

# Relationship Modeling: Graph Neural Networks (GNNs)

Ju Sun  
Computer Science & Engineering

Nov 29, 2023



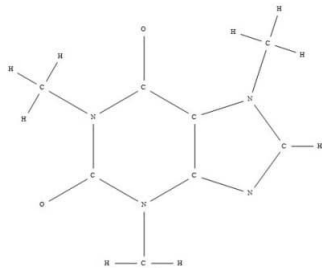
UNIVERSITY OF MINNESOTA  
Driven to Discover<sup>SM</sup>

# Outline

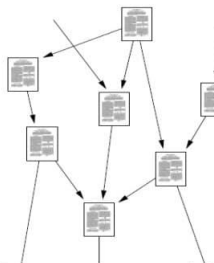
- Why graphs?
- Graphs: basic notions
- Graph neural networks
- Scaling up training

Why graphs?

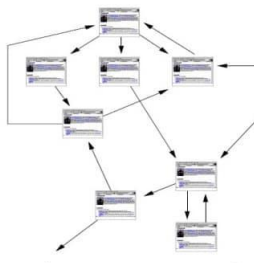
# Graphs are everywhere!



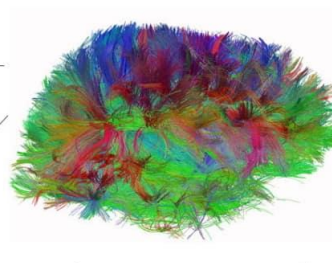
Molecules



Knowledge



Information



Brain/neurons

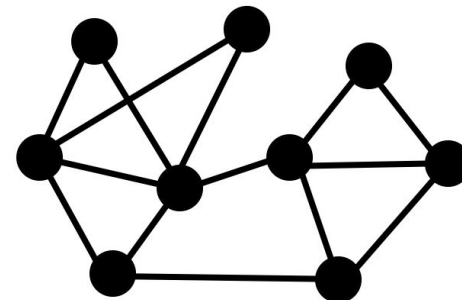
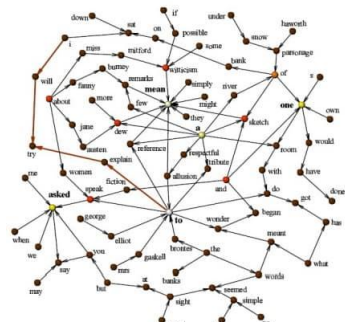


Image credit: Stanford CS224W



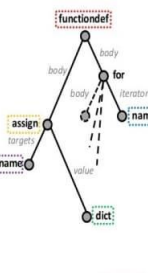
Genes



Communication

```
def encode(obj):  
    """  
    Encode a (possibly nested)  
    dictionary containing complex values  
    into a form that can be serialized  
    using JSON.  
    """  
    e = {}  
    for key, value in obj.items():  
        if isinstance(value, dict):  
            e[key] = encode(value)  
        elif isinstance(value, complex):  
            e[key] = {'type': 'complex',  
                    'r': value.real,  
                    'i': value.imag}  
    return e  
  
import ast  
tree = ast.parse("""  
...""")
```

Software



Social

Graphs model  
**relationships/  
interactions**

# Different tasks on graphs

The whole graph is **part of** all available data, i.e., a data point

**Graph prediction (classification/regression), graph generation**

A graph is a data point

Graph-level prediction,  
Graph generation

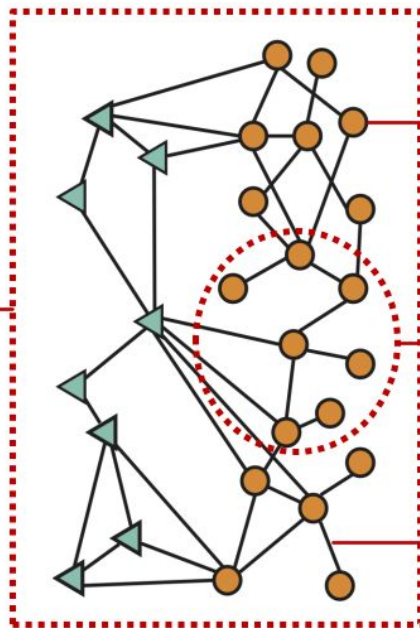


Image credit: Stanford CS224W

The whole graph is all available data

**Node level**

**Node prediction (classification/regression)**  
given labels over part of the graph

**Community (subgraph) level**

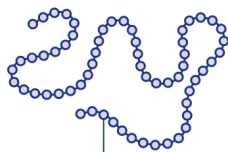
**Community detection/clustering**  
Clustering nodes/edges

**Edge-level**

**Link prediction**  
Predict links should exists or not

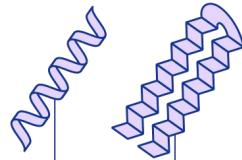
# Example task 1: Protein folding

Every protein is made up of a sequence of amino acids bonded together



Amino acids

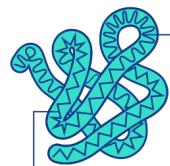
These amino acids interact locally to form shapes like helices and sheets



Alpha helix

Pleated sheet

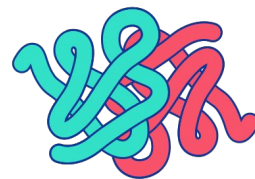
These shapes fold up on larger scales to form the full three-dimensional protein structure



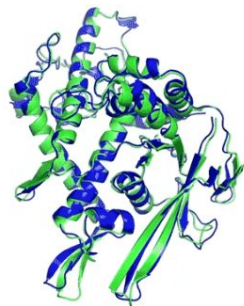
Pleated sheet

Alpha helix

Proteins can interact with other proteins, performing functions such as signalling and transcribing DNA



**Protein folding:** predict a protein's **3D structure** based on its **amino acid sequence**



T1037 / 6vr4

90.7 GDT

(RNA polymerase domain)



T1049 / 6y4f

93.3 GDT

(adhesin tip)

Image credit: Deep Mind

● Experimental result  
● Computational prediction

# Example task 1: Protein folding

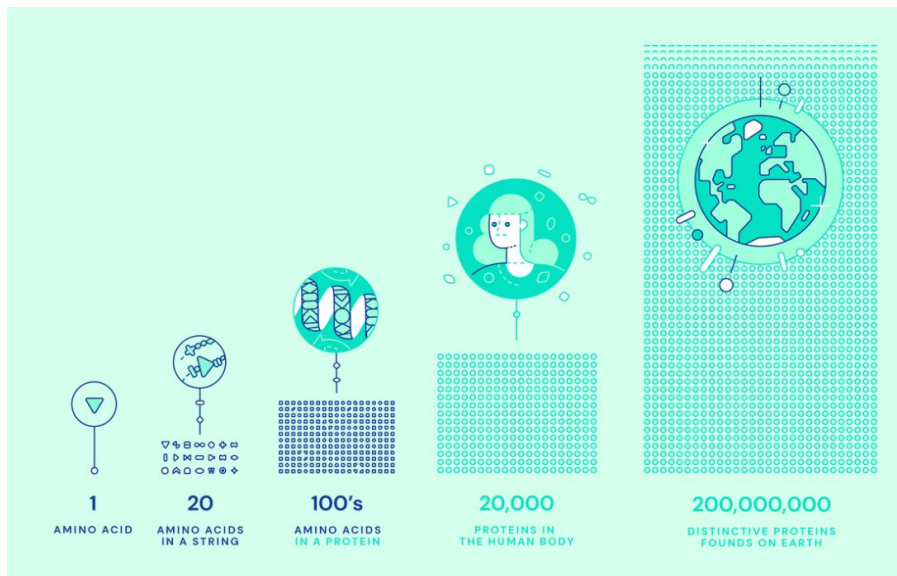
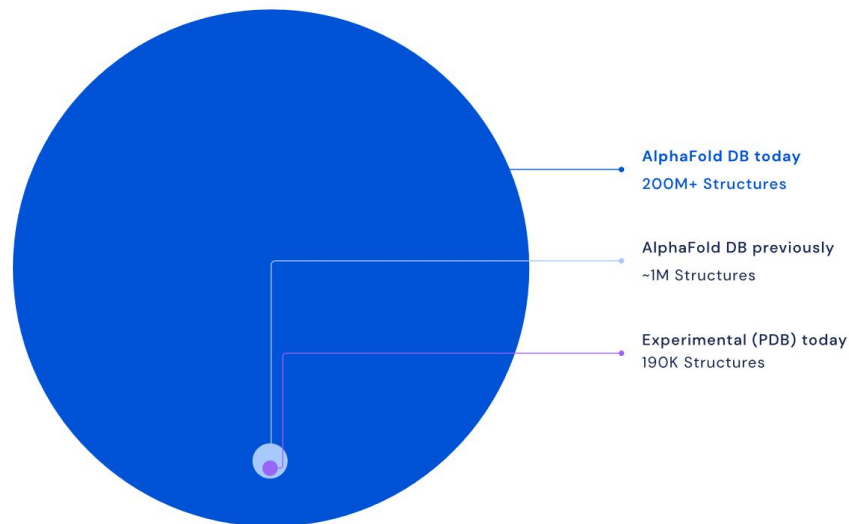
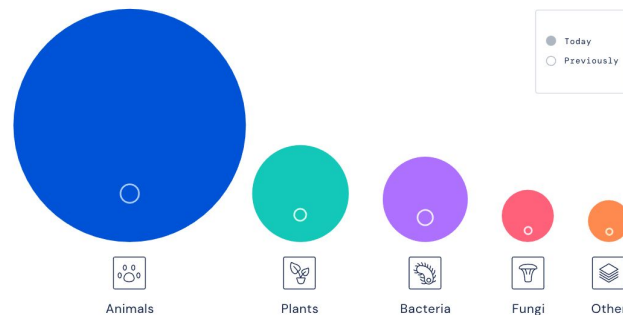


