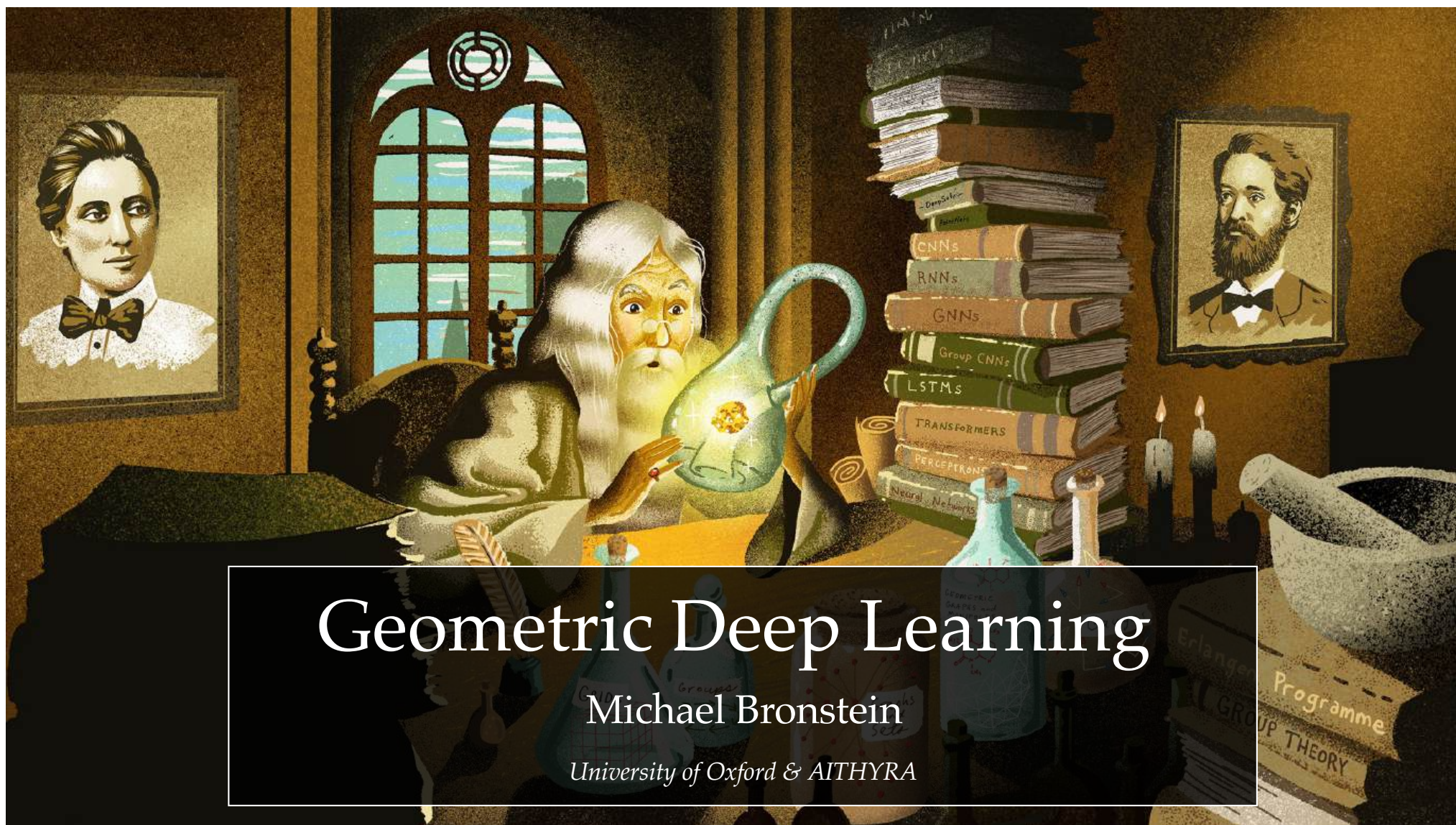




# Geometric Deep Learning

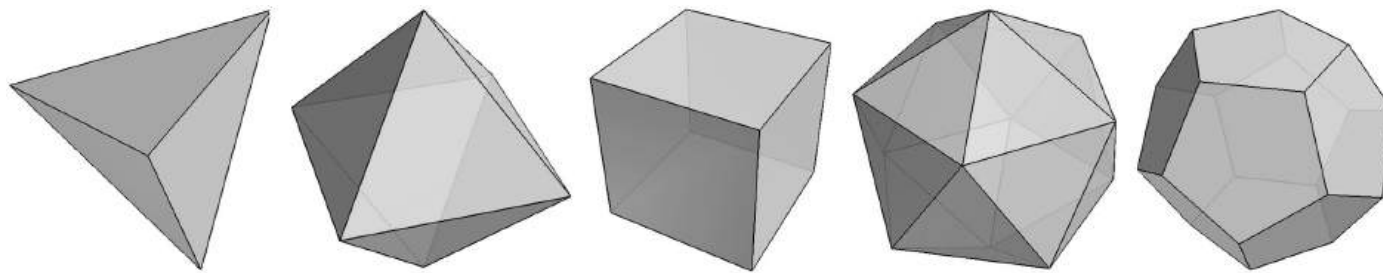
Michael Bronstein

*University of Oxford & AITHYRA*

“Symmetry, as wide or as narrow as you may define its meaning, is one idea by which man through the ages has tried to comprehend and create order, beauty, and perfection”



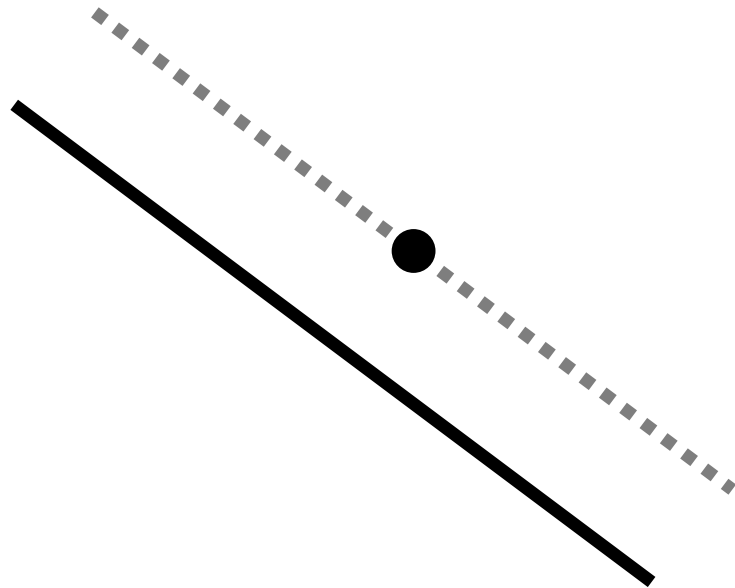
H. Weyl



**Plato**

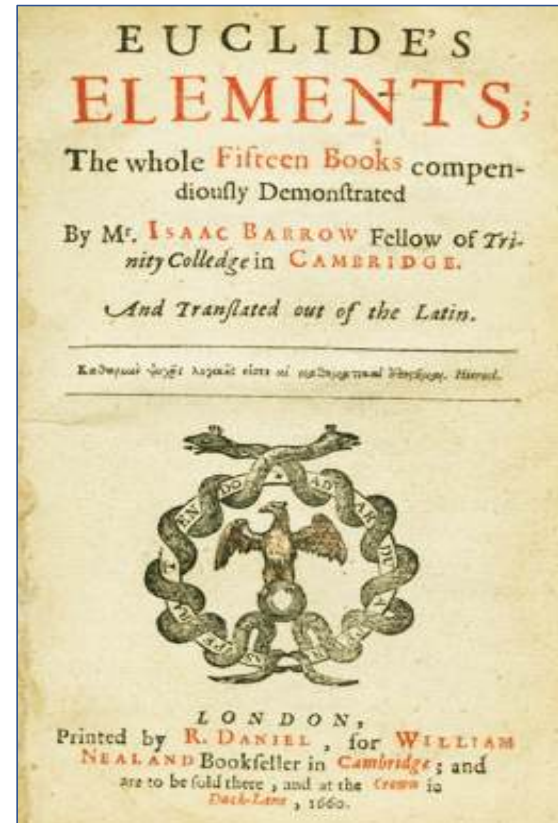
~370 BC

ΑΓΕΩΜΕΤΡΗΤΟΣ  
ΜΗΔΕΙΣ ΕΙΣΙΤΩ



Fifth Postulate

Portrait: Ihor Gorskyi

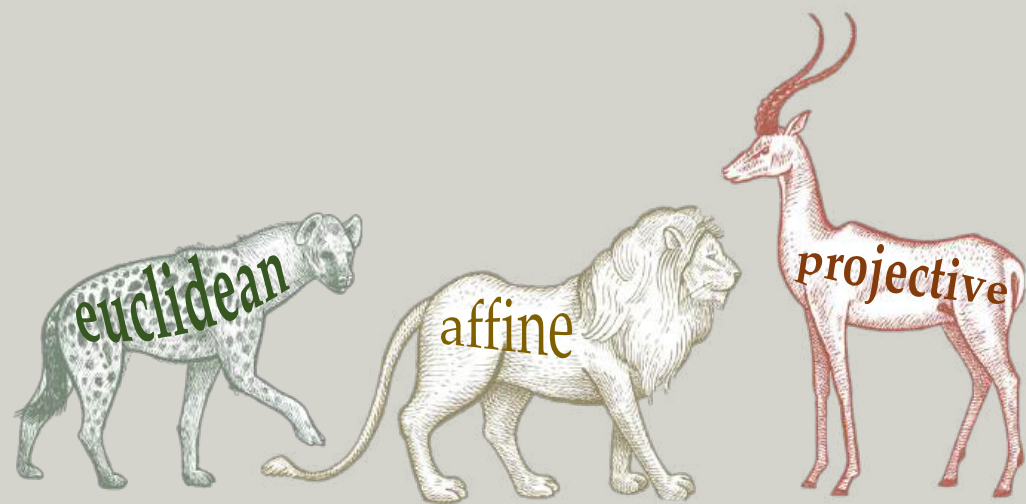


Euclid

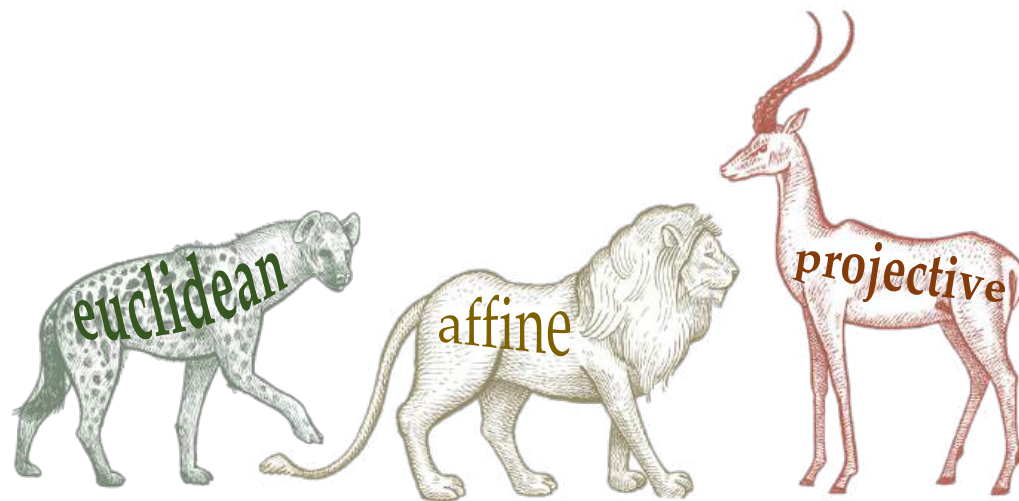
~300 BC

XIX century





# The Erlangen Programme



**Geometry = space + transformation group**



**F. Klein**

1872

## *Euclidean geometry*



$E(3)$

A horizontal arrow pointing from the original cat to the transformed cats.

Translation



Rotation



Reflection



**H. Poincaré**

1904



**H. Minkowski**

1907



**E. Noether**

1918



**H. Weyl**

1929

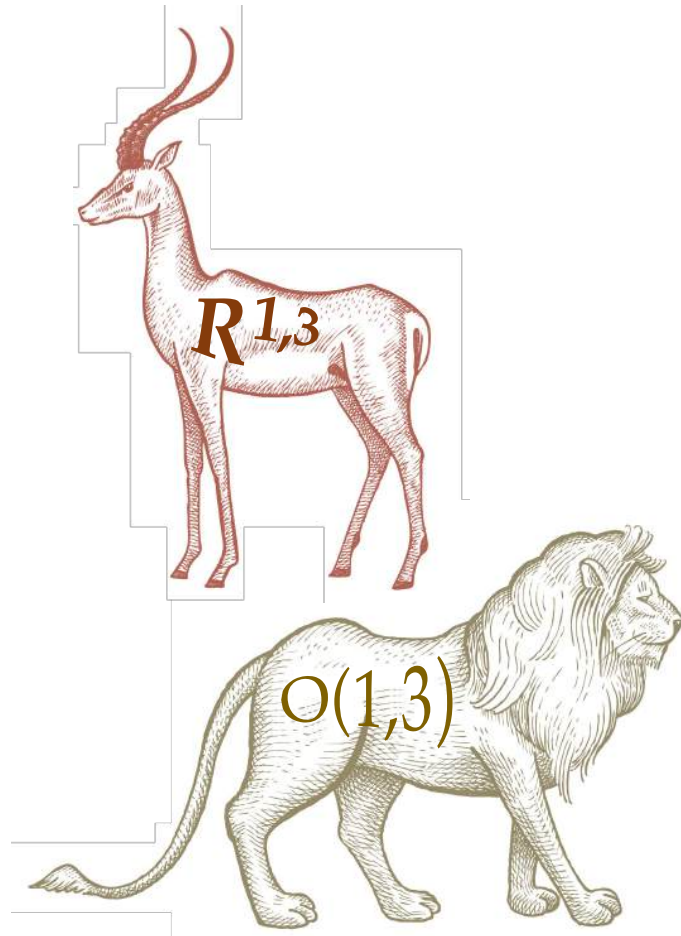


**C. N. Yang**

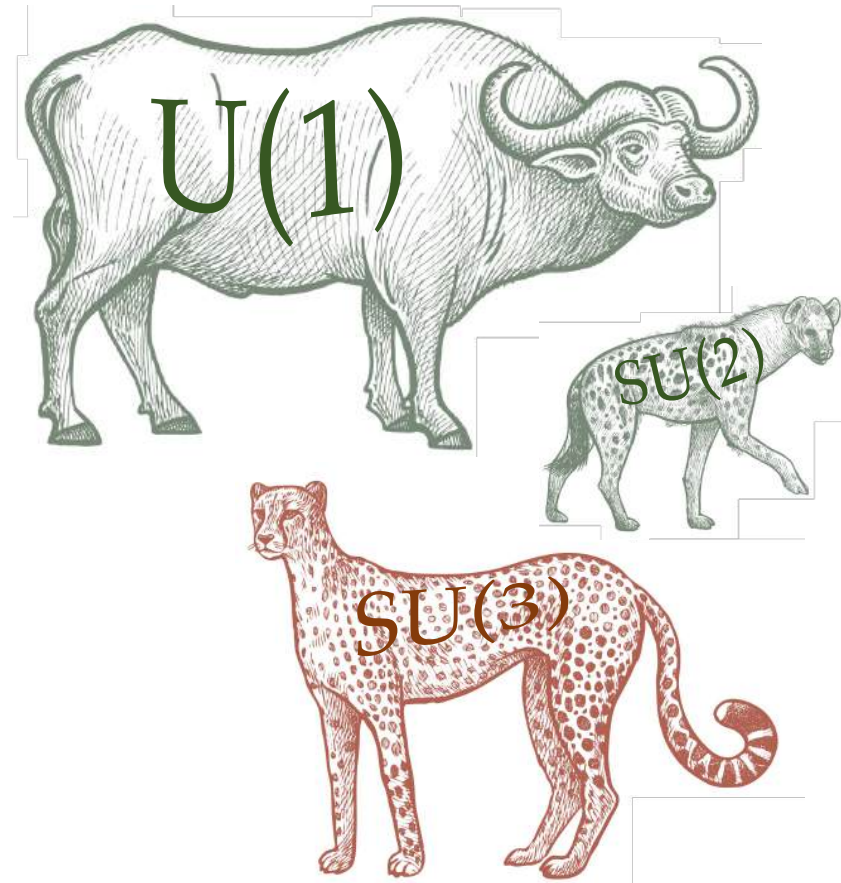
1954



**R. L. Mills**



External symmetry



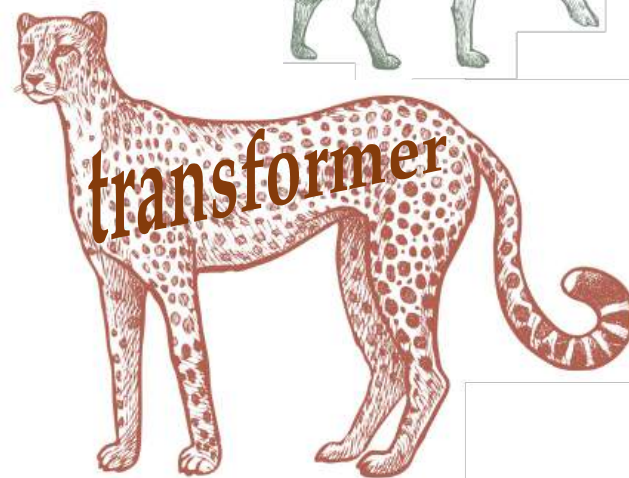
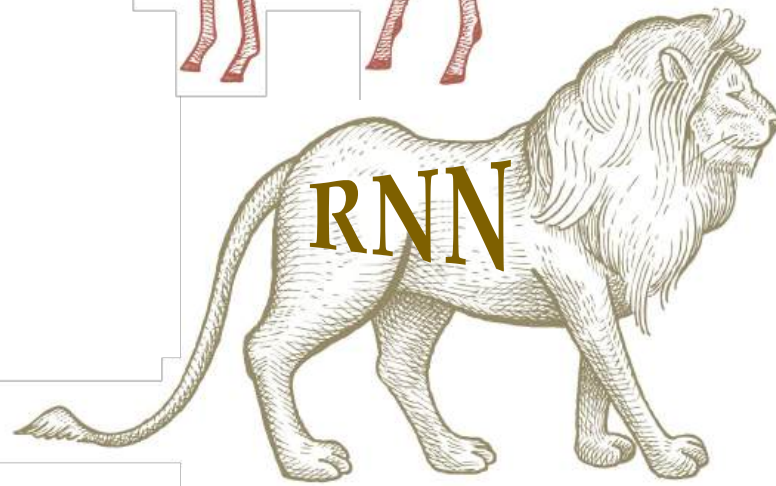
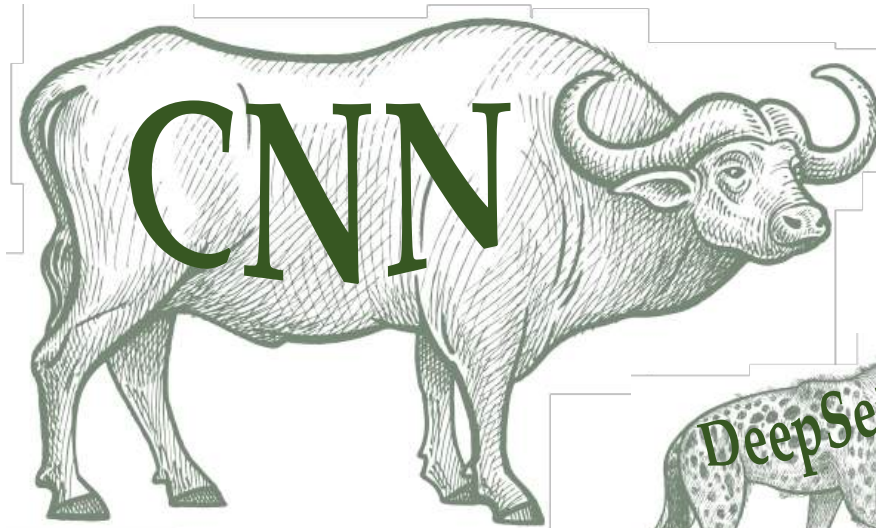
Internal symmetry

“It is only slightly overstating the case to say that Physics is the study of symmetry”

