BioMedical Learning through Graph Neural Networks

Dr. Nisha Pillai

Postdoctoral Associate @ Mississippi State University

nature Explore content About the journal Publish with us Subscribe

nature > news > article

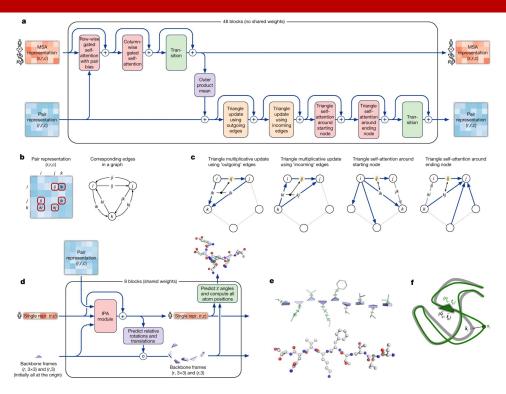
"What took us months and years to do, AlphaFold was able to do in a weekend."

Professor John McGeehan

Professor of Structural Biology and director for the centre, centre for enzyme innovation (CEI) at the University of Portsmouth

Source: @Nature, Deepmind

Graphs! Graphs!



Jumper, J., Evans, R., Pritzel, A. et al. Highly accurate protein structure prediction with AlphaFold. Nature 596, 583-589 (2021)

Today's Focus

1. Terminology and representations

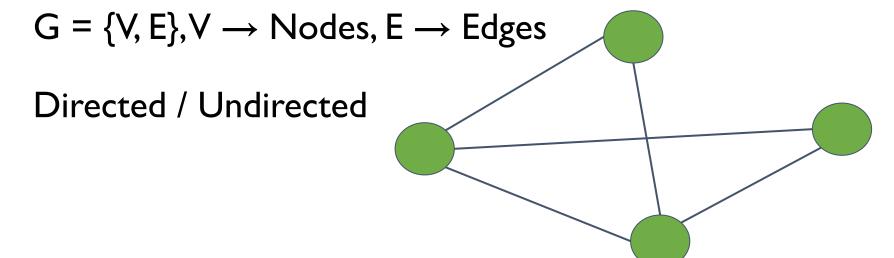
2. Popular architectures

3. An architecture demonstration

4. Related Work

Graphs

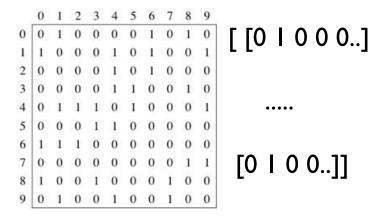
Real world objects, and their connections



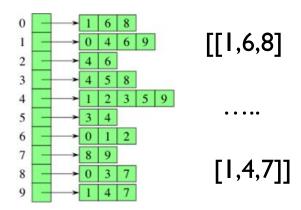
Representing Graphs

a) Edge lists
$$\rightarrow ((v_1, v_2)....(v_4, v_6))$$

b) Adjacency Matrices



c) Adjacency Lists



Source: Khan Academy

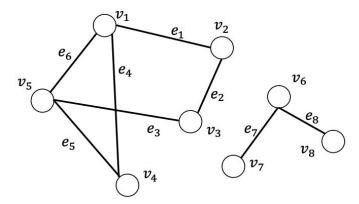
Properties

- \rightarrow Degree of a node \rightarrow Number of neighbours
- \rightarrow Distance between Node A and B \rightarrow shortest path
- → Eccentricity → Maximum distance between A to anynode
- → Connected components → Linked nodes
- Center of connected component

Connected Graphs

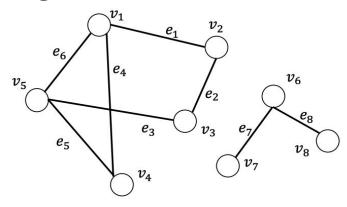
Trail → Walk with distinct edges

Path → Walk with distinct nodes



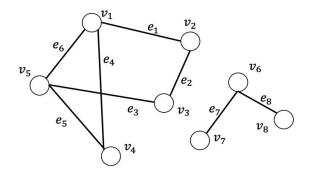
Node Centrality

- → Importance of a node
- → Degree based → Number of neighbour nodes
- → Eigenvector centrality
- → Catz centrality
- → Betweenness centrality



Node Centrality

- → Eigenvector centrality
 - largest eigenvalue of adjacency matrix
 - eigen vector as centrality score vector
- Betweenness centrality