Image credit: Deep Mind



Number of species represented in AlphaFold DB

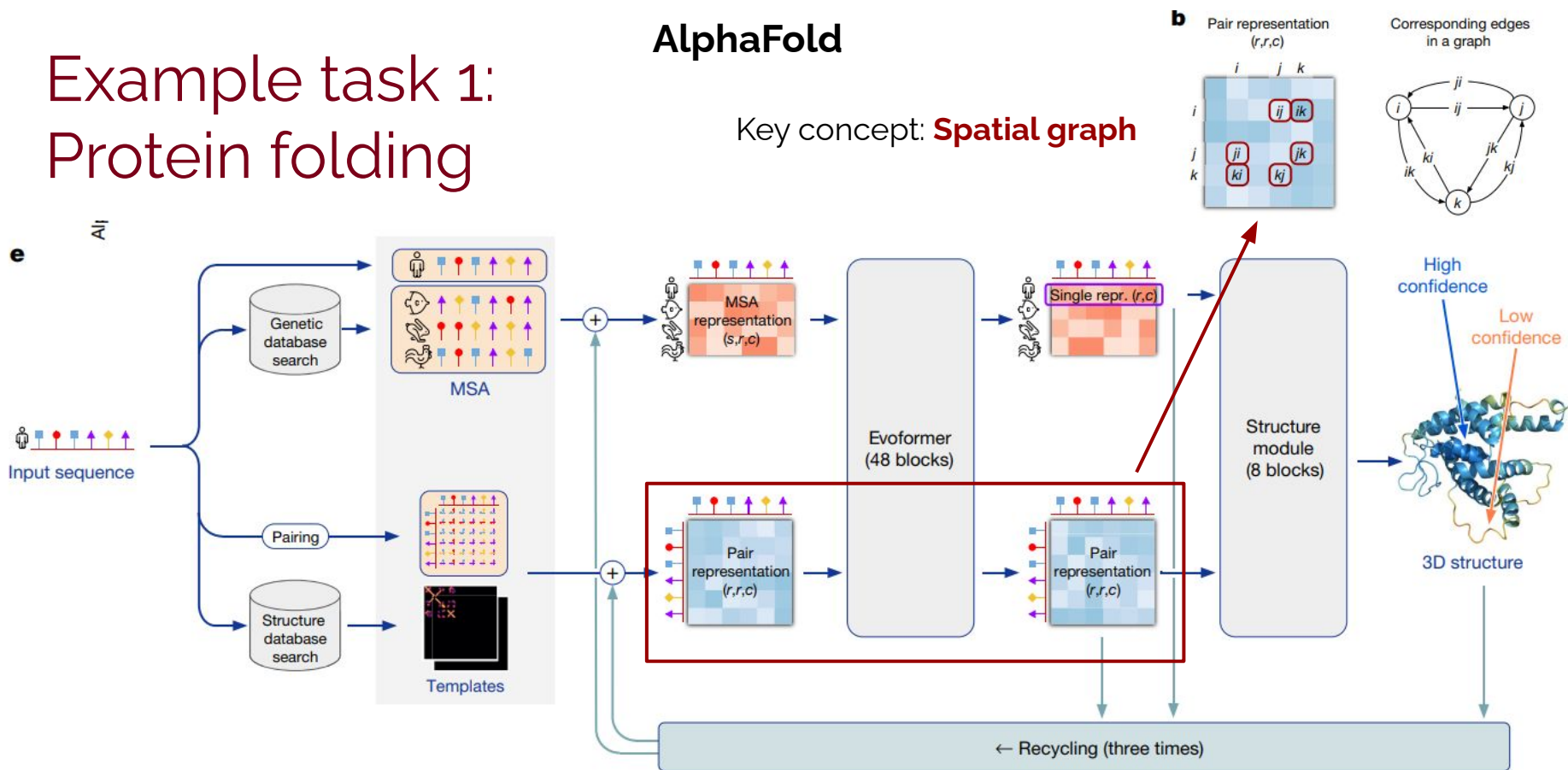
Total increase from ~10K to ~1M



# Example task 1: Protein folding

## AlphaFold

Key concept: **Spatial graph**

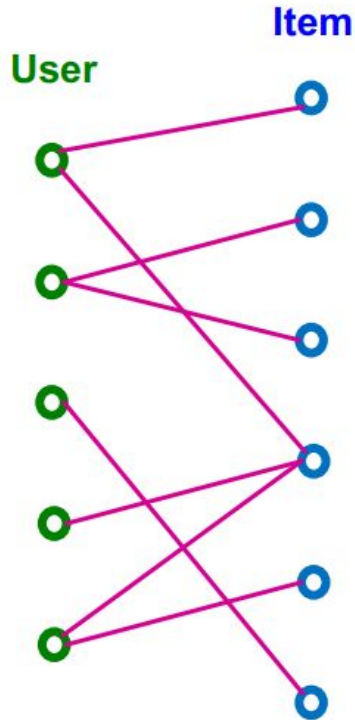


Complete story: <https://www.deepmind.com/research/highlighted-research/alphafold>

Paper: <https://www.nature.com/articles/s41586-021-03819-2>



# Example task 2: Recommendation systems



online shopping,  
music/movie  
recommendation

**Nodes:**  
Users, items  
**Edges:**  
User-item  
interactions

Image credit: Stanford CS224W

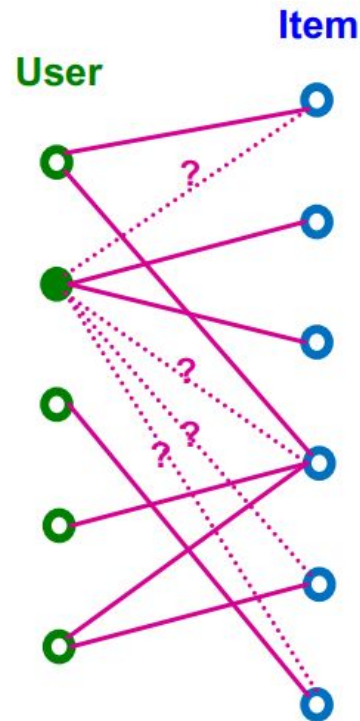
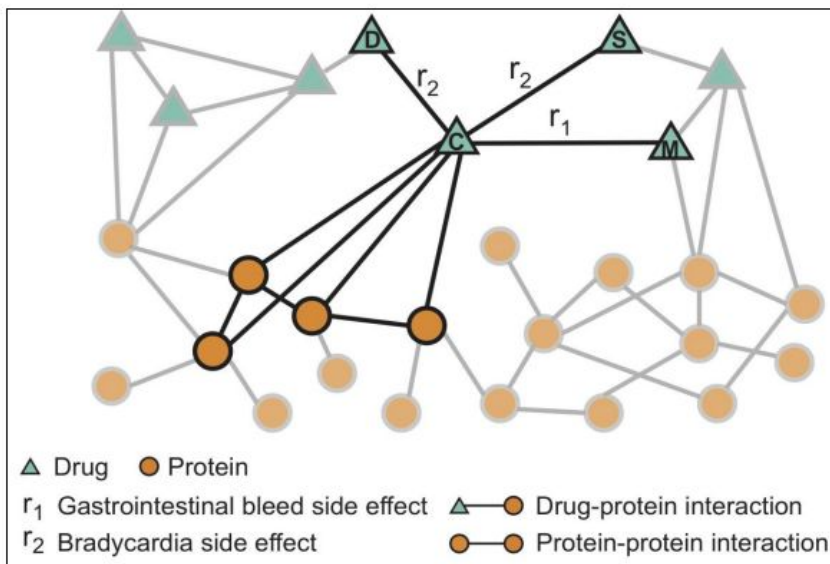


Image credit: Stanford CS224W

# Example task 3: Drug adverse effect discovery

- **Nodes:** Drugs & Proteins
- **Edges:** Interactions



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

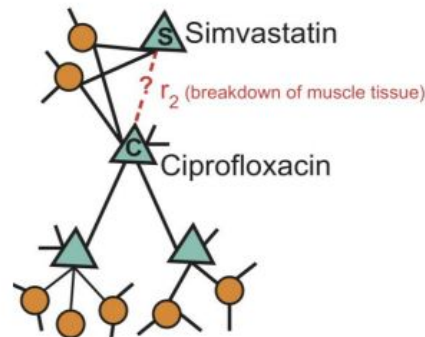


Image credit: Stanford CS224W

# Example task 4: Traffic prediction

☰

🗺️

🚗

🚝

🚶

🚲

✈️

✕

○

⋮

📍

Your location

Minneapolis Institute of Art, 2400 3rd Ave

↕

⊕

Leave now ▾

Options

📱

Send directions to your phone

🚝

⚠️ 1:50 PM—2:25 PM

35 min

🚶 > 🚗 2 > 🚶

1:54 PM from Washington Ave & Coffman Union

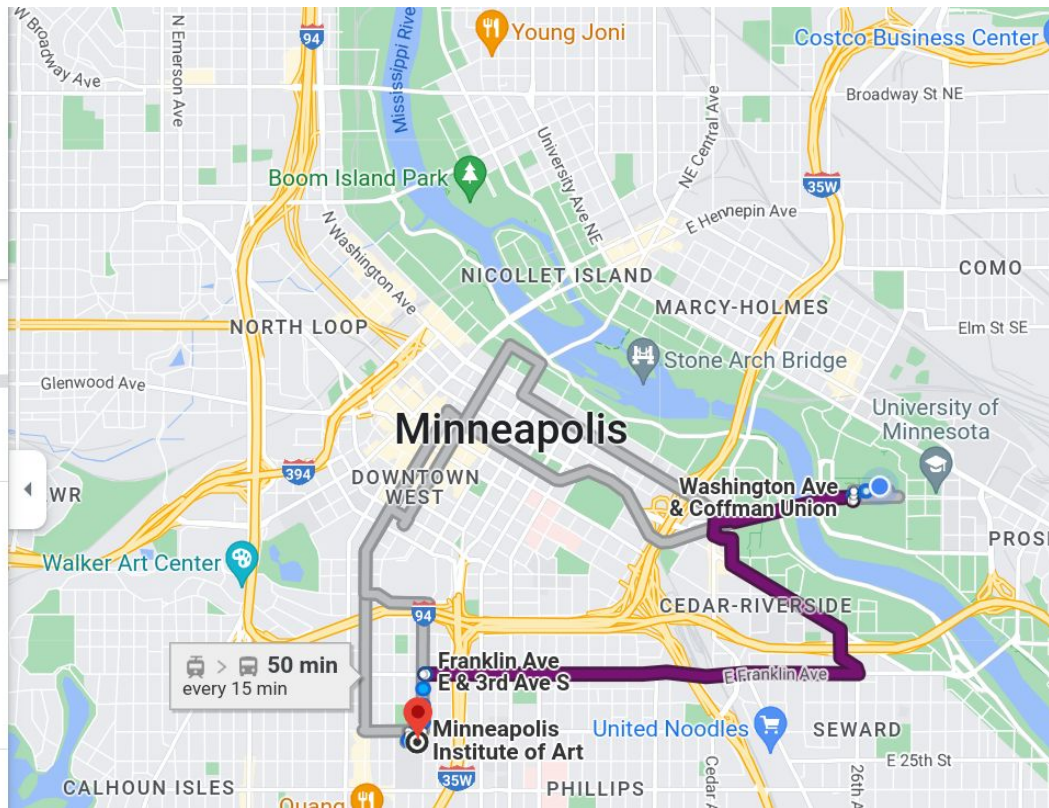
🚶 11 min every 15 min

Details

🚝

1:49 PM—2:30 PM

41 min



# Example task 4: Traffic prediction

- **Nodes:** Road segments
- **Edges:** Connectivity between road segments
- **Prediction:** Time of Arrival (ETA)

