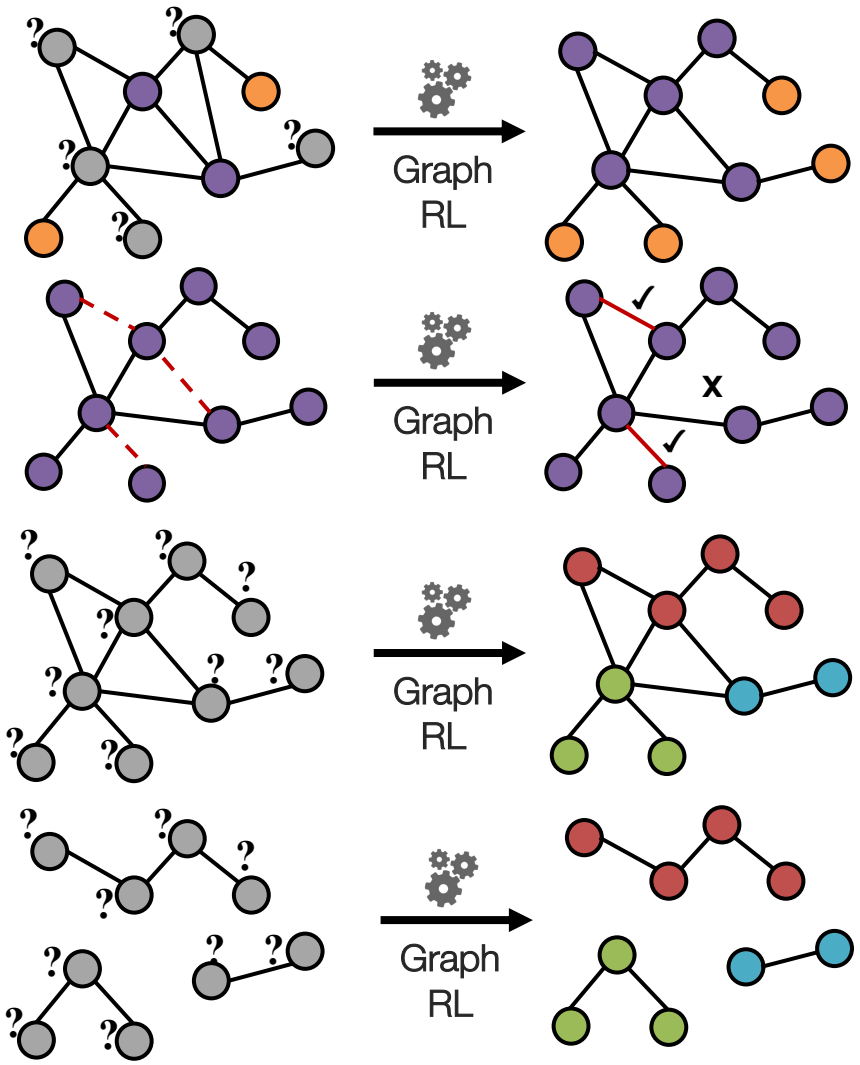
Graph Representation Learning for Biomedicine, *Nature Biomedical Engineering* (in press), 2022, arXiv:2104.04883

This Tutorial

1. Methods: Network diffusion, shallow network embeddings, graph neural networks, equivariant neural networks
2. Applications: Fundamental biological discoveries and precision medicine
3. Hands-on exercises: Demos, implementation details, tools, and tips

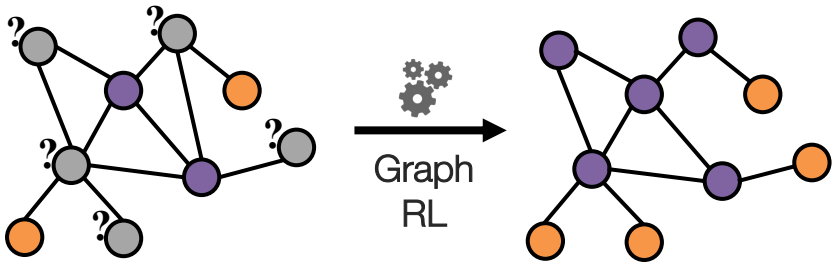
Graph representation learning tasks

- Node-level
  - Characteristics of a given node
- Edge-level
  - Whether or how two nodes are connected
- Subgraph-level
  - How clusters of nodes interact with each other and the rest of the graph
- Graph-level
  - Similarity of graph to other graphs



Graph representation learning tasks

- Node-level
  - Characteristics of a given node



Node classification: Example

Classifying the function of proteins in the interactome!

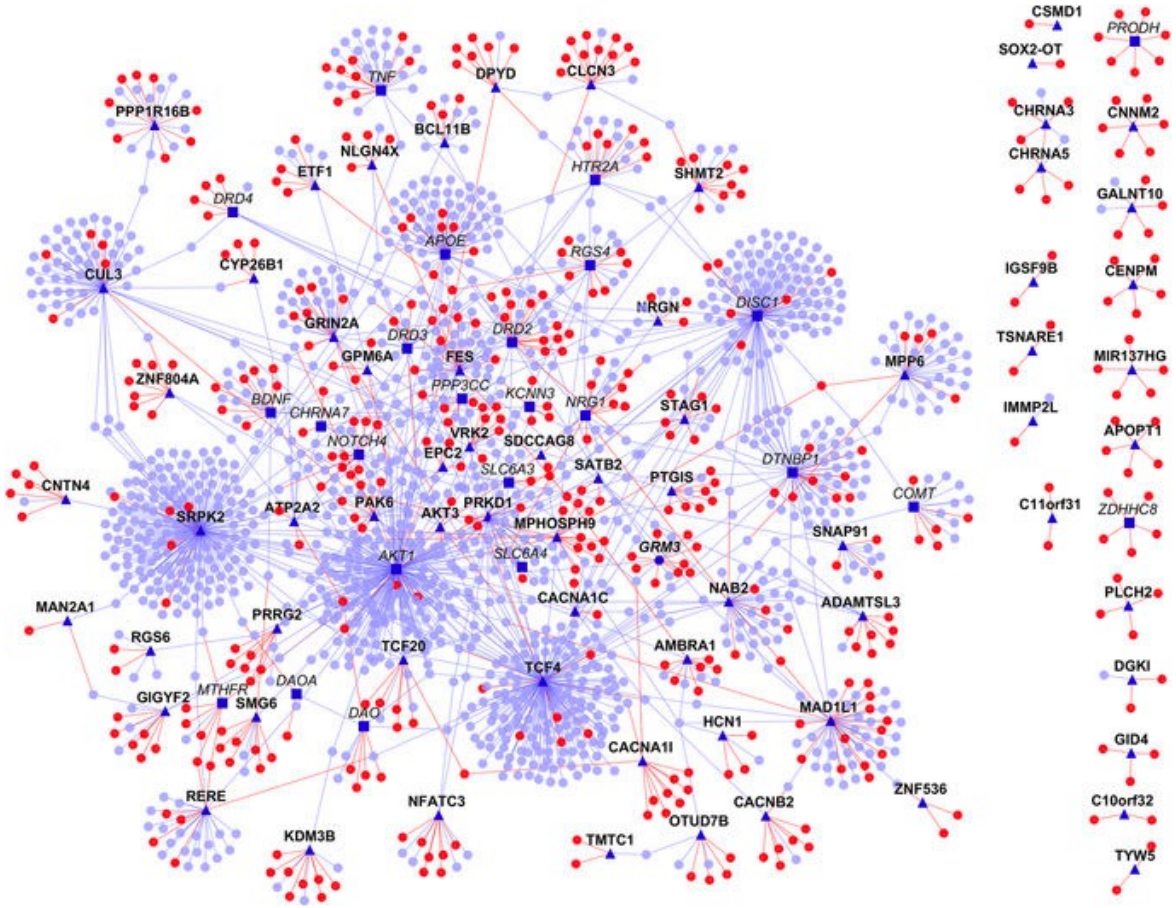
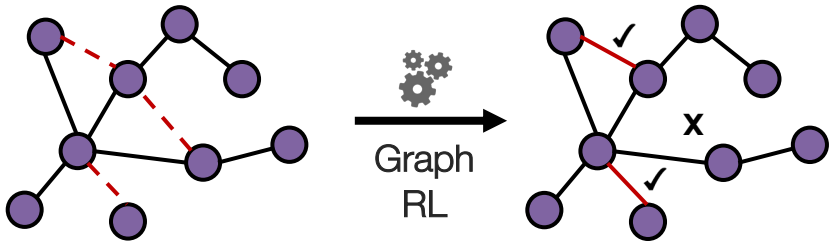


Image from Ganapathiraju et al. 2016. Schizophrenia interactome with 504 novel protein–protein interactions. *Nature*.

Graph representation learning tasks

- Edge-level
  - Whether or how two nodes are connected



Link prediction: Example

Predicting which diseases a new molecule might treat!

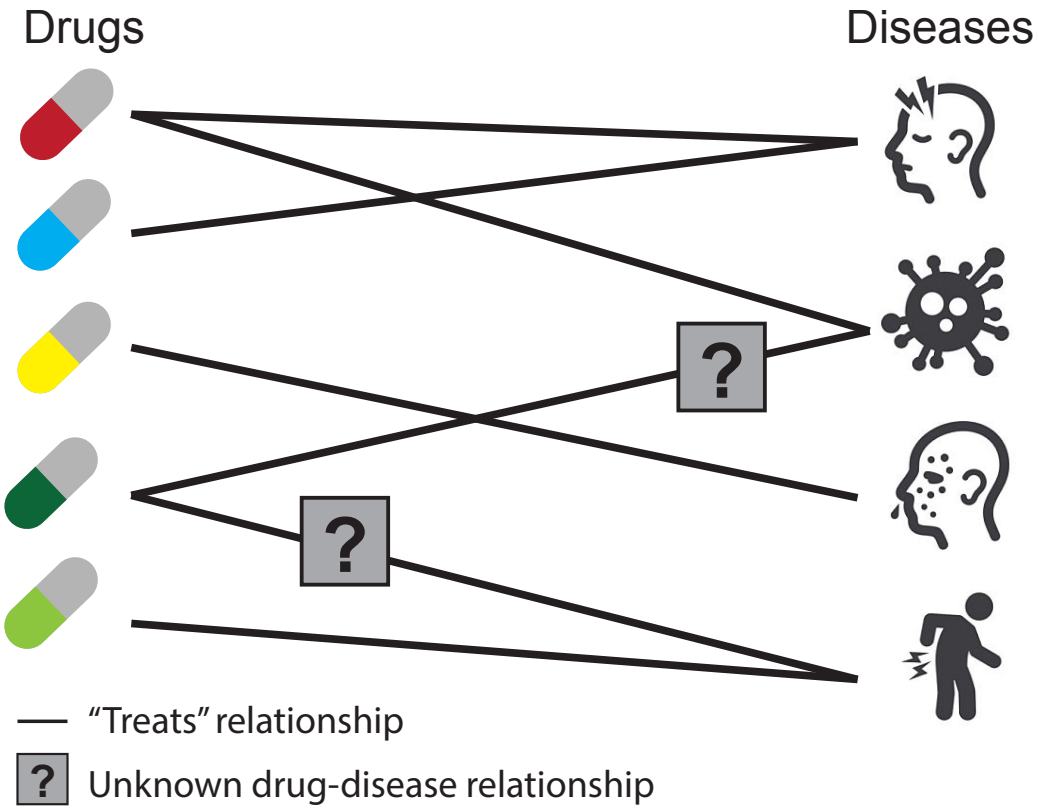
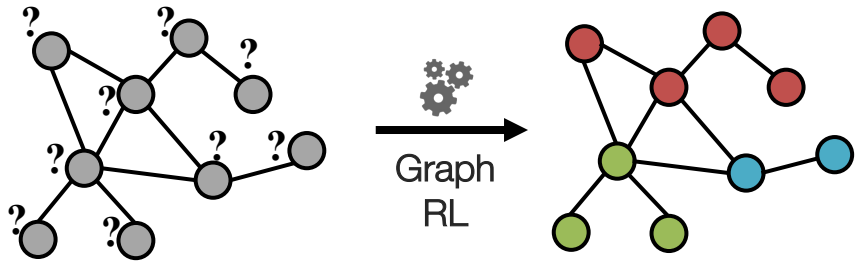


Image from: Zitnik et al. 2020. Network-based discovery of drug indications.

Graph representation learning tasks

- Subgraph-level
  - How clusters of nodes interact with each other and the rest of the graph



Subgraph classification: Example

Identifying disease proteins in the interactome!