— *More is different*



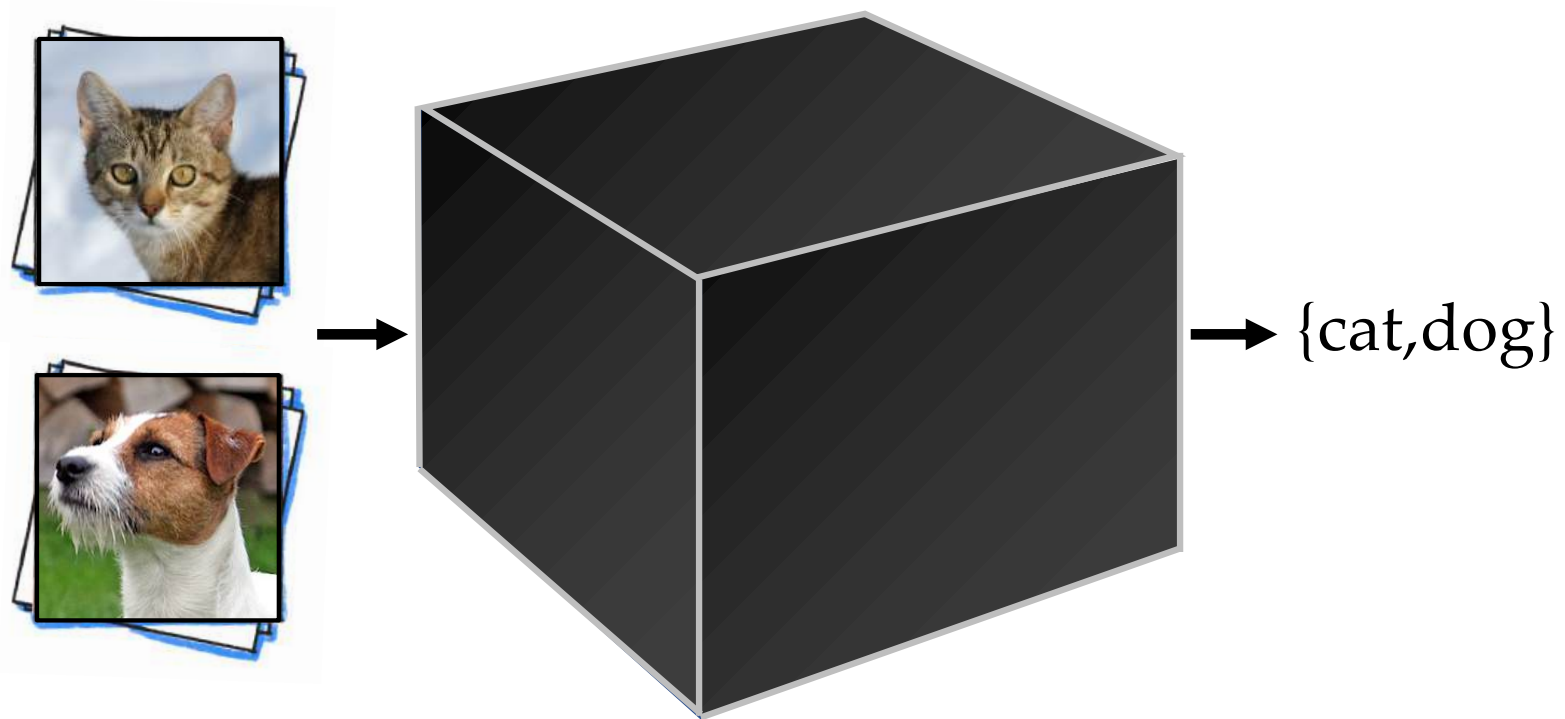
**P. Anderson**



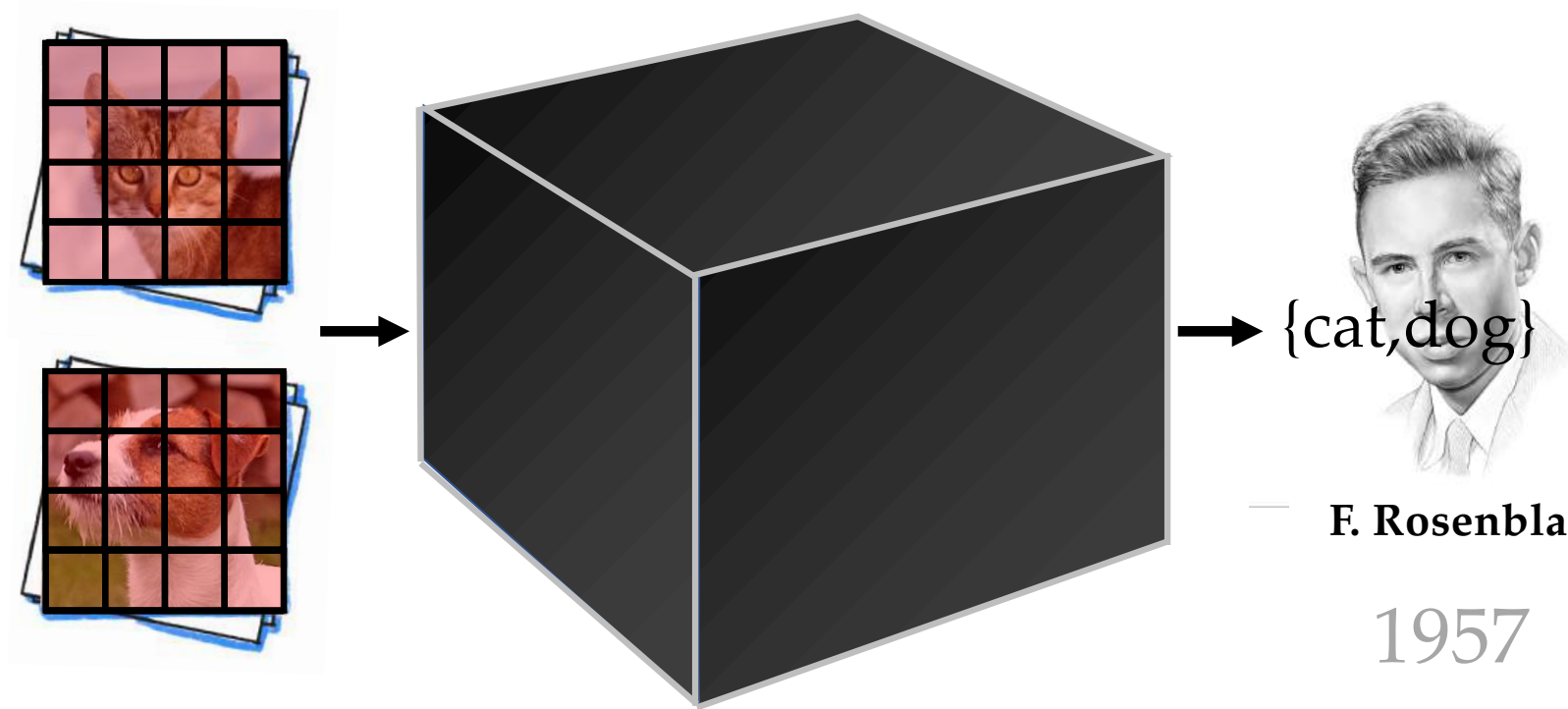
# Geometric Deep Learning



*Supervised ML = Function Approximation*



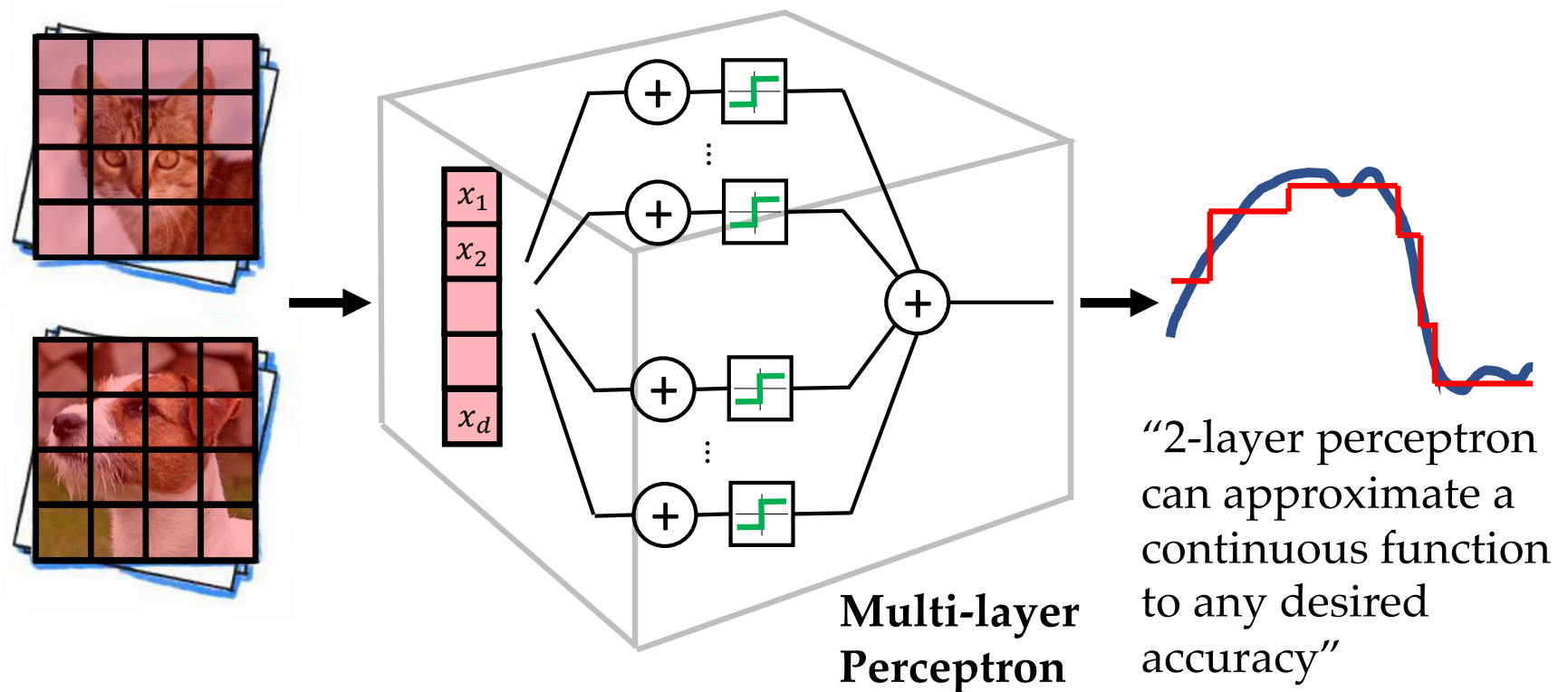
# *Supervised ML = Function Approximation*



— F. Rosenblatt —

1957

# Universal Approximation

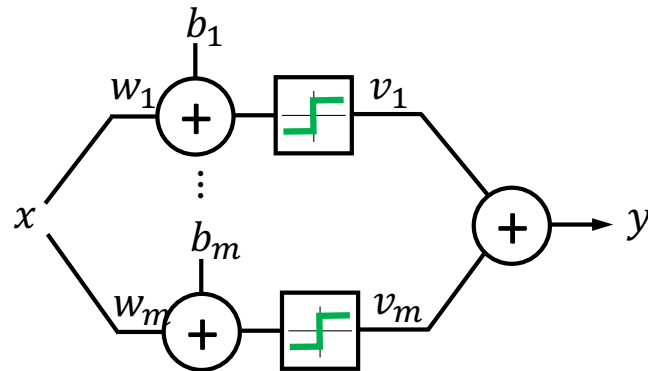


Universal Approximation: Hilbert's 13<sup>th</sup> problem 1900; Kolmogorov 1956; Arnold 1957; Cybenko 1989; Hornik 1991; Barron 1993; Leshno et al 1993; Maiorov 1999; Pinkus 1999

## *Shallow Perceptrons are universal approximators*

**Universal Approximation Theorem:**  $\sigma$  is not polynomial iff for every continuous function  $f: K \subset \mathbb{R}^d \rightarrow \mathbb{R}$  defined on a *compact set*  $K$  and  $\varepsilon > 0$ , there exists a two-layer Perceptron with  $m$  neurons and weights  $\mathbf{W}, \mathbf{b}, \mathbf{v}$  s.t.

$$\max_{x \in K} \left| f(x) - \sum_{j=1}^m v_j \sigma(w_j^T x + b_j) \right| < \varepsilon$$

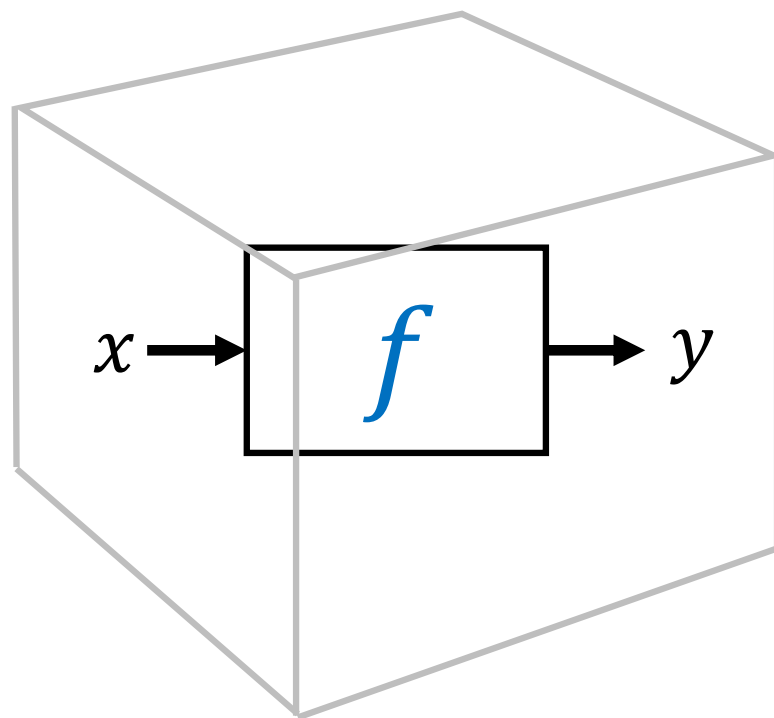


## *Shallow Perceptrons are universal approximators*

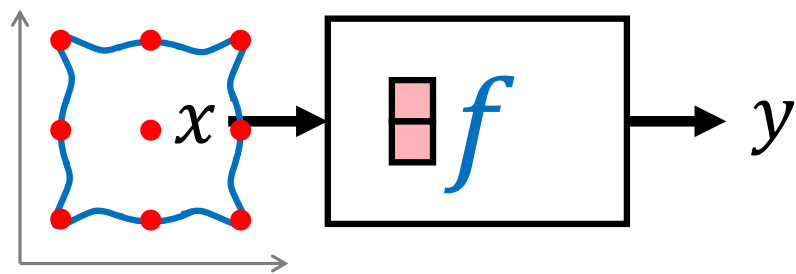
**Universal Approximation Theorem:**  $\sigma$  is not polynomial iff for every continuous function  $f: K \subset \mathbb{R}^d \rightarrow \mathbb{R}$  defined on a *compact set*  $K$  and  $\varepsilon > 0$ , there exists a two-layer Perceptron with  $m$  neurons and weights  $\mathbf{W}, \mathbf{b}, \mathbf{v}$  s.t.

$$\max_{x \in K} \left| f(x) - \sum_{j=1}^m v_j \sigma(w_j^T x + b_j) \right| < \varepsilon$$

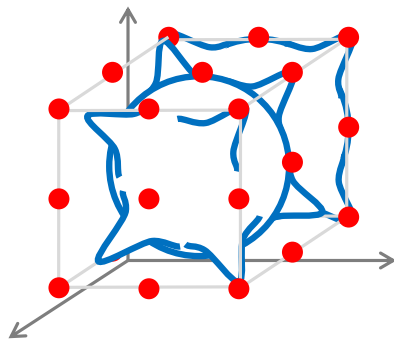
**What is the relation between dimension  $d$ ,  
number of neurons  $m$ , and the error  $\varepsilon$ ?**



2-dimensional



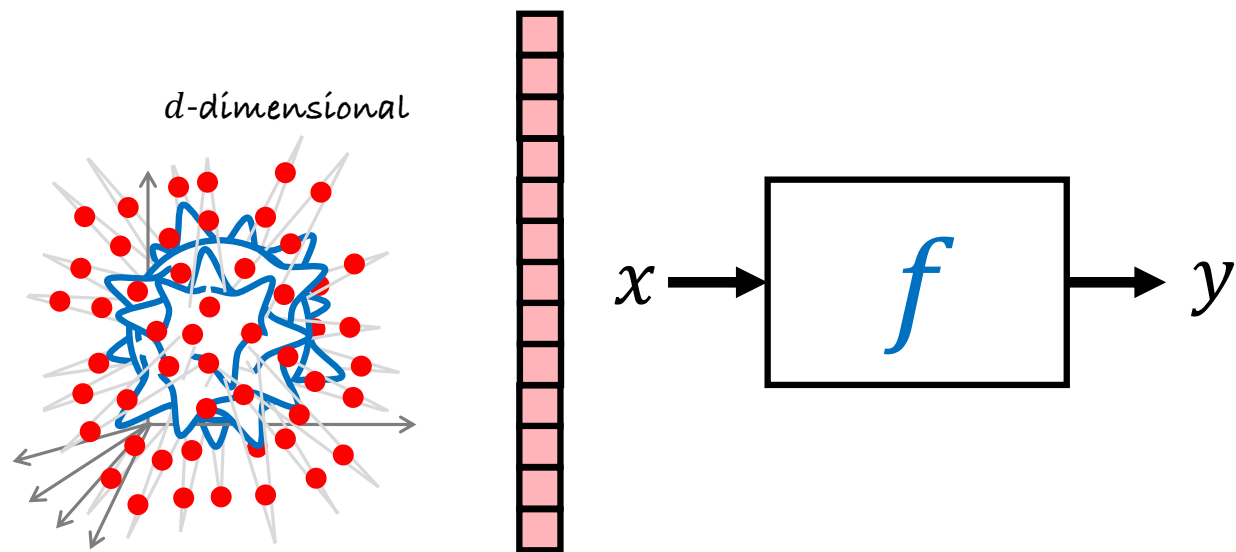
3-dimensional



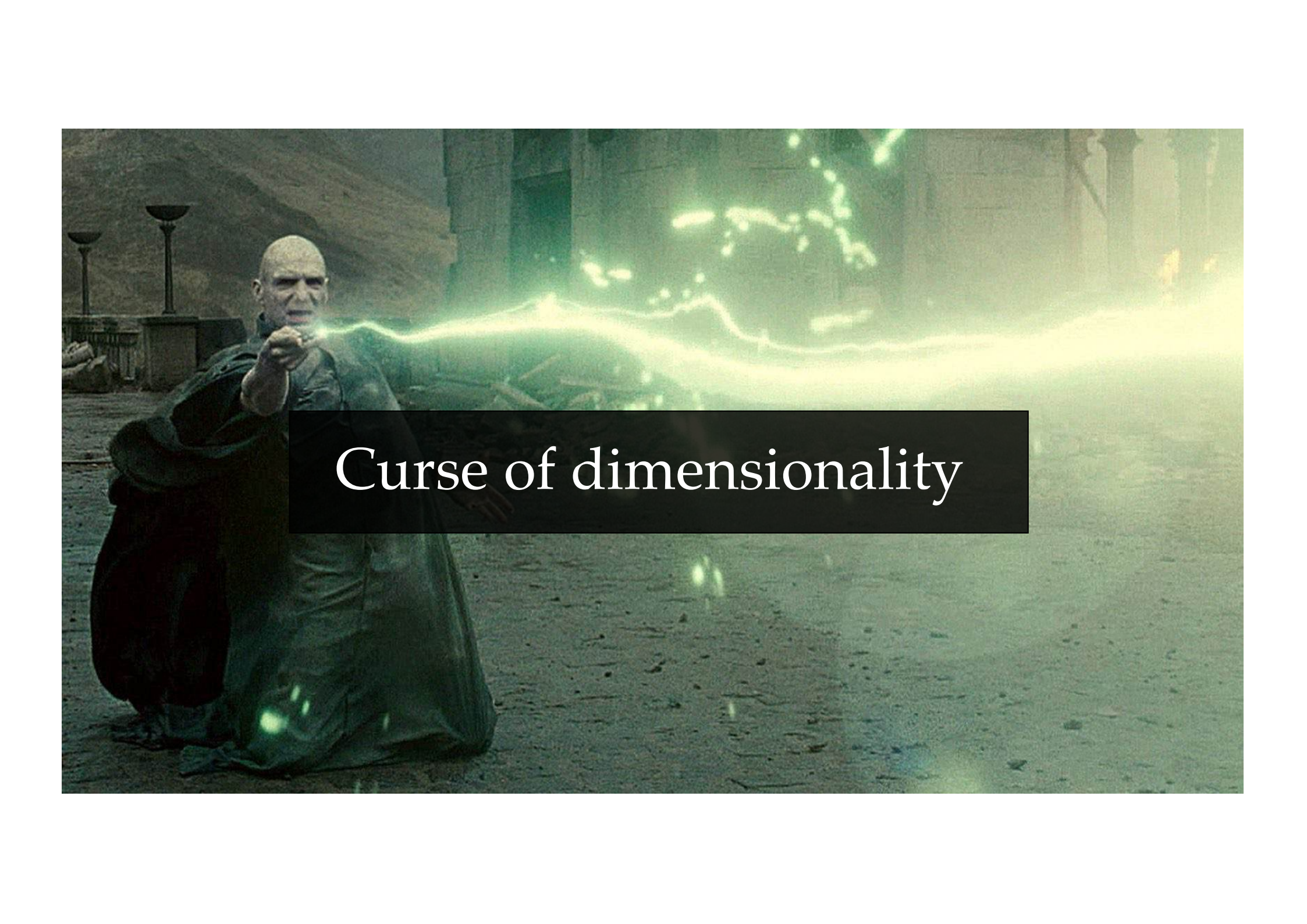
$x$



$y$



$O(\varepsilon^{-d})$  samples

A still from the Harry Potter movies showing Lord Voldemort in a dark, stone-walled corridor. He is wearing his black robe and is casting a powerful green lightning spell (the Avada Kedavra curse) towards the right. The spell is depicted as a bright green beam of light with jagged, lightning-like edges. The background shows the architecture of the corridor, including stone walls and a doorway. The overall atmosphere is dark and ominous.