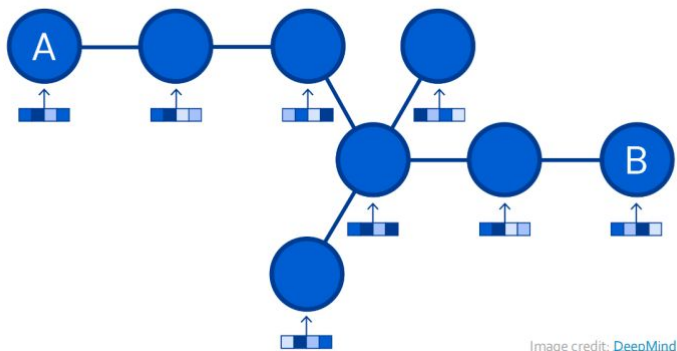


Image credit: Stanford CS224W

## Predicting Time of Arrival with Graph Neural Networks

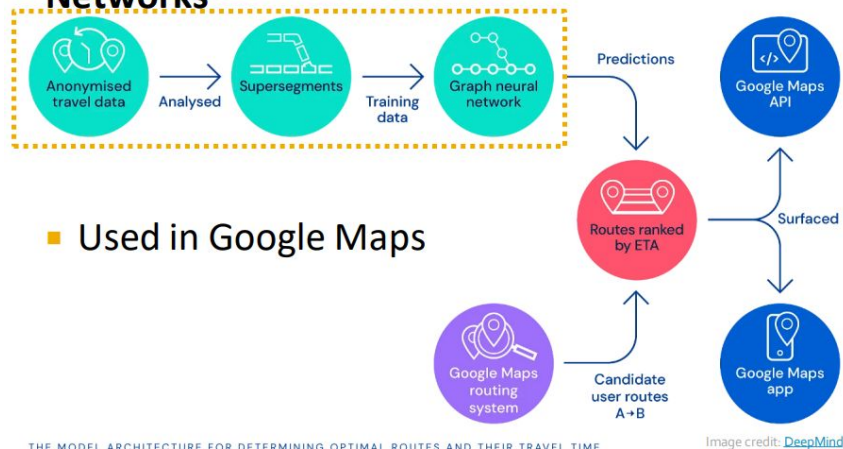


Image credit: Stanford CS224W

## Subgraph discovery

# Example task 5: Drug discovery

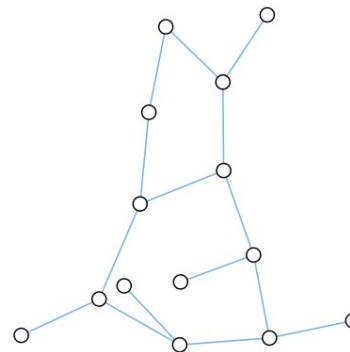
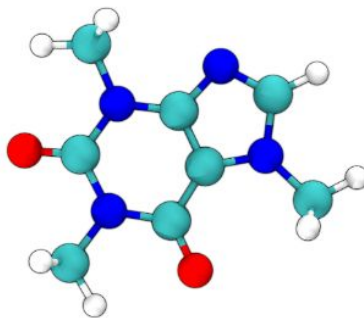
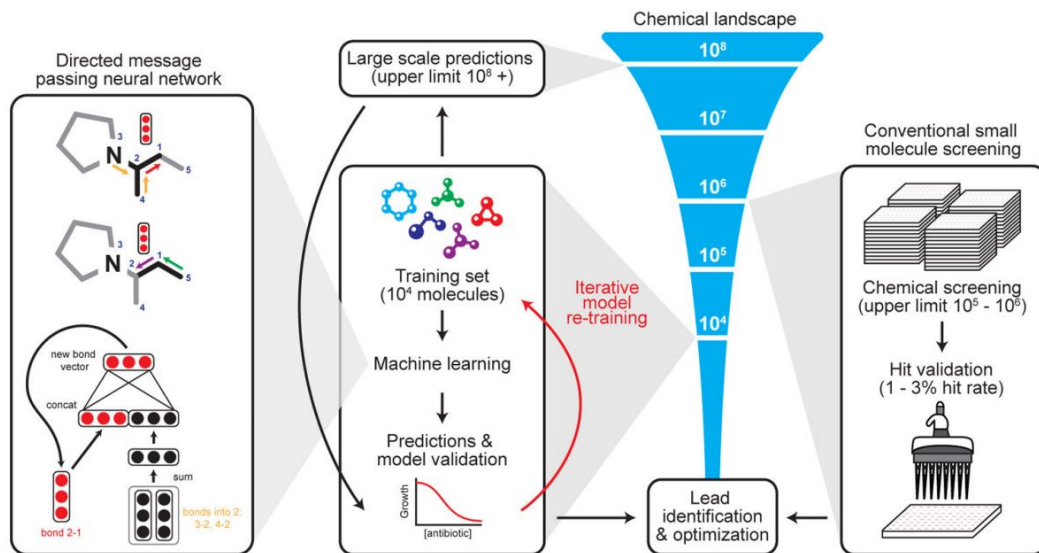


Image credit: <https://distill.pub/2021/gnn-intro/>

**Molecules as graphs:**

**Nodes:** atoms

**Edges:** chemical bounds



**full-graph prediction**

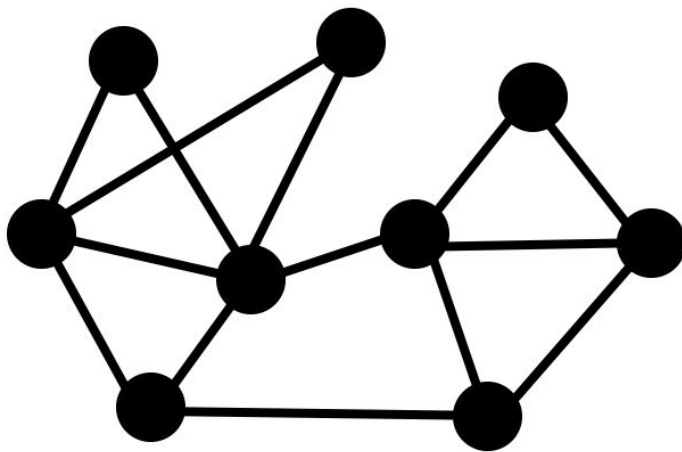
Image credit:

<https://pubmed.ncbi.nlm.nih.gov/32084340/>

# Graphs: basic notions



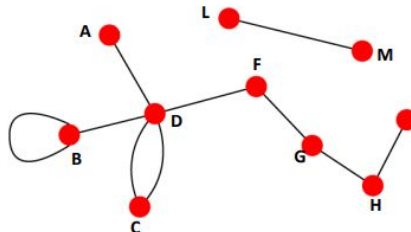
# Basic objects



- $N$  : Nodes (also vertices)
- $E$  : Edges (also links)
- $G(N, E)$  : Graph

## Undirected

- **Links:** undirected (symmetrical, reciprocal)

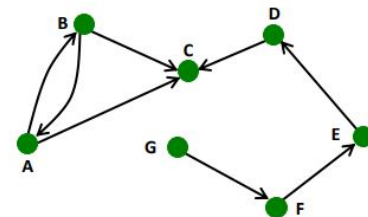


## Examples:

- Collaborations
- Friendship on Facebook

## Directed

- **Links:** directed (arcs)

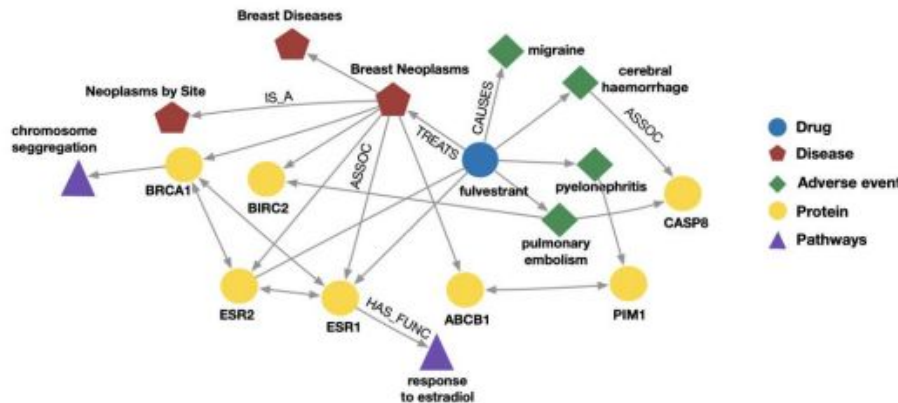


## Examples:

- Phone calls
- Following on Twitter

Image credit: Stanford CS224W

# Heterogeneous graphs



## Biomedical Knowledge Graphs

Example node: Migraine

Example edge: (fulvestrant, Treats, Breast Neoplasms)

Example node type: Protein

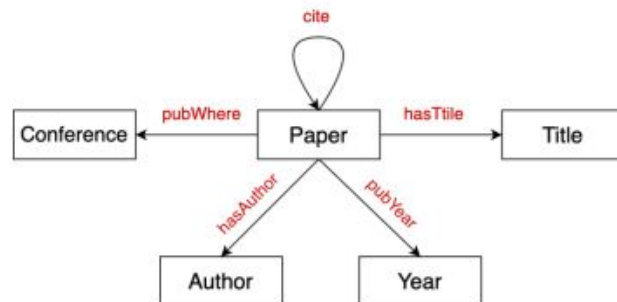
Example edge type (relation): Causes

Nodes/Edges are multi-typed

$$G(N, E, T, R)$$

T: types of nodes

R: types of relationships



## Academic Graphs

Example node: ICML

Example edge: (GraphSAGE, NeurIPS)

Example node type: Author

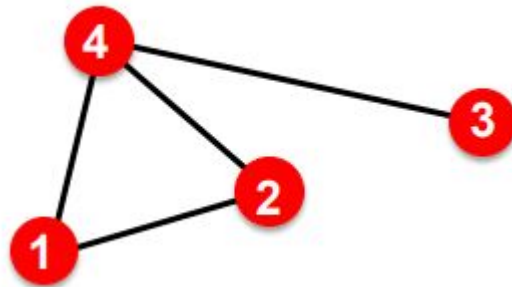
Example edge type (relation): pubYear

Image credit: Stanford CS224W



# Graph representation

Undirected graphs



$$A = \begin{pmatrix} 0 & 1 & 0 & 1 \\ 1 & 0 & 0 & 1 \\ 0 & 0 & 0 & 1 \\ 1 & 1 & 1 & 0 \end{pmatrix}$$

Adjacency matrix

(1, 4), (1, 2)  
(2, 1), (2, 4)  
(3, 4)  
(4, 1), (4, 2), (4, 3)

Edge list

1: 2, 4  
2: 1, 4  
3: 4  
4: 1, 2, 3

Adjacency list

# Graph representation

Directed graphs

$$A = \begin{pmatrix} 0 & 0 & 0 & 1 \\ 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 \end{pmatrix}$$

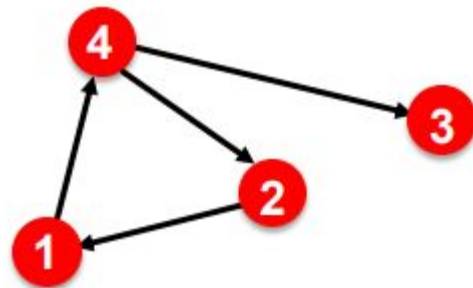
Adjacency matrix

(1, 4)

(2, 1)

(4, 2), (4, 3)

Edge list



1: 4

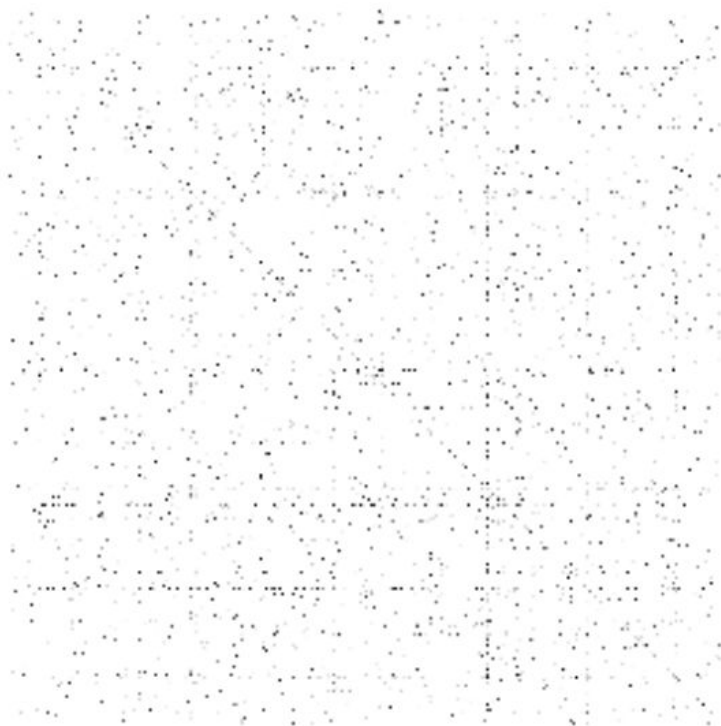
2: 1

3:

4: 2, 3

Adjacency list

# Adjacency matrix is often inefficient



NETWORK	NODES	LINKS	DIRECTED/ UNDIRECTED	N	E
Internet	Routers	Internet connections	Undirected	192,244	609,066
WWW	Webpages	Links	Directed	325,729	1,497,134
Power Grid	Power plants, transformers	Cables	Undirected	4,941	6,594
Phone Calls	Subscribers	Calls	Directed	36,595	91,826
Email	Email Addresses	Emails	Directed	57,194	103,731
Science Collaboration	Scientists	Co-authorship	Undirected	23,133	93,439
Actor Network	Actors	Co-acting	Undirected	702,388	29,397,908
Citation Network	Paper	Citations	Directed	449,673	4,689,479
E. Coli Metabolism	Metabolites	Chemical reactions	Directed	1,039	5,802
Protein Interactions	Proteins	Binding interactions	Undirected	2,018	2,930

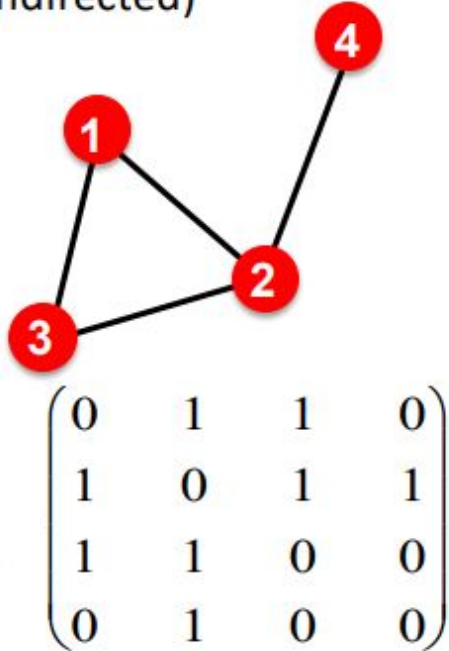
$$\text{Density} = |E|/|N|^2$$

**Real-world graphs are often very sparse**

# Weighted graphs

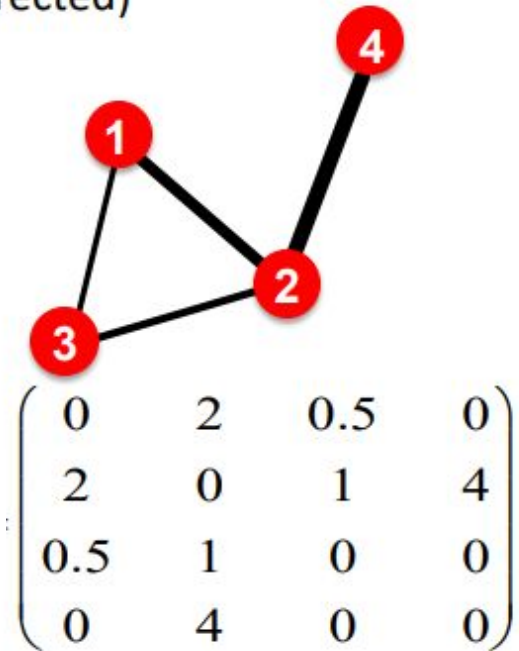
## ■ Unweighted

(undirected)

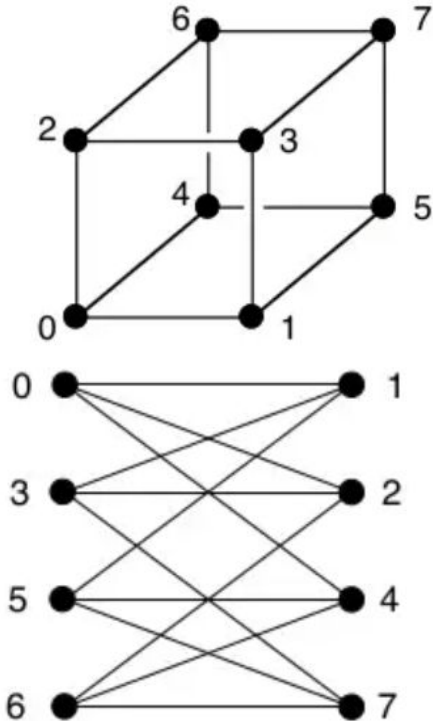


## ■ Weighted

(undirected)



# Graph isomorphism/equivalence



Graph G	Graph H	An isomorphism between G and H
		$f(a) = 1$ $f(b) = 6$ $f(c) = 8$ $f(d) = 3$ $f(g) = 5$ $f(h) = 2$ $f(i) = 4$ $f(j) = 7$

Image credit: Image credit: [https://en.wikipedia.org/wiki/Graph\\_isomorphism](https://en.wikipedia.org/wiki/Graph_isomorphism)

**Isomorphism:** there exists a bijective mapping, i.e., **permutation**, results in the same neighborhood structure

# Permutation invariance

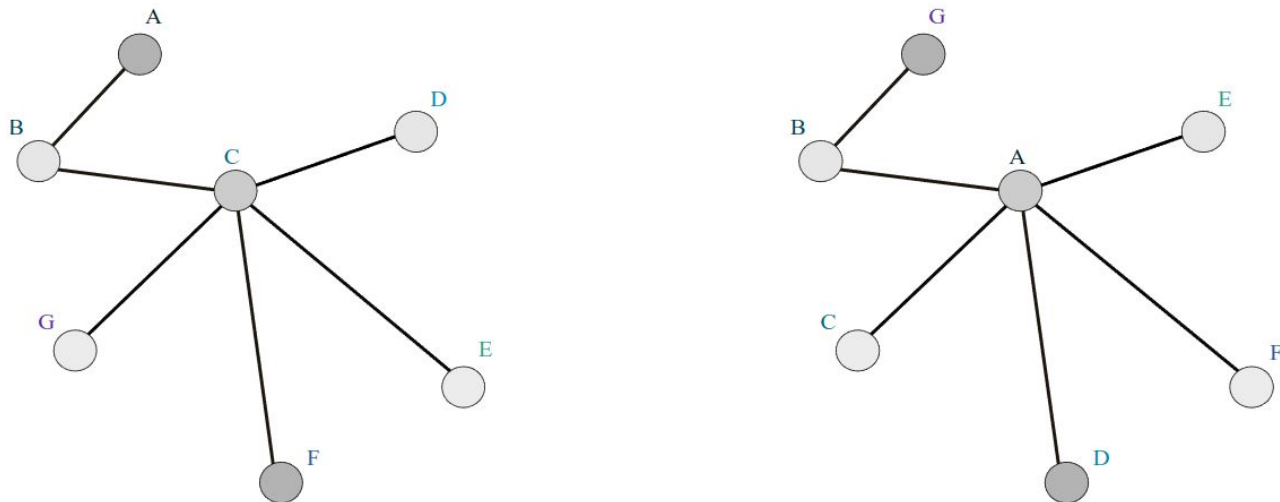


Image credit: Image credit: <https://distill.pub/2021/understanding-gnns/>

**Permutation invariance:** permuting the names of the nodes doesn't change the graph, as graph nodes are intrinsically orderless

**Mathematically:** if  $A$  is (the adjacency matrix of) a graph,  $\Pi A \Pi^T$  is (the adjacency matrix of) an equivalent graph for **any permutation matrix**  $\Pi$

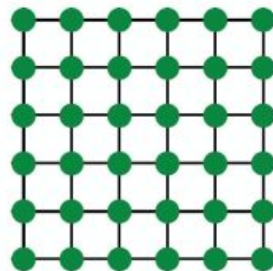
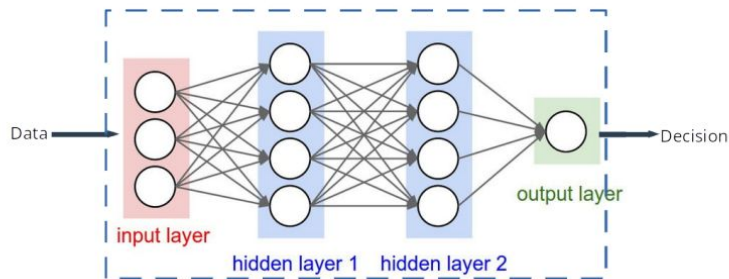
# Graph neural networks (GNNs)

# Representation learning for graphs

traditional learning pipeline



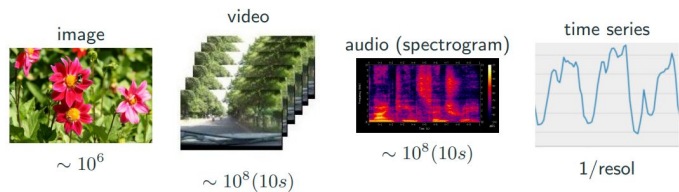
## modern learning pipeline



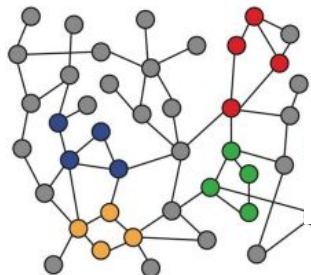
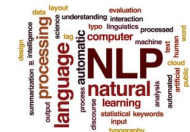
## Grid



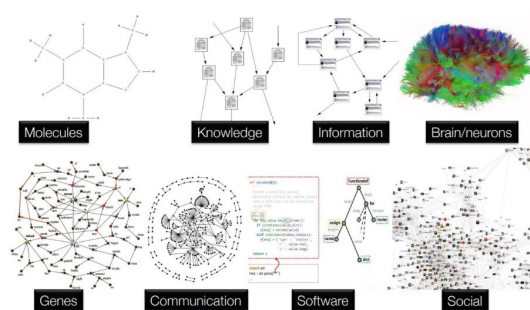
## List



- machine translation, e.g., English  $\leftrightarrow$  Chinese
- typing/writing prediction (smart compose)
- semantic classification

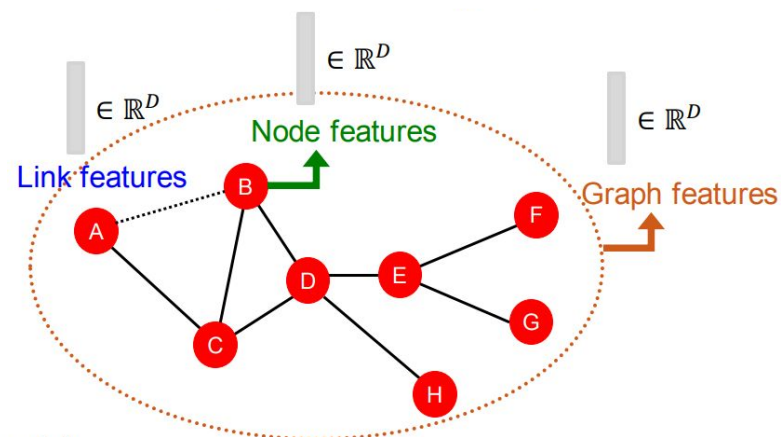
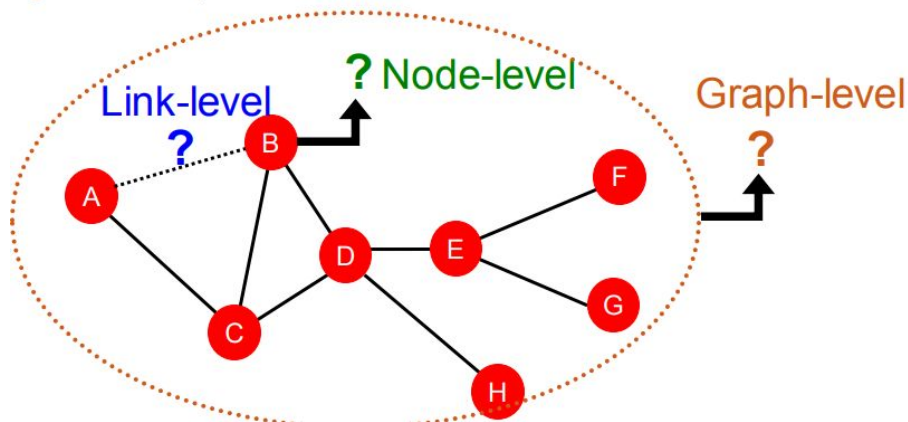


## Graph



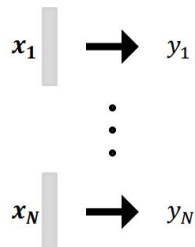


# Where to put the features?



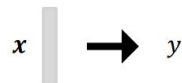
## ■ Train an ML model:

- Random forest
- SVM
- Neural network, etc.