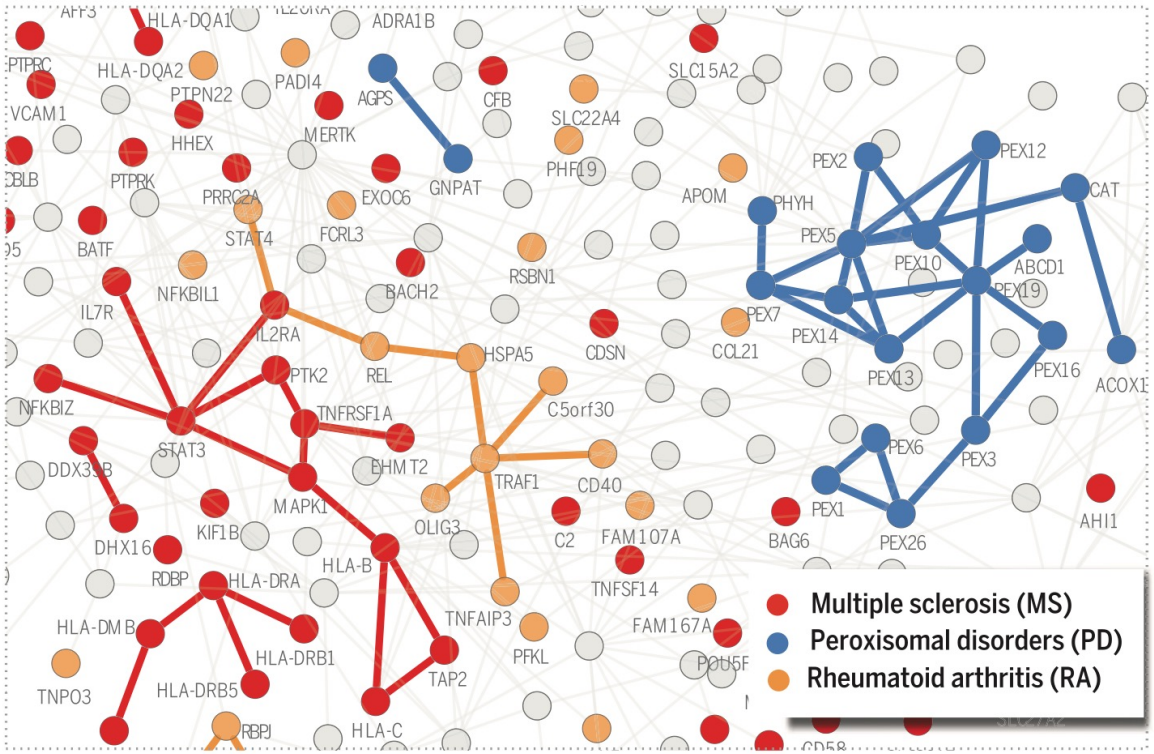
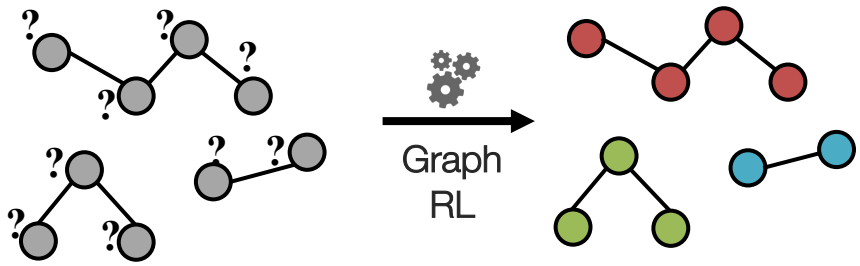


Image from: Menche et al. 2015. Uncovering disease-disease relationships through the incomplete interactome. *Science*.

Graph representation learning tasks

- Graph-level
  - Similarity of graph to other graphs



Graph classification: Example

Designing new small molecule compounds to treat a disease!

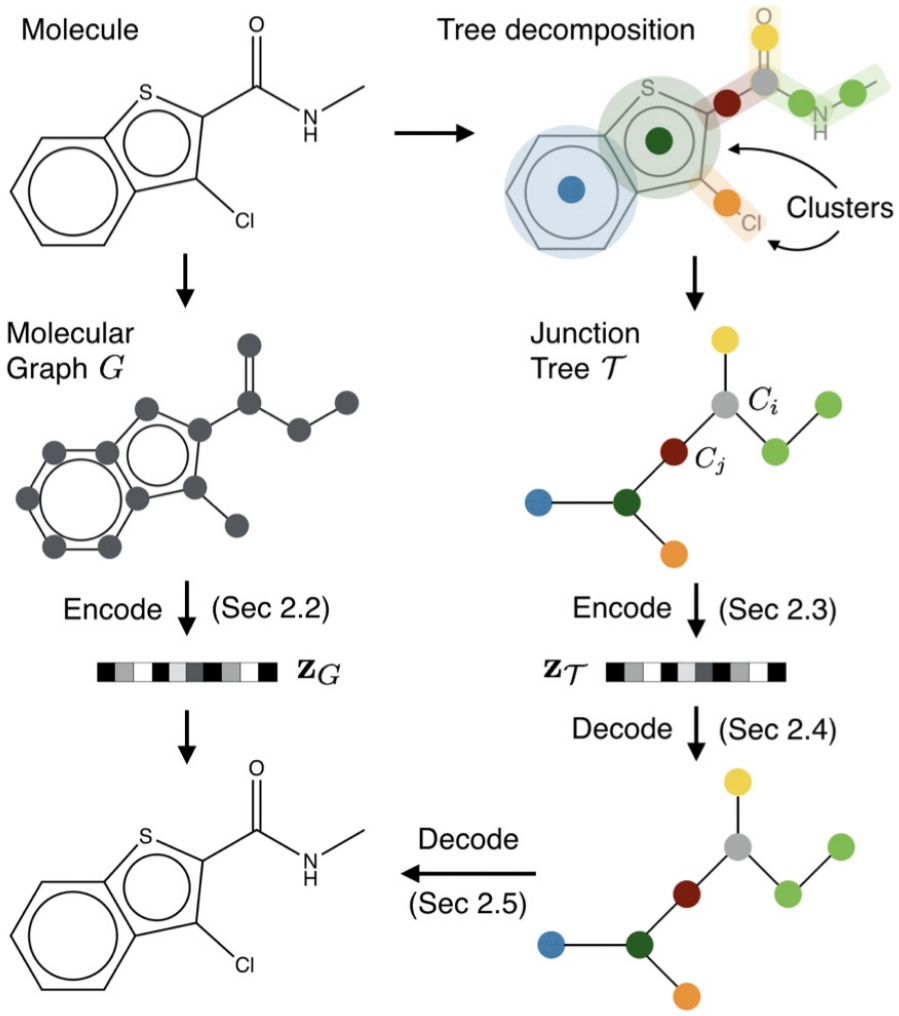
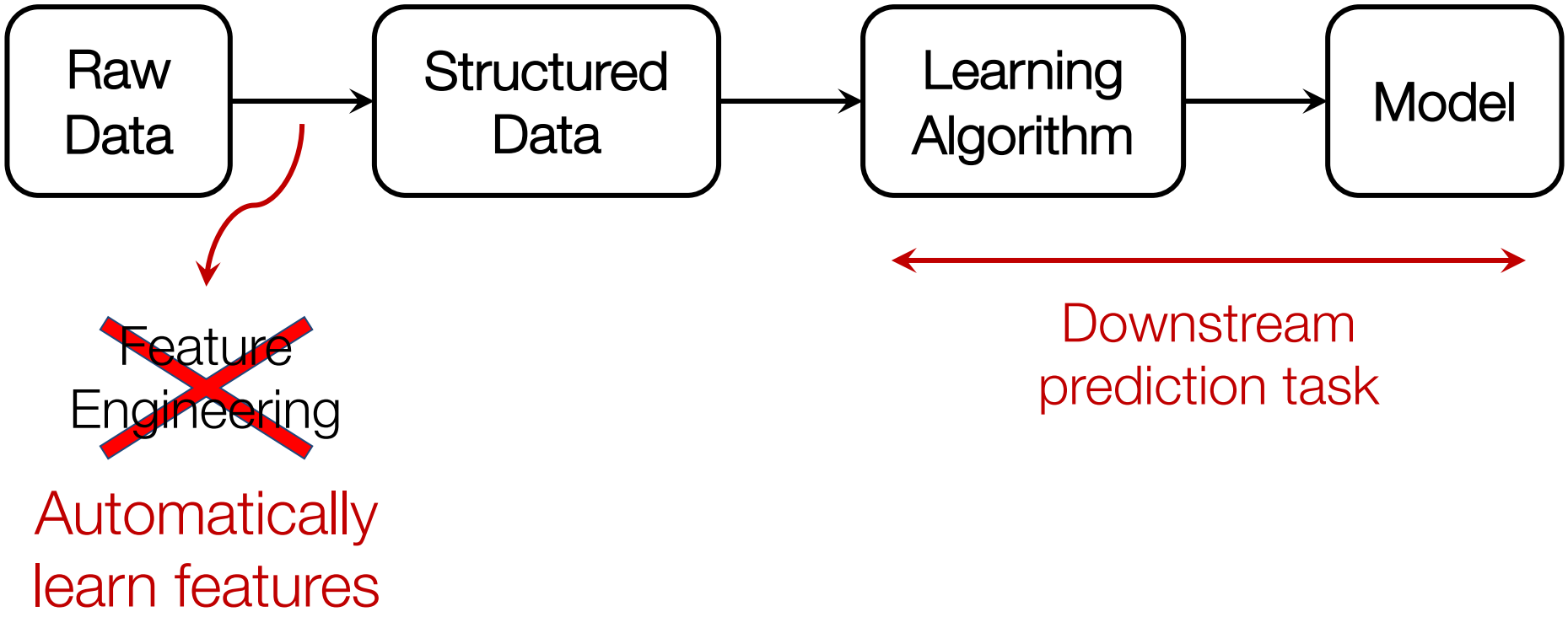


Image from: Jin et al. 2018. Junction Tree Variational Autoencoder for Molecular Graph Generation. *ICML.*

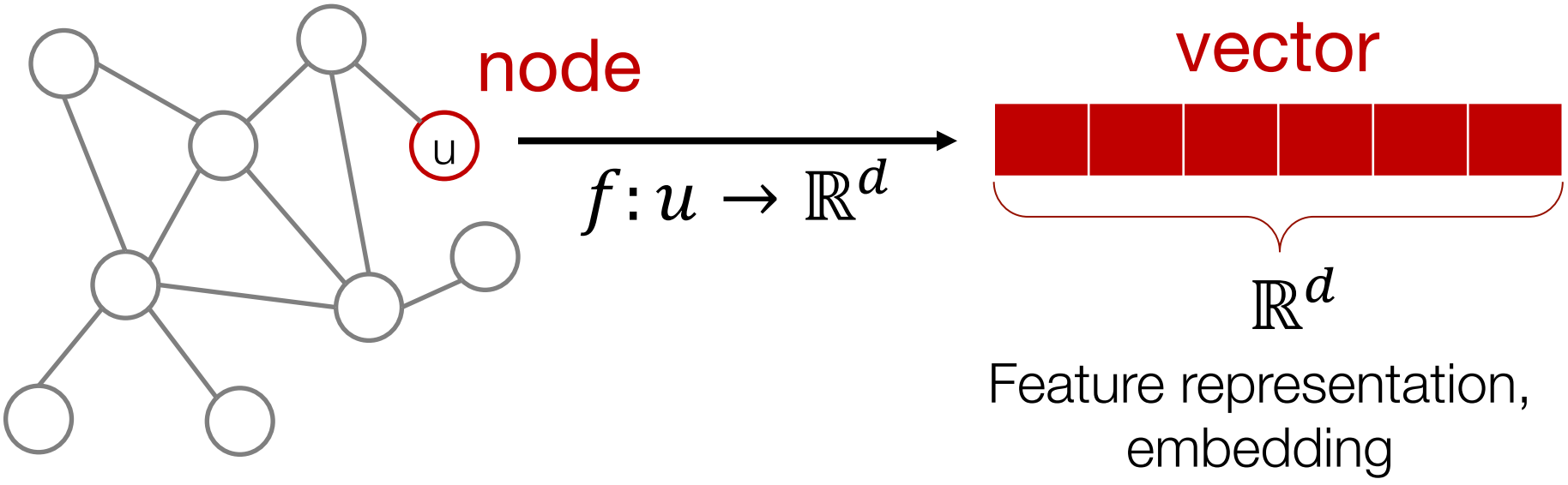
Predictive modeling lifecycle

(Supervised) Machine learning lifecycle: This feature, that feature. Every single time!



Feature learning in graphs

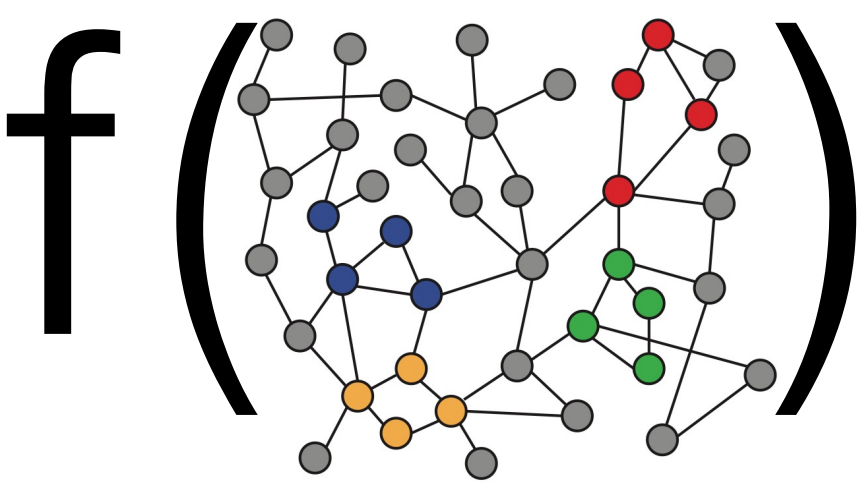
Goal: Efficient task-independent feature learning for machine learning in networks!



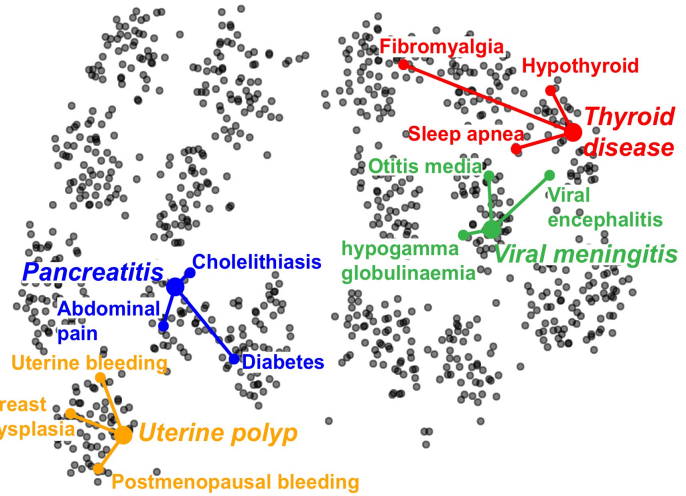
Embedding nodes

Intuition: Map nodes to embeddings such that similar nodes in graph are embedded close by

Input



Output



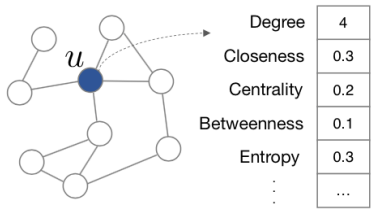
Disease similarity network

2D node embeddings

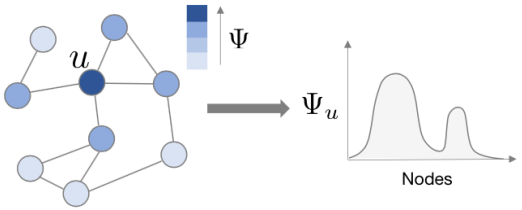
How to learn mapping function f?