Curse of dimensionality

## Approximation rates

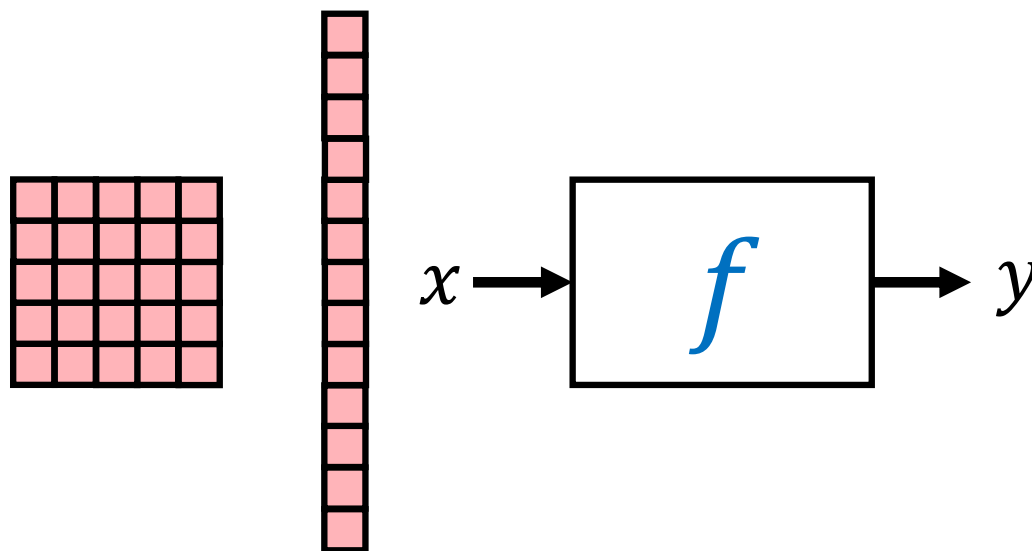
- Bound on the approximation error

$$\varepsilon = \inf_{g \in \mathcal{F}} \sup_{x \in K \subset \mathbb{R}^d} |f(x) - g(x)|$$

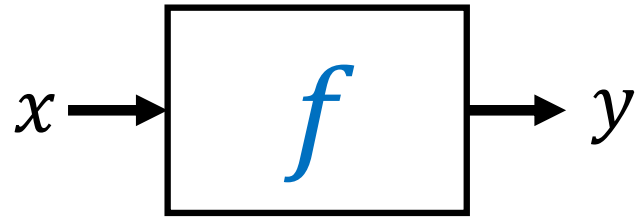
w.r.t.  $d$  (input dimension) and  $m$  (model complexity) for different classes of functions

- *Sobolev class*  $f \in H^s(\mathbb{R}^d) = \left\{ f \in L_2(\mathbb{R}^d) : \int_{\mathbb{R}^d} (1 + \|\omega\|^2)^s |\hat{f}(\omega)|^2 d\omega < \infty \right\}$   
error is exponential  $\varepsilon = \mathcal{O}(m^{-s/d})$  **dimensionality-cursed!**
- *Barron class*  $f \in \left\{ f \in L_2(\mathbb{R}^d) : \int_{\mathbb{R}^d} \|\omega\|^2 |\hat{f}(\omega)|^2 d\omega < \infty \right\}$   
error is  $\varepsilon = \mathcal{O}(m^{-1})$  **too strong assumption in practice!**

*Geometric priors*

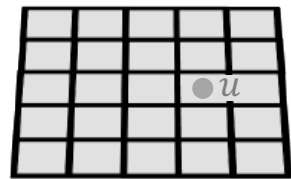


*Geometric priors*



## *Geometric priors*

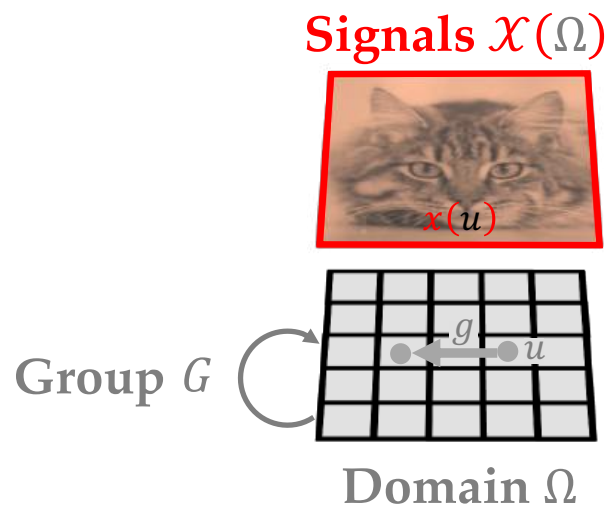
Signals  $\mathcal{X}(\Omega)$



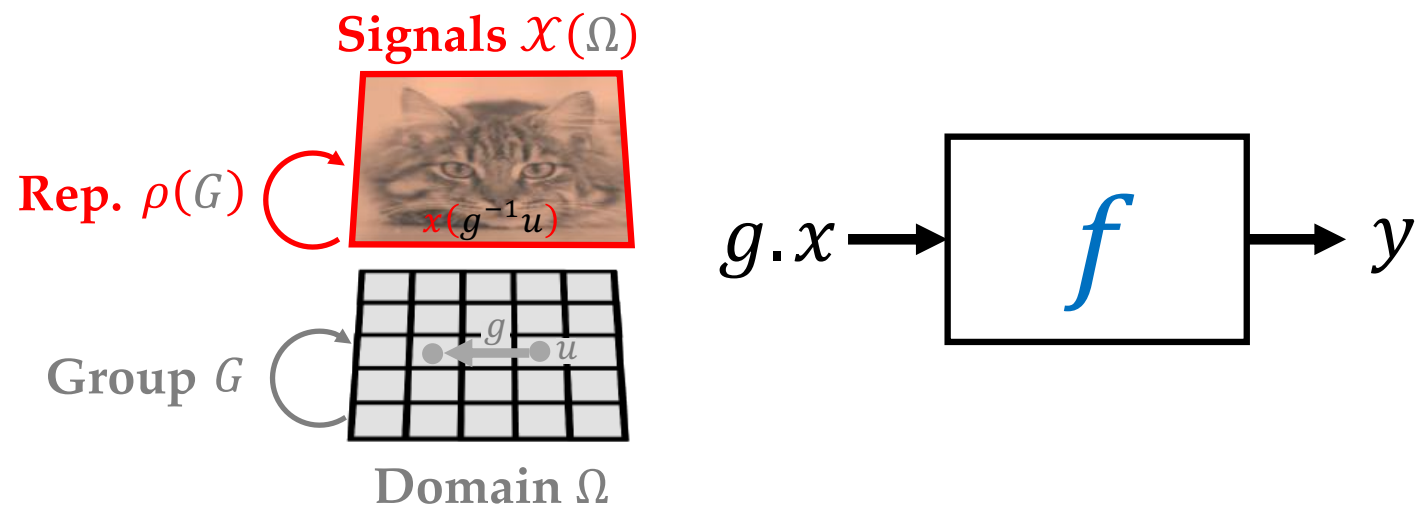
Domain  $\Omega$



## *Geometric priors*

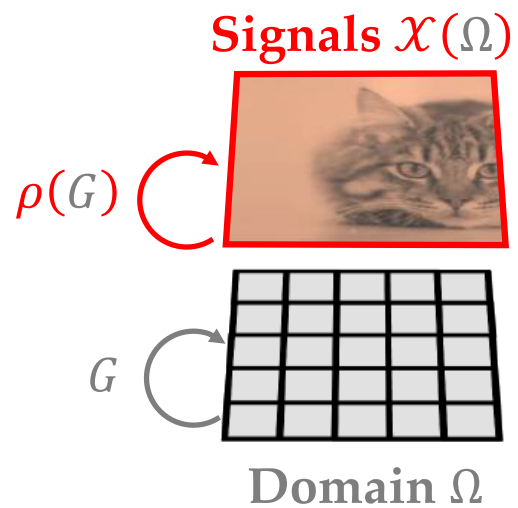


## *Geometric priors*



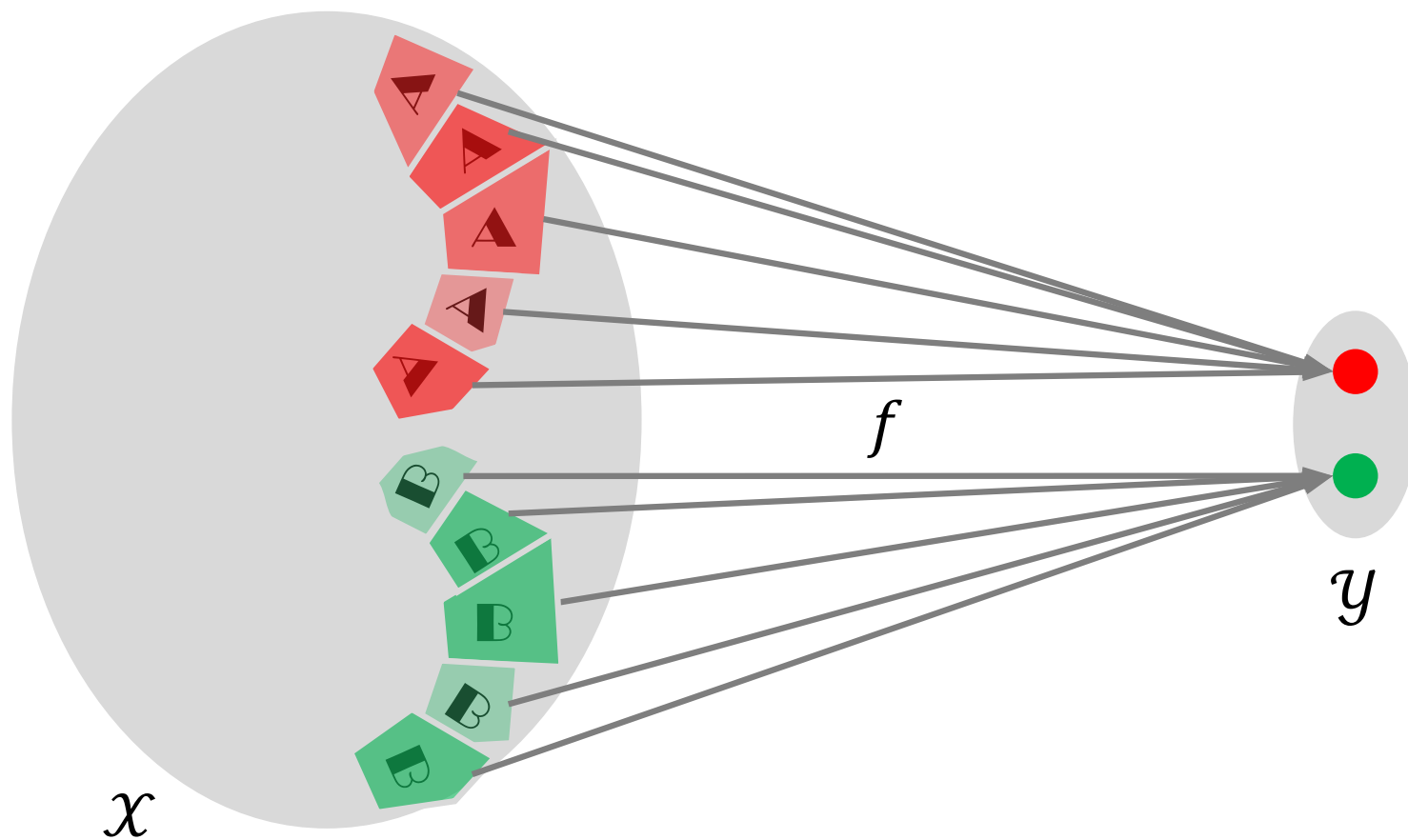
*“How  $f$  interacts with the group  $G$ ?”*