Number of shortest paths passing through a

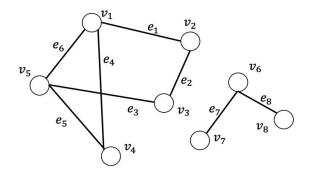
node

Katz Centrality

Variant of eigenvector centrality

$$c_k(v_i) = \alpha \sum_{j=1}^N \mathbf{A}_{i,j} c_k(v_j) + \beta,$$

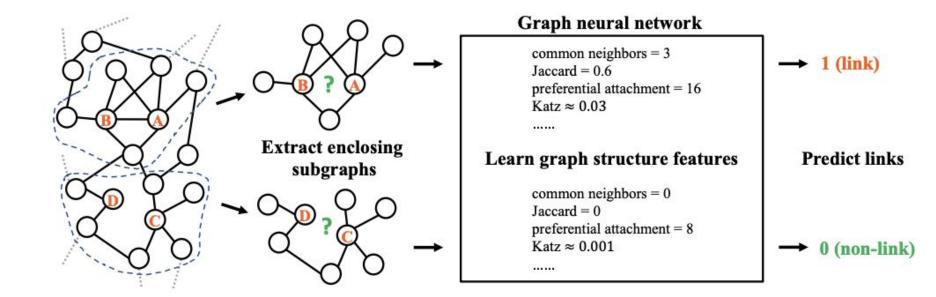
$$\mathbf{c}_k = (\mathbf{I} - \alpha \cdot \mathbf{A})^{-1} \boldsymbol{\beta}.$$



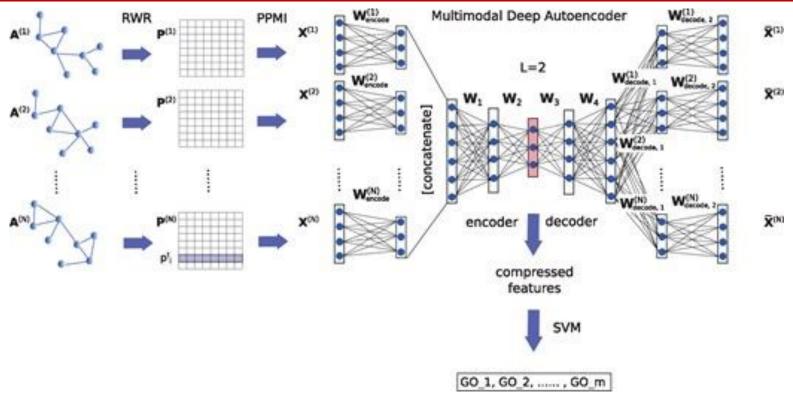
Applications in Biology

- → Protein-Protein Interaction (PPI)
 - Interactions among proteins, Proteins as nodes, interactions as edges
- → Gene regulatory networks
 - Regulating gene expression, generating proteins from DNA sequence
- Metabolic networks
 - Metabolic reactions in a living organisms, enzymes as edges
- → Drug drug interaction networks

Link Prediction

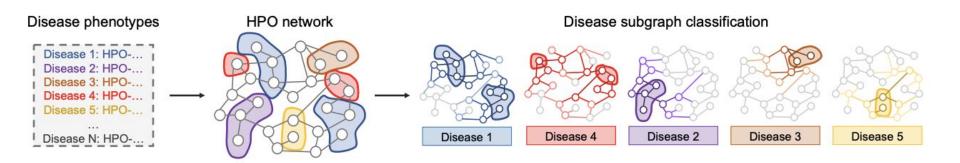


Node Classification



Gligorijević V, Barot M, Bonneau R. deepNF: deep network fusion for protein function prediction. Bioinformatics, 2018.

Graph Classification



Michelle M. Li, Kexin Huang, Marinka Zitnik, Graph Representation Learning in Biomedicine, 2021