Predominant graph learning paradigms

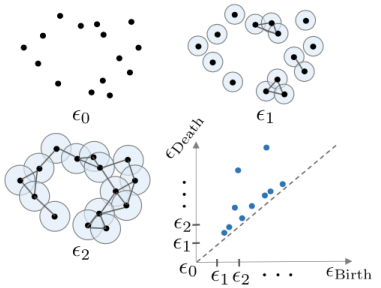
a Graph theoretic techniques



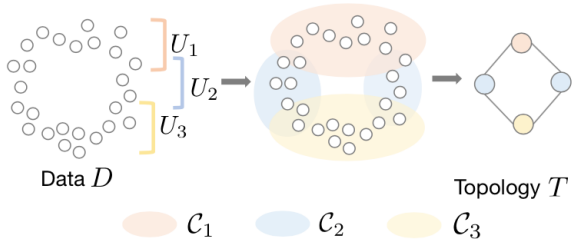
b Random walks and diffusion



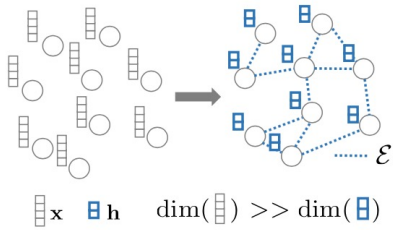
c Persistent homology



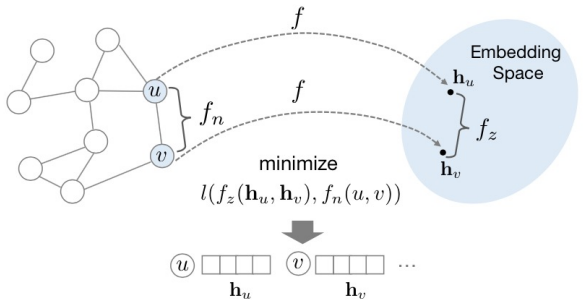
d Geometrical and topological representations



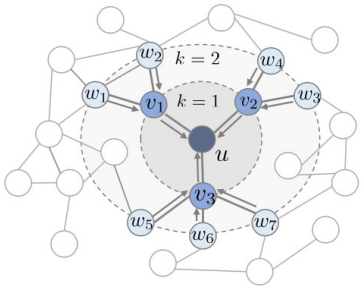
e Manifold learning



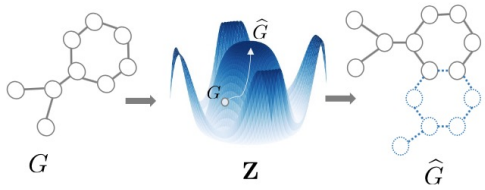
f Shallow network embeddings



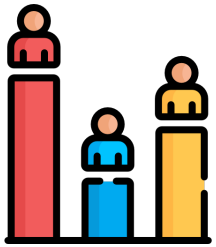
g Graph neural networks



h Graph generative models



Graph Representation Learning for Biomedicine, *Nature Biomedical Engineering* (in press), 2022, arXiv:2104.04883

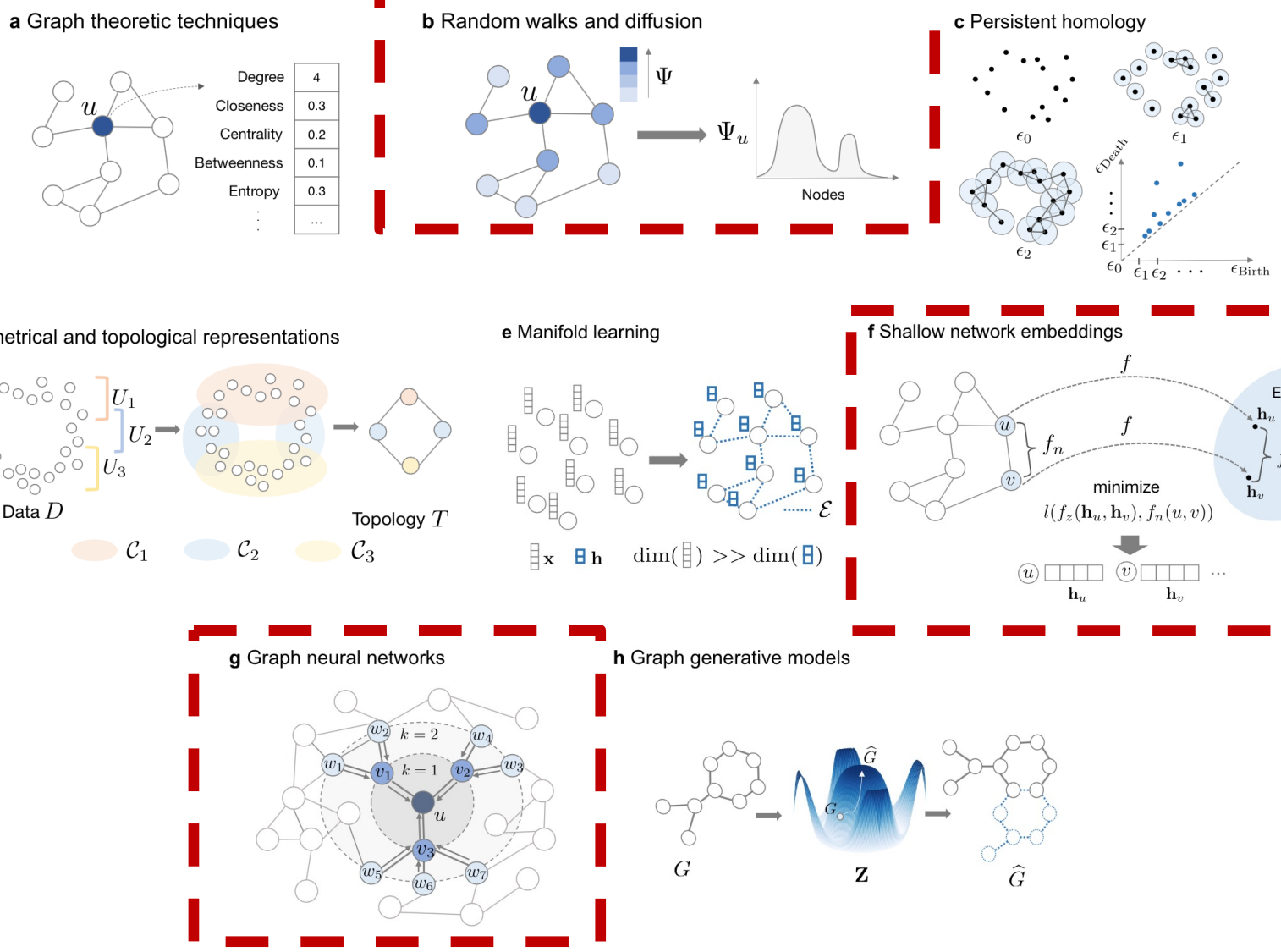


Time for a poll question about…

GRAPH MACHINE LEARNING TASKS

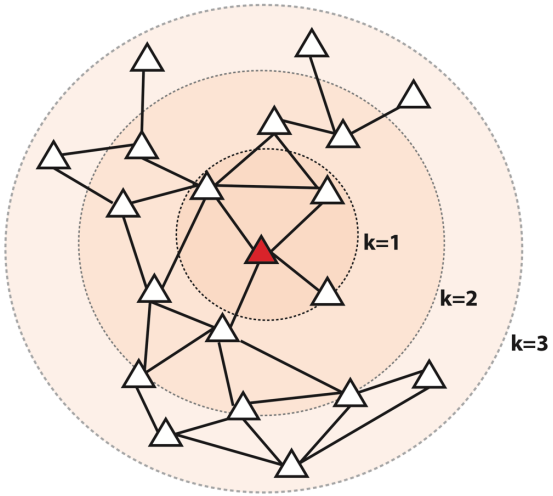
1. Which of the following is an example of a node-level task? *Multiple choice*
2. Which of the following is an example of a graph-level task? *Multiple choice*

Predominant graph learning paradigms



Random walks and diffusion

- Nodes in a graph influence each other along paths
- Diffusion measures these spreads of influences

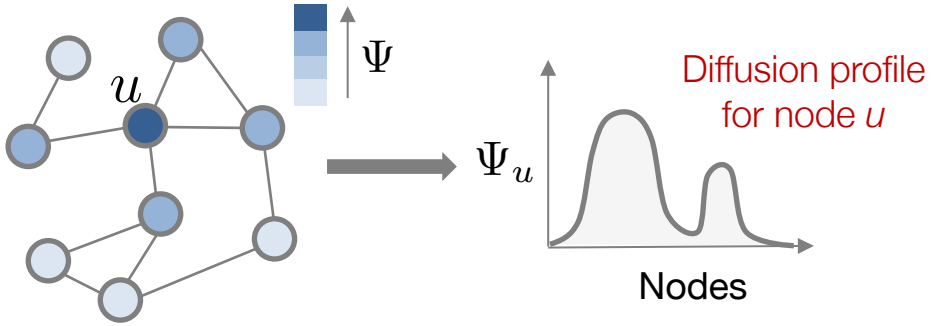


Red: Target node
k = 1: 1-hop neighbors
k = 2: 2-hop neighbors
k = 3: 3-hop neighbors

- Intuition
  - Capture the local connectivity patterns for each node
  - Define node similarity function based on higher-order neighborhoods

Random walks and diffusion

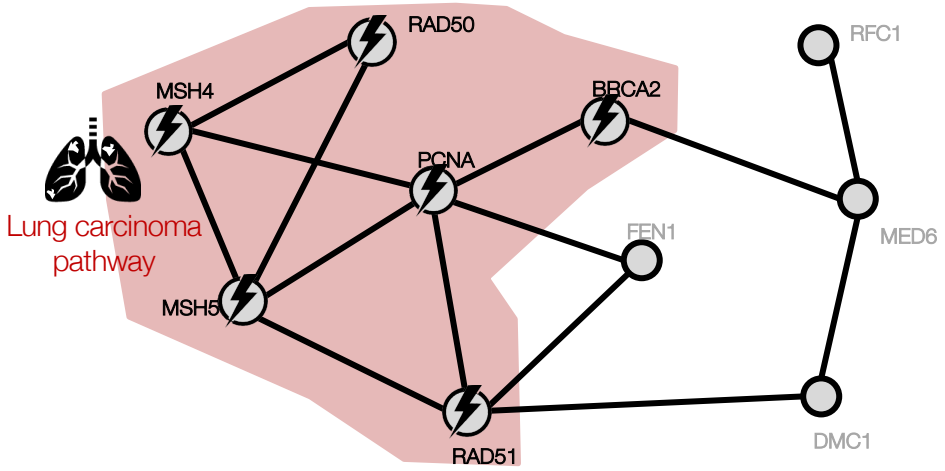
- Method: Diffusion state distance (DSD)
  - Simulate random walks from source node *u*
  - Count the number of random walks of length *k* that start at *u* and visit a destination node *v*
- Node representation: Each node *u* has vector Ψ_u that represents its influence on its *k*-hop neighborhood

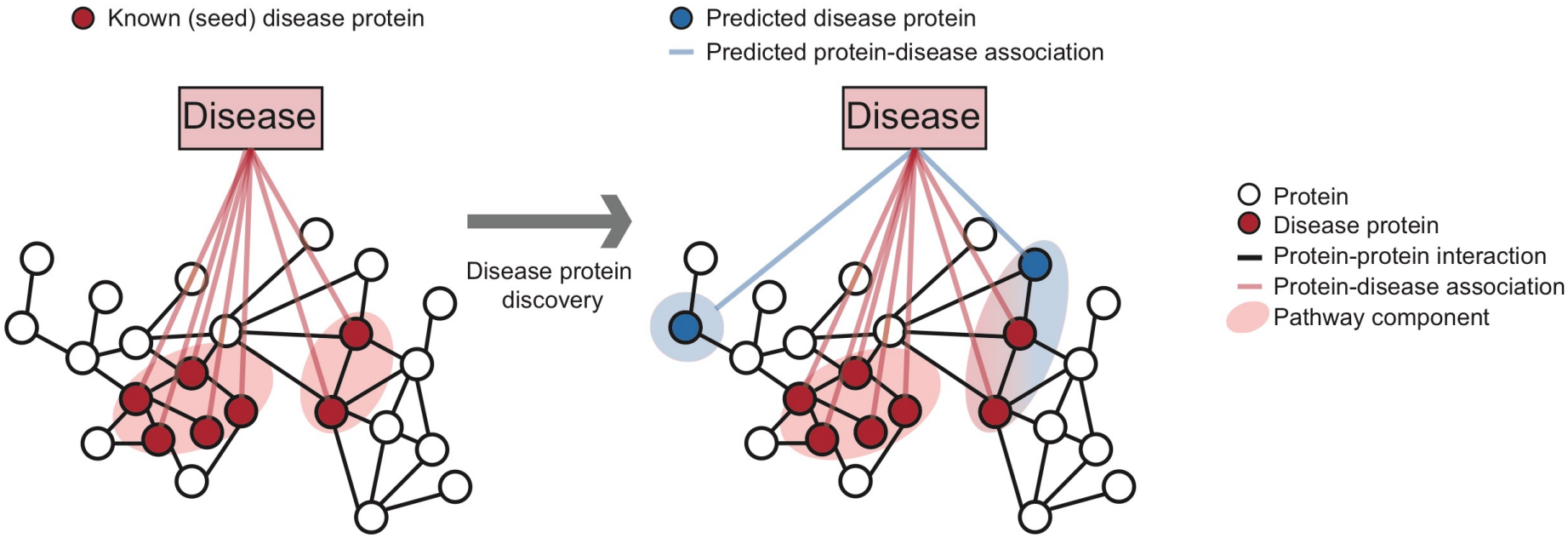


- Comparison: Calculate whether nodes *u* and *v* have similar local connectivity by $DSD(u, v) = \| \Psi_u - \Psi_v \|_1$