## *Geometric priors: Invariance*

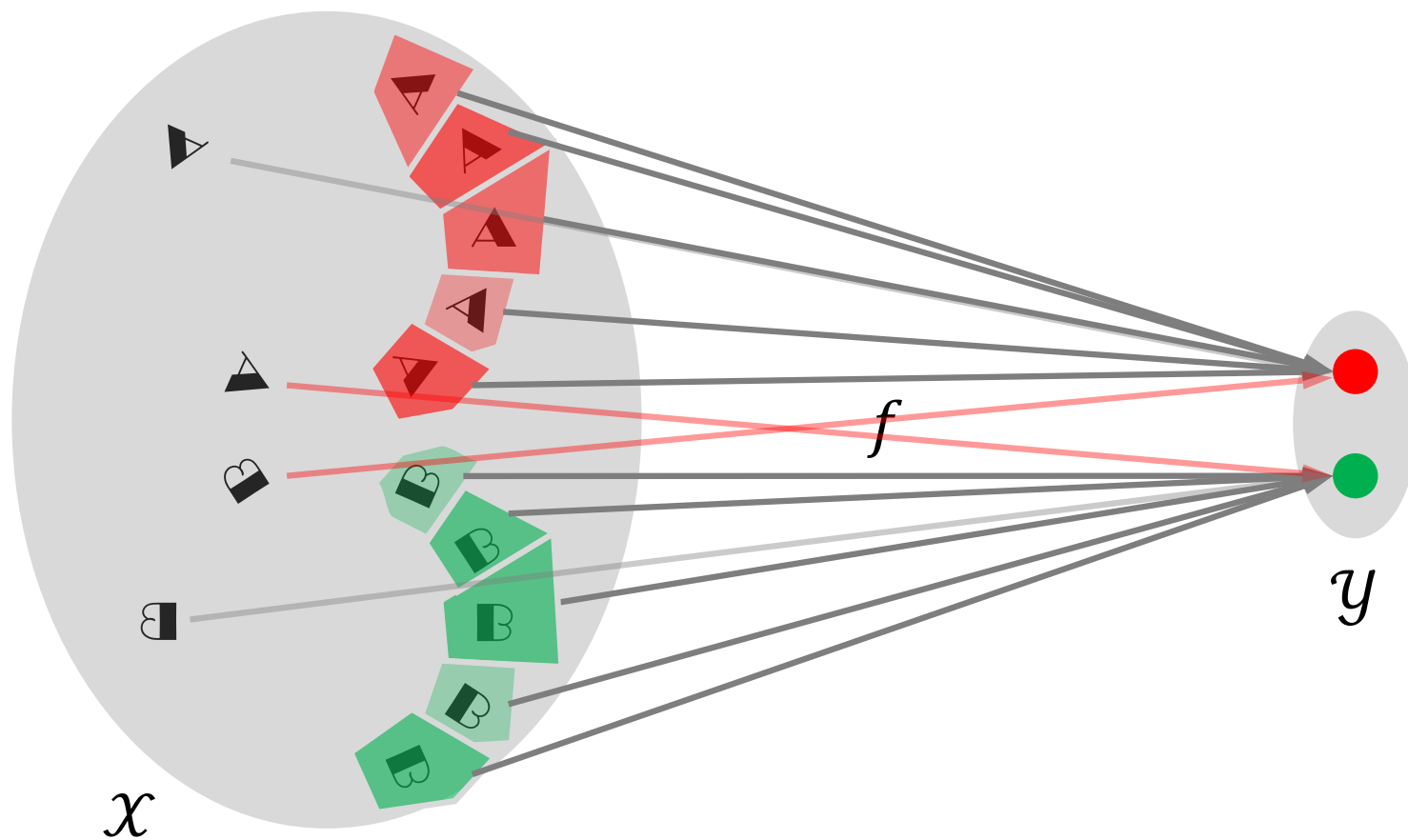


$$f(\rho(g)x) = f(x) \quad \forall g \in G$$

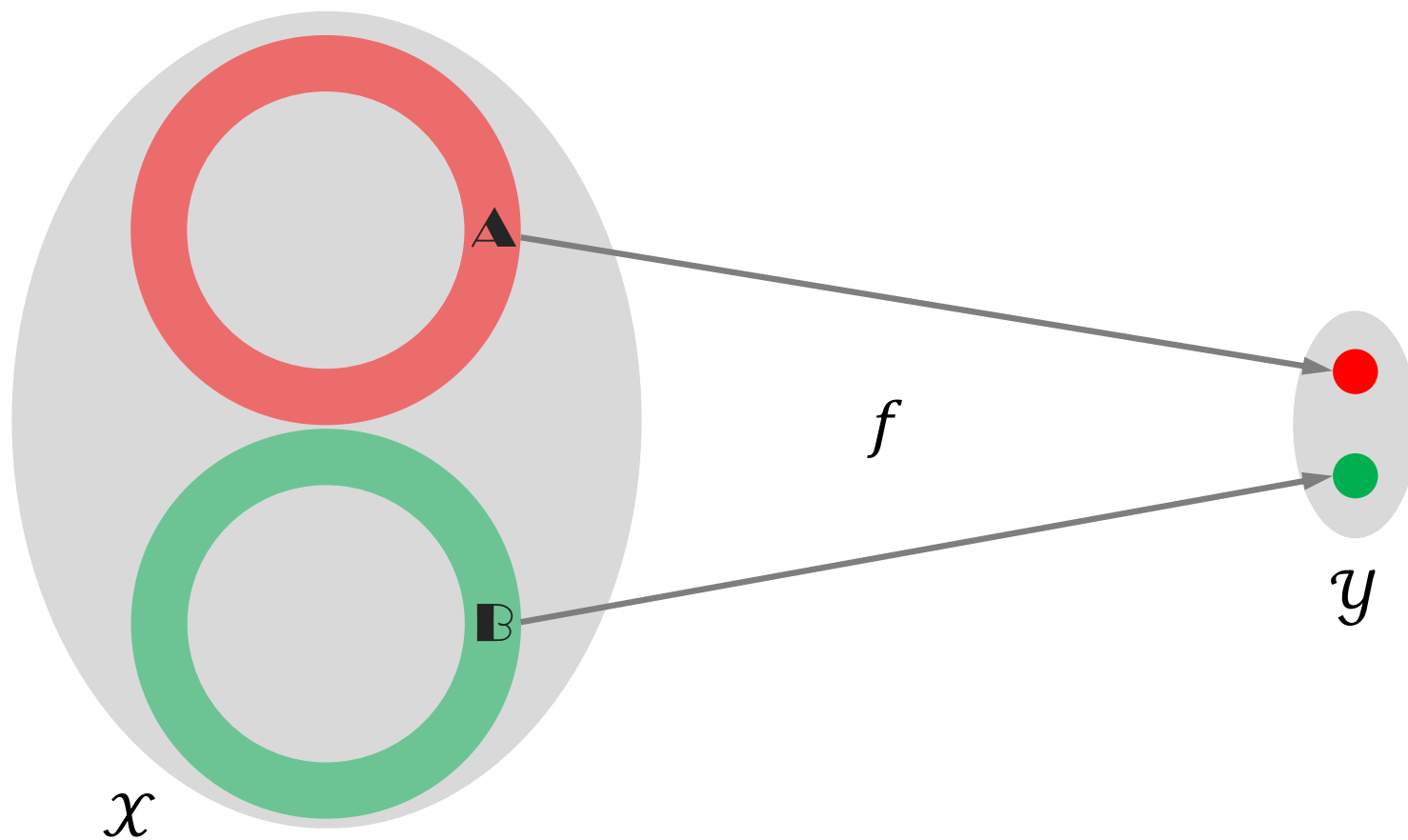
# *Symmetries of the Label Function*



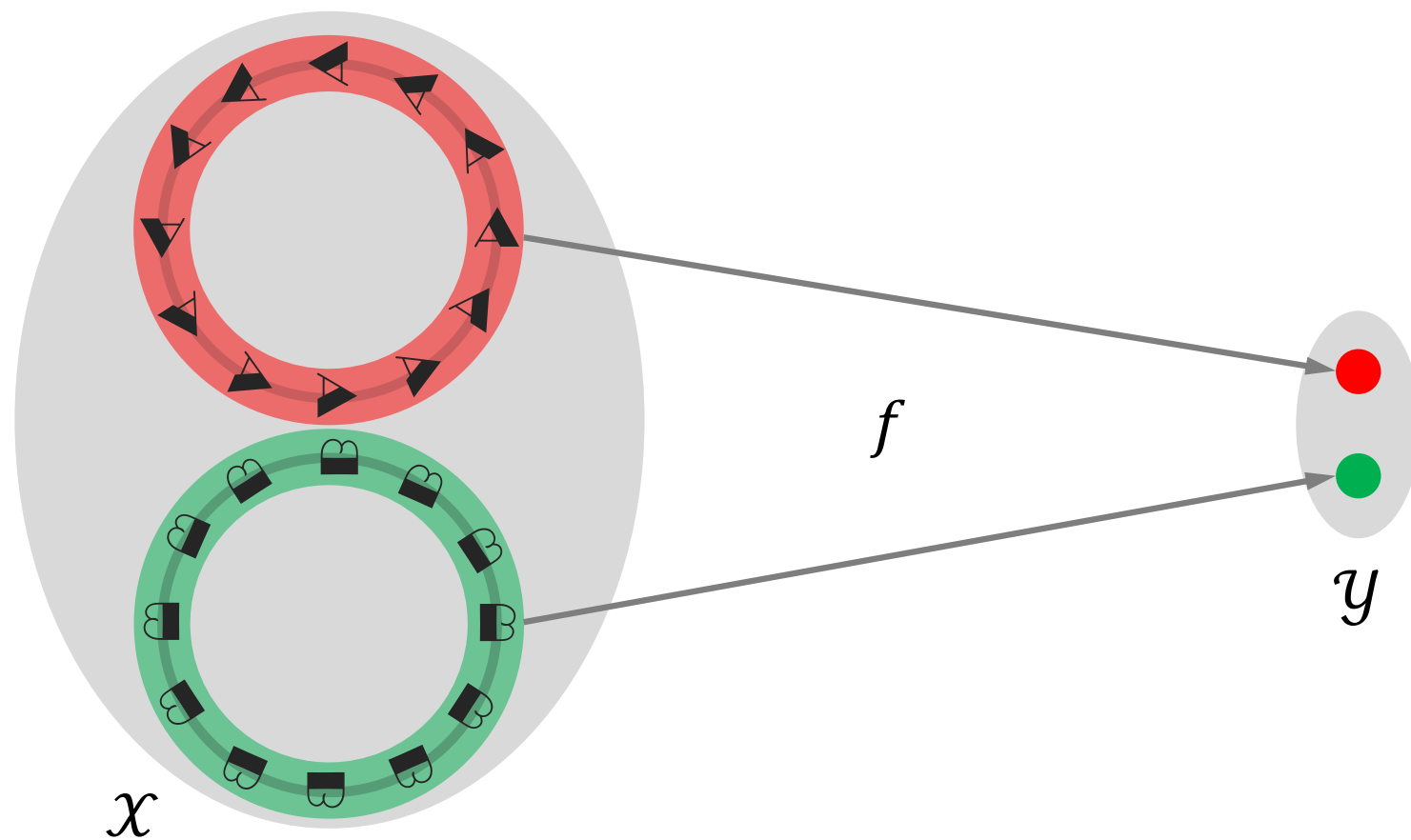
# *Symmetries of the Label Function*



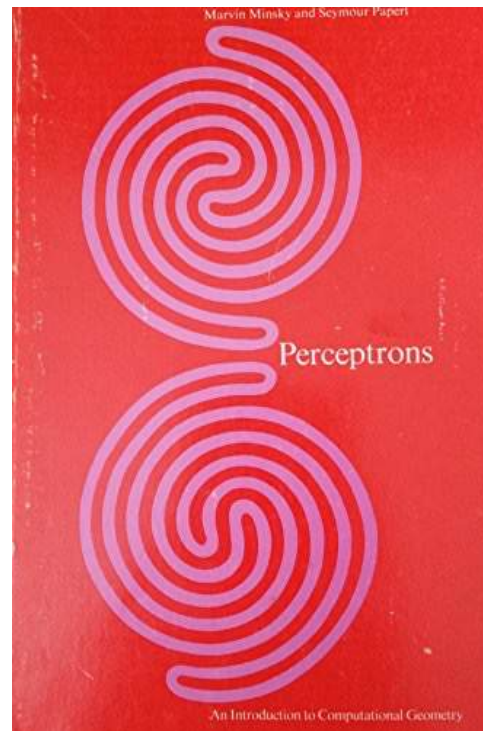
# *Symmetries of the Label Function*



# *Symmetries of the Label Function*



## *First “geometric” machine learning*



**M. Minsky**



**S. Papert**

1969

Minsky, Papert 1969

## *First “geometric” machine learning*

**Group Invariance Theorem:** “if a neural network is invariant to a group, then its output can be expressed as functions of the orbits of the group”

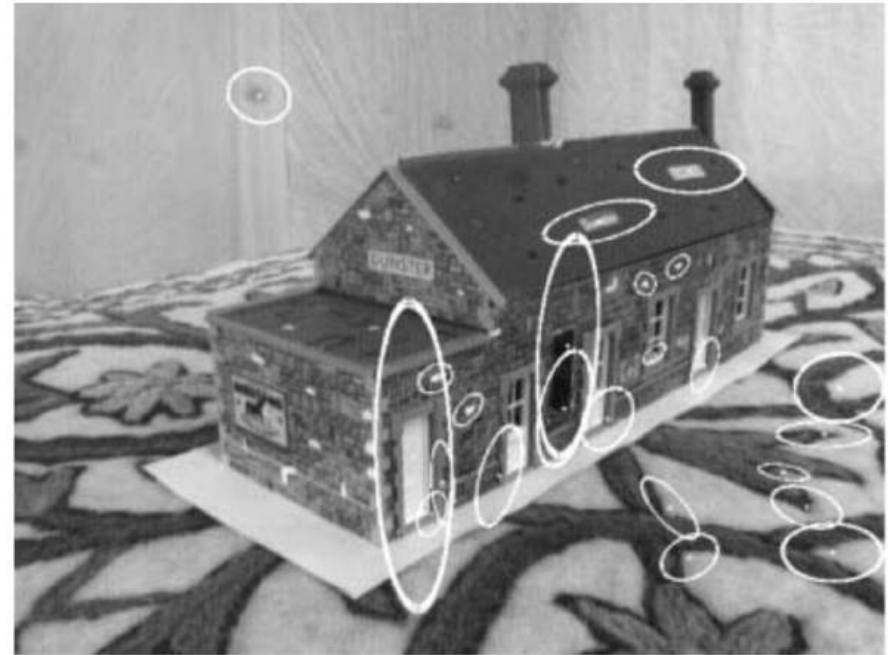
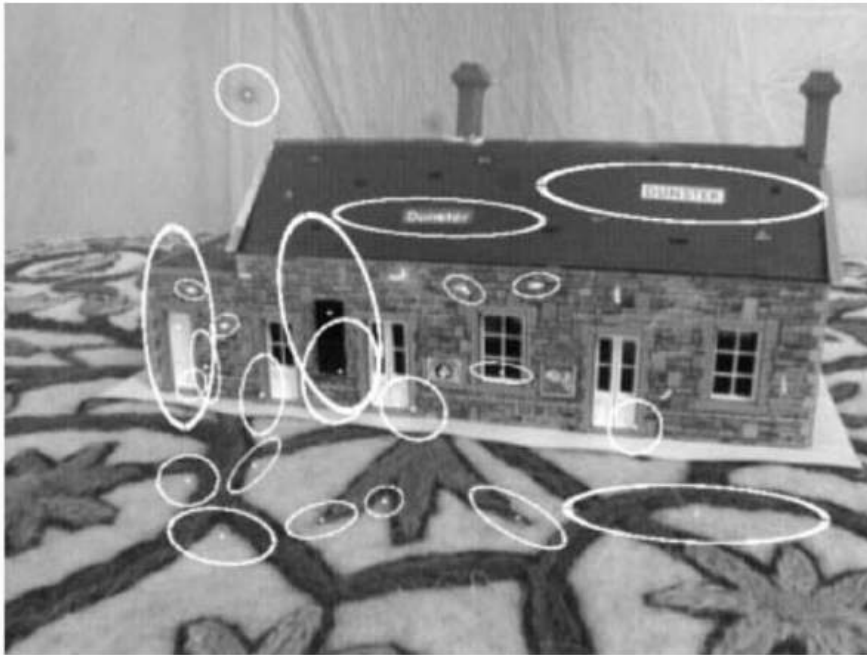


**M. Minsky**

**S. Papert**

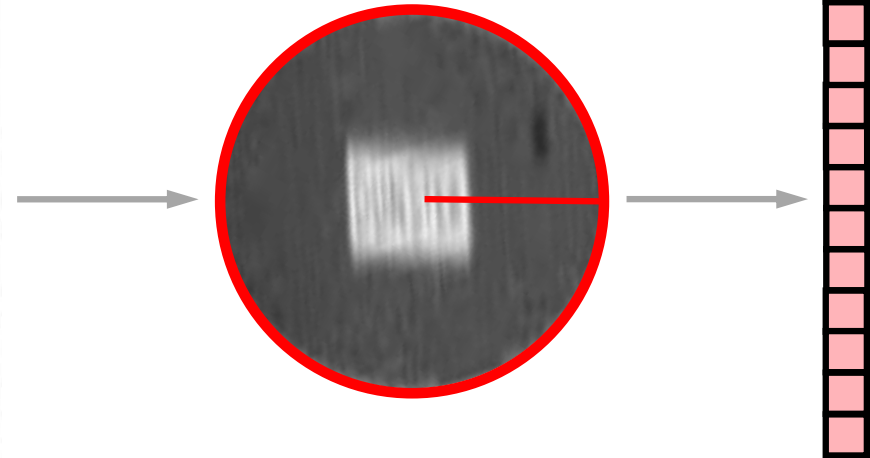
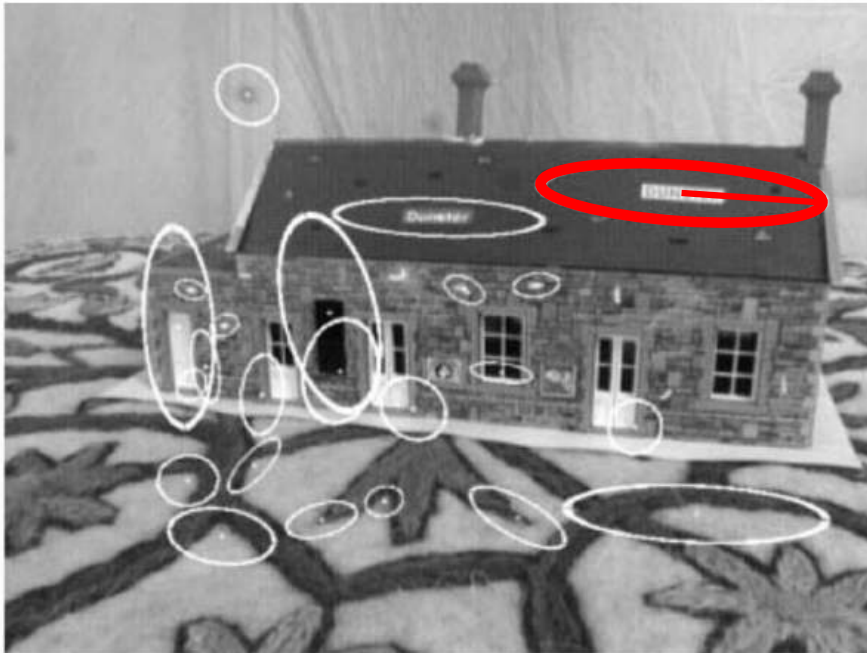
1969

