

# Graph Neural Networks (GNNs)

## Concepts, Implementations and Applications

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Graph: Represents the relations between a collection of objects.

## Example: Molecule-molecule interactions

- Objects: a set of molecules
- Relations: interactions between different molecules

## Example: Atom-level interactions within a molecule

- Objects: a set of atoms
- Relations: different bonds between the atoms

# Graphs

Where else can we find graphs?

- Images as graphs

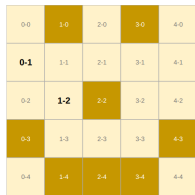
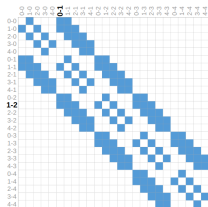
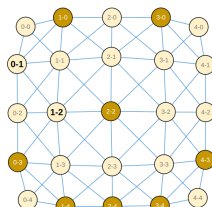


Image Pixels

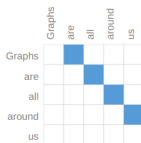
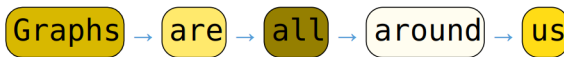


Adjacency Matrix



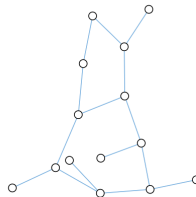
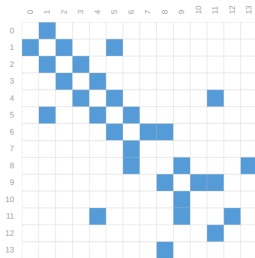
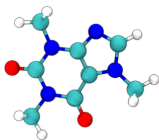
Graph

- Text as graphs



- Images and texts have some regular structures:
  - Pixels are connected in a grid.
  - Texts have line-like structure.

- There are, however, more complicated (heterogeneous) structures:



- Similar structures are seen in social networks as well.

And, the simple definitions (let's just recall it):

## Graph

- 1 A graph  $G$  is a pair  $(V, E)$  where  $V$  is a set of vertices (representing **objects**,  $E$  is a set of edges (representing **relations** and a subset of  $V \times V$ .
- 2  $G$  is undirected if for every  $(u, v) \in E$ ,  $(v, u) \in E$ .
- 3 A convenient way to represent a graph is by using a *adjacency matrix*  $\mathbf{A} \in \mathbb{R}^{|V| \times |V|}$ , where  $\mathbf{A}[u, v] = 1$  if  $(u, v) \in E$  and  $\mathbf{A}[u, v] = 0$  otherwise.

**Q.** In practice, what can go wrong with representing graphs by adjacency matrix?

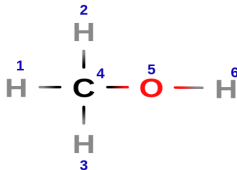
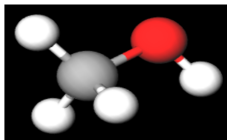
A. Memory requirement:  $O(|V|^2)$

- Representing large graphs
- Representing sparse graphs

S. Use adjacency list:  $O(|E|)$

# Graphs

Labelled graph: *Feature* information associated with a graph



Something like this, for the vertices:

$v_1$	:	$[0, 1, 0]$
$v_2$	:	$[0, 1, 0]$
$v_3$	:	$[0, 1, 0]$
$v_4$	:	$[1, 0, 0]$
$v_5$	:	$[0, 0, 1]$
$v_6$	:	$[0, 1, 0]$



Now,

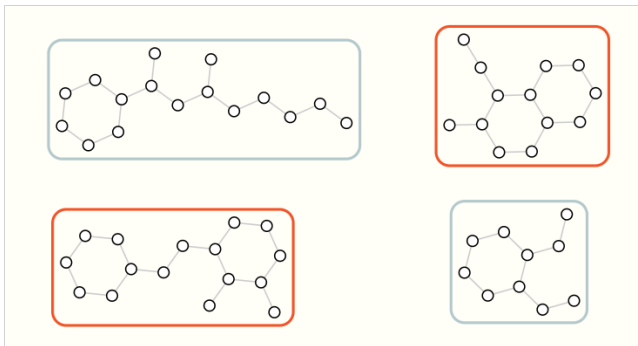
## Labelled Graph

A labelled graph  $G \in \mathcal{G}$  is represented as:  $(V, E, \sigma, \psi, \epsilon)$ , where