Application: Identify disease pathways

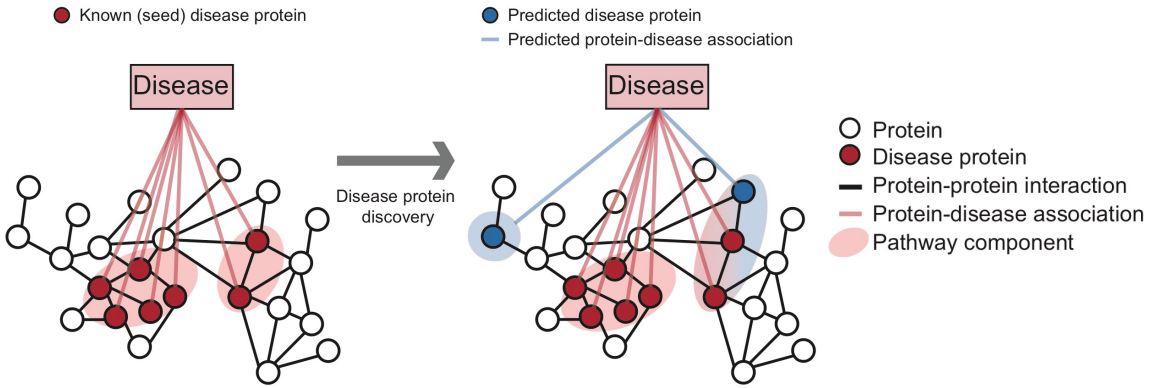
- Pathway: Subnetwork of interacting proteins associated with a disease





Large-scale analysis of disease pathways in the human interactome, *Pacific Symposium on Biocomputing, 2018*

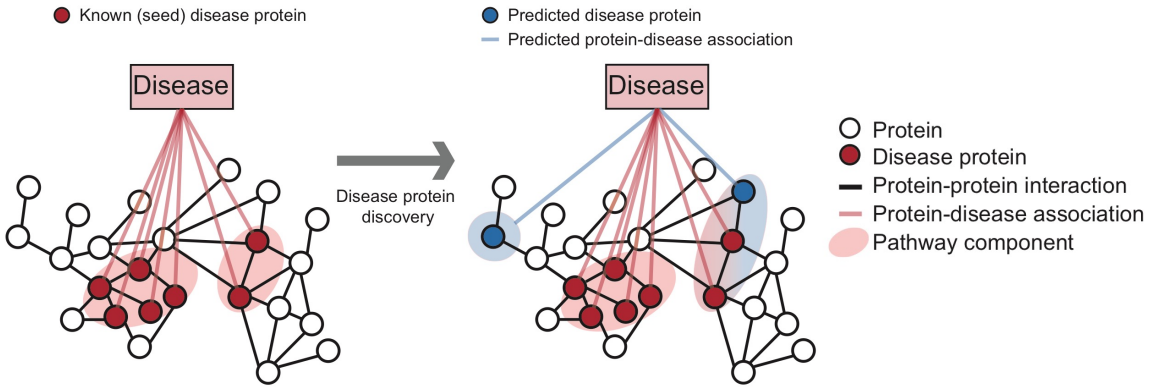
Disease pathway dataset



- Protein-protein interaction (PPI) network culled from 15 knowledge databases:
  - 350k physical interactions
    - Examples: metabolic enzyme-coupled interactions, signaling interactions, protein complexes
  - All protein-coding human genes (21k)
- Protein-disease associations
  - 21k associations split among 519 diseases
- Multi-label node classification
  - Every node (i.e. protein) can have 0, 1, or more labels (i.e. disease associations)

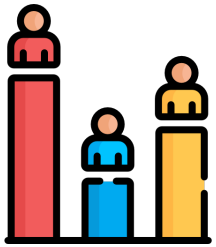
Large-scale analysis of disease pathways in the human interactome, *Pacific Symposium on Biocomputing, 2018*

Experimental setup



- Two main stages:
  1. Take the PPI network and use DSD to compute a vector representation for every node
  2. For each disease, fit a logistic regression classifier that predicts disease proteins based on the vector representations:
     - Train the classifier using training proteins
     - Predict disease proteins in the test set (i.e. the probability that a particular protein is associated with the disease)

Large-scale analysis of disease pathways in the human interactome, *Pacific Symposium on Biocomputing, 2018*

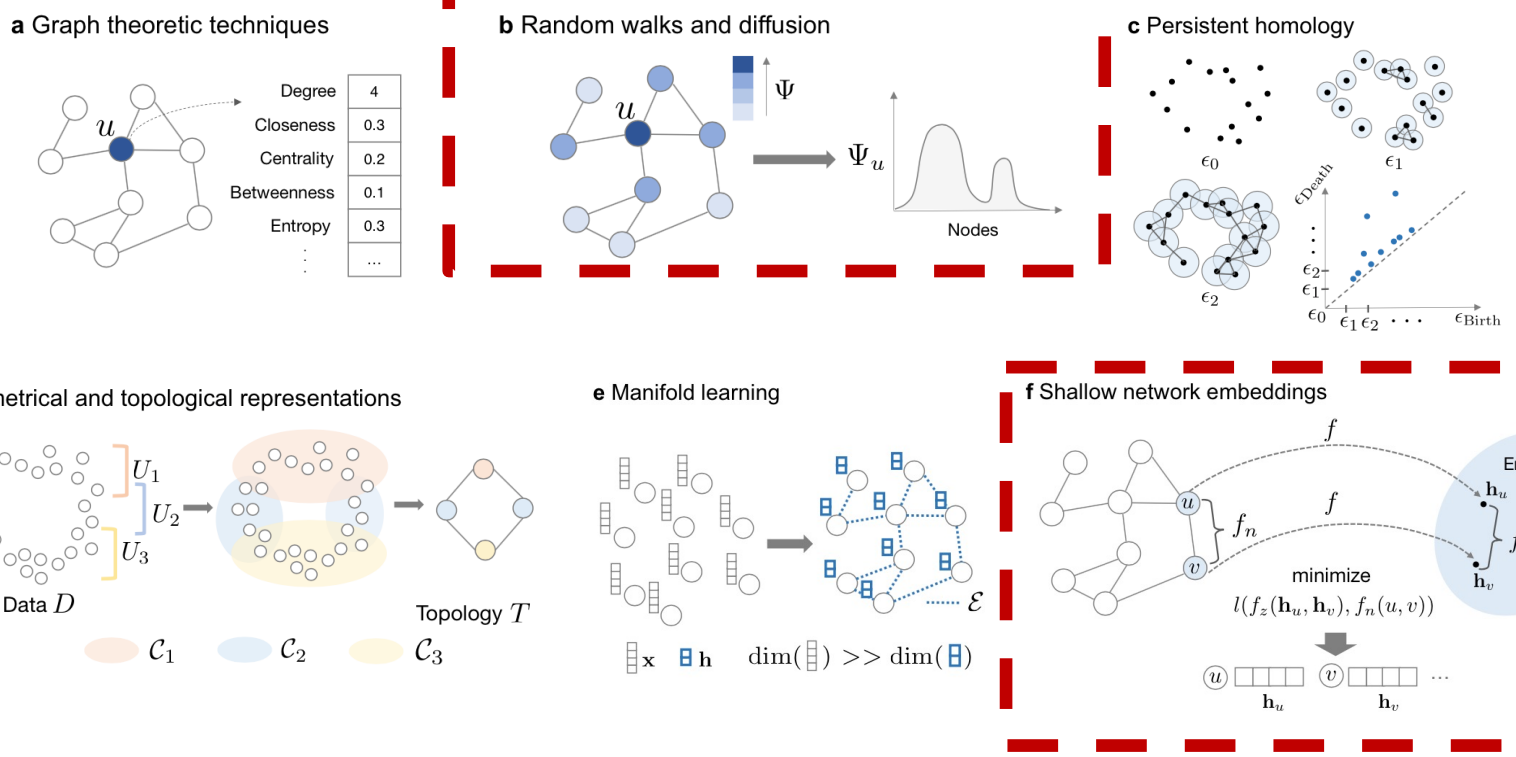


Time for a poll question about…

RANDOM WALKS & DIFFUSION

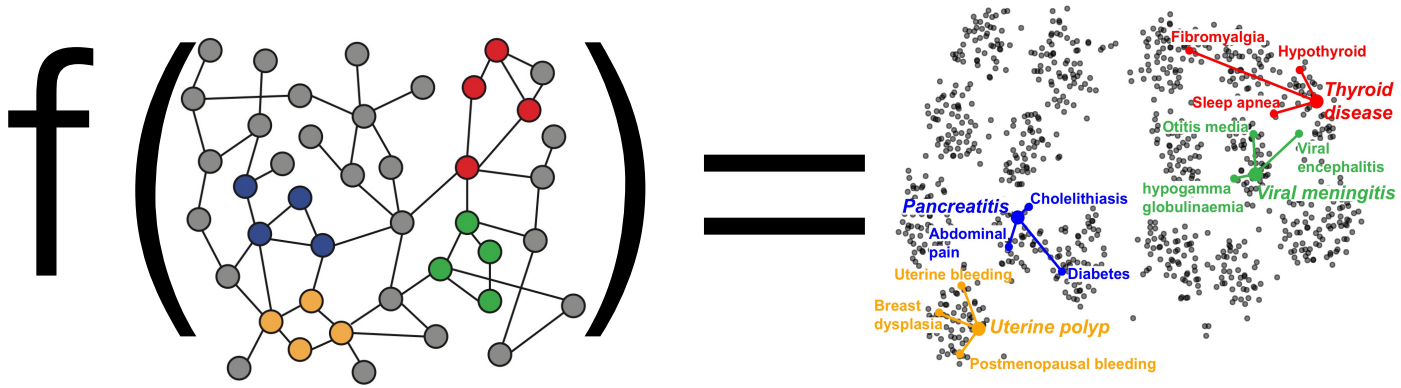
1. Which of the following describes how random walks can be used to generate representations of nodes? *Multiple choice*

Predominant graph learning paradigms



Shallow network embeddings

- Intuition: Map nodes to *d*-dimensional embeddings such that similar nodes in the graph are embedded close together
- Assume we have a graph $\mathbf{G}$:
  - $\mathbf{V}$ is the vertex set
  - $\mathbf{A}$ is the adjacency matrix (assume binary)
  - No node features or extra information is used!

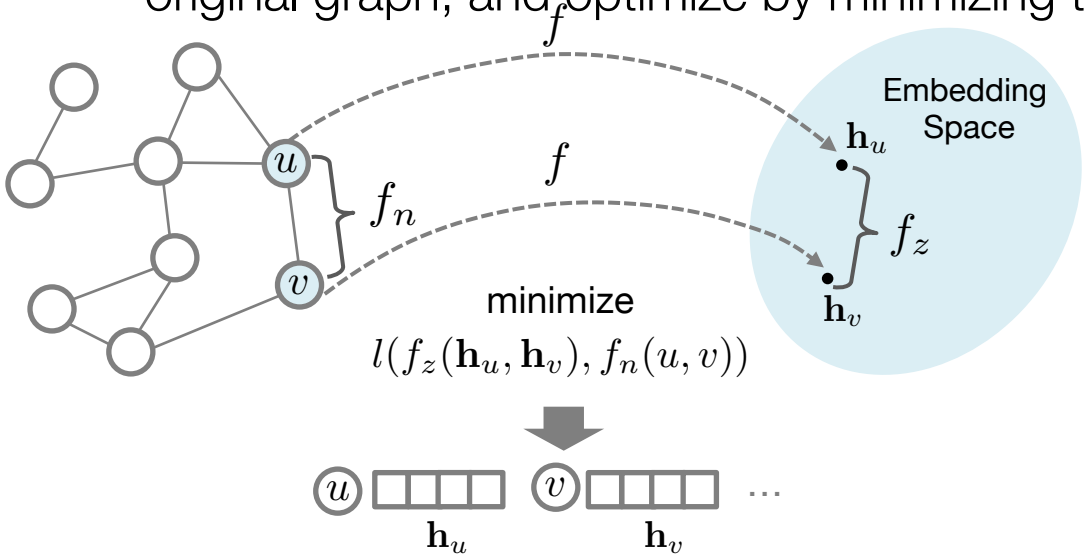


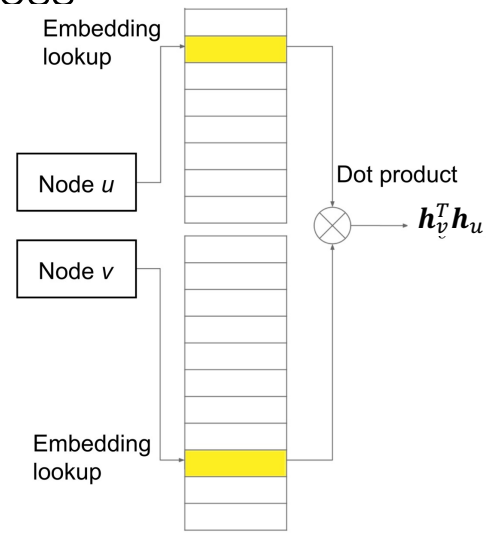
Disease similarity network

2-dimensional node embeddings

Shallow network embeddings

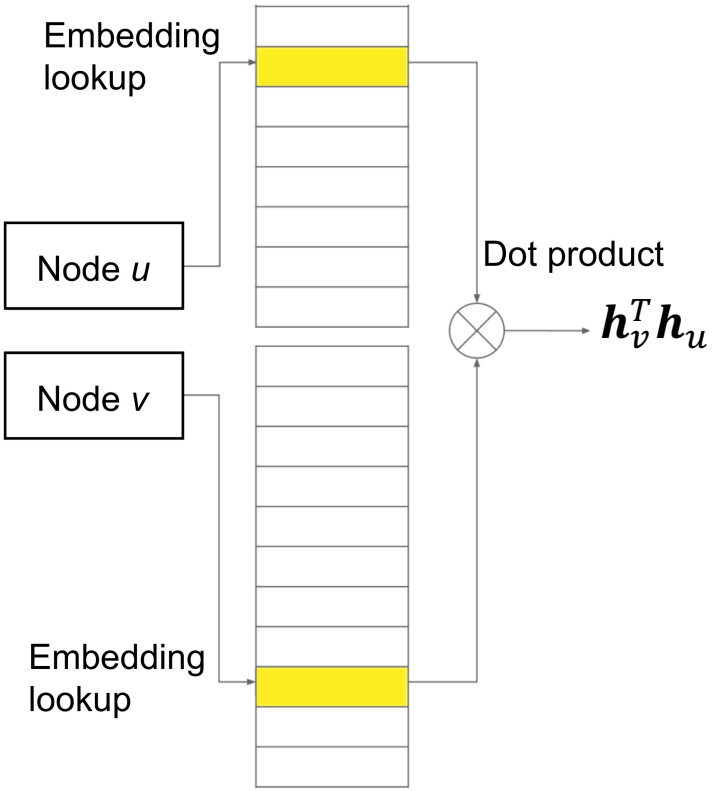
- Goal: Similarity in the embedding space approximates similarity in the network
- Three main stages:
  1. Given a pair of nodes *u*, *v* in network *G*, obtain function *f* to map these nodes to an embedding space to generate $\mathbf{h}_u$ and $\mathbf{h}_v$
  2. Define network similarity $f_n(u,v)$ and embedding similarity $f_z(\mathbf{h}_u, \mathbf{h}_v)$
  3. Define loss l to measure whether embedding preserves distance in original graph, and optimize by minimizing the loss