## *Canonisation*



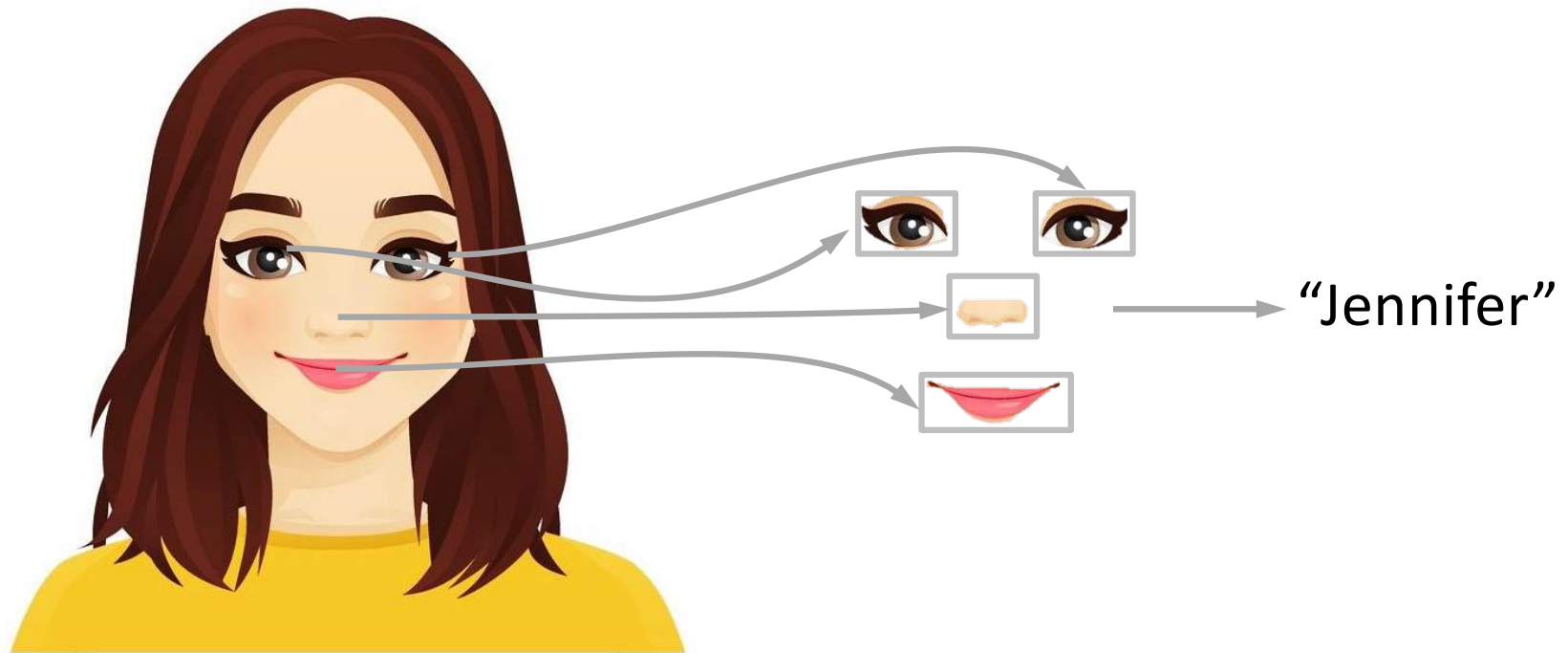
Mikolajczyk, Schmid 2004

# *Canonisation*

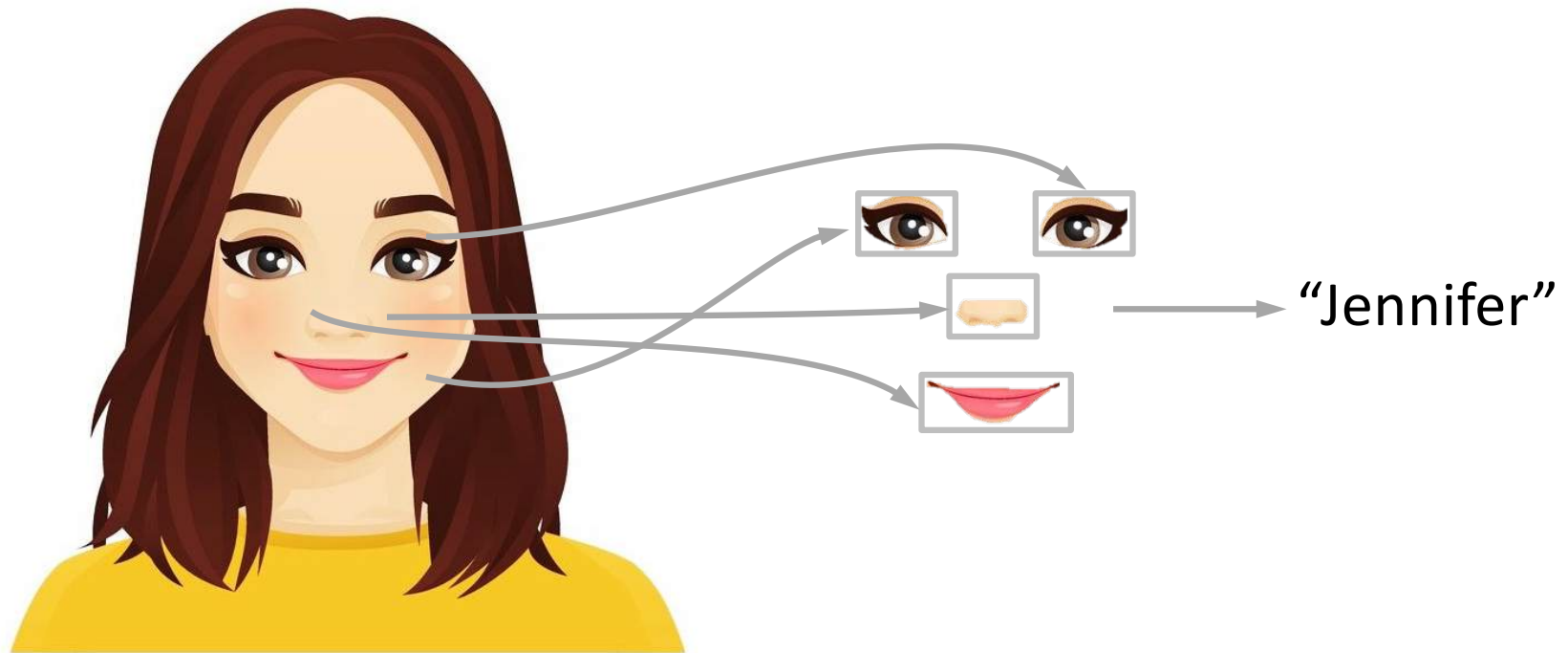


**canonisation**

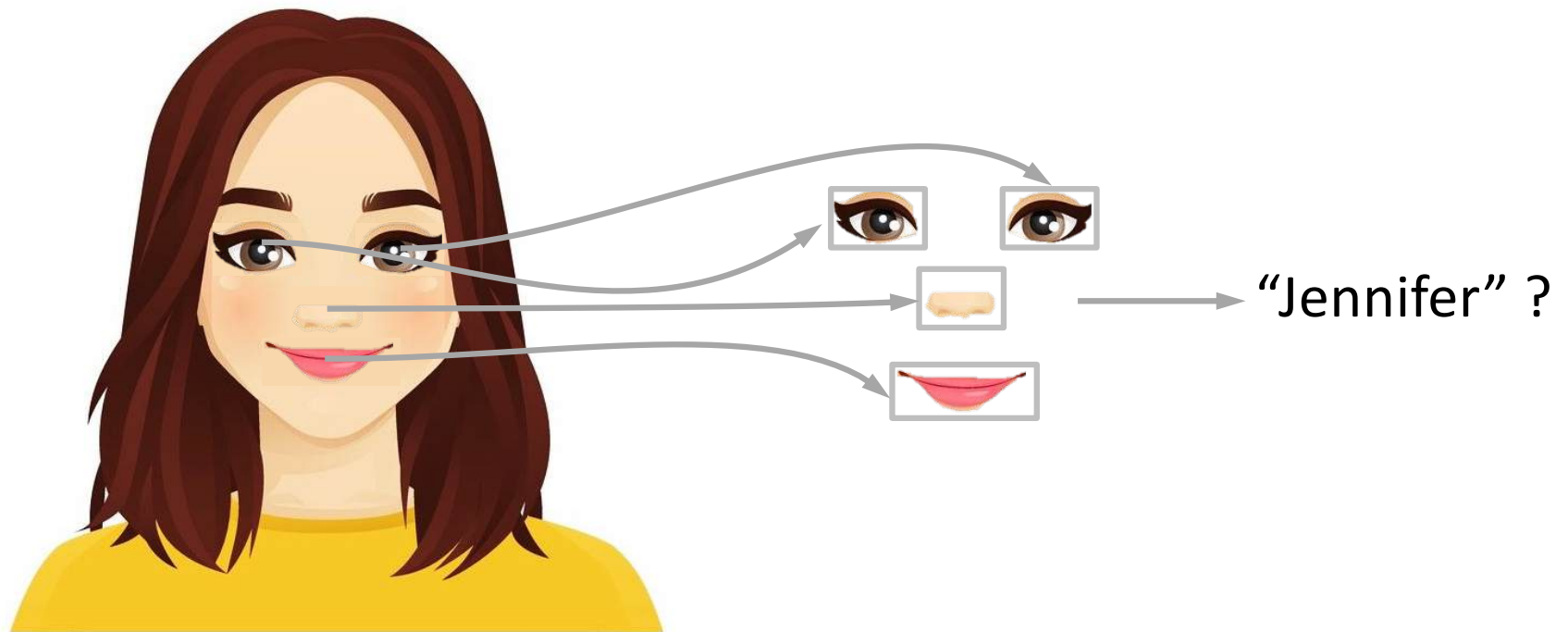
## *Canonisation*

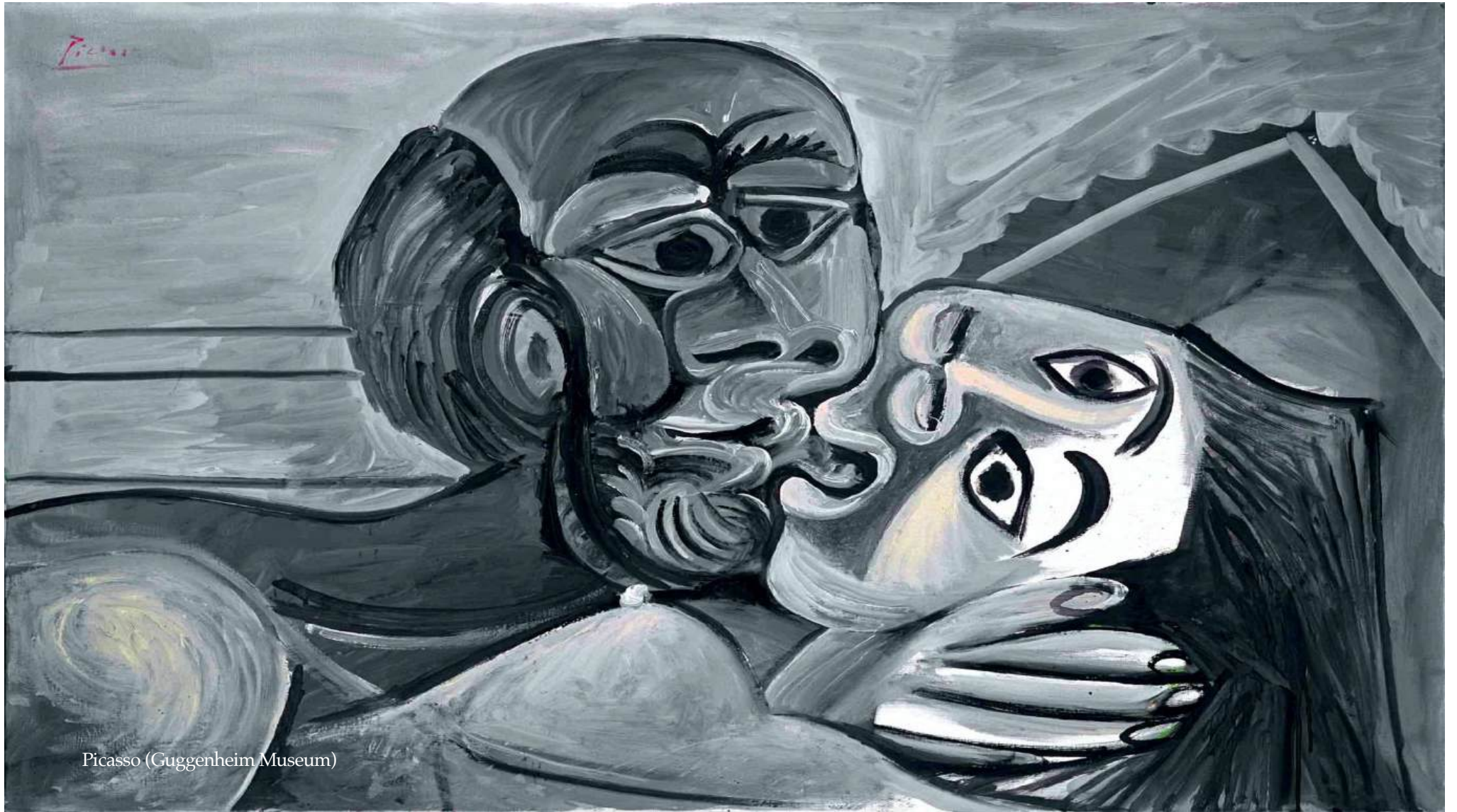


## *Canonisation*



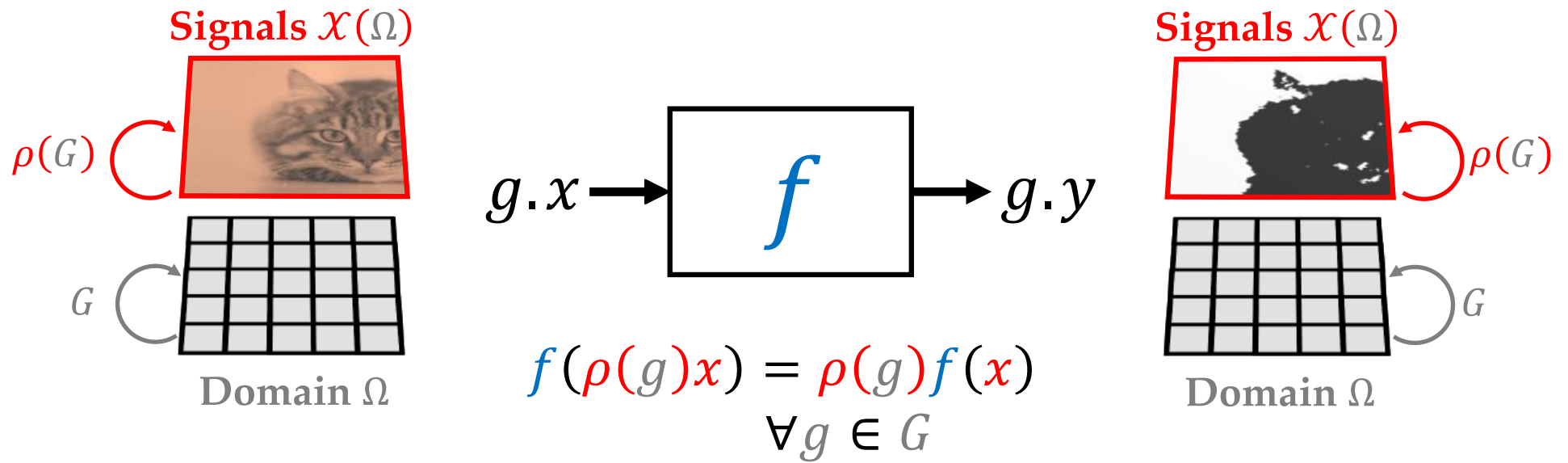
## *Canonisation*



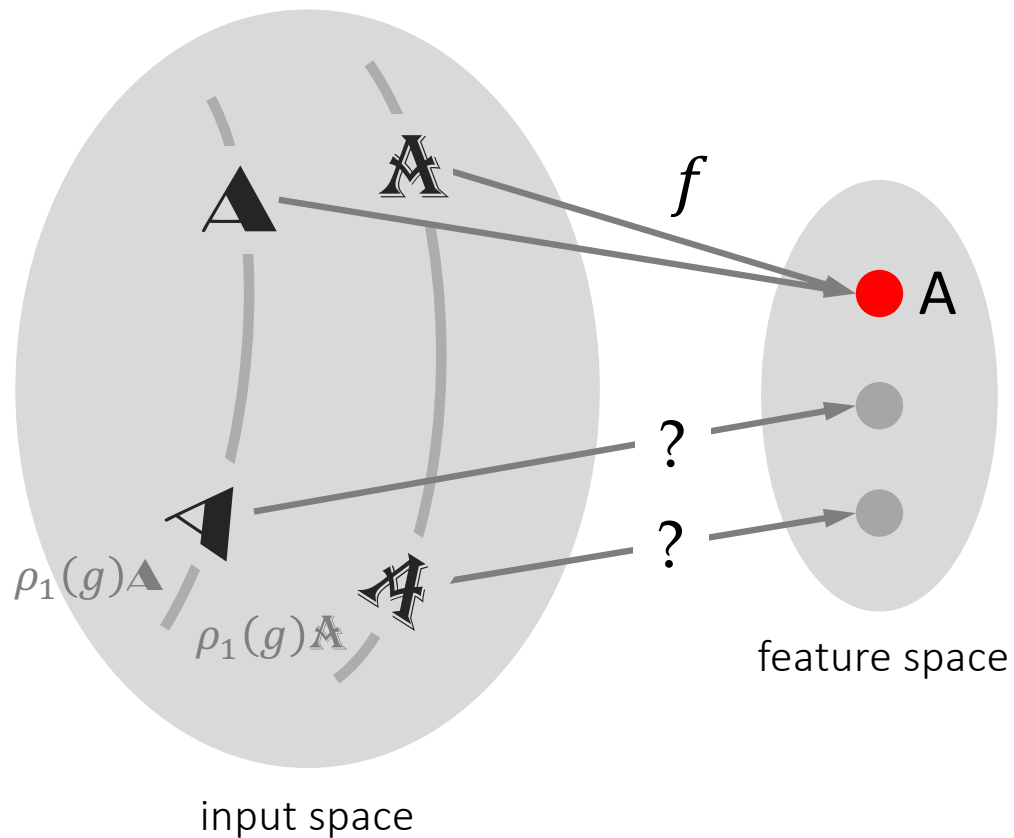


Picasso (Guggenheim Museum)

## Geometric priors: Equivariance



*Equivariance = Symmetry-consistent generalisation*

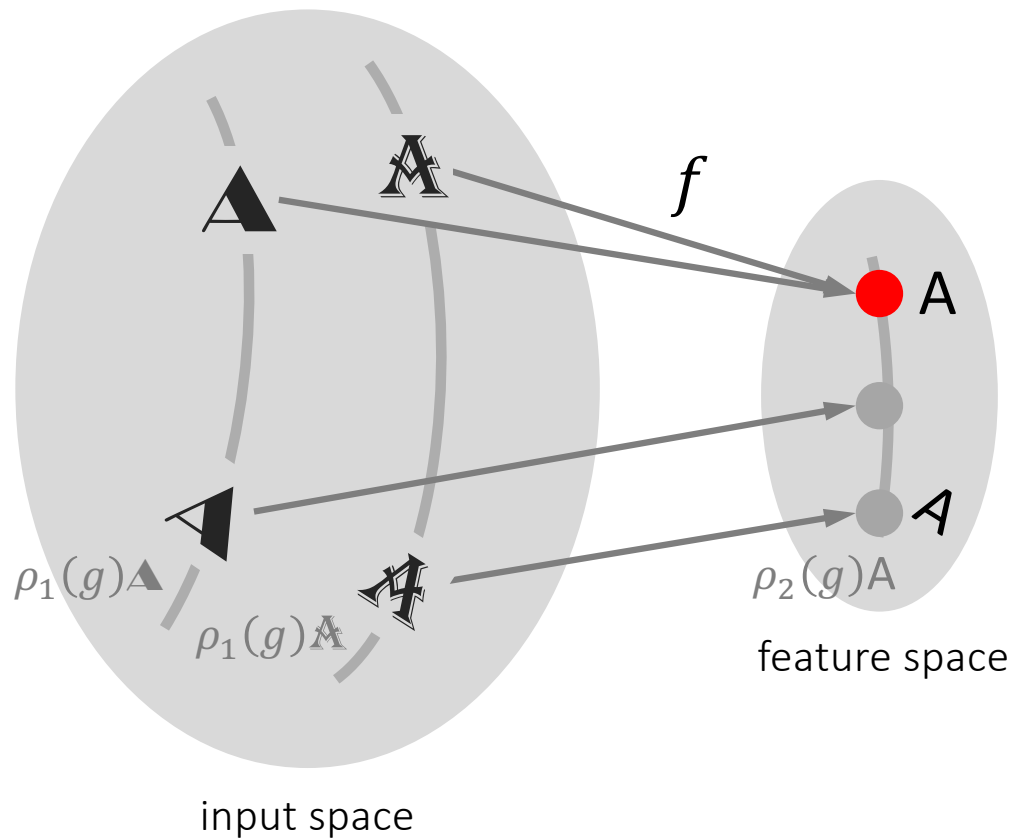


$$f(\rho_1(g)\blacktriangle) = \rho_2(g) \textcolor{red}{f(\blacktriangle)}$$

$$\parallel$$

$$f(\rho_1(g)\mathbb{A}) = \rho_2(g) \textcolor{red}{f(\mathbb{A})}$$

*Equivariance = Symmetry-consistent generalisation*

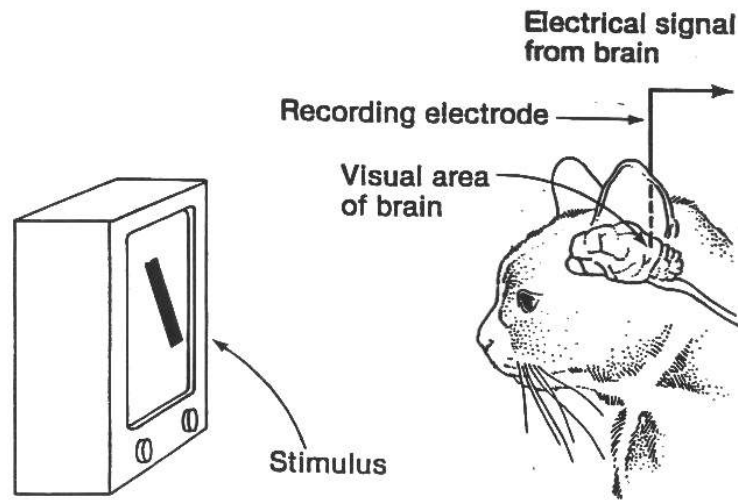


$$f(\rho_1(g)A) = \rho_2(g) f(A)$$

$$\parallel$$

$$f(\rho_1(g)\tilde{A}) = \rho_2(g) f(\tilde{A})$$

## *Early Geometric Architectures*

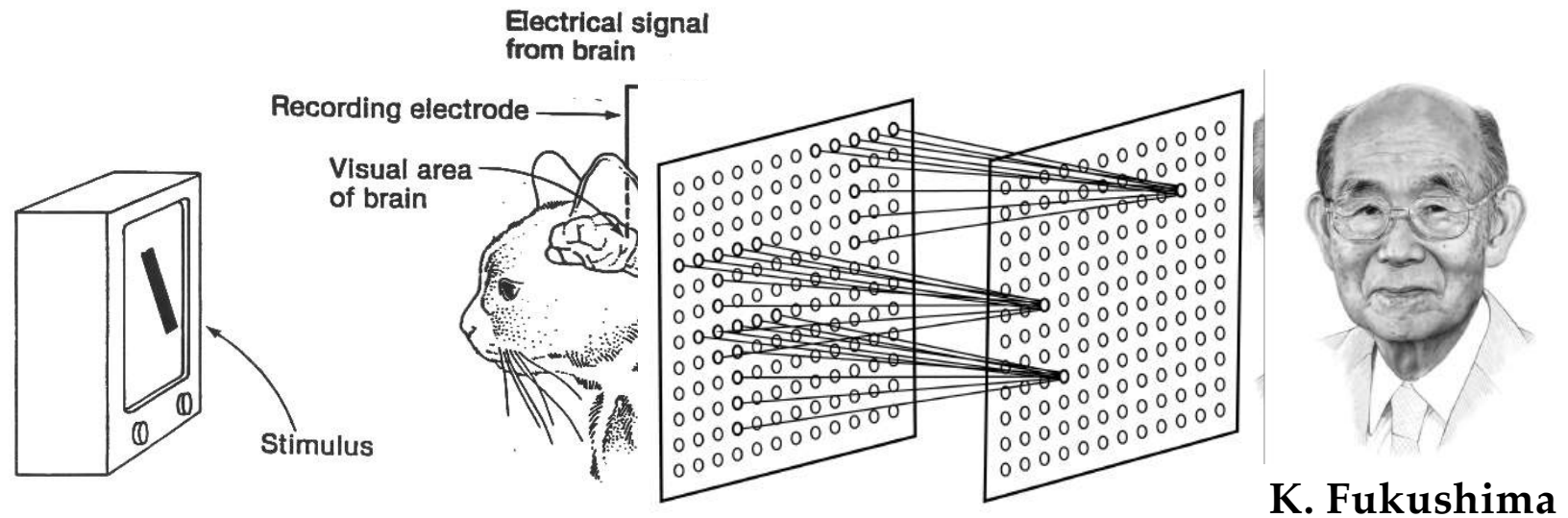


**D. Hubel**

**T. Wiesel**

1959

## *Early Geometric Architectures*



1959 1980

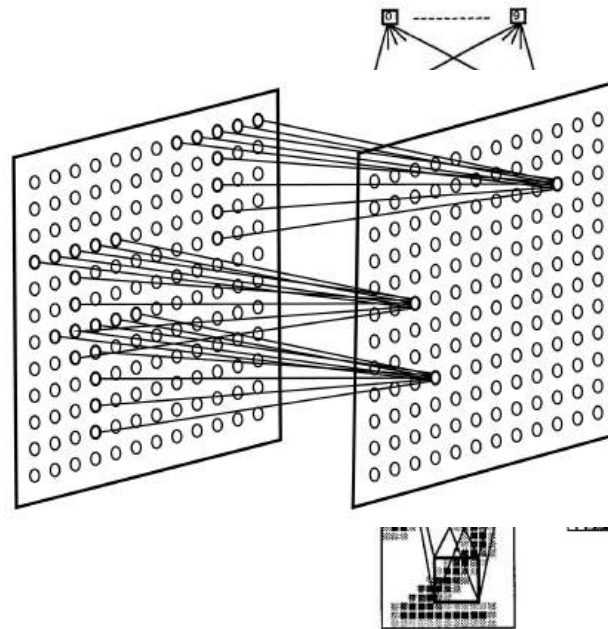
## *Early Geometric Architectures*



**D. Hubel**

**T. Wiesel**

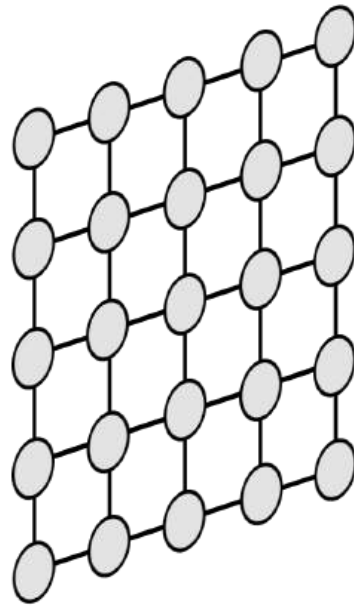
1959



**K. Fukushima**

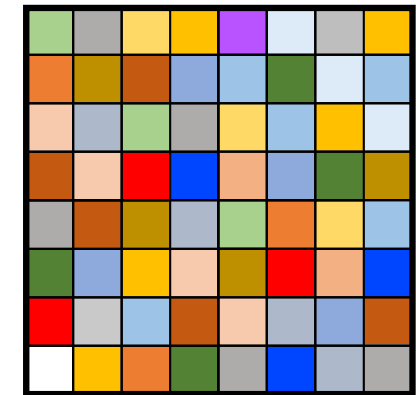
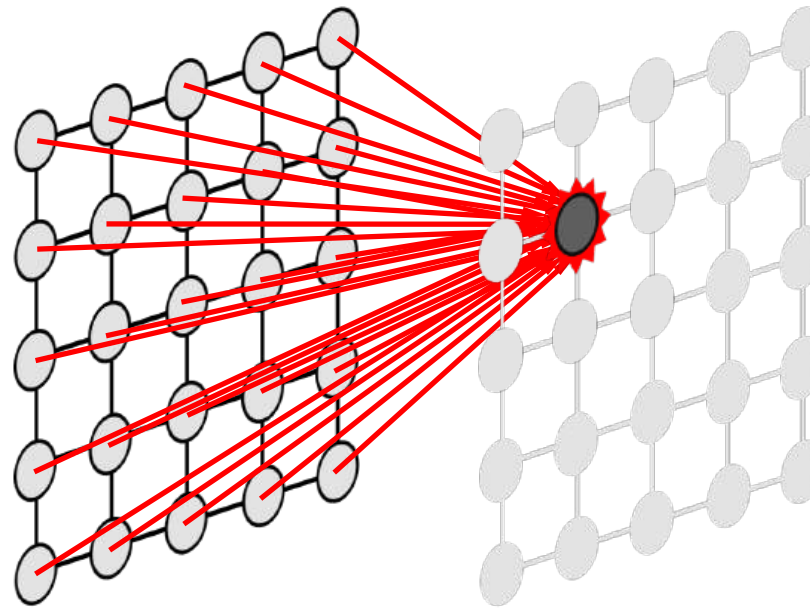
1980