- $V$ : a set of vertices
- $E$ : a set of edges
- $\sigma$ : neighbourhood function  $\sigma : V \rightarrow 2^V$
- $\psi$ : vertex-labelling function  $\psi : V \rightarrow 2^V$
- $\epsilon$ : edge-labelling function  $\epsilon : E \rightarrow 2^E$

# Learning Tasks on Graphs

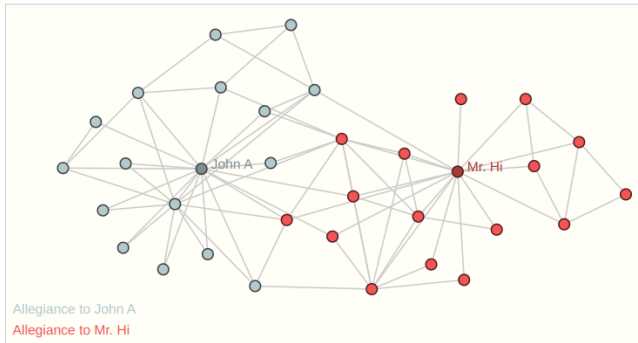
- Graph-level task: Predicting a property of the whole graph



- Predicting *efficacy* of a drug molecule

# Learning Tasks on Graphs

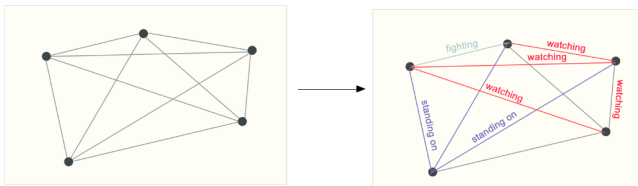
- Node-level task: Predicting a property of a node



- Predicting whether an aminoacid will be in an *interacting* chain

# Learning Tasks on Graphs

- Edge-level task: Predicting a property of an edge (node-node pair)



- Predicting what drug *treats* what disease

## Node Statistics:

- Node degree: Measures the influence of a node on its neighbours
- Node centrality: Measures the importance of a node in the graph
- Clustering coefficient: Measures the differences in properties of two nodes
- etc.

Kernel methods:

- Bag of nodes: Aggregates node-level statistics
- The Weisfeiler-Lehman (WL) kernel: Computes and compares two graph representations

WL Kernel: Iterative neighbourhood aggregation

- 1 Assign an initial labelling to each node (usually, its degree):

$$\ell^{(0)}(v) = d_v \quad \forall v \in V$$

- 2 Iteratively assign a new labelling to each node by hashing the multiset of the current labels within the node's neighborhood:

$$\ell^{(i)} = \text{HASH}(\{\{\ell^{(i-1)}(u)\} \mid u \in \mathcal{N}(v)\})$$

- 3 After running  $K$  iterations of re-labelling (i.e., Step 2), we now have a label  $\ell^{(K)}(v)$  for each node that summarizes the structure of its  $K$ -hop neighbourhood.