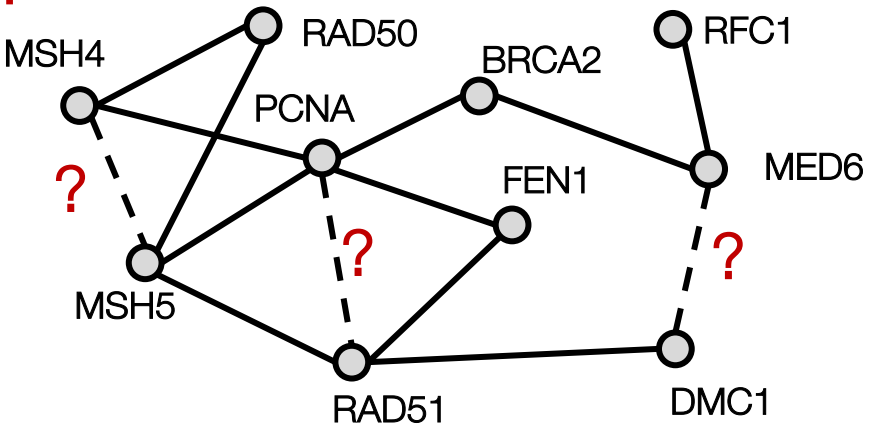
Shallow network embeddings

- Summary:
  - One-layer of data transformation
  - A single hidden layer maps node u to embedding $\boldsymbol{h}_u$ via function f
- Limitations:
  - O(|V|) parameters are needed:
    - No sharing of parameters between nodes
    - Every node has its own unique embedding
  - Inherently "transductive"
    - Cannot generate embeddings for nodes **not** seen during training
  - Do not incorporate node features
    - Many graphs have features that we can and should leverage



Application: Predict protein interactions

- Human PPI network:
  - Experimentally validated physical protein-protein interactions (BioGRID)
- Link prediction: Given two proteins, predict probability that they interact



How to address tasks involving pairs of nodes (e.g., link prediction)?

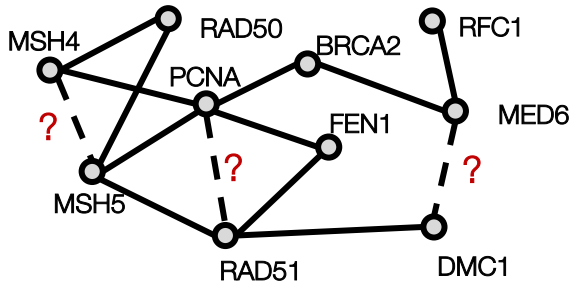
- Given u and v, define an operator g that generates an embedding for pair (u, v):

$$\boldsymbol{h}_{(u,v)} = g(u, v)$$

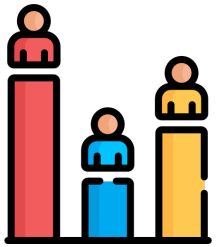
- Examples of choices for g

Scoring node pairs	Definition
(a) Average	$[\mathbf{z}_u \boxplus \mathbf{z}_v]_i = \frac{\mathbf{z}_u(i)+\mathbf{z}_v(i)}{2}$
(b) Hadamard	$[\mathbf{z}_u \boxdot \mathbf{z}_v]_i = \mathbf{z}_u(i) * \mathbf{z}_v(i)$
(c) Weighted-L1	$\|\mathbf{z}_u \cdot \mathbf{z}_v\|_{\bar{1}i} = \|\mathbf{z}_u(i) - \mathbf{z}_v(i)\|$
(d) Weighted-L2	$\|\mathbf{z}_u \cdot \mathbf{z}_v\|_{\bar{2}i} = \|\mathbf{z}_u(i) - \mathbf{z}_v(i)\|^2$

Experimental Setup



- We are given a PPI network with a certain fraction of edges removed:
  - Remove about 50% of edges
  - Randomly sample an equal number of node pairs that have no edge connecting them
  - Explicitly removed edges and non-existent (or false) edges form a balanced test data set
- Two main stages:
  1. Learn an embedding for every node in the filtered PPI network
  2. Predict a score for every protein pair in the test set based on the embeddings

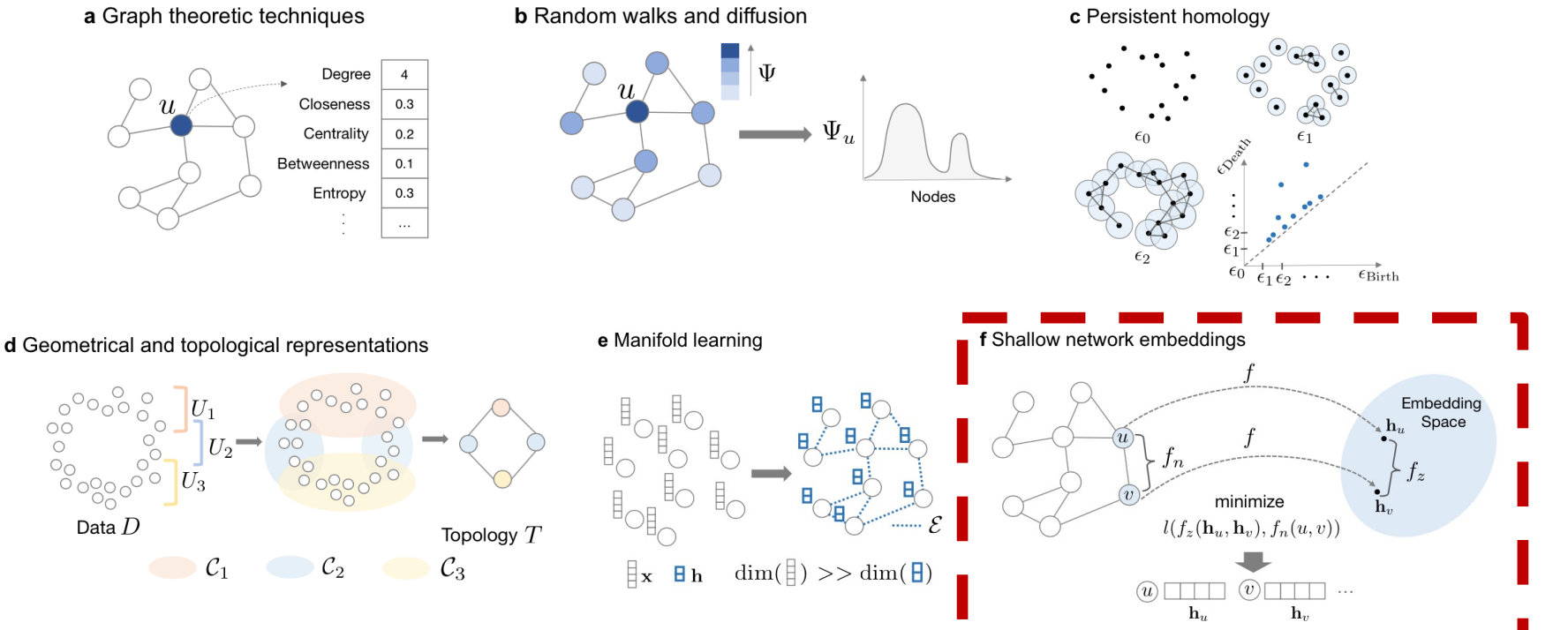


Time for a poll question about…

SHALLOW NETWORK EMBEDDINGS

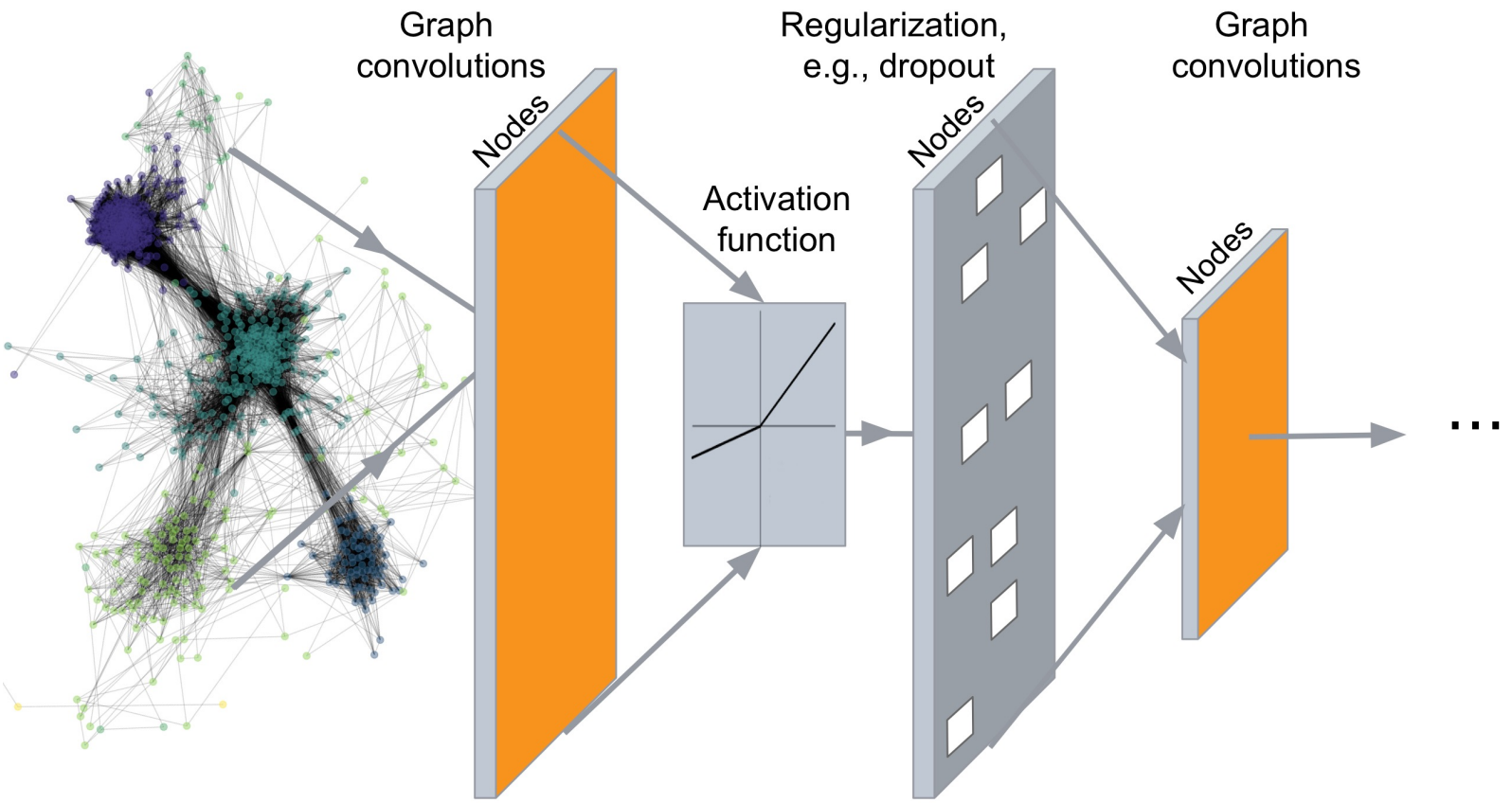
1. Which of the following are true about shallow network embeddings? *Select many*

Predominant graph learning paradigms



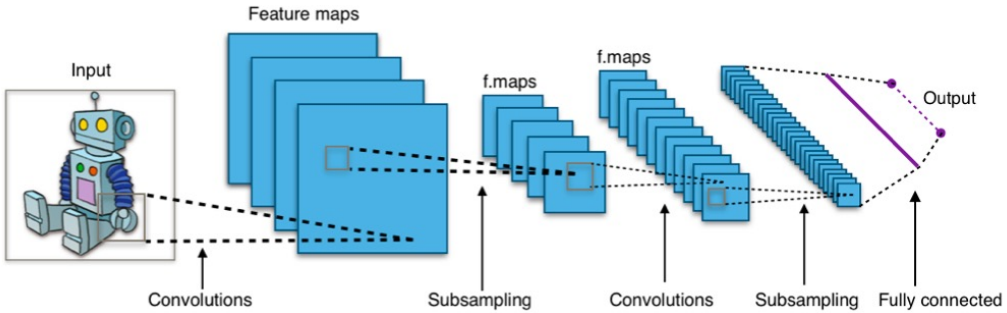
Graph neural networks

- Encoder: Multiple layers of nonlinear transformation of graph structure



Convolutional networks

- Let's start with convolutional networks on an image:



- Single convolutional network with a 3x3 filter:

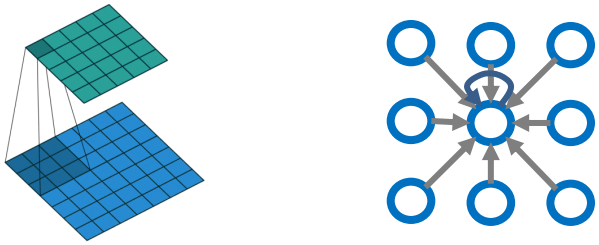
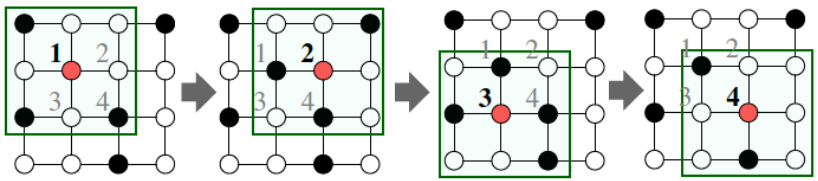


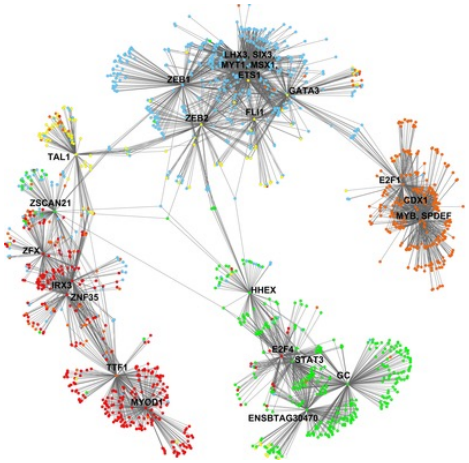
Image Graph

- Transform information (or messages) from the neighbors and combine them: $\sum_i W_i \, h_i$

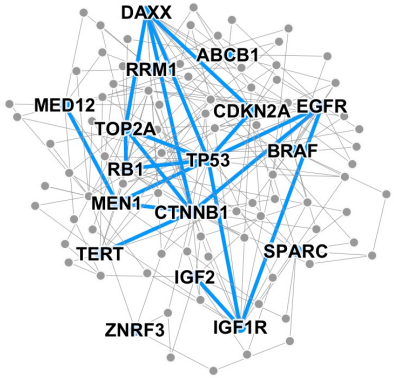


Real world graphs

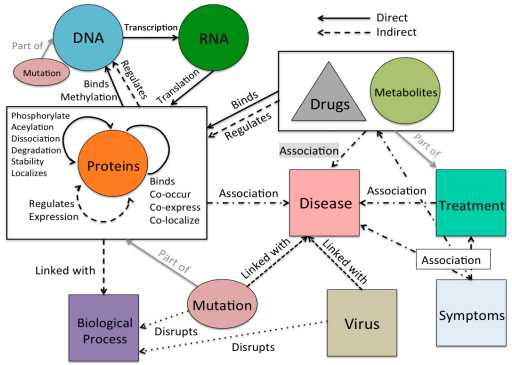
- But what if your graphs look like this?