## ■ Apply the model:

- Given a new node/link/graph, obtain its features and make a prediction



# Node embedding

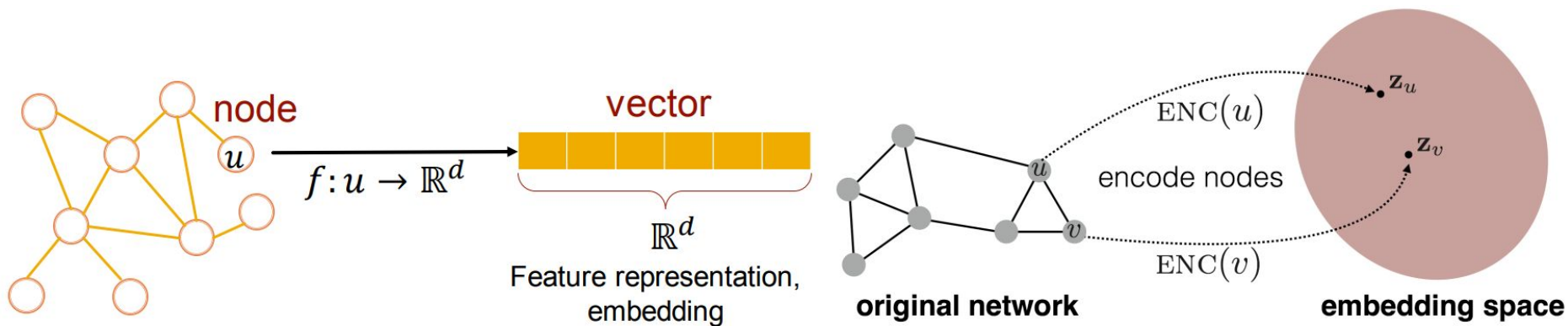


Image credit: Stanford CS224W

$N$  : set of nodes

$A$  : adjacency matrix

$X \in \mathbb{R}^{|N| \times d}$  : node (raw) features

$u, v$  : nodes in  $N$

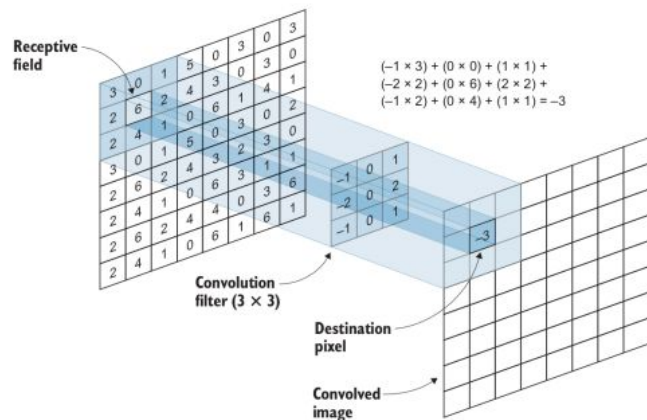
$\mathcal{N}(u)$  : neighbors of  $u$

**Node raw features: e.g.,**

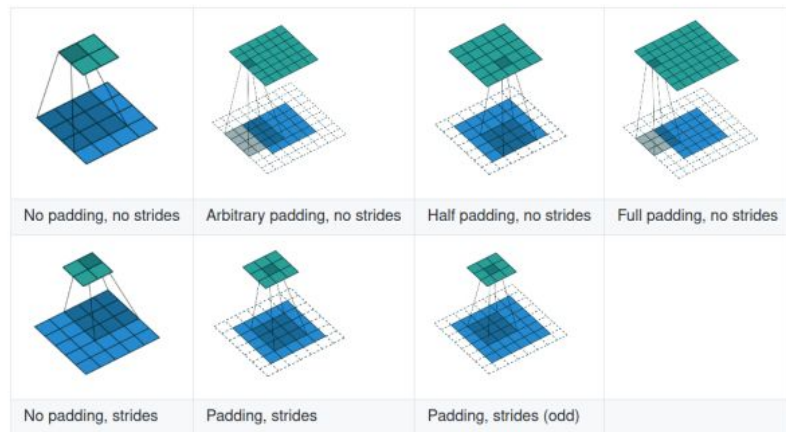
- Biomedical graphs: patient's EHR
- Social network graphs: user profile and images
- When no features: node indicator vector, constant vector

# How to define the $f$ ?

We'll bypass fully connected networks directly



(Credit: [Elgandy, 2020])



[https://github.com/vdumoulin/conv\\_arithmetic](https://github.com/vdumoulin/conv_arithmetic)

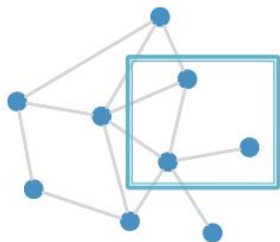
Convolution as performing **local info aggregation** (or **message passing**):

- Each time, the conv window focus on a **local neighborhood** of the current pixel
- Conv effectively **aggregates** the local info by **weighted summation**

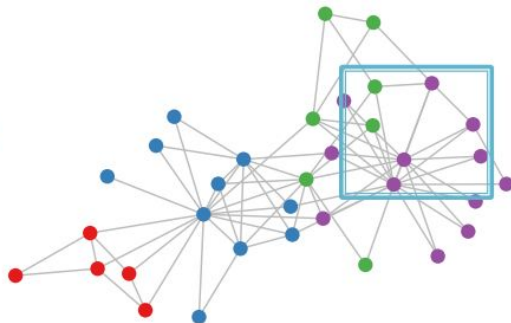
# How to define the $f$ ?

Convolution as performing **local info aggregation** (or **message passing**):

- **Neighborhood**: Each time, the conv window focus on a **local neighborhood** of the current pixel
- **Aggregation**: Conv effectively **aggregates** the local info by **weighted summation**

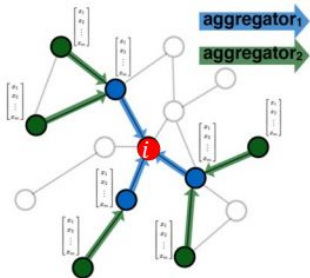
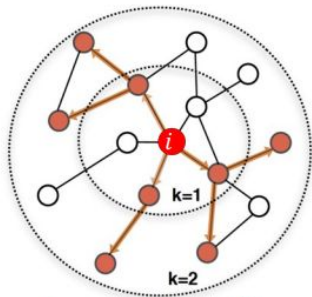


or this:



We need neighbors on the graph!

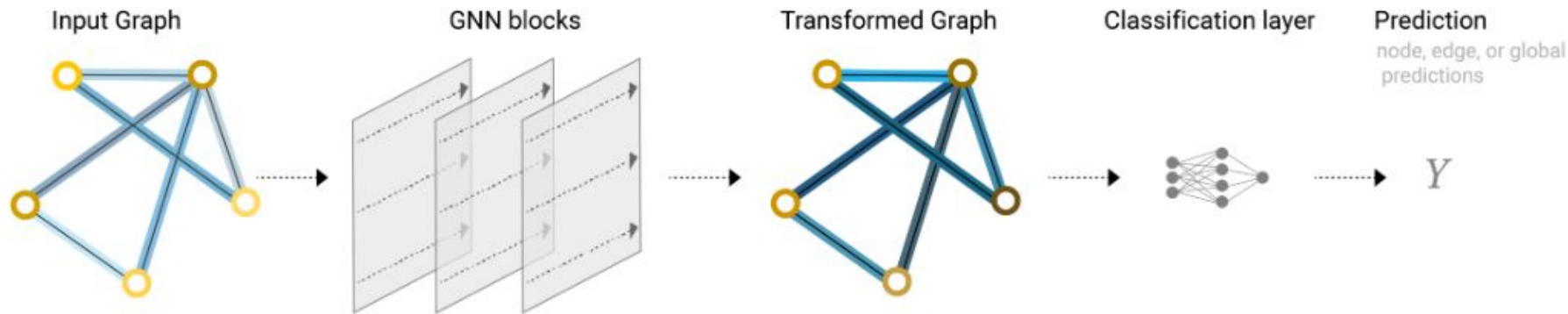
The rigid, grid-based neighborhood doesn't work!



**One layer of a graph  
neural network (GNN)!**

Image credit: Stanford CS224W

# Graph in, graph out

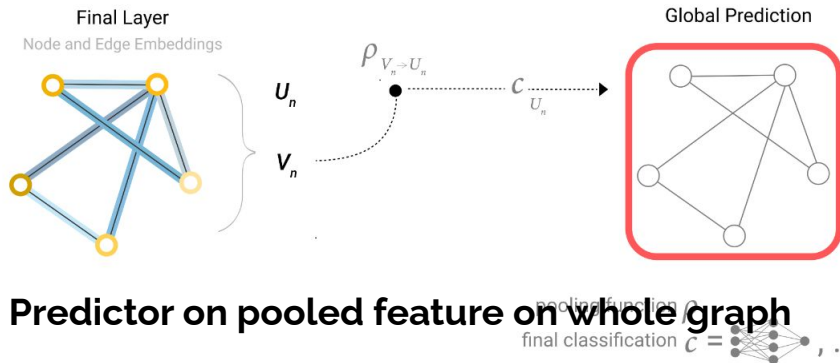
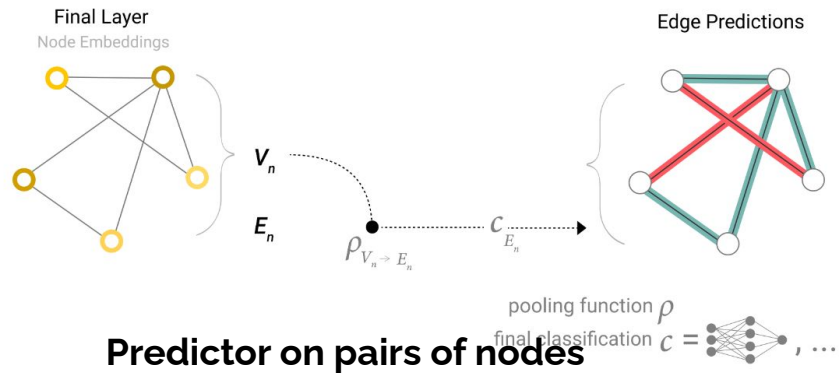
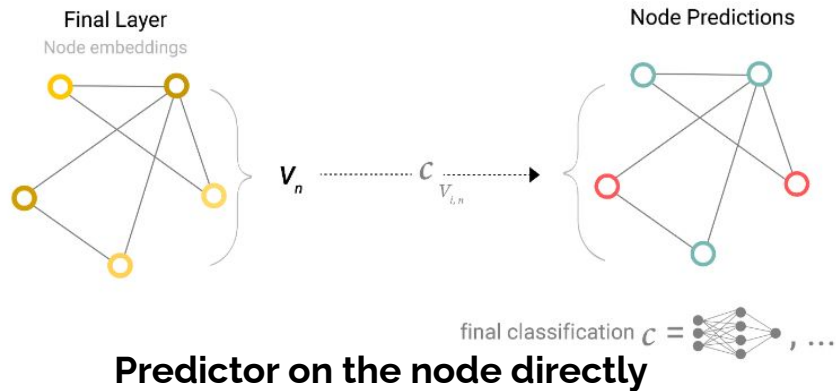


An end-to-end prediction task with a GNN model.