# *Multi-Layer Perceptron*



LeCun et al. 1989

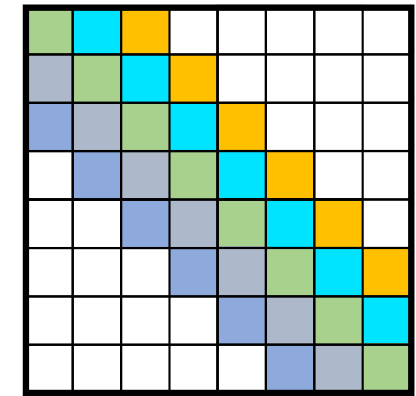
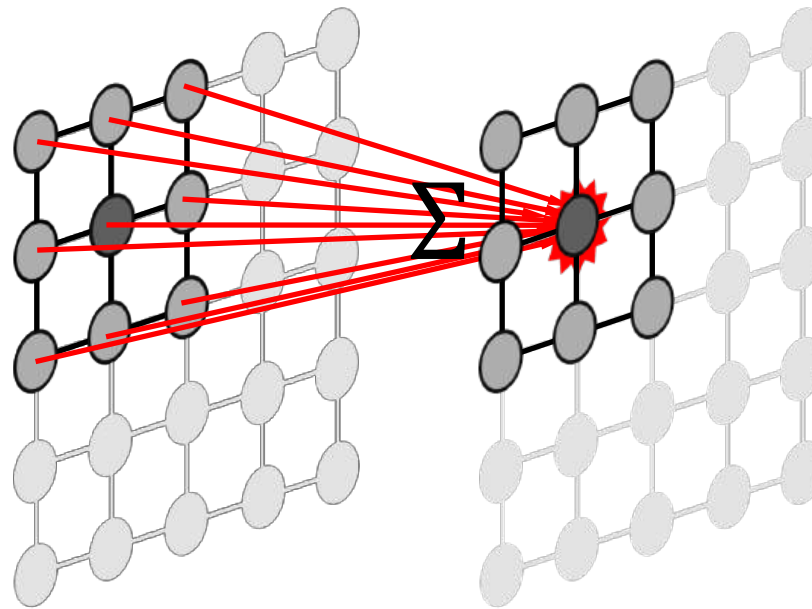
# Multi-Layer Perceptron



**weight matrix**  
 $\mathcal{O}(n^2)$  DOF

*Fully connected layer*

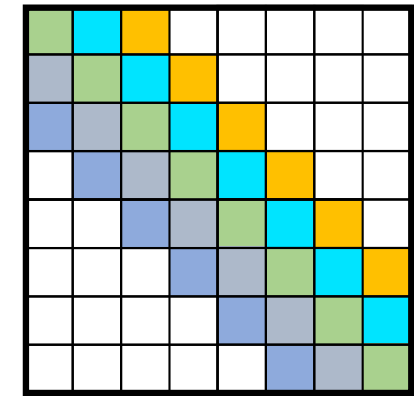
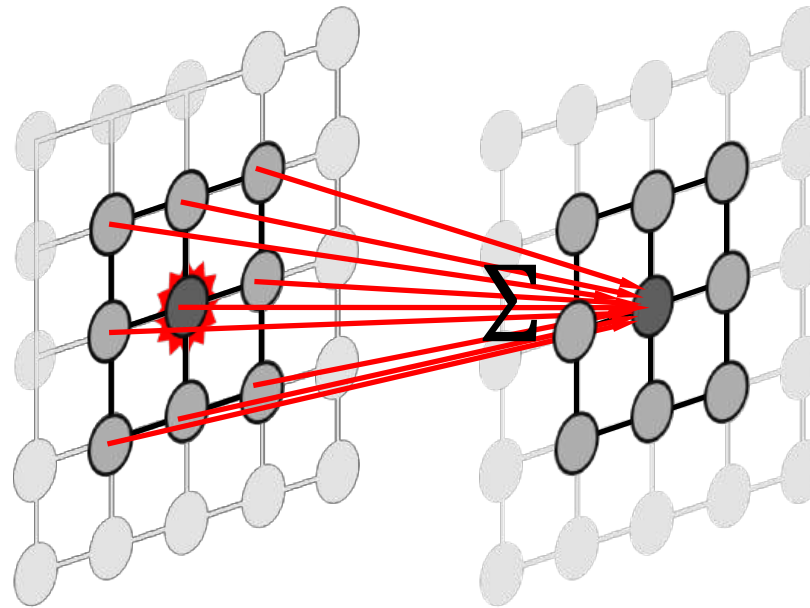
# Convolutional Neural Networks



**weight matrix**  
 $\mathcal{O}(1)$  DOF

*Locality + Shared parameters*

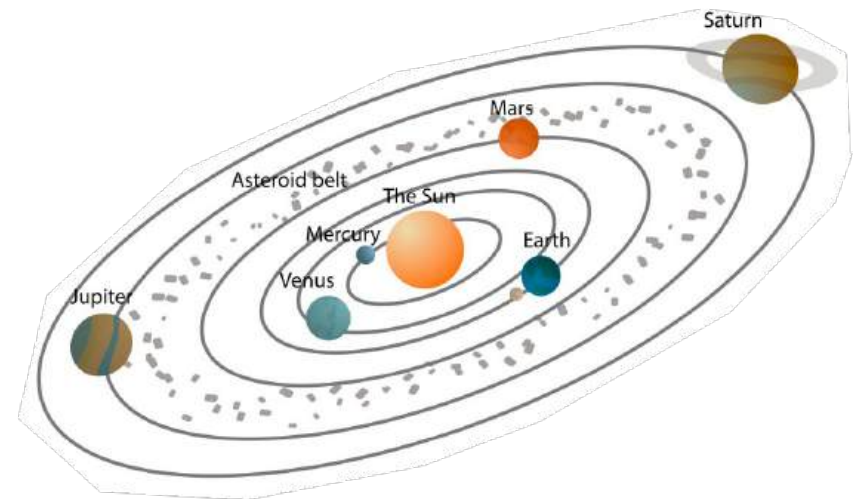
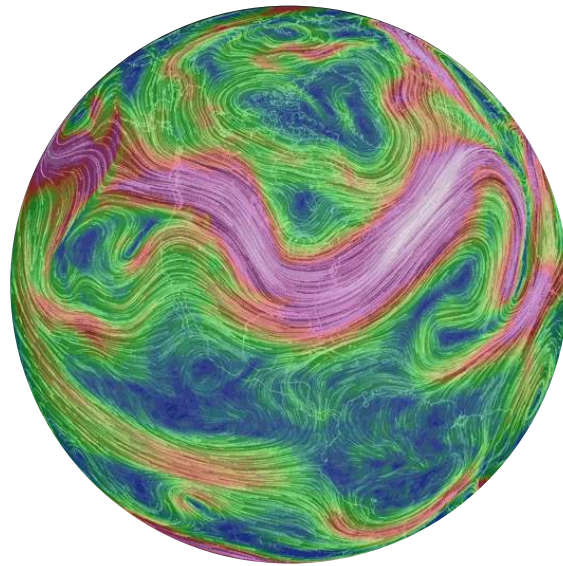
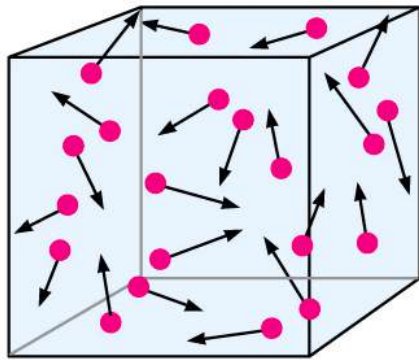
# Convolutional Neural Networks



**weight matrix**  
 $\mathcal{O}(1)$  DOF

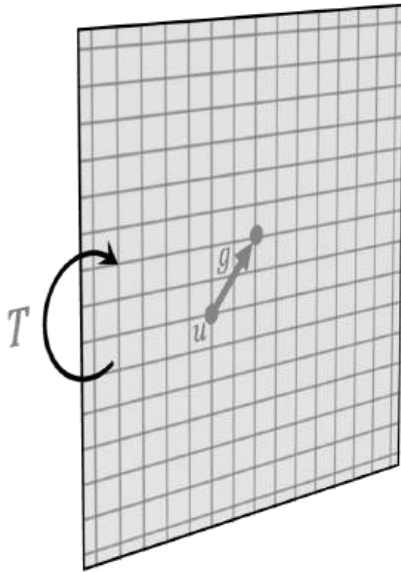
*Locality + Shared parameters*

## *Scale Separation*



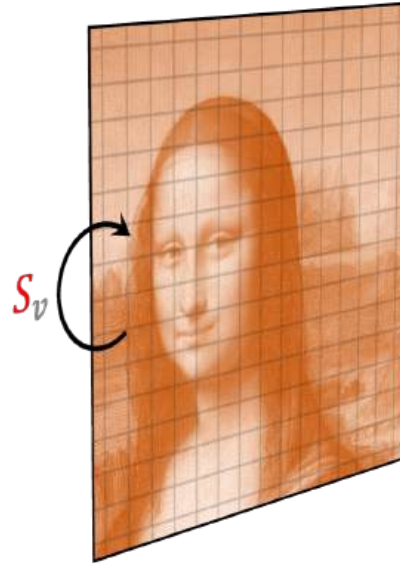
# Convolutional Neural Networks

Plane  $\mathbb{R}^2$



Translation group  $T(2)$

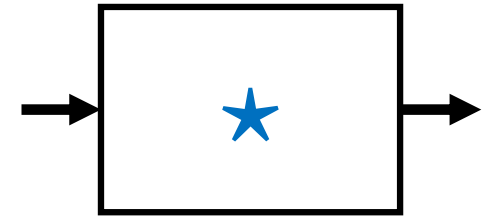
Images  $\mathcal{X}(\mathbb{R}^2)$



Shift operator  $S$

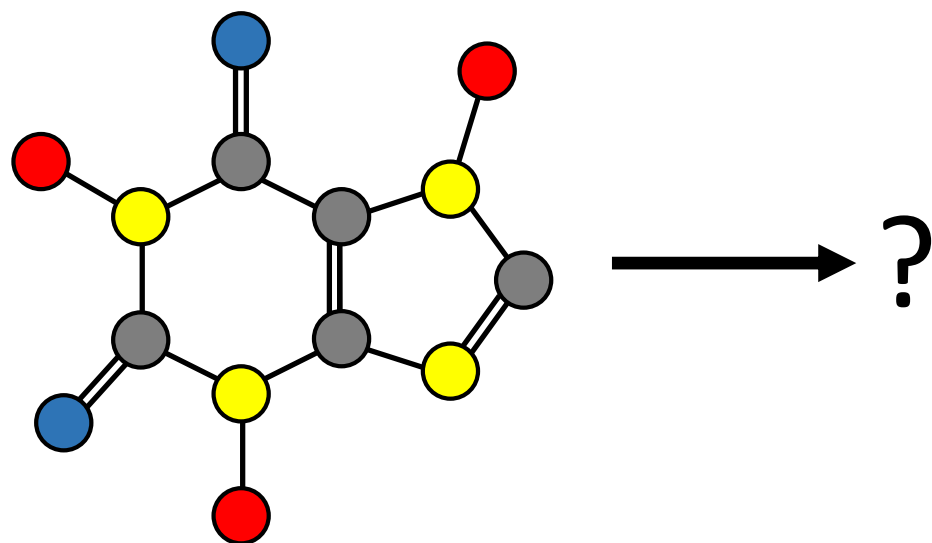
$$S_v x(u) = x(u - v)$$

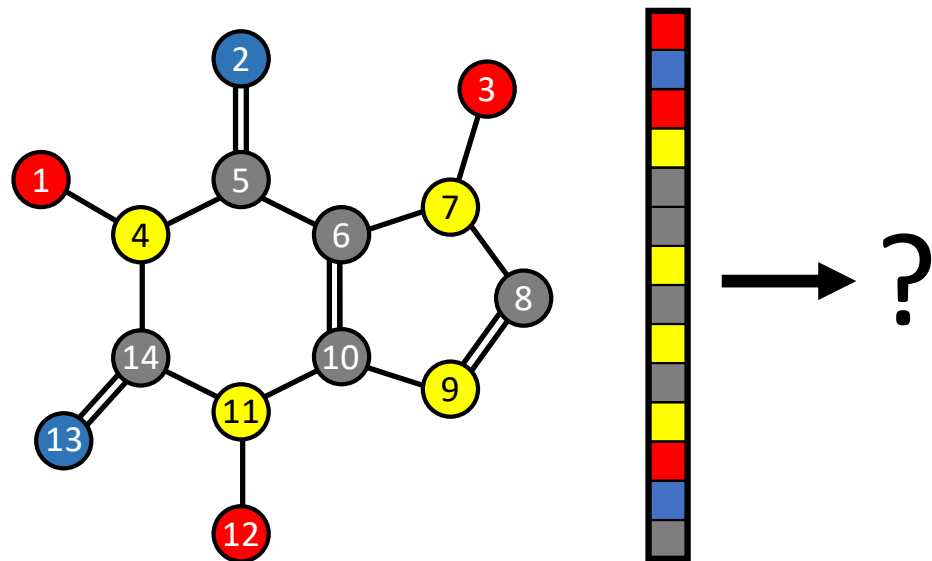
Functions  $\mathcal{F}(\mathcal{X}(\mathbb{R}^2))$

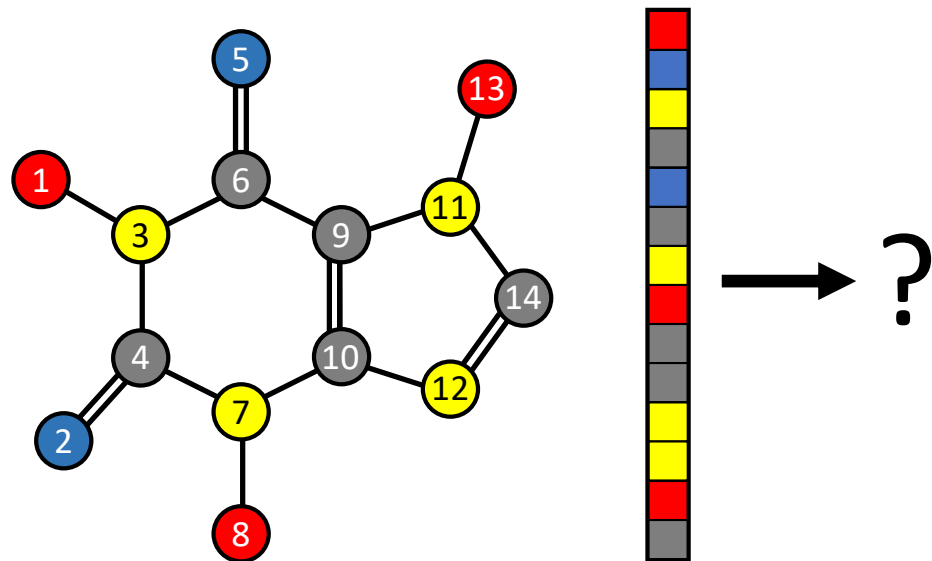


Convolution

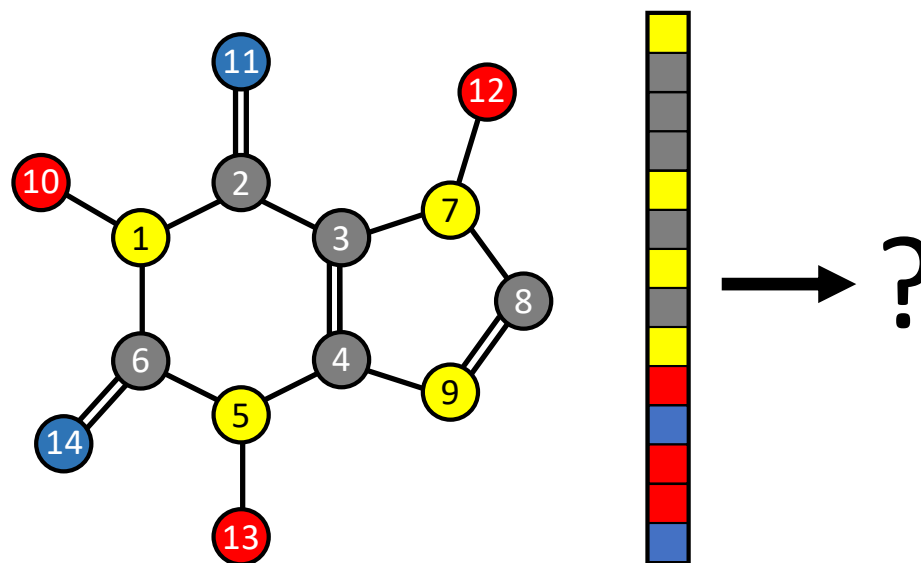
$$(Sx \star y) = S(x \star y)$$





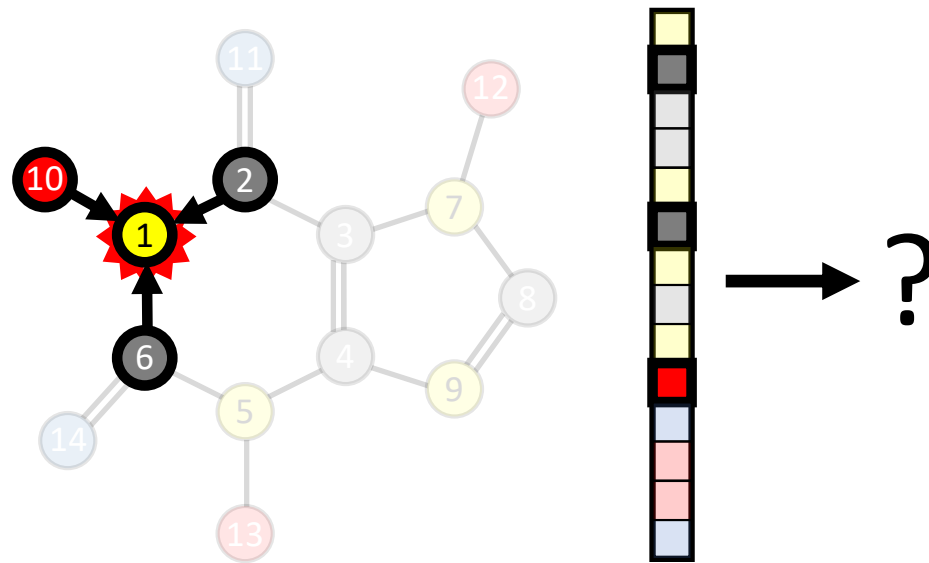


## *Permutation Invariance*



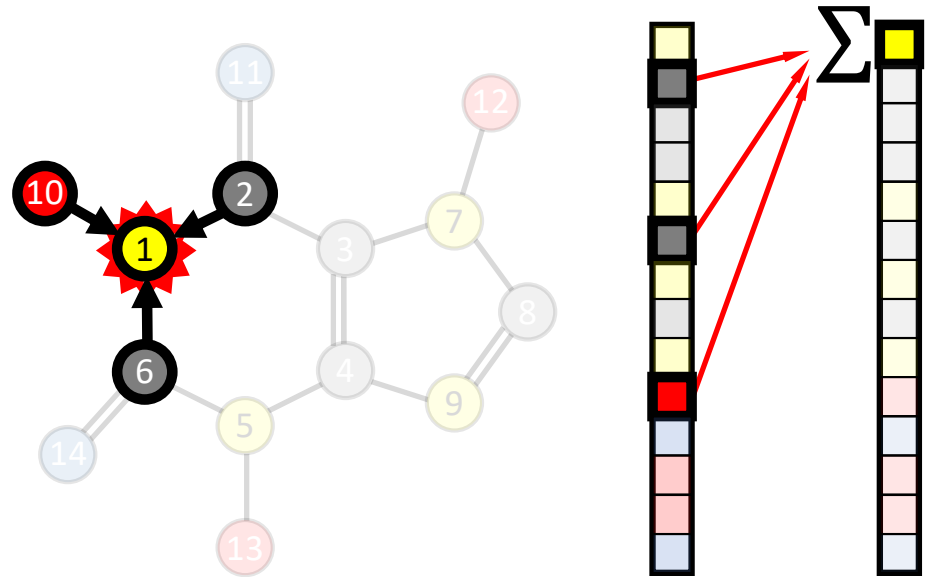
*“properties of a molecule do not change if we reorder the atoms”*