Gene interaction network



Disease pathways

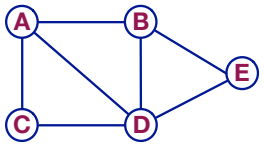


Biomedical knowledge graphs

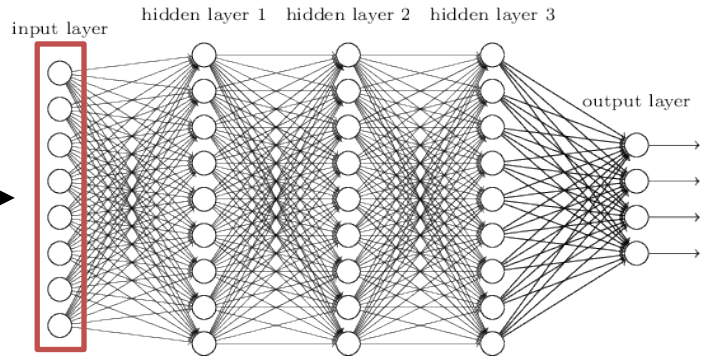
- Examples:
  - Biological or medical networks
  - Social networks
  - Information networks
  - Knowledge graphs
  - Communication networks
  - Web graphs
  - …

Naïve approach

- Join adjacency matrix and features
- Feed them into a deep neural network:



	A	B	C	D	E	Feat	
A	0	1	1	1	0	1	0
B	1	0	0	1	1	0	0
C	1	0	0	1	0	0	1
D	1	1	1	0	1	1	1
E	0	1	0	1	0	1	0

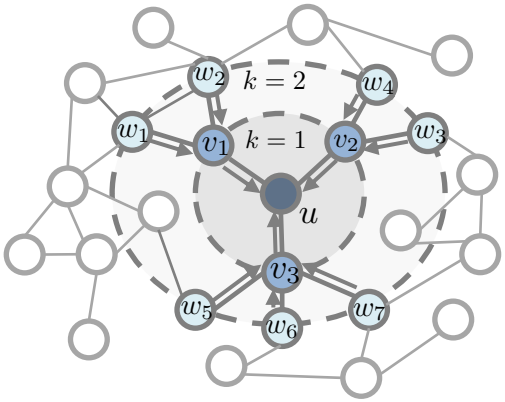


?

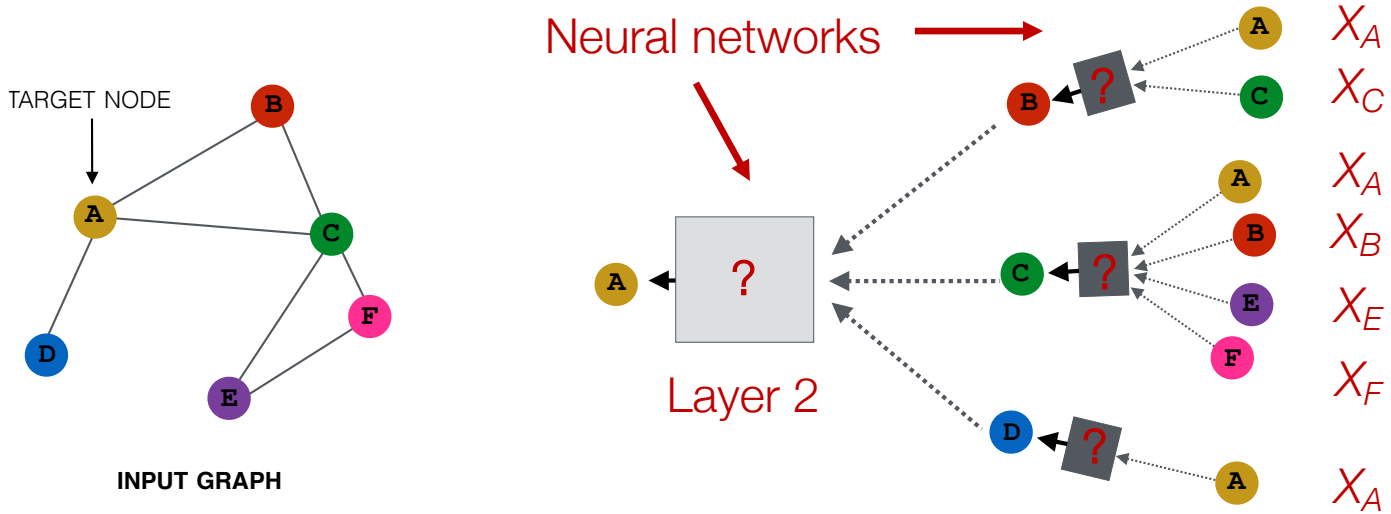
- Issues with this idea:
  - $O(N)$ parameters
  - Not applicable to graphs of different sizes
  - Not invariant to node ordering

Graph neural networks

- Intuition:
  - Each node's neighborhood defines a computational graph
  - Generate node embeddings based on local network neighborhoods

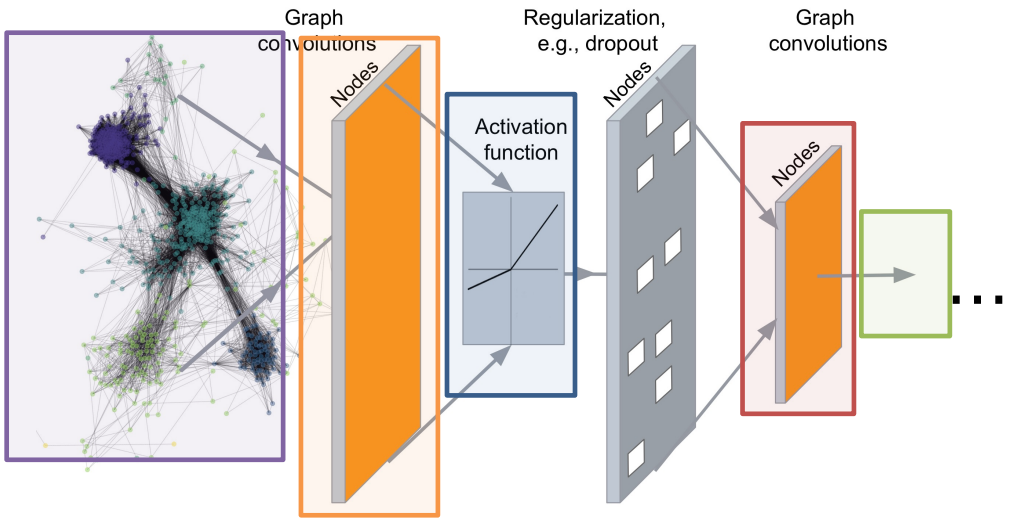


- Neighborhood aggregation:



  - Model can be of arbitrary depth
    - Nodes have embeddings at each layer
    - Layer 0 embedding of node *u* is its input features X_u
- Basic neighborhood aggregation approach (i.e. □): Average information from neighbors and apply a neural network

Basic approach



Initial 0-th layer embeddings are equal to node features

$$\mathbf{h}_v^0 = \mathbf{x}_v$$

Previous layer embedding of v

$$\mathbf{h}_v^k = \sigma\left(\mathbf{W}_k \sum_{u \in N(v)} \frac{\mathbf{h}_u^{k-1}}{|N(v)|} + \mathbf{B}_k \mathbf{h}_v^{k-1}\right), \quad \forall k \in \{1, ..., K\}$$

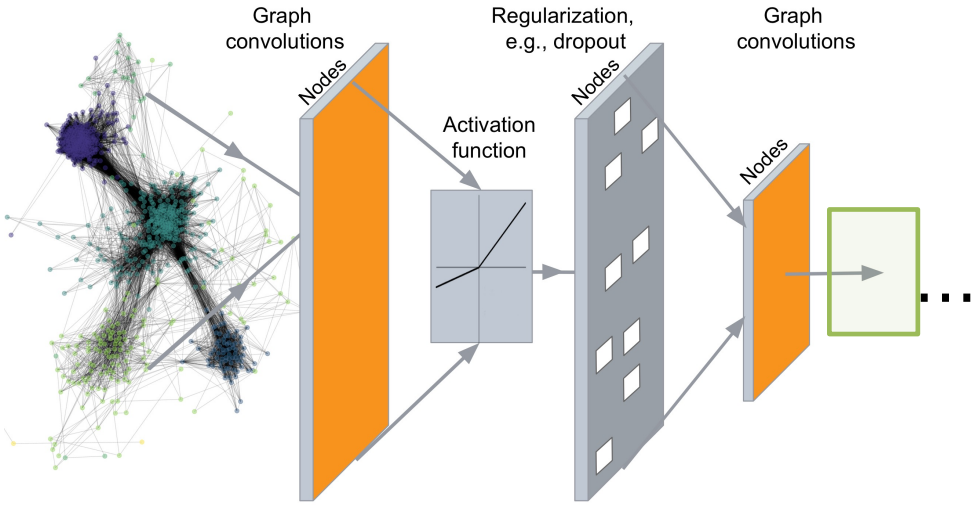
Average of neighbor's previous layer embeddings

$$\mathbf{z}_v = \mathbf{h}_v^K$$

Embedding after K layers of neighborhood aggregation

Non-linearity (e.g., ReLU)

Basic approach



trainable weight matrices
(i.e., what we learn)

$$\mathbf{h}_v^0 = \mathbf{x}_v$$

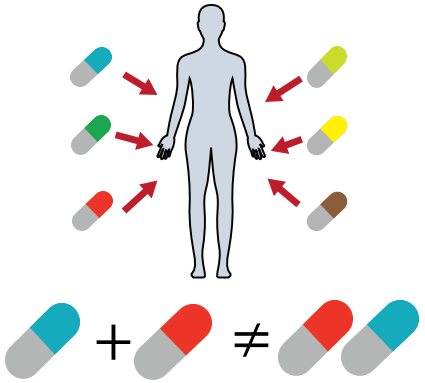
$$\mathbf{h}_v^k = \sigma\left(\mathbf{W}_k \sum_{u \in N(v)} \frac{\mathbf{h}_u^{k-1}}{|N(v)|} + \mathbf{B}_k \mathbf{h}_v^{k-1}\right), \quad \forall k \in \{1, ..., K\}$$

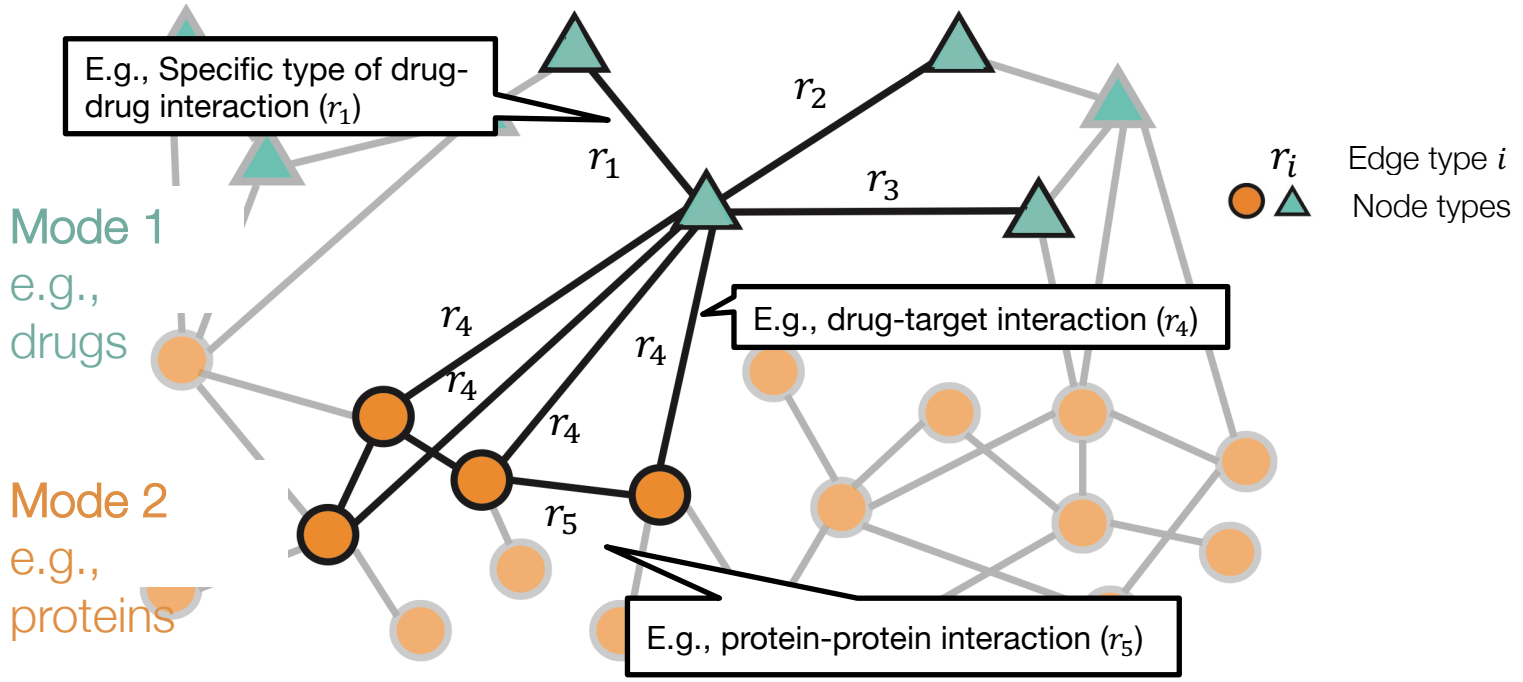
$$\mathbf{z}_v = \mathbf{h}_v^K$$

We can feed these into any loss function and run stochastic gradient descent to train the weight parameters