Image credit: <https://distill.pub/2021/gnn-intro/>

# How to make supervised predictions?

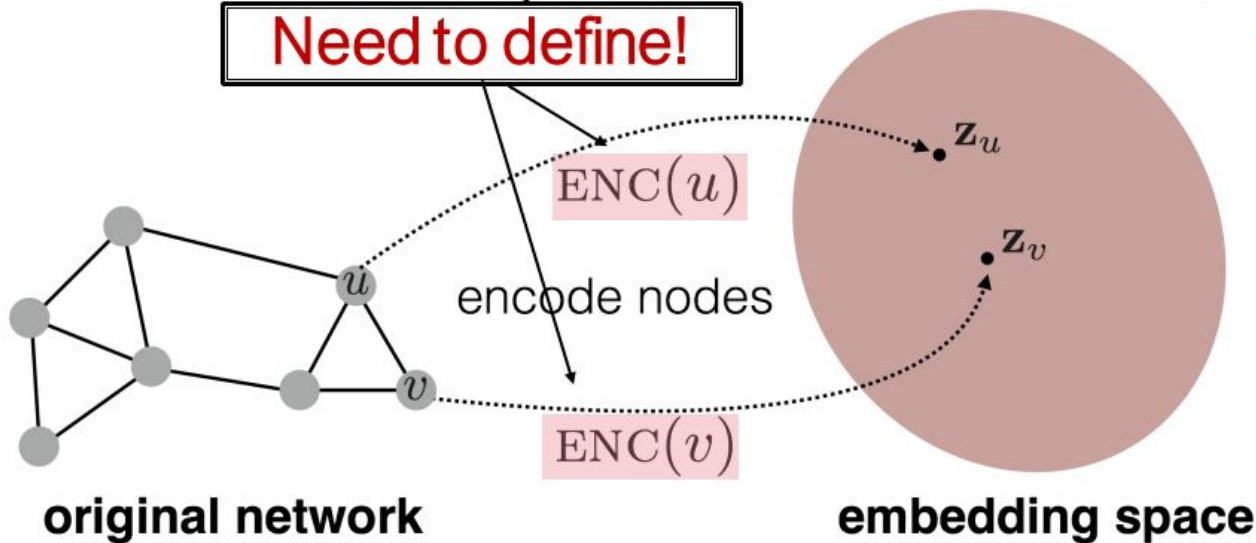
Image credit: <https://distill.pub/2021/gnn-intro/>



# How to perform unsupervised learning?

Goal:  $\text{similarity}(u, v)$  in the original network  $\approx \mathbf{z}_v^T \mathbf{z}_u$  Similarity of the embedding

**Need to define!**



$$\mathcal{L} = \sum_{z_u, z_v} \text{CE}(y_{u,v}, \text{DEC}(z_u, z_v))$$

# Look into GNN layers

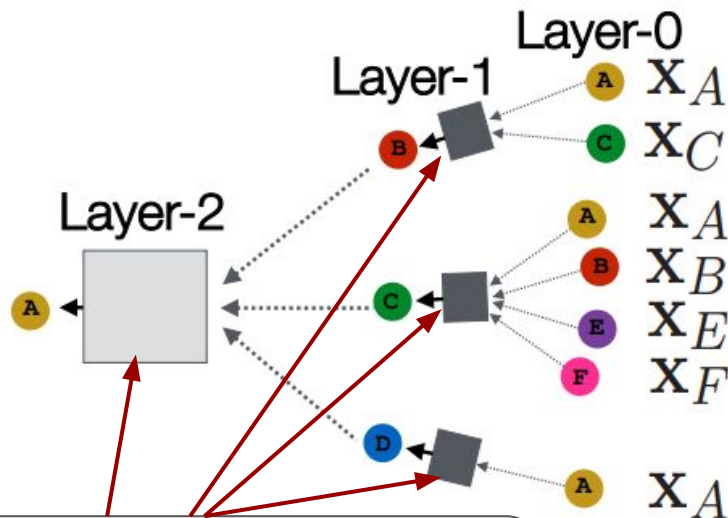
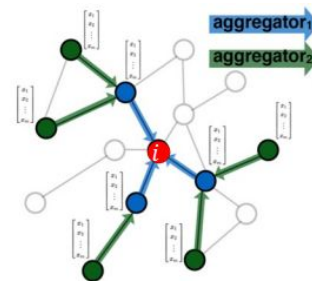
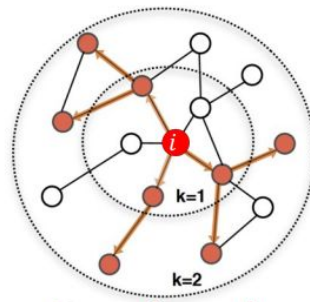
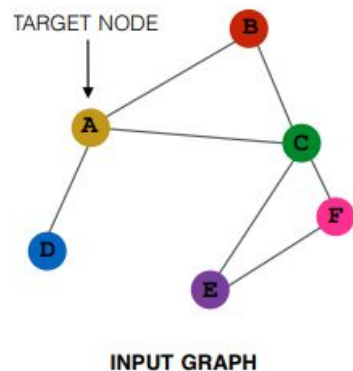


Image credit: Stanford CS224W

These **aggregators** sum up neighboring info, and can be represented by **DNNs**



# Permutation invariance

Feature vector for the  
**whole graph**

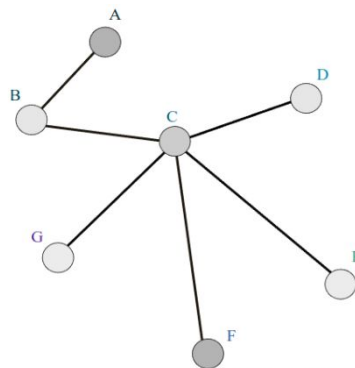
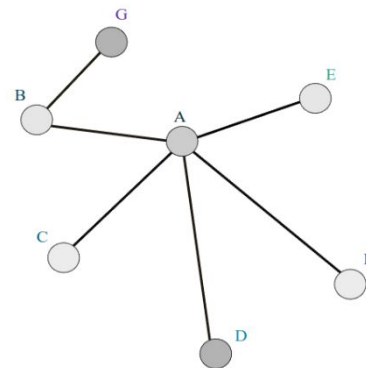


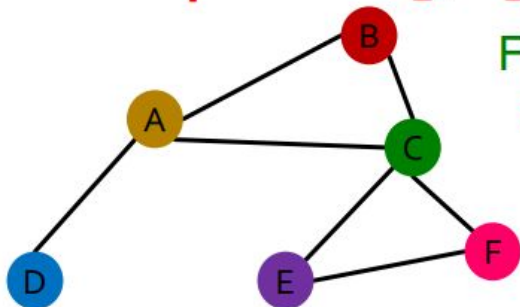
Image credit: Image credit: <https://distill.pub/2021/understanding-gnns/>



**Permutation invariance:** permuting the names of the nodes doesn't change the graph, as graph nodes are intrinsically orderless

For  $f : G(A, X) \mapsto h$  ,  $f(A_1, X_1) = f(A_2, X_2)$

**Order plan 1:  $A_1, X_1$**



For two order plans,  
output of  $f$  should  
be the same!

**Order plan 2:  $A_2, X_2$**

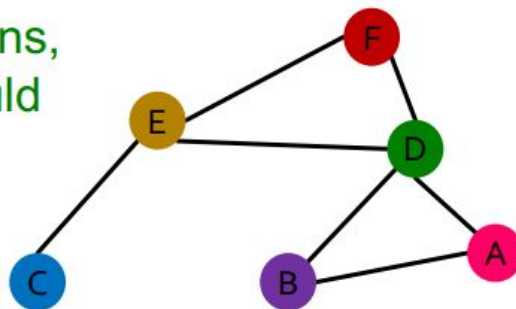


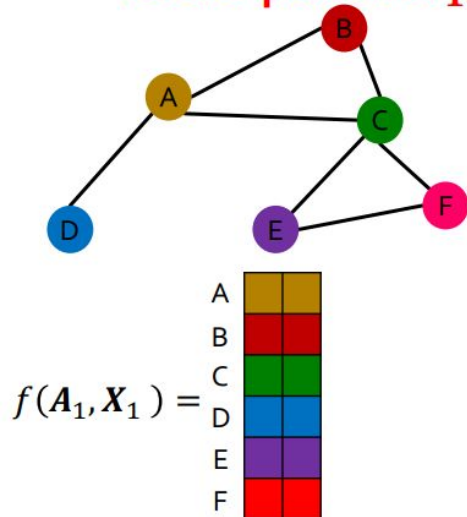
Image credit: Stanford CS224W

# Permutation equivariance

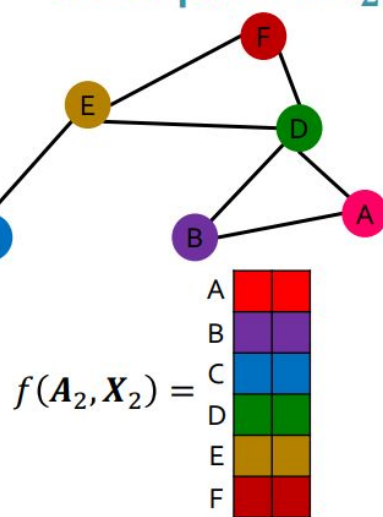
For  $f : G(\mathbf{A}, \mathbf{X}) \mapsto \mathbf{H} \in \mathbb{R}^{|N| \times d}$   
 $f(\mathbf{\Pi A \Pi}^\top, \mathbf{\Pi X}) = \mathbf{\Pi f(A, X)}$   
 for any permutation  $\mathbf{\Pi}$