# *Graph Neural Networks*



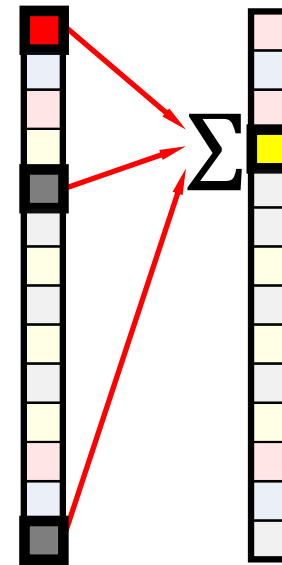
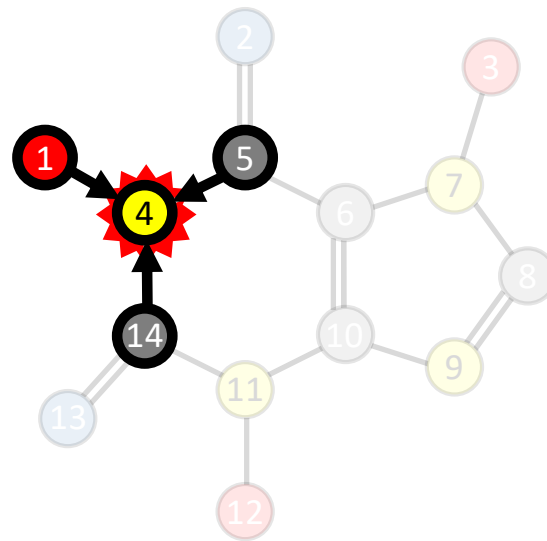
*Locality + Shared parameters*

# *Graph Neural Networks*



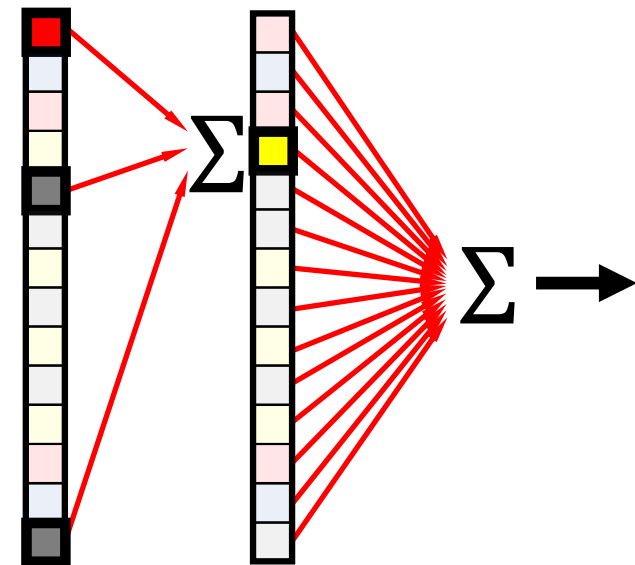
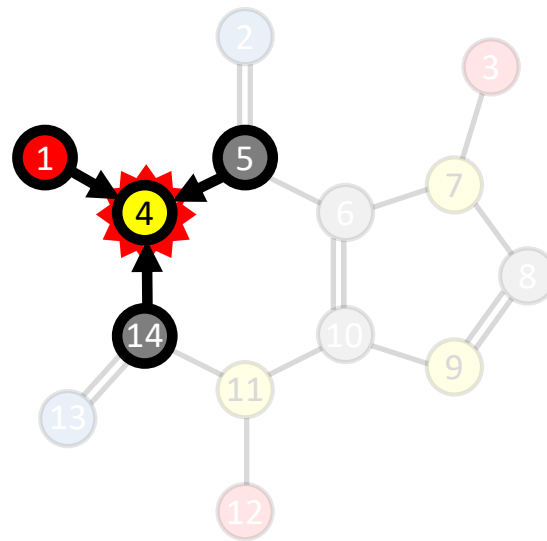
Permutation-  
equivariant layer

# *Graph Neural Networks*



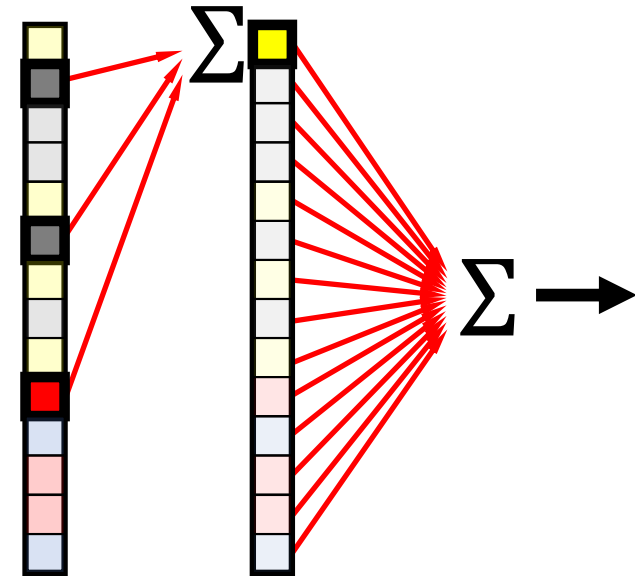
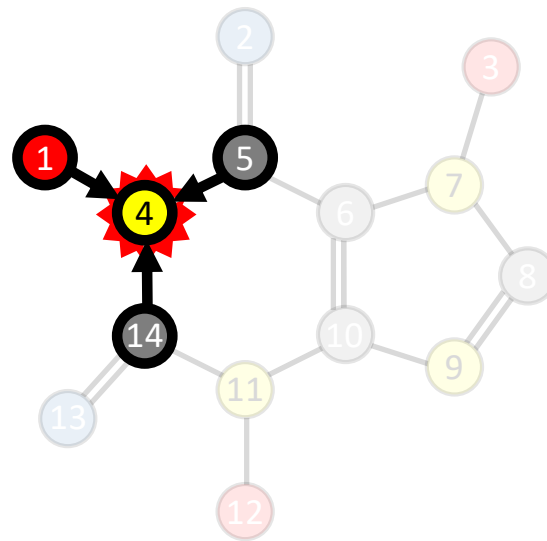
Permutation-  
equivariant layer

# Graph Neural Networks



Permutation-  
invariant readout

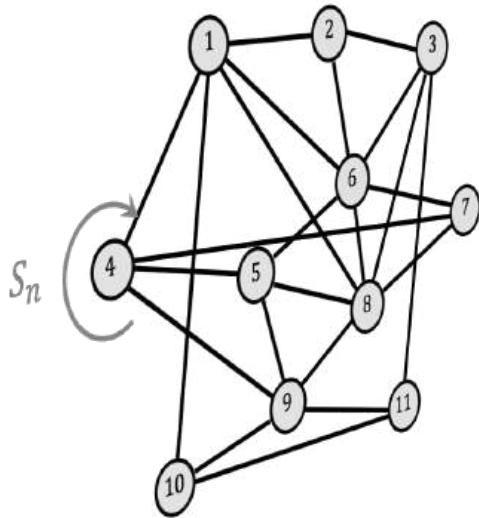
# Graph Neural Networks



Permutation-  
invariant readout

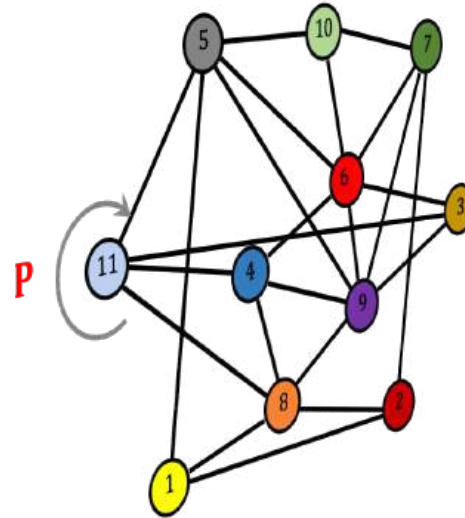
# Graph Neural Networks

Graph  $G = (V, E)$



Permutation group  $S_n$

Node features  $\mathcal{X}(G)$



Permutation matrix  $\mathbf{P}$

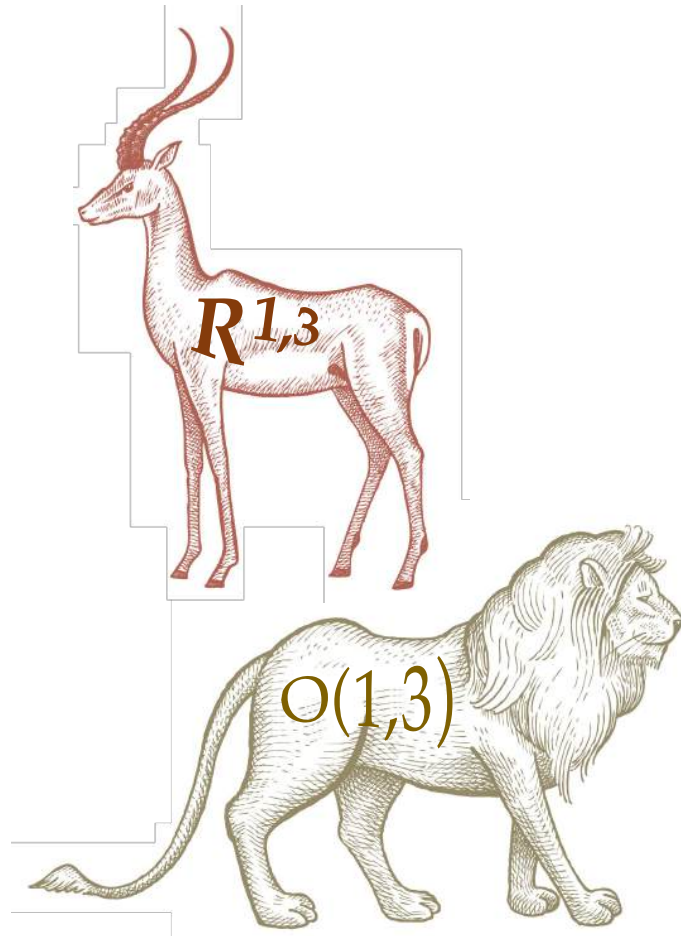
$$\mathbf{PX} = (x_{\pi^{-1}(i),j})$$

Functions  $\mathcal{F}(\mathcal{X}(G))$

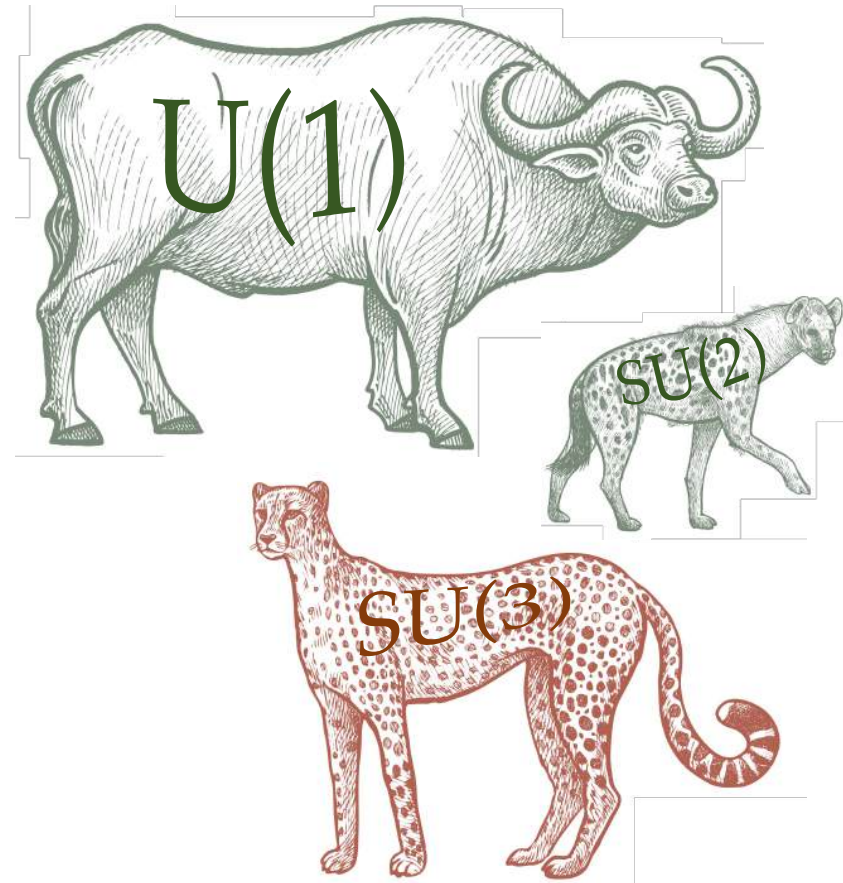


Message passing

$$\mathbf{F}(\mathbf{PX}, \mathbf{PAP}^\top) = \mathbf{PF}(\mathbf{X}, \mathbf{A})$$

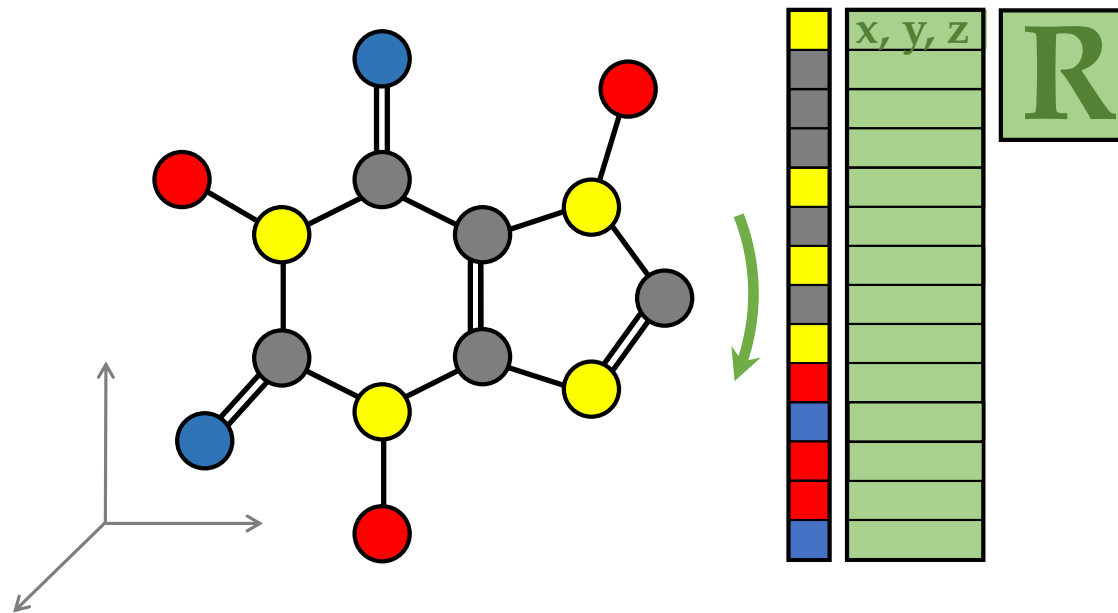


External symmetry



Internal symmetry

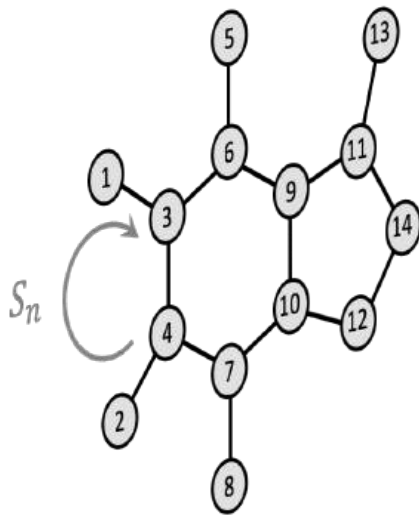
$SO(3)$ -invariance



*“properties of a molecule do not change if we rotate it”*

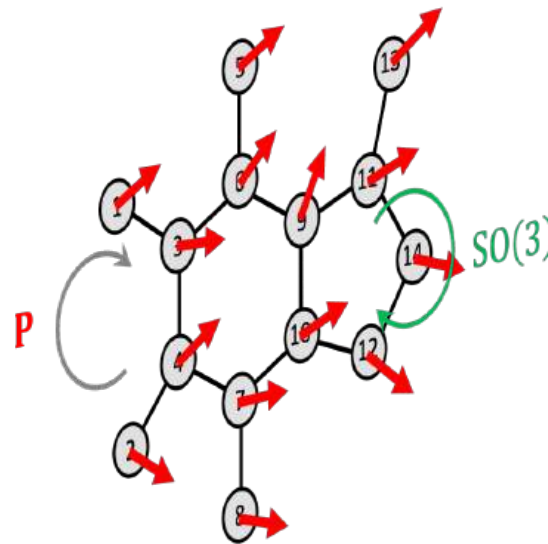
# Geometric (“Equivariant”) Graph Neural Networks

Geometric Graph  $G$



Permutation group  $S_n$   
“domain symmetry”

Node features  $\mathcal{X}(G)$



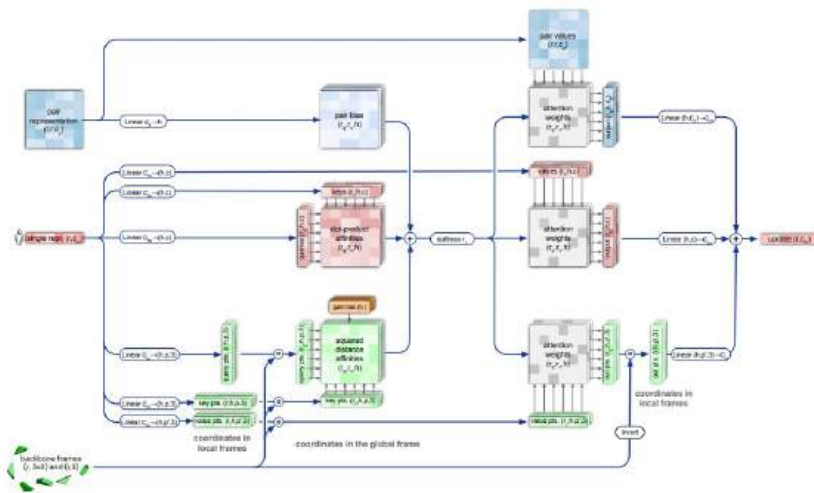
Permutation matrix  $P$   
Rotation  $R$   
“data symmetry”

Functions  $\mathcal{F}(\mathcal{X}(G))$



Geometric message passing  
$$F(PXR, PAP^T) = PF(X, A)R$$

# Revolution in Structural Biology



Jumper et al. 2021

# AlphaFold 2

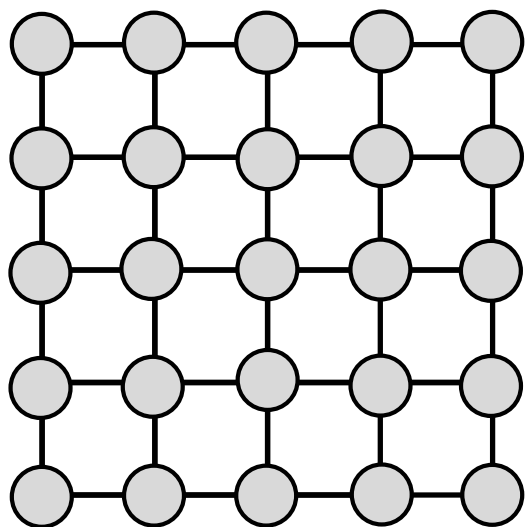
## “Invariant point attention”