Application: Prioritize drug combos

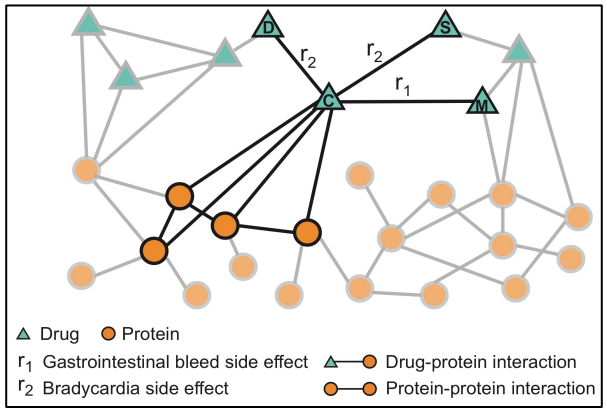
- Combinatorial explosion
  - >13 million possible combinations of 2 drugs
  - >20 billion possible combinations of 3 drugs
- Non-linear & non-additive interactions
  - Different effect than the additive effect of individual drugs
- Small subsets of patients
  - Side effects are interdependent
  - No info on drug combinations not yet used in patients





Modeling Polypharmacy Side Effects with Graph Convolutional Networks, Bioinformatics, 2018

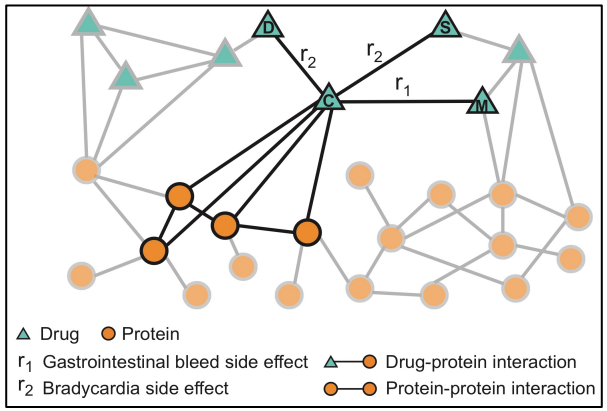
Polypharmacy dataset



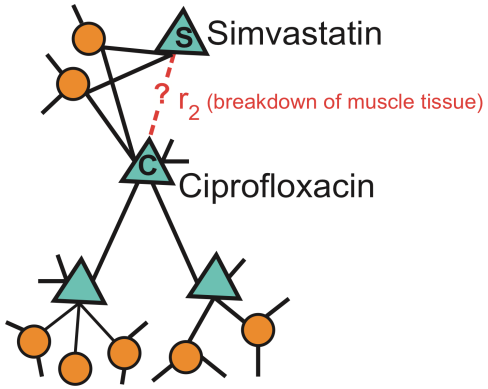
- Molecular, drug, and patient data for all drugs prescribed in US
  - 4,651,131 drug-drug edges: Patient data from adverse event system, tested for confounders [FDA]
  - 18,596 drug-protein edges
  - 719,402 protein-protein edges: Physical, metabolic enzyme-coupled, and signaling interactions
  - Drug and protein features: drugs' chemical structure, proteins' membership in pathways
- Gives multimodal network with over 5 million edges separated into 1,000 different edge types

Modeling Polypharmacy Side Effects with Graph Convolutional Networks, Bioinformatics, 2018

Experimental setup

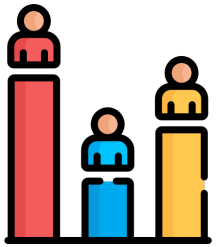


- Two main stages:
  1. Learn an embedding for every node in polypharmacy network
  2. Predict a score for every drug-drug, drug-protein, protein-protein pair in the test set based on the embeddings



Example: How likely will Simvastatin and Ciprofloxacin, when taken together, break down muscle tissue?

Modeling Polypharmacy Side Effects with Graph Convolutional Networks, Bioinformatics, 2018



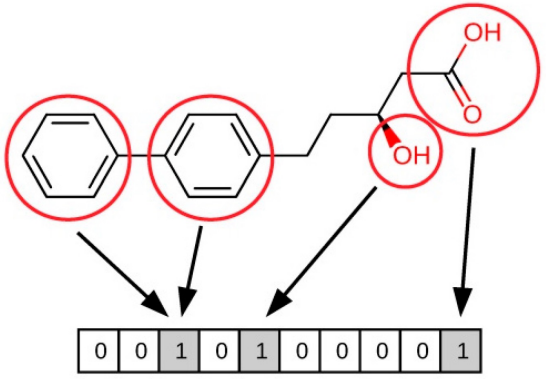
Time for a poll question about…

GRAPH NEURAL NETWORKS

1. Which of the following are false about graph neural networks? *Select many*

Molecular graphs and structures (xyz coordinates) are fundamental features in molecules

Often these are converted into molecular descriptors or some other representations



Why is that? Why can we not work with the data directly?

Illustrative example (1/2)

- Let's say we have a butane molecule and would like to predict its potential energy from its position. We could train a linear model $\hat{E}$ that predicts energy:

$$\hat{E} = XW + b$$

  where X is 14 (atoms) × 3 (xyz coordinates) matrix containing positions and W, b are trainable parameters
- Now what if we translate all the coordinates by -10:

$$(X - 10)W + b = X + b \; - 10|W|$$

- We know the energy should not change if we translate all the coordinates equally – the molecule is not changing conformations
- However, our linear regression will change by $-10|W|$
- We have accidentally made our model sensitive to the origin of our coordinate system, which is not physical. This is **translational variance** – the model changes when we translate the coordinates

Illustrative example (2/2)

- Consider another example from our butane molecule. What if we swapped the order of the atoms in our
- The of our mo
- Ho ch wei nergy will
- Thi es if we kno
- We have accidentally made the model sensitive to the ordering of the atoms

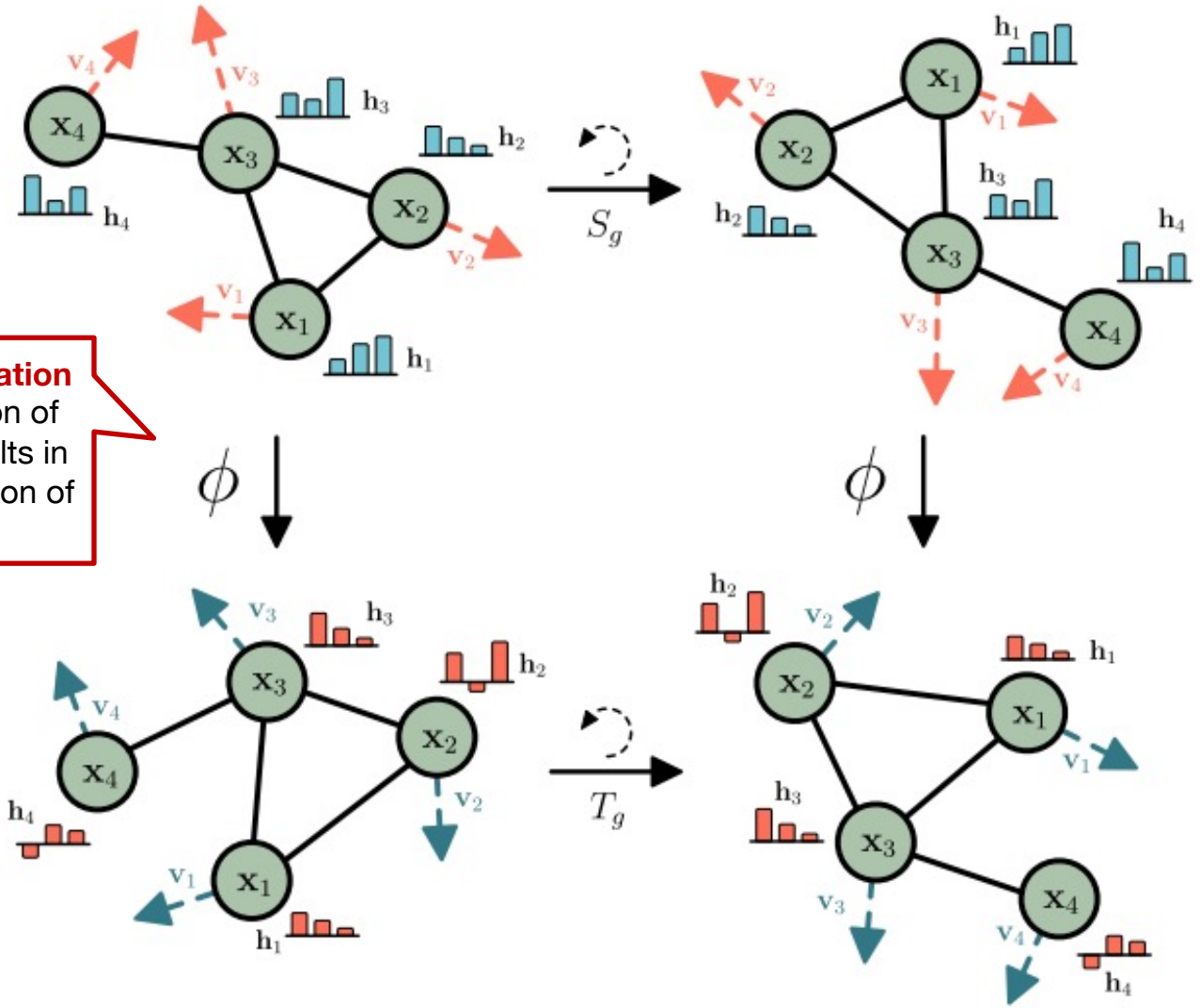
Take-away message: We want models predicting potential energy of molecules from their position to be insensitive to the translation and rotation of molecular coordinated — namely, they should be **permutation invariant** and **translationally invariant.**

Methods so far presented in Tutorial

- **Method presented so far:** Neural networks that process input data in a way that is invariant to node and edge permutations
- **Next:** Neural networks that process input data in a way that is sensitive to some type of transformations
  - Equivariant neural networks!
  - Permutation equivariant: If you rearrange the order of atoms, the output changes in the same way
  - Translationally equivariant: If you translate the input to a neural network the output will be translated in the same way

Example of rotational equivariance

Equivariant to rotation means that rotation of input features results in an equivalent rotation of outputs.



Example of rotation equivariance on a graph with a graph neural network ϕ

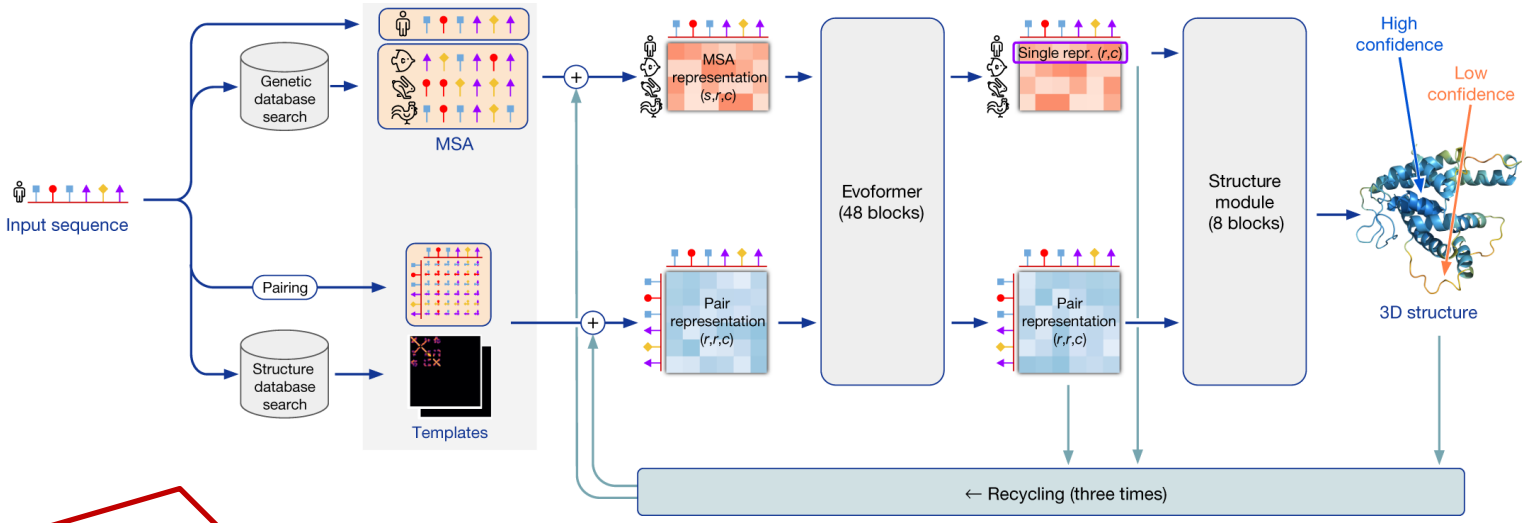
Equivariant neural networks

- Equivariant neural networks are part of a broader topic of **geometric deep learning**, which is learning with data that has some underlying geometric relationships
  - Geometric deep learning is a broad-topic and includes the "5Gs": grids, groups, graphs, geodesics, and gauges
  - Typical nomenclature in current literature:
    - Point clouds (gauges) → equivariant neural networks
    - Graphs → graph neural networks
    - Grids → convolutional neural networks

Highly-active research area, especially for predicting energies, forces, protein docking, and structures of molecules

Why should I care about equivariant neural networks?