Graph representation: Aggregate the updated node labellings

Limitations of Pre-GNN (or traditional) approaches:

- Require careful, hand-engineered statistics and measures
- Designing these features is time-consuming
- Hand-engineered features are not very flexible: May not adapt through the learning process



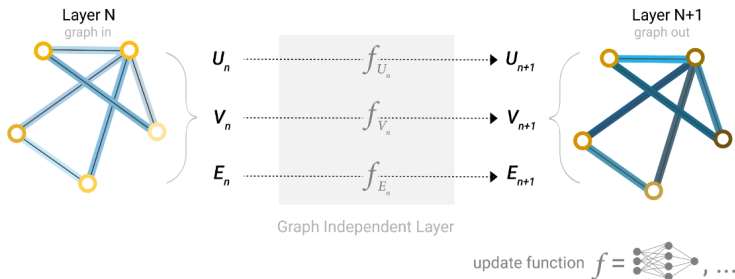
GNN is a special kind of deep neural network (DNN) where

- The input is a labelled graph;
- Its output is *permutation equivariant*\*;
- It follows a “Graph-in, Graph-out” principle.

\*Output of the GNN is unaffected by permutation (ordering) of the vertices or their labellings.

# ML on Graphs using GNNs

A simple GNN convolution step (also, called a 'layer') can be visualised this way:



Notice that the change is only to the descriptions associated with the graph (nodes, edges and graph), and not the structure of the graph.

We can describe this using a function:

## Relabel function

A Relabel function is defined as

$$\textit{Relabel} : \mathcal{G} \rightarrow \mathcal{G}'.$$

That is,

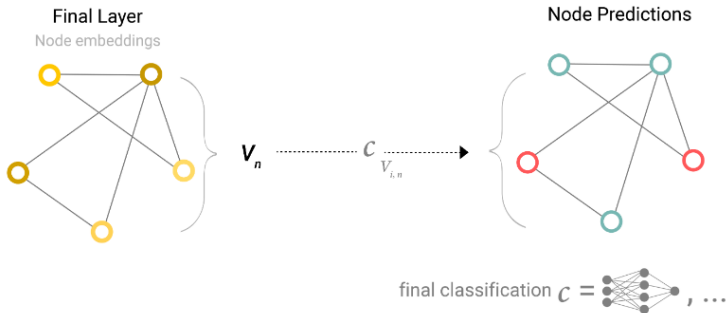
$$\textit{Relabel}((V, E, \sigma, \psi, \epsilon)) = (V, E, \sigma, \psi', \epsilon')$$

- *Relabel* is implemented using AGGREGATE-COMBINE procedures.
  - Graph convolution and pooling operations

# ML on Graphs using GNNs

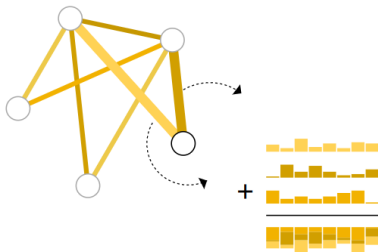
Now, how do we deal with various learning tasks: Prediction for nodes, edges, graphs?

**Node-level prediction:** Apply a classifier on the node attribute.



# ML on Graphs using GNNs

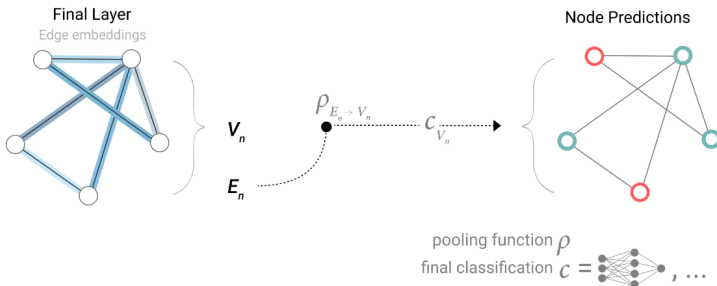
Things can be quite complicated: What if we don't have node-level information, just the edge-information and we want to do **node-level prediction**?