Collection of feature vectors on all nodes

Order plan 1:  $\mathbf{A}_1, \mathbf{X}_1$

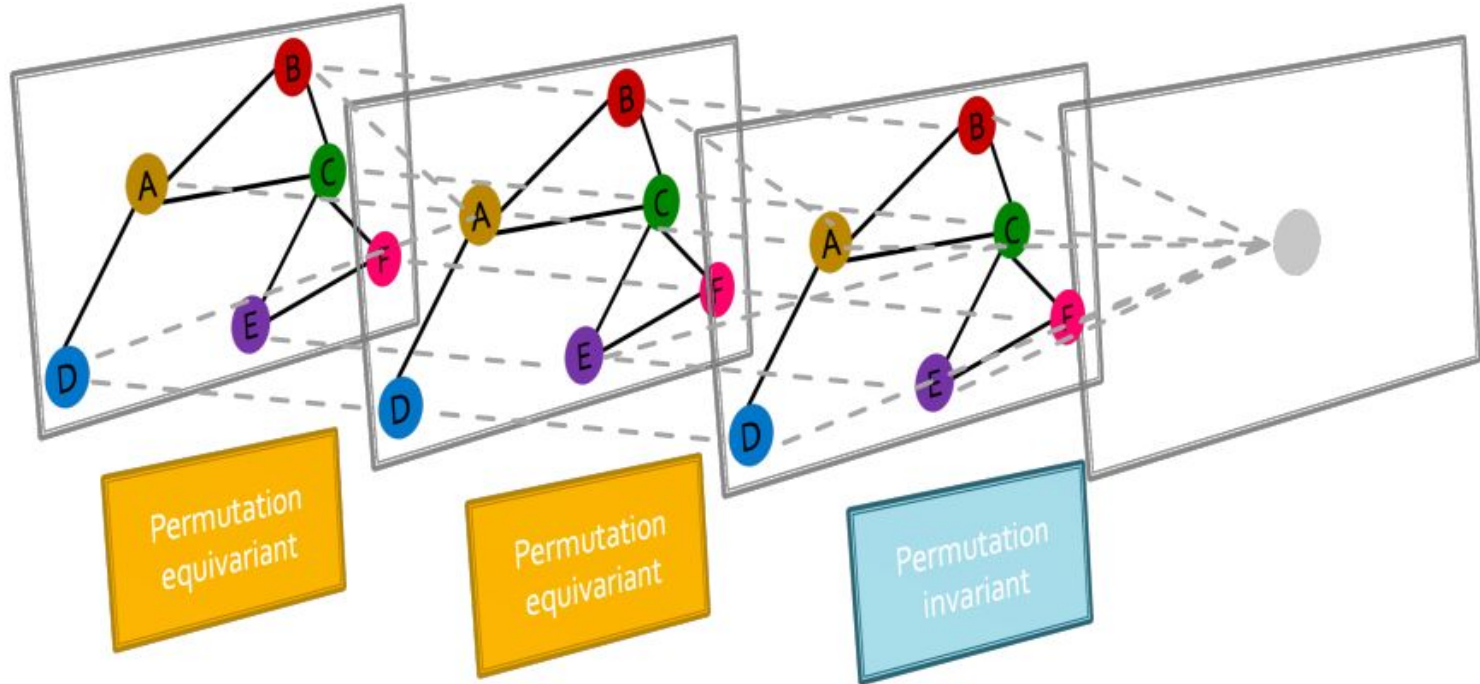


Order plan 2:  $\mathbf{A}_2, \mathbf{X}_2$



In other words, if the nodes are re-ordered, the learned features are re-ordered accordingly, **so features are attached to nodes not their names**

A typical GNN consists of multiple permutation equivariant/invariant layers



# Graph convolutional networks (GCNs)

$$h_v^{(0)} = x_v \quad \text{for all } v \in V.$$

Node  $v$ 's initial embedding. ... is just node  $v$ 's original features.

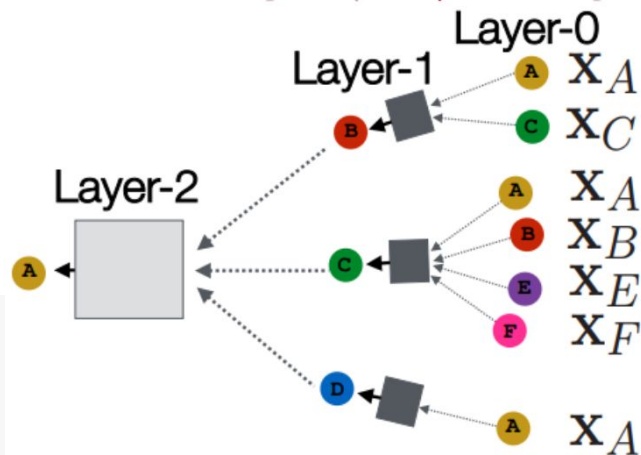
and for  $k = 1, 2, \dots$  upto  $K$ :

$$h_v^{(k)} = f^{(k)} \left( W^{(k)} \cdot \frac{\sum_{u \in \mathcal{N}(v)} h_u^{(k-1)}}{|\mathcal{N}(v)|} + B^{(k)} \cdot h_v^{(k-1)} \right) \quad \text{for all } v \in V.$$

Node  $v$ 's embedding at step  $k$ .      Mean of  $v$ 's neighbour's embeddings at step  $k - 1$ .      Node  $v$ 's embedding at step  $k - 1$ .

Color Codes:

- Embedding of node  $v$ .
- Embedding of a neighbour of node  $v$ .
- (Potentially) Learnable parameters.



# Graph attention networks (GATs)

$$h_v^{(0)} = x_v \quad \text{for all } v \in V.$$

Node  $v$ 's initial embedding. ... is just node  $v$ 's original features.

and for  $k = 1, 2, \dots$  upto  $K$ :

$$h_v^{(k)} = f^{(k)} \left( W^{(k)} \cdot \left[ \sum_{u \in \mathcal{N}(v)} \alpha_{vu}^{(k-1)} h_u^{(k-1)} + \alpha_{vv}^{(k-1)} h_v^{(k-1)} \right] \right) \quad \text{for all } v \in V.$$

Node  $v$ 's embedding at step  $k$ .

Weighted mean of  $v$ 's neighbour's embeddings at step  $k - 1$ .

Node  $v$ 's embedding at step  $k - 1$ .

where the attention weights  $\alpha^{(k)}$  are generated by an attention mechanism  $A^{(k)}$ , normalized such that the sum over all neighbours of each node  $v$  is 1:

$$\alpha_{vu}^{(k)} = \frac{A^{(k)}(h_v^{(k)}, h_u^{(k)})}{\sum_{w \in \mathcal{N}(v)} A^{(k)}(h_v^{(k)}, h_w^{(k)})} \quad \text{for all } (v, u) \in E.$$

Color Codes:

- Embedding of node  $v$ .
- Embedding of a neighbour of node  $v$ .
- (Potentially) Learnable parameters.

Image credit: <https://distill.pub/2021/understanding-gnns/>

# Graph sample and aggregate (GraphSAGE)

$$h_v^{(0)} = x_v \quad \text{for all } v \in V.$$

Node  $v$ 's  
initial  
embedding.

... is just node  $v$ 's  
original features.

and for  $k = 1, 2, \dots$  upto  $K$ :

$$h_v^{(k)} = f^{(k)} \left( W^{(k)} \cdot \left[ \text{AGG}(\{h_u^{(k-1)}\}), h_v^{(k-1)} \right] \right) \quad \text{for all } v \in V.$$

Node  $v$ 's  
embedding at  
step  $k$ .

Aggregation of  $v$ 's  
neighbour's  
embeddings at  
step  $k - 1$  ...

... Node  $v$ 's  
embedding at  
step  $k - 1$ .

... concatenated  
with ...

Color Codes:

- Embedding of node  $v$ .
- Embedding of a neighbour of node  $v$ .
- (Potentially) Learnable parameters.

# Graph isomorphism networks (GINs)

$$h_v^{(0)} = x_v \quad \text{for all } v \in V.$$

Node  $v$ 's  
initial  
embedding.

... is just node  $v$ 's  
original features.

and for  $k = 1, 2, \dots$  upto  $K$ :

$$h_v^{(k)} = f^{(k)} \left( \sum_{u \in \mathcal{N}(v)} h_u^{(k-1)} + (1 + \epsilon^{(k)}) \cdot h_v^{(k-1)} \right) \quad \text{for all } v \in V.$$

Node  $v$ 's  
embedding at  
step  $k$ .

Sum of  $v$ 's  
neighbour's  
embeddings at  
step  $k - 1$ .

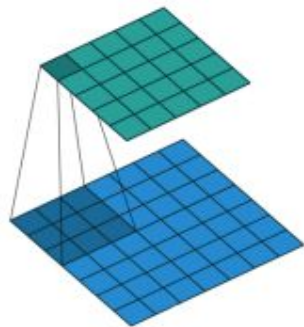
Node  $v$ 's  
embedding at  
step  $k - 1$ .

Color Codes:

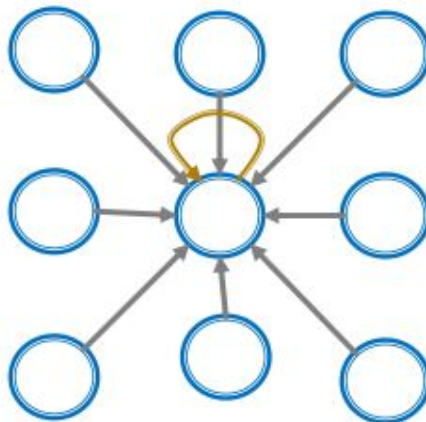
- Embedding of node  $v$ .
- Embedding of a neighbour of node  $v$ .
- (Potentially) Learnable parameters.

# Connection to CNNs and Transformers

filter:



Image



Graph

- CNN is GNN that keeps local ordering
- CNN not permutation-invariant

$$\text{GNN formulation: } h_v^{(l+1)} = \sigma(\mathbf{W}_l \sum_{u \in N(v)} \frac{h_u^{(l)}}{|N(v)|} + B_l h_v^{(l)}), \forall l \in \{0, \dots, L-1\}$$

$$\text{CNN formulation: } h_v^{(l+1)} = \sigma(\sum_{u \in N(v)} \mathbf{W}_l^u h_u^{(l)} + B_l h_v^{(l)}), \forall l \in \{0, \dots, L-1\}$$



# Connection to CNNs and Transformers

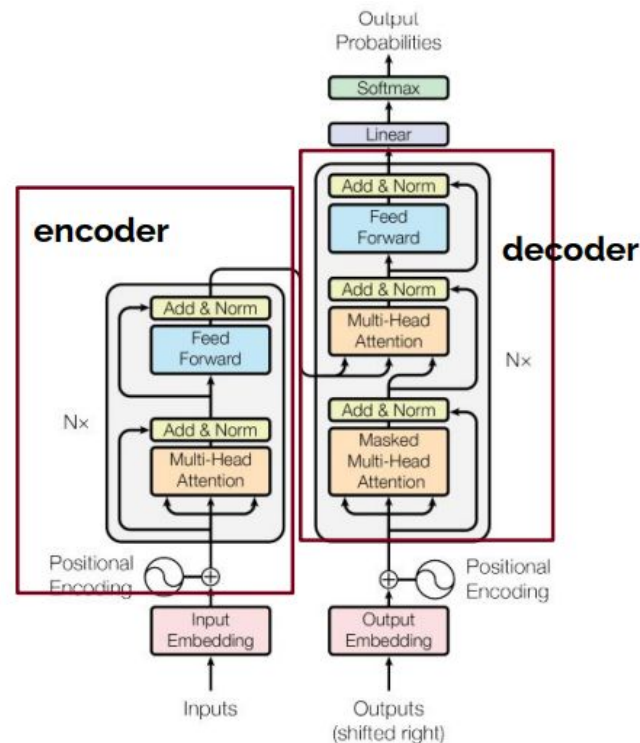
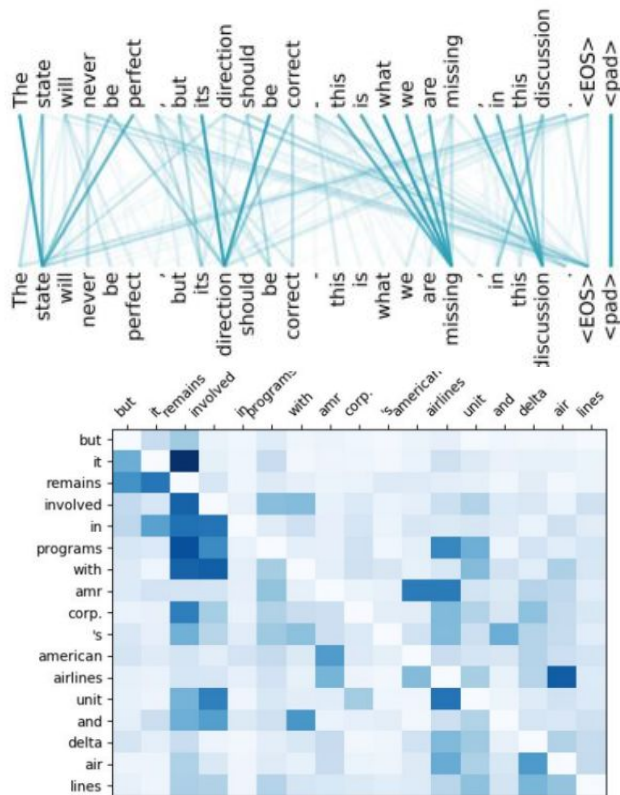