Popular Datasets

Drugbank Protein Interaction Network Analysis

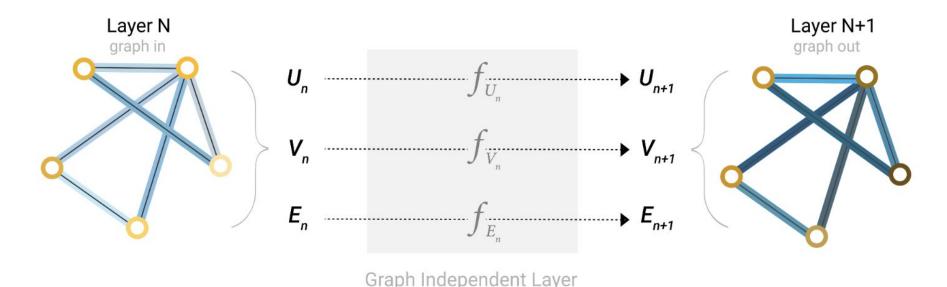
MUTAG Molecular INTeraction

PubChem's BioAssay database DREAM4

Protein Data Bank Tox21

Human Protein Reference Database

Graph Neural Network Model



update function f =

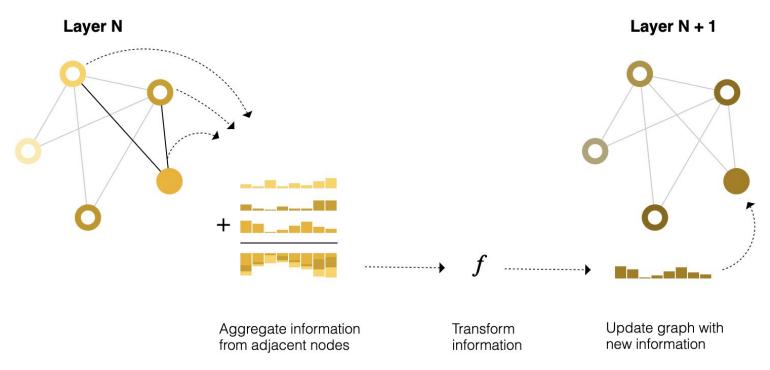
Graph Predictions

- → Pooling → Gather all information in matrix, Average/Sum
- → Node prediction with no node features → Pooling with edges
- → Edge prediction with no properties → Pooling with nodes
- → Global Average Pooling → Graph embedding

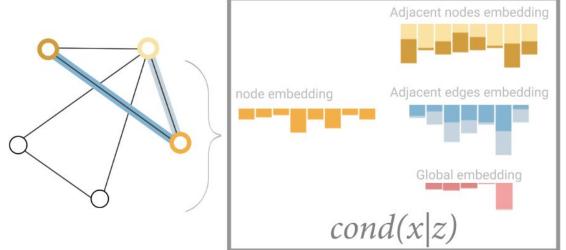
Message Passing

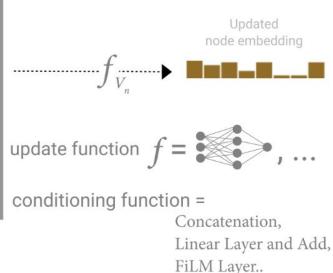
- → Gather neighbour node information
- → Aggregate them
- → Update function → an NN method

Message Passing

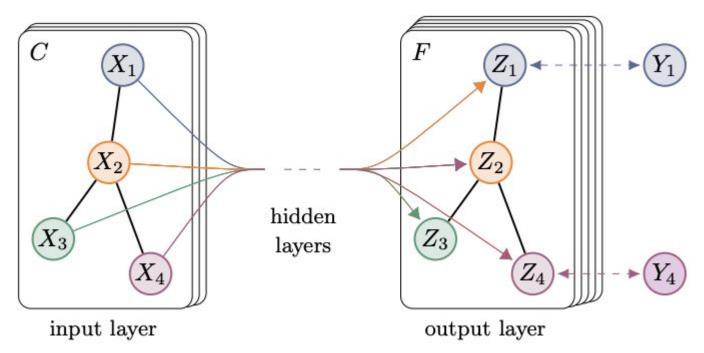


Global Representation





Graph Convolutional Networks



Thomas N. Kipf, Max Welling, "Semi-Supervised Classification with Graph Convolutional Networks, 2016.

Graph Convolutional Networks

Inputs: Initial feature vector for nodes, adjacency list

$$H^{l+1} = f(H^l, A)$$
, L - number of layers

Let the "f" be ReLU,

$$H^{l+1} = ReLU(AH^lW^l)$$
, W is the weight matrix,

ReLU is a non-linear activation function, To normalize, $1/D_i^{1/2}$ A $1/D_j^{1/2}$

Implementations

Pytorch:

https://pytorch-geometric.readthedocs.io/en/1.3.2/ modul es/torch geometric/nn/conv/gcn conv.html

Tensorflow:

https://github.com/stellargraph/stellargraph/blob/develop/stellargraph/layer/gcn.py

Deep Walk

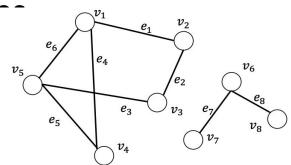
Adjacent nodes ←→ Similar representations

Transductive algorithm

Random walks of "L" length, "k" times

2. SkipGram method

Gradient descent to update neighbour node



GraphSage

Dynamic graph learning - No need to retrain

Context based similarity representations

- Random Walks
- Learning weights using aggregate function
- 3. Neural network layer to learn weights