Aggregate information  
from adjacent edges

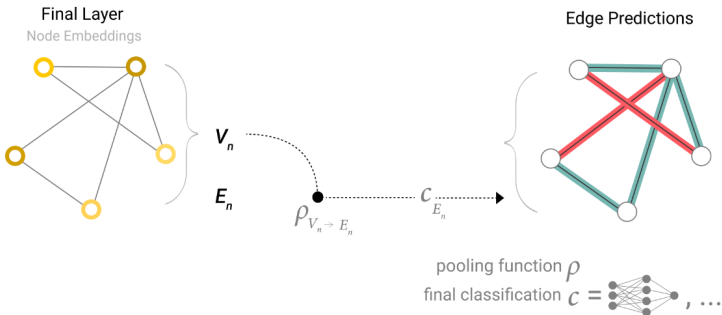
# ML on Graphs using GNNs

*Pooling*: collect information from edges and give them to nodes for prediction.



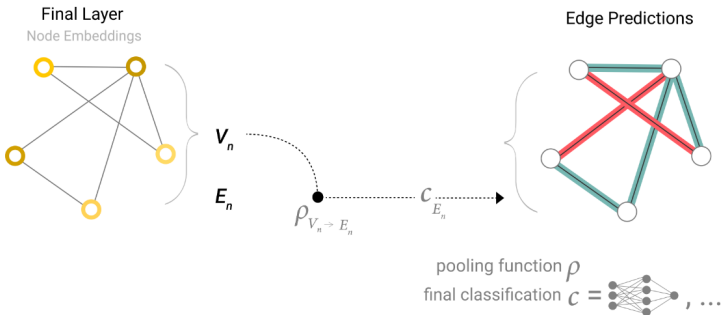
# ML on Graphs using GNNs

Similarly, we can use only the node-level information and use it for edge-level prediction.



# ML on Graphs using GNNs

Further, we can use only the node-level information and use it for **graph-level prediction**.



*Global average pooling:* Gather all available node information together and aggregate them and use it for prediction by a classifier\*.

\*A differentiable function (an MLP, mostly).



This process of obtaining a graph-level representation can be described using a *vectorise* function:

## Vec function

A vectorise function is defined as

$$\text{Vec} : \mathcal{G}' \rightarrow \mathbb{R}^d$$

- This function implemented by a READOUT procedure.
  - Global or hierarchical pooling operations

Then, a graph-level prediction can be described as:

## NN function

A NN function is defined as

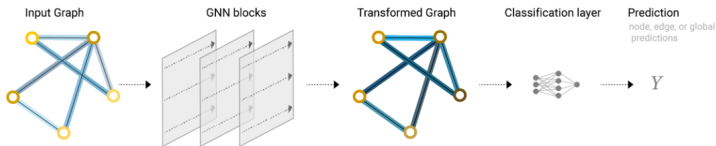
$$NN : \mathbb{R}^d \rightarrow \mathcal{Y}$$

where  $\mathcal{Y}$  denotes a set of class-labels or it is simply  $\mathbb{R}$  for regression.

- This function is implemented using a multilayered perceptron (MLP).

# ML on Graphs using GNNs

That's it! We are now familiar with the basic principles of GNNs.



Some things to always remember:

- Representations are *tensors*.
- GNN operations are on those tensors.

GCN [[Kipf and Welling, ICLR 2017](#)]:

- Weighted aggregation of neighbour node information

$$\mathbf{x}^{(\ell)} = \sigma \left( \tilde{D}^{-\frac{1}{2}} \tilde{\mathbf{A}} \tilde{D}^{-\frac{1}{2}} \mathbf{x}^{(\ell-1)} \mathbf{w}^{(\ell)} \right)$$

- For a single node in the graph,  $v_i$  the equation is simply,

$$\mathbf{x}_{im} = \sigma \left( \frac{1}{d_i} \tilde{a}_{ij} x_{jk} w_{mk} \right)$$

Here:

- $j$ : index for the neighbour node
- $k$ : index for the node feature
- $m$ : index for the *output* node feature
- $w_{mk}$ : trainable weight parameter
- $\tilde{\mathbf{A}} = \mathbf{A} + \mathbf{I}_N$ : Adjacency matrix with added self-connections ( $N$  is the number of nodes in the graph)

- Some things to note:
  - The equation, as before, communicates with the immediate neighbours, only once.  
Meaning: One layer of computation  $\leftrightarrow$  1-hop communication
  - In many real-world problems, the information from distant neighbours may be useful.  
Meaning: Multilayer computation  $\leftrightarrow$  Multihop communication
  - Stack multiple layers of GNNs with different lengths of output node feature vectors.