Equivariant neural networks underly several breakthroughs, including AlphaFold 2 for protein structure prediction

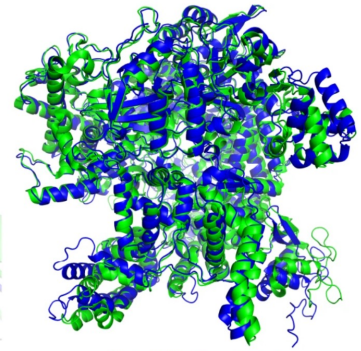


Equivariant neural networks are receiving increasing interest from the natural and medical sciences as they represent a new tool for analyzing molecules and their properties

Motivation: AlphaFold network (1/2)

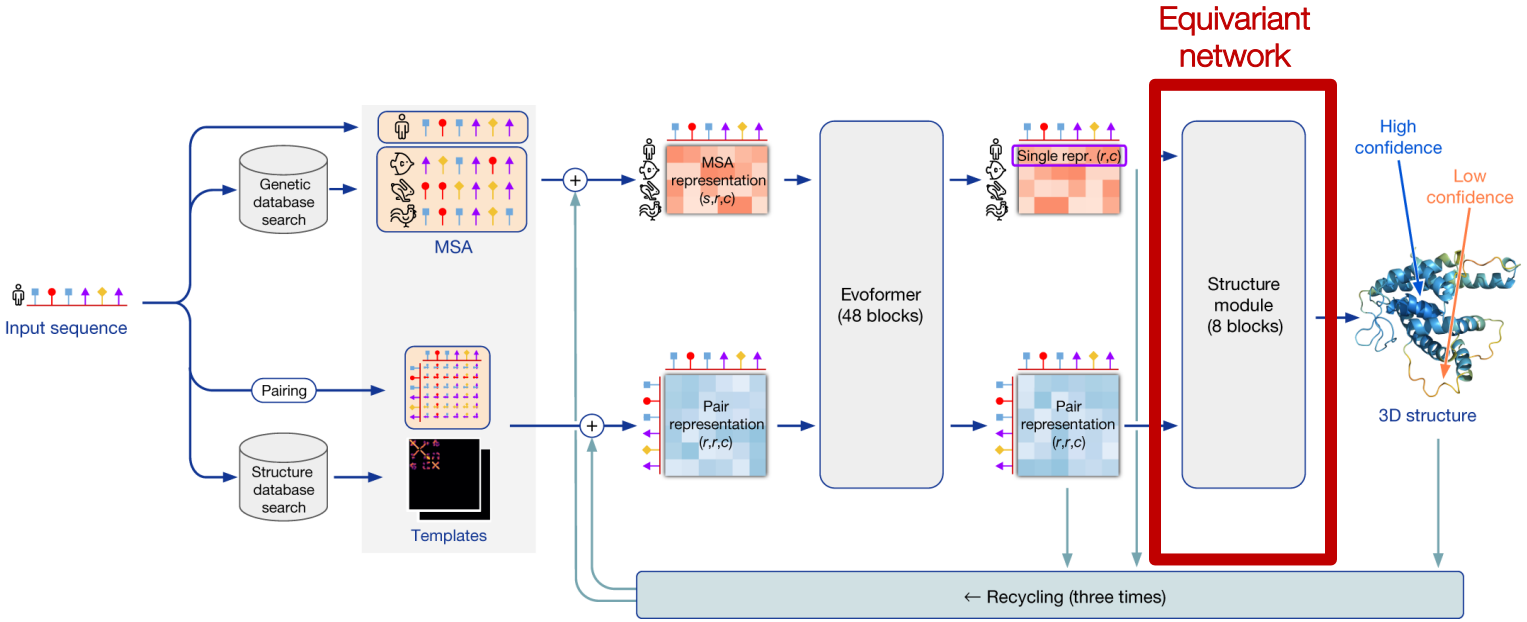
- What drives accurate protein structure prediction?
  - Novel neural architecture based on the evolutionary, physical and geometric constraints of protein structures
- Input:
  - Primary AA sequence of a given protein
  - Aligned sequences of homologues

- Output:
  - Predicted 3D coordinates of all heavy atoms in the protein



Motivation: AlphaFold network (2/2)

- **Structure module** in the AlphaFold network:
  - It introduces an explicit 3D structure in the form of a rotation and translation for each residue of the protein
  - Representations are initialized in a trivial state with all rotations set to the identity and all positions set to the origin
  - Representations rapidly develop and refine a highly accurate protein structure with precise atomic details



Problem definition

- **Setup:**
  - Graph $G = (V, E)$ with nodes $v_i \in V$ and edges $e_{ij} \in E$
  - In addition to node embeddings $h_i \in R^d$ we also consider a n-dimensional coordinate $x_i \in R^n$ associated with each node
- **Goal:**
  - Model that will **preserve equivariance to rotations and translations** on these set of coordinates x_i
  - Model that will preserve equivariance to permutations on the set of nodes V in the same fashion as GNNs

E(n) Equivariant Graph Neural Networks, ICML, 2021

Approach: Equivariant GNN (EGNN)

- EGNN model has multiple neural layers
- Layer l is an equivariant graph convolutional layer:
  - Input:
    - Set of node embeddings $h^l = \{h_0^l, \ldots, h_{M-1}^l\}$
    - Coordinate embeddings $x^l = \{x_0^l, \ldots, x_{M-1}^l\}$
    - Edge information $E = (e_{ij})$
  - Output:
    - Updated node embeddings $h^{l+1} = \{h_0^{l+1}, \ldots, h_{M-1}^{l+1}\}$
    - Updated coordinate embeddings $x^{l+1} = \{x_0^{l+1}, \ldots, x_{M-1}^{l+1}\}$
- Concisely: $h^{l+1}, x^{l+1} = \mathrm{EGCL}(h^l, x^l, E)$

E(n) Equivariant Graph Neural Networks, ICML, 2021

Approach: EGC layer

Main difference with the original GNN

Update coordinate embeddings: Update the position of each particle x_i as a vector field in a radial direction

Aggregate coordinate info: We choose to aggregate coordinates according to the relative squared distance between two coordinates

$$\mathbf{m}_{ij} = \phi\left(\mathbf{h}_i^l, \mathbf{h}_j^l, \left\|\mathbf{x}_i^l - \mathbf{x}_j^l\right\|^2, a_{ij}\right)$$

$$\mathbf{x}_i^{l+1} = \mathbf{x}_i^l + C\sum_{j\neq i}\left(\mathbf{x}_i^l - \mathbf{x}_j^l\right)\phi_x\left(\mathbf{m}_{ij}\right)$$

$$\mathbf{m}_i = \sum_{j\neq i}\mathbf{m}_{ij}$$

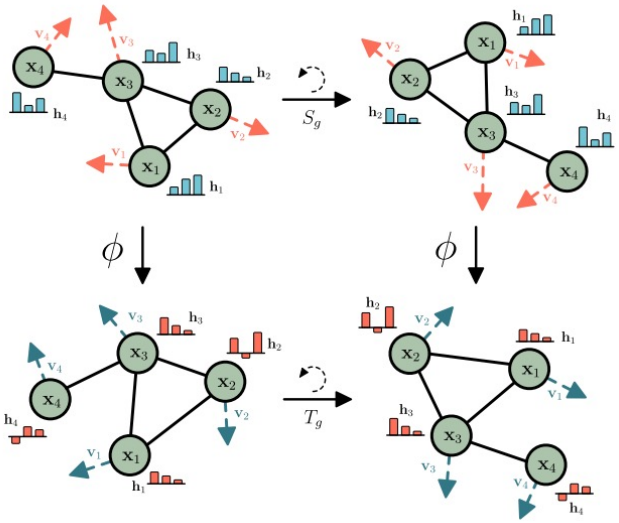
Aggregate node info: We choose to aggregate messages from all other nodes $j \neq i$. Alternatively, we could limit the message exchange to a given neighborhood $j \in N(i)$

$$\mathbf{h}_i^{l+1} = \phi_h\left(\mathbf{h}_i^l, \mathbf{m}_i\right)$$

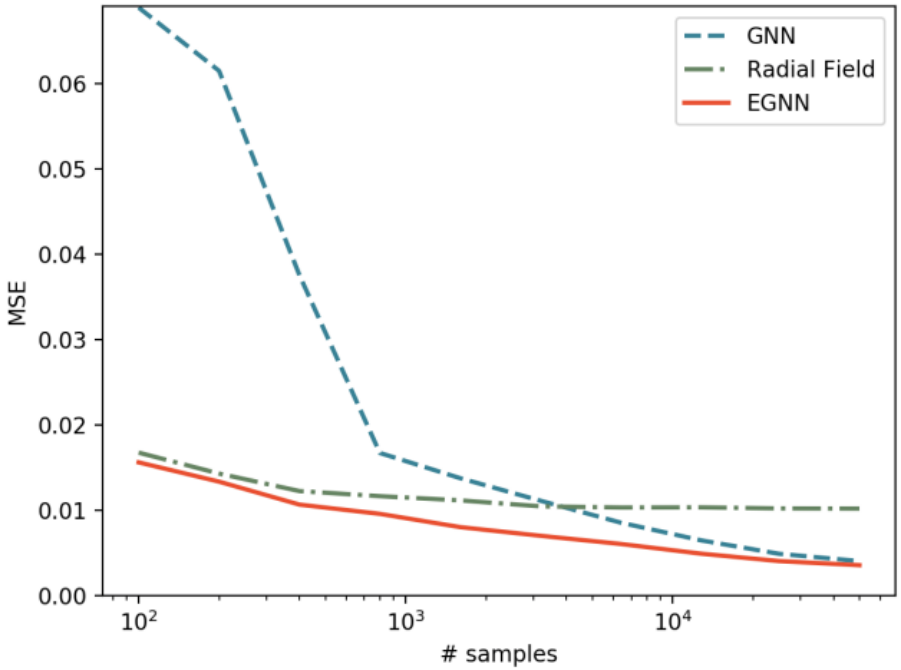
Update node embeddings: It takes as input the aggregated message, the node embedding from layer l and outputs the updated node embedding at layer $l+1$

E(n) Equivariant Graph Neural Networks, ICML, 2021

Recap: Equivariant neural network

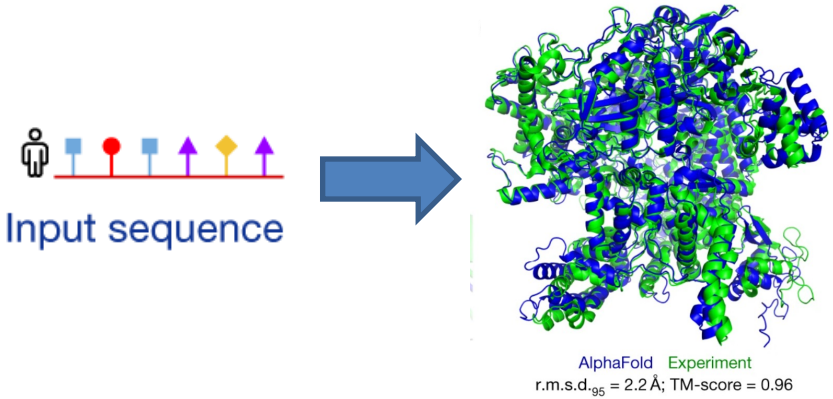


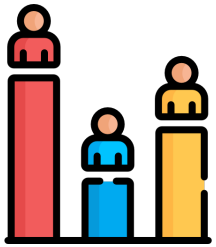
Example of rotation equivariance on a graph with a graph neural network ϕ



Mean Squared Error in the N-body experiment for the Radial Field, GNN and **EGNN** methods when sweeping over different amounts of training data

E(n) Equivariant Graph Neural Networks, ICML, 2021





Time for a poll question about…

EQUIVARIANT NEURAL NETWORKS

1. Which of the following are applicable to equivariant neural networks? *Select many*

This Tutorial

✓ 1. Methods: Network diffusion, shallow network embeddings, graph neural networks, equivariant neural networks

2. Applications: Fundamental biological discoveries and precision medicine

3. Hands-on exercises: Demos, implementation details, tools, and tips

Resources

- Books & survey papers
  - William Hamilton, *Graph Representation Learning* (morganclaypool.com/doi/abs/10.2200/S01045ED1V01Y202009AIM046)
  - Li et al., Graph Representation Learning for Biomedicine (arxiv.org/abs/2104.04883)

- Keynotes & seminars
  - Michael Bronstein, "Geometric Deep Learning: The Erlangen Programme of ML" (ICLR 2021 keynote) (youtube.com/watch?v=w6Pw4MOzMuo)
  - Broad Institute Models, Inference & Algorithms: Actionable machine learning for drug discovery; Primer on graph representation learning (youtube.com/watch?v=9YpTYdru0Rg)
  - Stanford University (CS224W Lecture): Graph neural networks in computational biology (youtube.com/watch?v=_hy9AgZXhbQ)
  - AI Cures Drug Discovery Conference (youtube.com/watch?v=wNXSkISMTw8)

- Conferences & summer schools
  - London Geometry and Machine Learning Summer School (logml.ai)
  - Learning on Graphs Conference (logconference.github.io)

Resources

- **Software & packages**
  - PyTorch Geometric
  - NetworkX
  - Stanford Network Analysis Platform (SNAP)

- **Tutorials & code bases**
  - Pytorch Geometric Colab Notebooks (pytorch-geometric.readthedocs.io/en/latest/notes/colabs.html)
  - Zitnik Lab Graph ML Tutorials (github.com/mims-harvard/graphml-tutorials)
  - Stanford University's CS224 (web.stanford.edu/class/cs224w)

- **Datasets**
  - Precision Medicine Oriented Knowledge Graph (PrimeKG) (zitniklab.hms.harvard.edu/projects/PrimeKG)
  - Therapeutic Data Commons (TDC) (tdcommons.ai)
  - BioSNAP (snap.stanford.edu/biodata/)
  - Open Graph Benchmark (OGB) (ogb.stanford.edu)