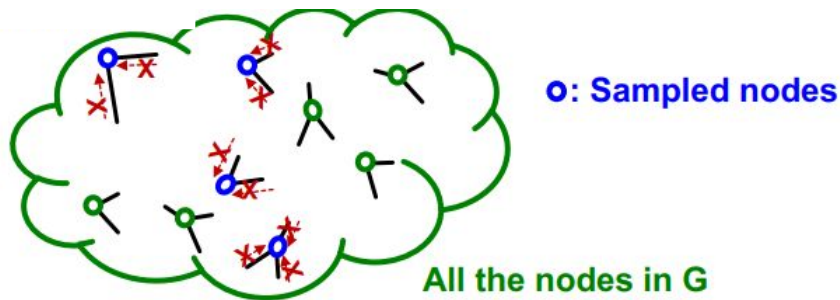
Figure 1: The Transformer - model architecture.

Self-attention (plus feed forward) is a layer of GAT on a complete graph!

# Scaling up training

# Practical graphs are large yet sparse

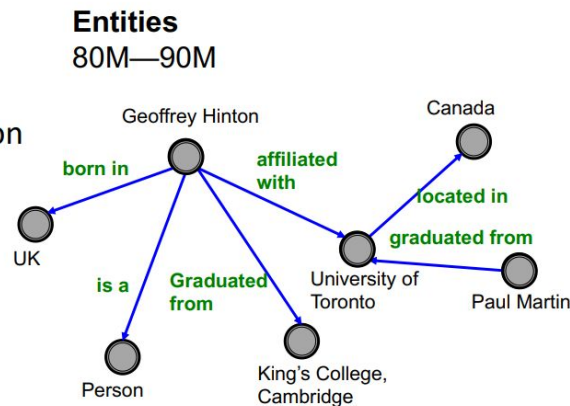
How to perform mini-batch training?



- Mini-batch subsampling induces isolated nodes
- No info to aggregate inside the mini-batch for most nodes

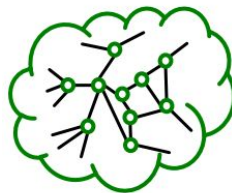
## Knowledge Graphs (KGs):

- Wikidata
- Freebase
- **ML tasks:**
  - KG completion
  - Reasoning



**Solution:** structured subsampling

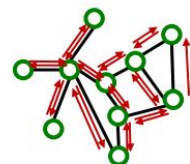
Large graph



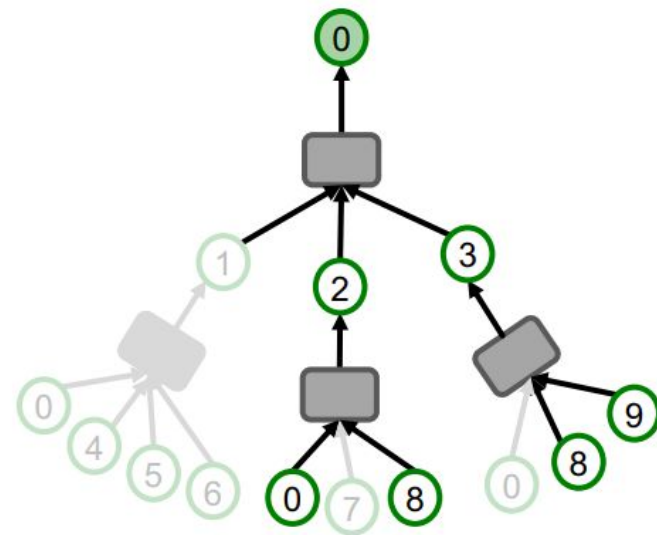
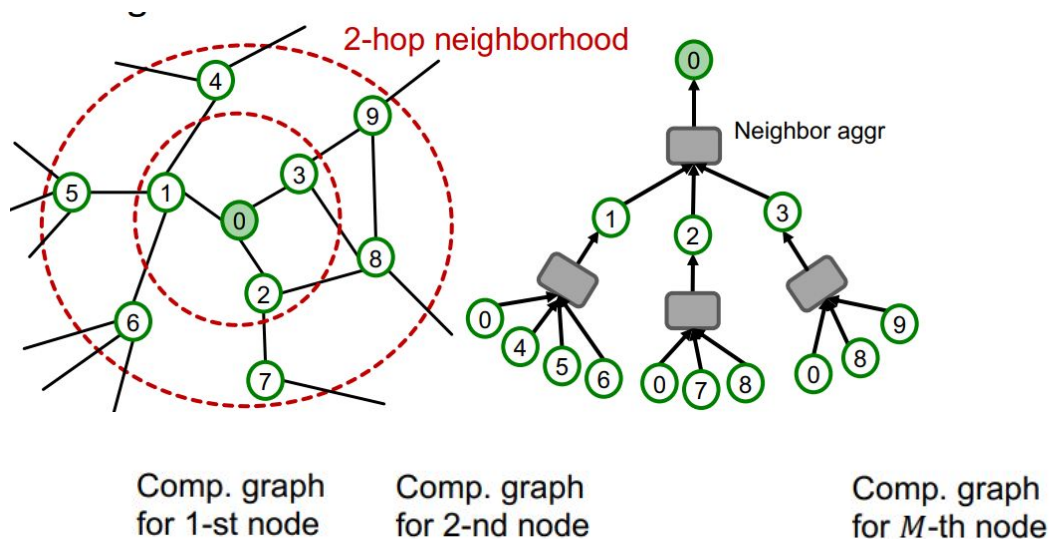
Sampled subgraph  
(small enough to be put on a GPU)



Layer-wise  
node embeddings  
update on the GPU



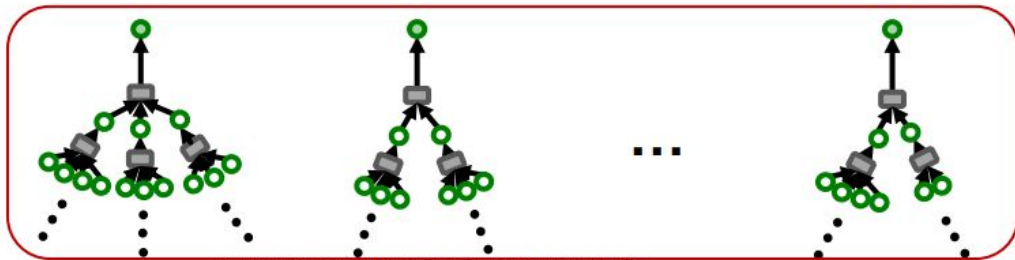
# Two structured sub-sampling strategies—I



i.e., **neighborhood sampling**,  
instead of iid uniform sampling

Image credit: Stanford CS224W

Mini-batch

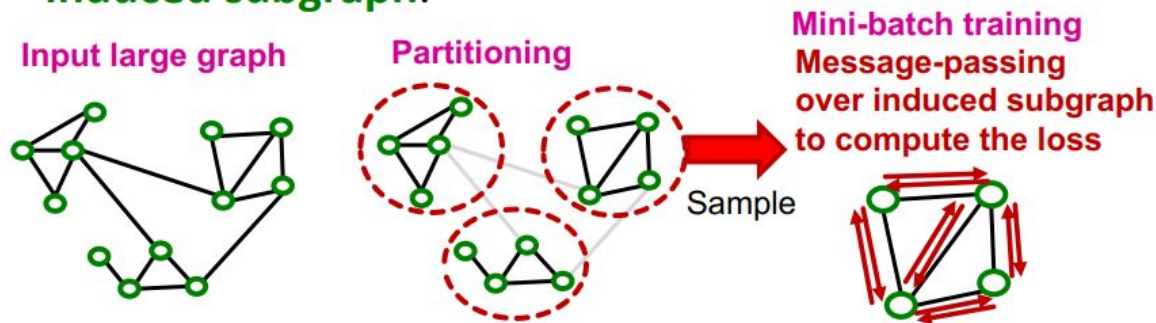


# Two structured sub-sampling strategies—II

**Cluster-GCN** consists of two steps:

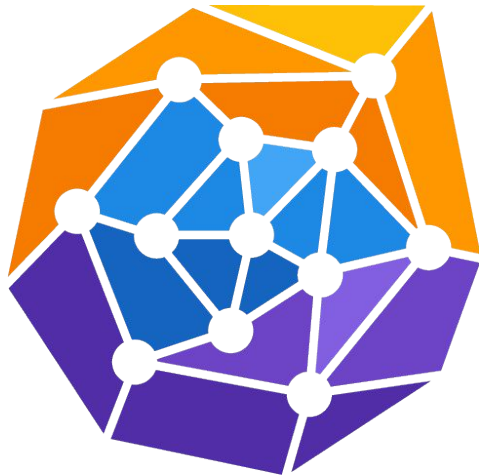
- **Pre-processing**: Given a large graph, partition it into groups of nodes (i.e., subgraphs).
- **Mini-batch training**: Sample one node group at a time. Apply GNN's message passing over the **induced subgraph**.

Rationale: important to keep the community structures, i.e., keep the “backbone” nodes



# Software

PyTorch Geometric (PyG)



<https://pytorch-geometric.readthedocs.io/en/latest/>

Deep Graph Library (DGL)



<https://www.dgl.ai/>

# Further reading

- What are graph neural networks?  
<https://blogs.nvidia.com/blog/2022/10/24/what-are-graph-neural-networks/>
- A Gentle Introduction to Graph Neural Networks  
<https://distill.pub/2021/gnn-intro/>
- Understanding Convolutions on Graphs  
<https://distill.pub/2021/understanding-gnns/>
- Graph Neural Networks: A Review of Methods and Applications  
<https://arxiv.org/abs/1812.08434>
- Stanford CS224W: Machine Learning with Graphs  
<https://web.stanford.edu/class/cs224w/index.html>
- Graph Representation Learning [https://www.cs.mcgill.ca/~wlh/grl\\_book/](https://www.cs.mcgill.ca/~wlh/grl_book/)