- There are now numerous implementations of GNN layers. Some popular ones are:
  - GCN [[Kipf and Welling, ICLR 2017](#)]
  - GraphSAGE [[Hamilton et al., NIPS 2017](#)]
  - GAT [[Veličković et al., ICLR 2018](#)]
  - $k$ -GNN [[Morris et al., AAAI 2019](#)]
  - ARMA [[Bianchi et al., IEEE TPAMI 2021](#)]
  - ...
- Similarly, there are different implementations of pooling layers.
- A comprehensive survey on various GNN layers can be found here: [[Wu et al., IEEE TNNLS 2020](#)].

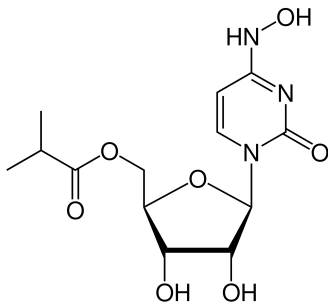
We have prepared a notebook for you to play with:

[GNN Tutorial](#)

Contributors:

- [Shreyas Bhat](#)
- [Soham Chitnis](#)





Q. Is this molecule effective against Covid-19 virus (*pos*)?

GNNs have been successfully used for solving many real-world problems, including the one being discussed here.

But, there have been none or only a few attempts at incorporating domain-knowledge into GNNs.

Why is the inclusion of domain-knowledge into GNNs important?

- The incorporation of domain-knowledge is the first of the 3 Grand Challenges in developing AI systems:

‘‘ML and AI are generally domain-agnostic.... Off-the-shelf practice treats [each of these] datasets in the same manner and ignores domain knowledge...

Improving our ability to systematically incorporate diverse forms of domain knowledge can impact every aspect of AI ...’’



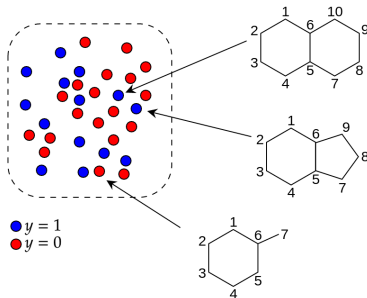
(AI for Sc. Report,  
2020)

Read the [AI for Science Report](#).

Our interest is in real-world scientific problems where:

- Data are relational, naturally represented as graphs;
- Domain-knowledge is available.

## Application 1: The discriminative problem

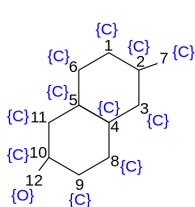


Graph space: Each instance (● or ●) is a graph.

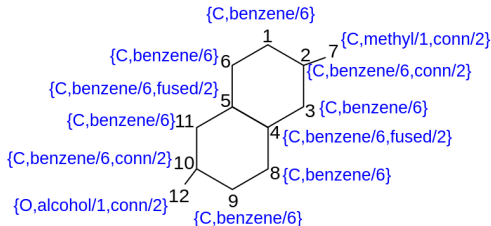
Let's assume we are dealing with problems in drug-discovery.

We have some domain-knowledge: Knowledge about various functional groups and various other structures.