GraphSage

```
Algorithm 1: GraphSAGE embedding generation (i.e., forward propagation) algorithm
```

```
Input: Graph \mathcal{G}(\mathcal{V}, \mathcal{E}); input features \{\mathbf{x}_v, \forall v \in \mathcal{V}\}; depth K; weight matrices
                     \mathbf{W}^k, \forall k \in \{1, ..., K\}; non-linearity \sigma; differentiable aggregator functions
                     AGGREGATE_k, \forall k \in \{1, ..., K\}; neighborhood function \mathcal{N}: v \to 2^{\mathcal{V}}
    Output: Vector representations \mathbf{z}_v for all v \in \mathcal{V}
\mathbf{h}_{v}^{0} \leftarrow \mathbf{x}_{v}, \forall v \in \mathcal{V};
2 for k = 1...K do
           for v \in \mathcal{V} do
               \mathbf{h}_{\mathcal{N}(v)}^k \leftarrow \text{AGGREGATE}_k(\{\mathbf{h}_u^{k-1}, \forall u \in \mathcal{N}(v)\});
4
                \mathbf{h}_v^k \leftarrow \sigma\left(\mathbf{W}^k \cdot \text{CONCAT}(\mathbf{h}_v^{k-1}, \mathbf{h}_{\mathcal{N}(v)}^k)\right)
           end
    \mathbf{h}_v^k \leftarrow \mathbf{h}_v^k / \|\mathbf{h}_v^k\|_2, \forall v \in \mathcal{V}
8 end
\mathbf{g} \ \mathbf{z}_v \leftarrow \mathbf{h}_v^K, \forall v \in \mathcal{V}
```

Hamilton, Will, Zhitao Ying, and Jure Leskovec. "Inductive representation learning on large graphs.", NeuIPS, 2017.

Graph Attention Networks

Attention mechanism → higher weight for important nodes

- 1. Linear transformation, W^IH^I
- 2. Additive attention
 - a. Concatenate 2 neighbour features
 - b. Multiply with weight vector, a.
 - c. Apply LeakyReLU
- 3. Normalize with softmax
- 4. GCN

Graph Encoder

To find a representative embedding

Encoder layer → Graph convolutional layers, non-linear activations

Decoder layer - Graph convolutional layers

Reconstruction loss to find the difference.

Demonstration

Brain Decoding

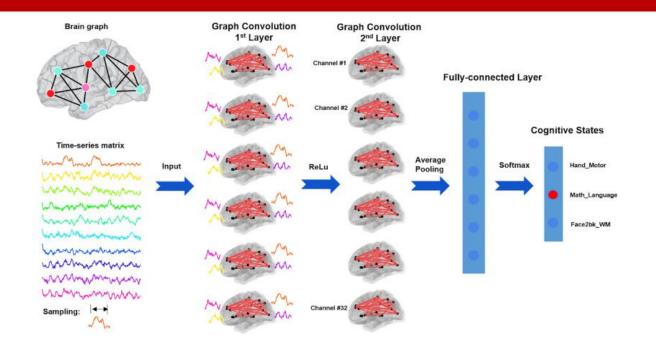
- → Multidomain brain decoder for brain response
- → Graph classification
- → Human Connectome Project task-fMRI database
 - ◆ 1200 participants, 21 different experimental conditions
 - 6 cognitive domain: emotion, language, motor, relational, social, and working memory.

Yu Zhang, Loïc Tetrel, Bertrand Thirion, Pierre Bellec

"Functional annotation of human cognitive states using deep graph convolution", 2021

BioMedical Learning through Graph Neural Networks: A hands-on Approach

Brain Decoding



6 GCN layers with 32 graph filters

Global average pooling layer,

2 fully connected layers

Softmax layer

Yu Zhang, Loïc Tetrel, Bertrand Thirion, Pierre Bellec

"Functional annotation of human cognitive states using deep graph convolution", 2021

Autism Spectrum Disorder

Graph node classification

Autism Brain Imaging Data Exchange (ABIDE) dataset

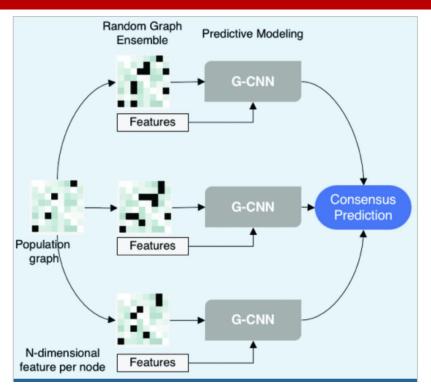
Gender and site information → Population Graph

Imaging features → Node feature vector

Anirudh, R., and Thiagarajan, J

Bootstrapping graph convolutional neural networks for autism spectrum disorder classification, 2019

Autism Spectrum Disorder



Anirudh, R., and Thiagarajan, J

Bootstrapping graph convolutional neural networks for autism spectrum disorder classification, 2019

Conclusion

Introduction to graph notations

Basic architectures

Some application