Simplified inclusion of domain-knowledge into GNNs:



(Before inclusion)

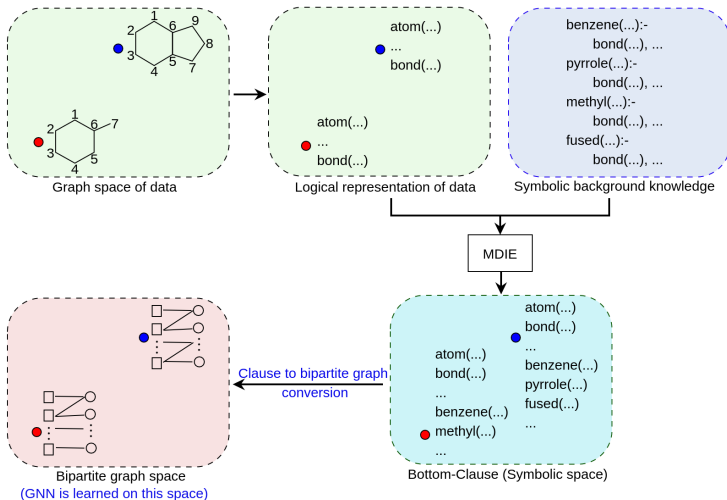


(After inclusion)

Based on: Vertex-Enrichment [Dash et al., MLJ 2021].

# Application of GNNs in Science

Complete inclusion of domain-knowledge into GNNs:



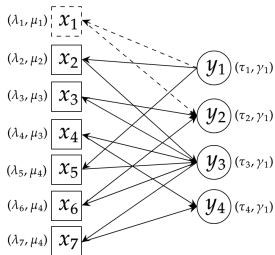


# Application of GNNs in Science

An example, on a simple family relation:

$gparent(henry, john) \leftarrow$   
 $father(henry, jane),$   
 $mother(jane, john)$

(Before inclusion)



(After inclusion)

Background knowledge:

$parent(X, Y) \leftarrow father(X, Y)$   
 $parent(X, Y) \leftarrow mother(X, Y)$   
 $mother(jane, alice) \leftarrow$

Based on: [Dash et al., MLJ 2022].

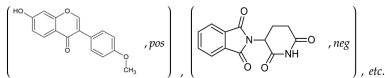
## Large-scale Empirical Evaluation of GNNs

**Datasets.** NCI-50 datasets (chemical compounds and their activities)

- Number of datasets: 73 (approx. 220,000 instances)
- A summary:

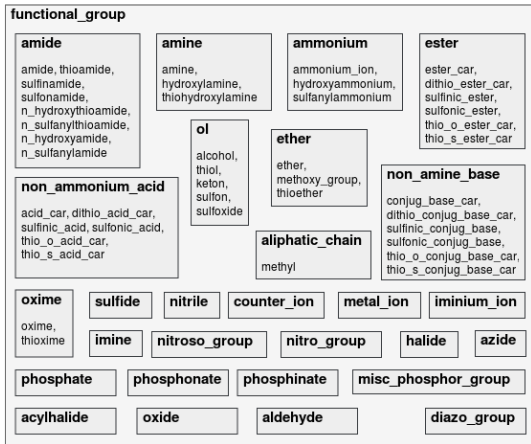
Avg. # of instances	Avg. # of atoms per instance	Avg. # of bonds per instance	% of positives
3032	24	51	0.4–0.9

- Each compound has an associated anti-cancer activity (positive or negative).

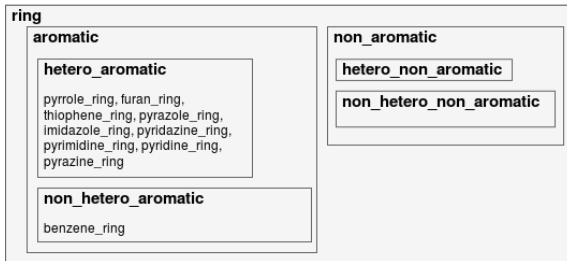


# Application of GNNs in Science

**Background Knowledge.** Facts and definitions of chemical structures



# Application of GNNs in Science



In overall, we have about 100 domain-relations.

GNNs. 5 different variants (as discussed before, GCN, GAT, etc.)

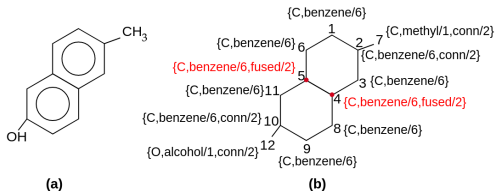
## Evaluation of VEGNNs:

- GNNs with domain-knowledge (VEGNNs) are better than GNNs without domain-knowledge.

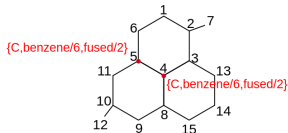
GNN Variant	Accuracy ( <i>VEGNN</i> vs. <i>GNN</i> ) Higher/Lower/Equal ( <i>p</i> -value)
$GNN_1$	48/14/11 ( $< 0.001$ )
$GNN_2$	48/19/6 (0.005)
$GNN_3$	53/11/9 ( $< 0.001$ )
$GNN_4$	54/12/7 ( $< 0.001$ )
$GNN_5$	43/19/11 (0.002)

But, there are some limitations:

- Vertex-enrichment simplifies domain-knowledge.



Similarly,



## Evaluation of BotGNNs:

- GNNs with domain-knowledge (BotGNNs) are better than GNNs without domain-knowledge.

GNN Variant	Accuracy ( <i>BotGNN</i> vs. <i>GNN</i> ) Higher/Lower/Equal ( <i>p</i> -value)
1	59/5/9 ( $< 0.001$ )
2	59/8/6 ( $< 0.001$ )
3	61/2/10 ( $< 0.001$ )
4	63/1/9 ( $< 0.001$ )
5	60/4/9 ( $< 0.001$ )



also:

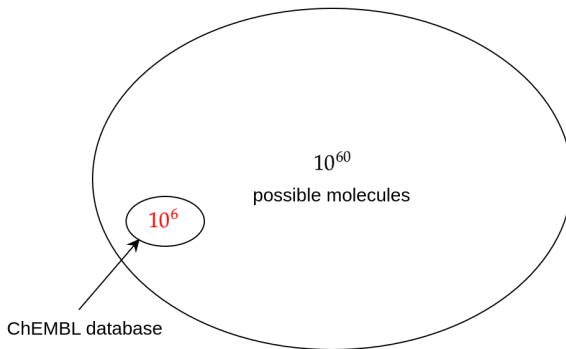
- BotGNNs are superior to VEGNNs.

GNN Variant	Accuracy ( <i>BotGNN</i> vs. <i>VEGNN</i> ) Higher/Lower/Equal ( $p$ -value)
1	54/11/8 ( $< 0.001$ )
2	61/9/3 ( $< 0.001$ )
3	54/10/9 ( $< 0.001$ )
4	55/11/7 ( $< 0.001$ )
5	52/9/12 ( $< 0.001$ )

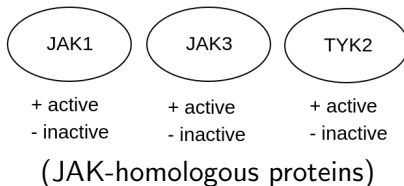
## Application 2: The generative problem

- To generate new small molecules which could act as inhibitors of a biological target (e.g. JAK2 protein).
- There is limited prior information on the target-specific inhibitors.
- We want to investigate whether domain-knowledge can assist in generating such molecules.

It is a hard problem: Searching the space of molecules

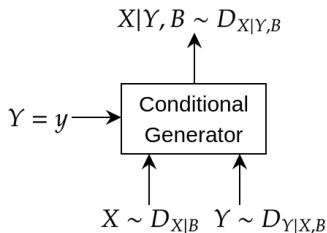


However, we have some information of some of the inhibitors for some related proteins:



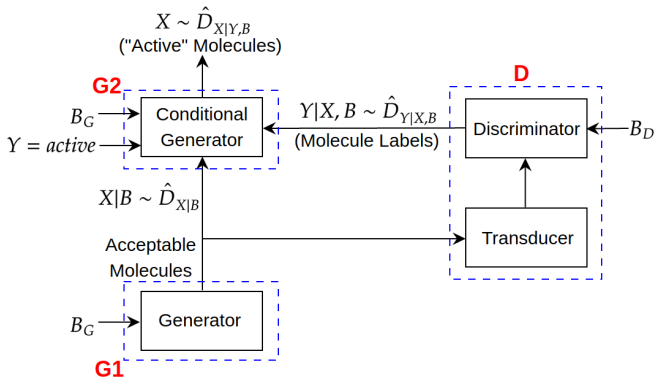
## The Idea.

- Molecules and their activities are instances of r.v.  $X$  and  $Y$  (resp.)
- We want to draw instances from the conditional distribution  $D_{X|Y,B}$



(Conditional generation of data)

## System Design. Approximating the distributions



## Empirical Evaluation of the System

### Data.

- $\Delta$ : ChEMBL database (1.9M unlabelled SMILES)
- JAK2-Homologues: 4300 labelled SMILES
- JAK2 data: 4100 labelled SMILES (for the proxy model)

### Background Knowledge.

- $B_G$ : Constraints on bulk-molecular properties from the literature
- $B_D$ : Functional groups, rings, fused and connected structures

### Generators.

- $G_1$  and  $G_2$ : LSTM-based VAEs
- $D$ : BotGNN

## Evaluation: Quantitative

As compared to the state-of-the-art approach:

- Our system generates significantly higher proportion of *active* molecules that are *active* for JAK2 inhibition.
- Our system generates significantly higher proportion of molecules that are *similar* to JAK2 inhibitors


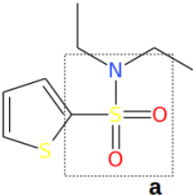
Comparison is against [[Krishnan et al, JCIM 2021](#)].



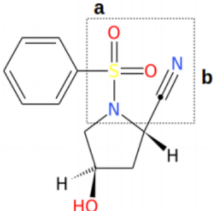
## Evaluation: By an expert (computational chemist)

- 10 generated molecules were evaluated:
  - 5 similar to JAK2 inhibitors
  - 5 dissimilar to JAK2 inhibitors
- The expert picked 3 molecules, dissimilar to JAK2 inhibitors that were novel and worth investigating further.

- Dissimilar and highly active molecules:

ID	Structure	Descriptors	Assessment
551		$Act = 9.12$ $Sim = 0.15$	This molecule has very low similarity to known JAK2 inhibitors. Also none of the groups specific to JAK2 could be identified by the substructure search. Discard this molecule.
1548		$Act = 9.04$ $Sim = 0.22$	This molecule has very low similarity to known JAK2 inhibitors. Also none of the groups specific to JAK2 could be identified by the substructure search. However, the sulfonamide group commonly found in JAK family inhibitors was found to be present (highlighted)

# Application of GNNs in Science

1562		$Act = 9.49$ $Sim = 0.32$	Despite low similarity to existing JAK2 inhibitors, 1562 had one JAK2-selective subgroup and a group common to JAK inhibitors, indicating potential to act as JAK family inhibitor, but the selectivity to JAK2 cannot be confirmed. <u>Possibly interesting new scaffold (highlighted) and worth pursuing further.</u>
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## Fan mail:

*I just saw your preprint ... **the last molecule seems indeed quite promising.***

From: a researcher at a prominent research lab in Europe

# Summary of the Talk

We discussed some

- Concepts
- Implementations and
- Real-world scientific Applications

of Graph Neural Networks or GNNs.

Follow our research on neuro-symbolic learning:

<https://github.com/tirtharajdash/NeSy>

Reach me at:

🏠 <https://tirtharajdash.github.io>  
@ [tdash@\[health.\]ucsd.edu](mailto:tdash@[health.]ucsd.edu)

Some contents are based on:

- [https://www.cs.mcgill.ca/~wlh/grl\\_book/](https://www.cs.mcgill.ca/~wlh/grl_book/)
- <https://distill.pub/2021/gnn-intro/>
- <https://distill.pub/2021/understanding-gnns/>
- <https://dmol.pub/dl/gnn.html>

Some contents of the notebooks are based on:

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