Baek et al. 2021

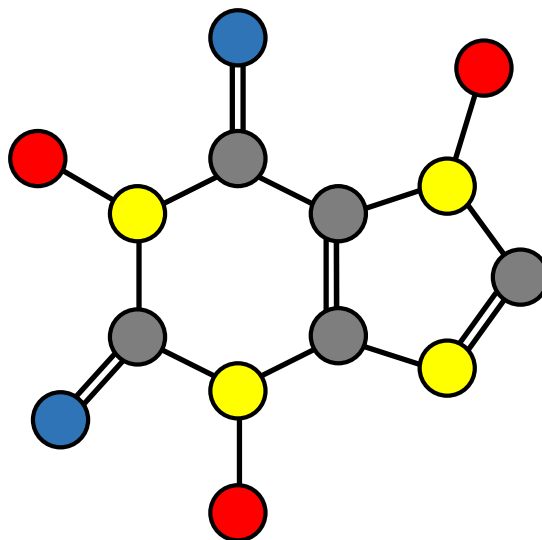
# RosettaFold SE(3)-equivariant Transformer

## Grids



*Translation*

## Graphs



*Permutation*

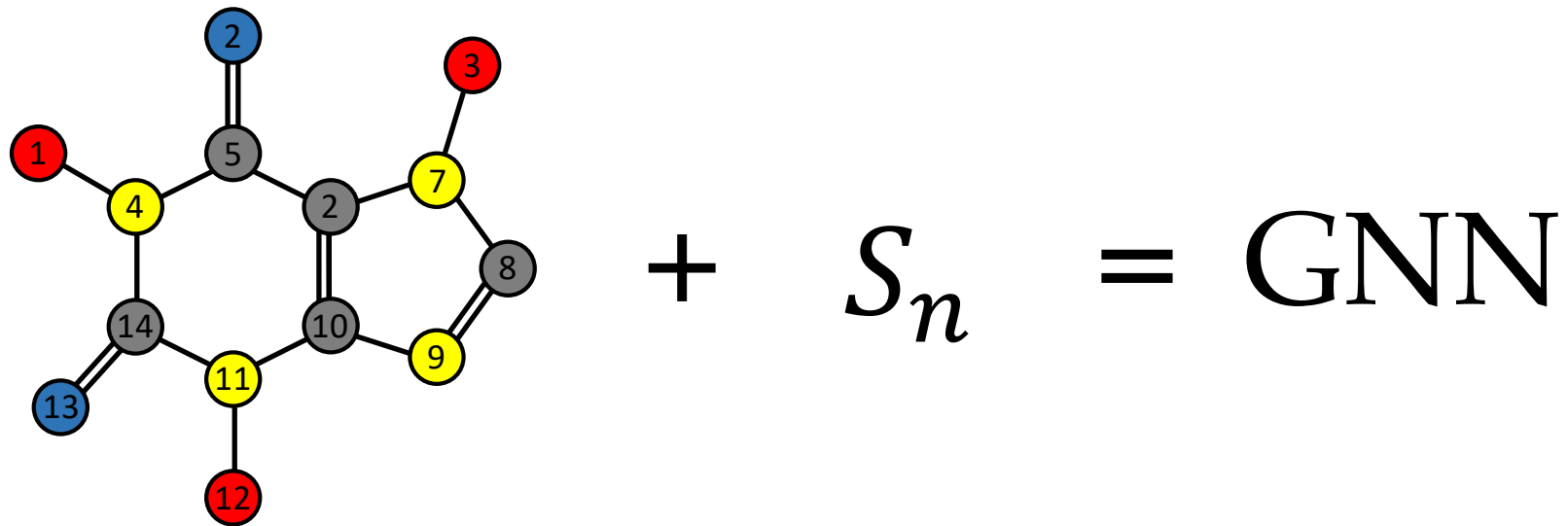
## Meshes



*Local Rotation*

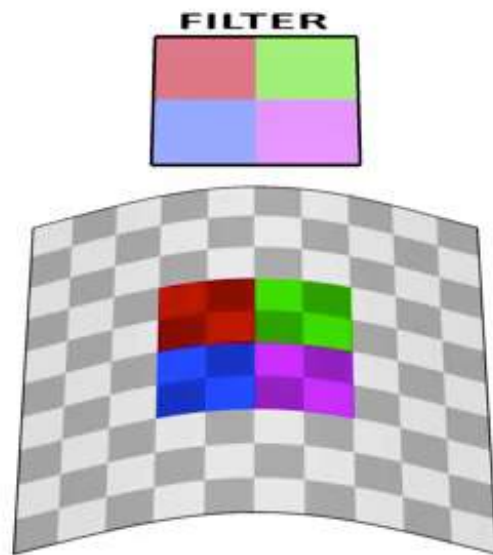


$$+ T(2) = \text{CNN}$$

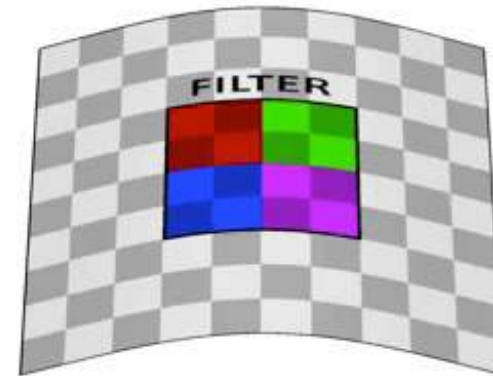




+  $SO(2)$  = MeshCNN



**Euclidean (extrinsic)  
convolution**

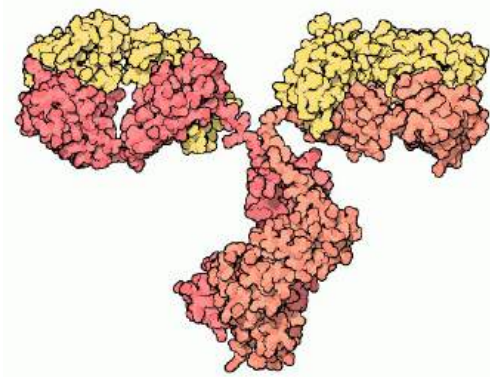


**Geometric (intrinsic)  
convolution**

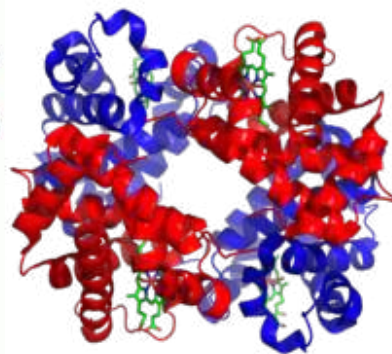


## Snap Acquires Ariel AI To Enhance AR Features

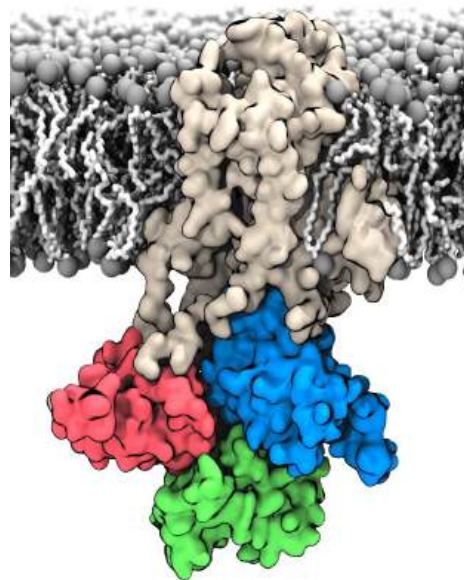




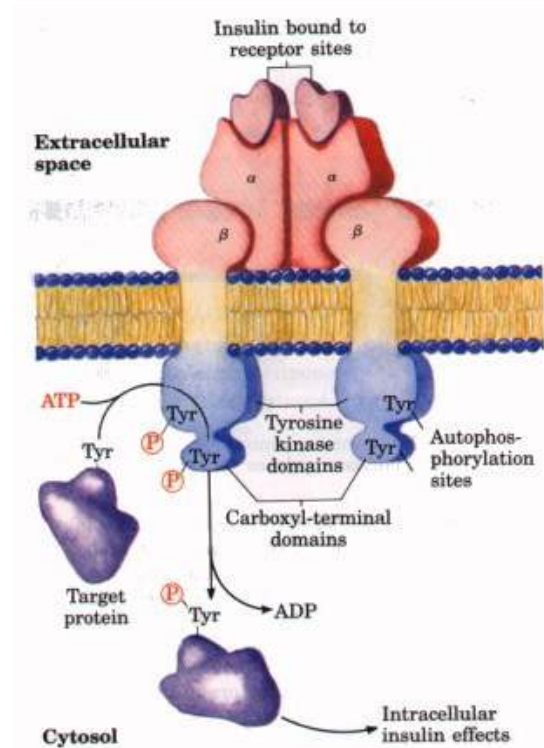
Defense (antibody)



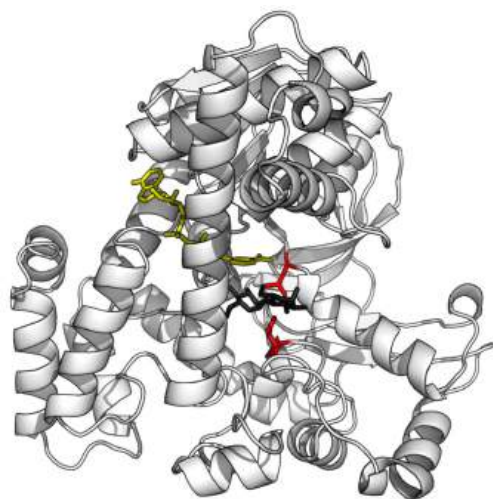
Storage (haemoglobin)



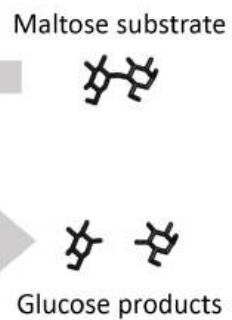
Transport (calcium pump)



Communication (insulin)



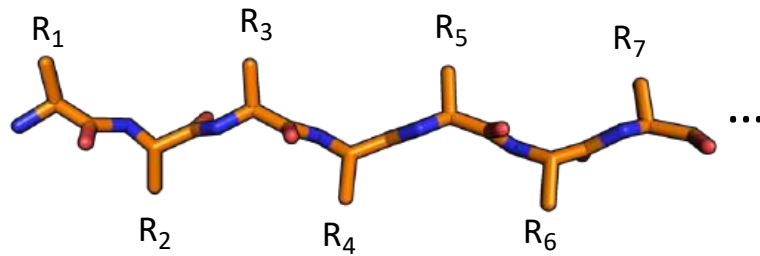
Catalysis (enzyme)



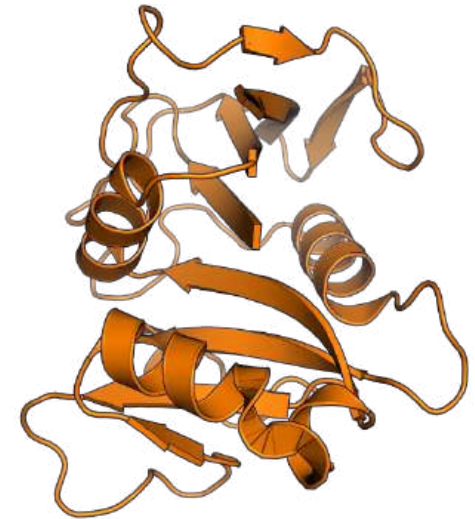
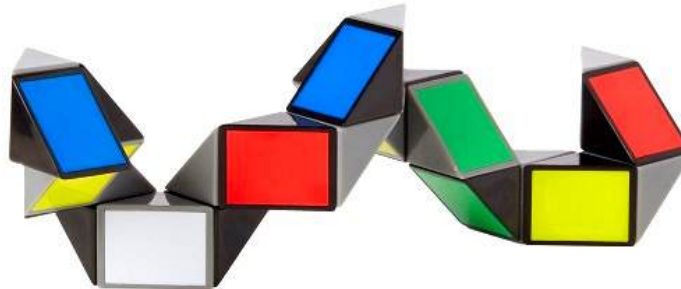
Structure (collagen)

# *Protein Folding*

Protein folding

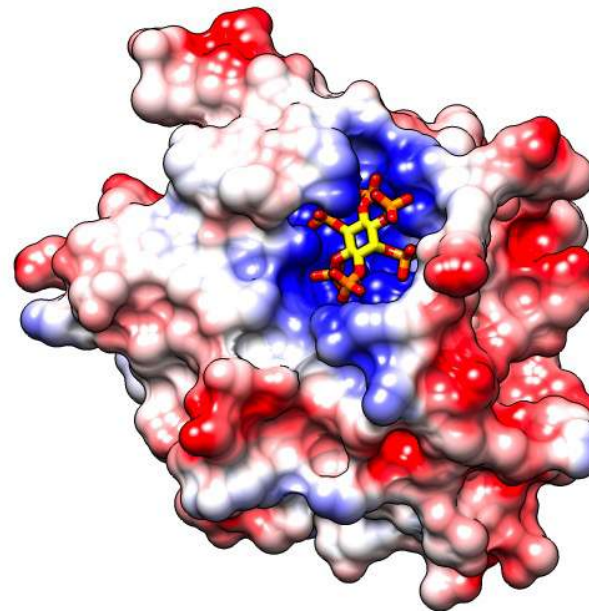
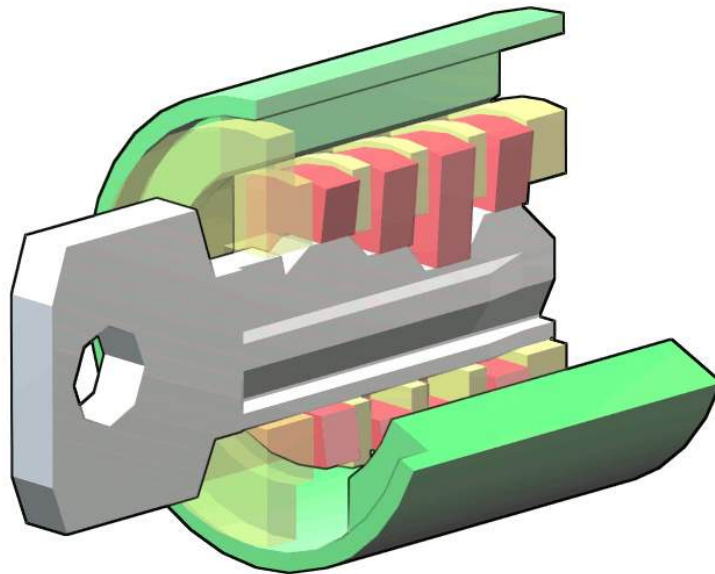


Sequence of  
amino acids



3D structure

# Lock-Key Metaphor



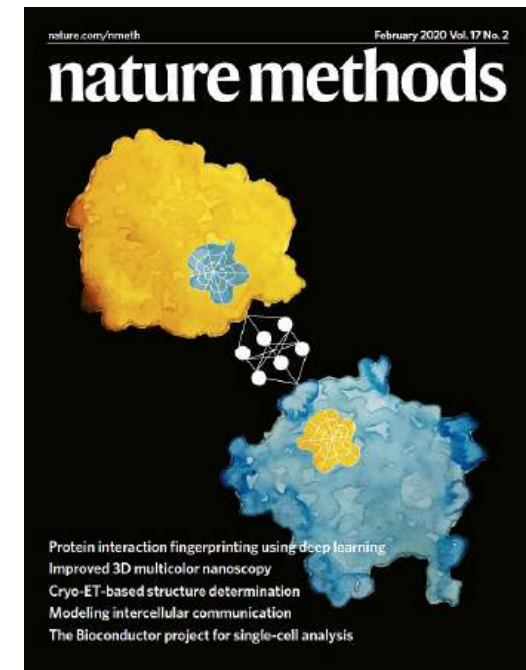
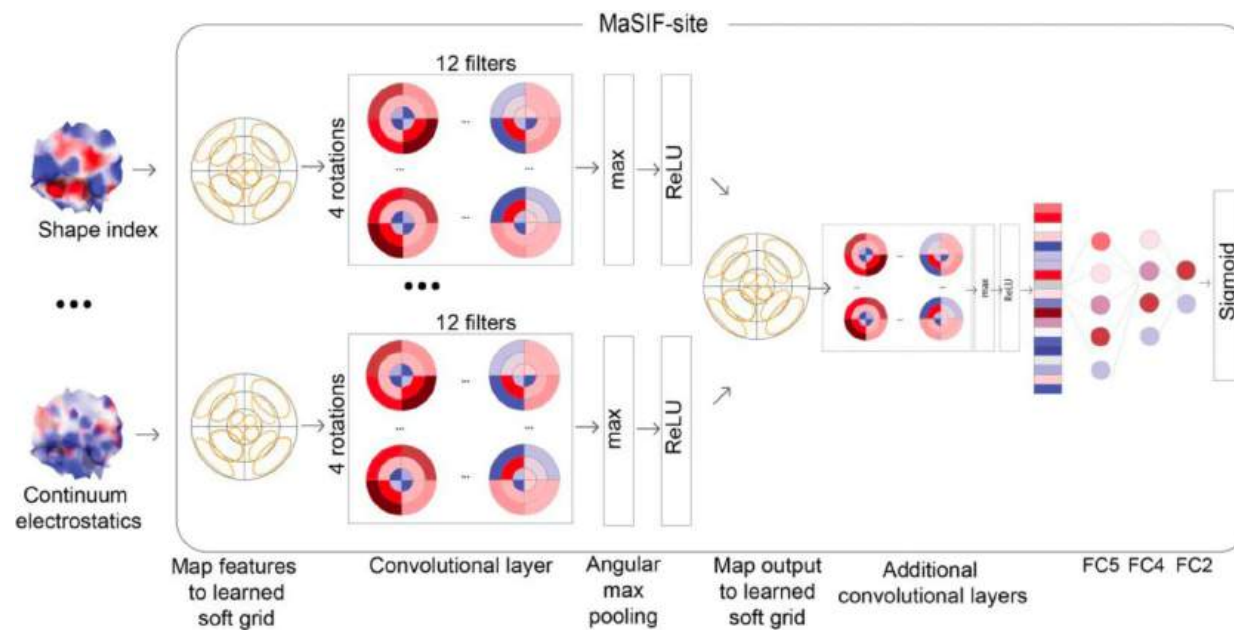
Emil Fischer "Schlüssel-Schloss-Prinzip" 1894

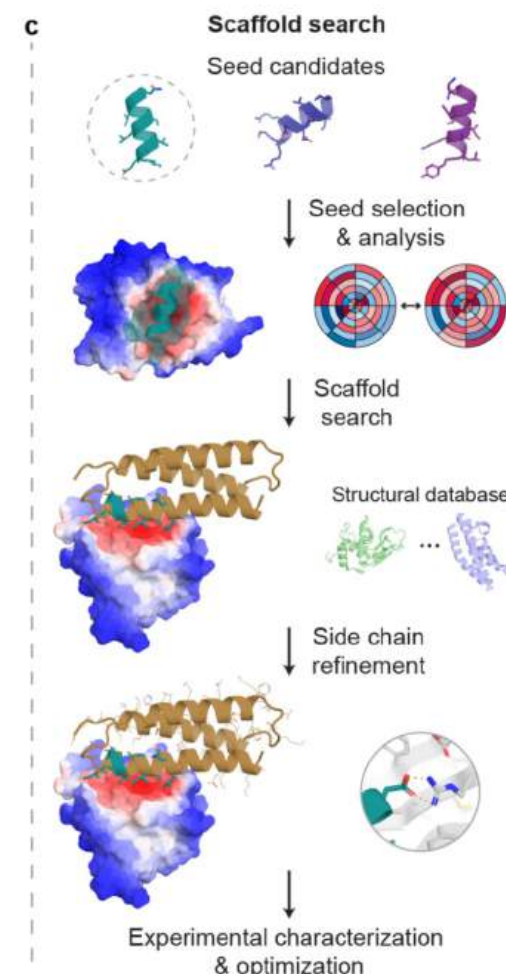
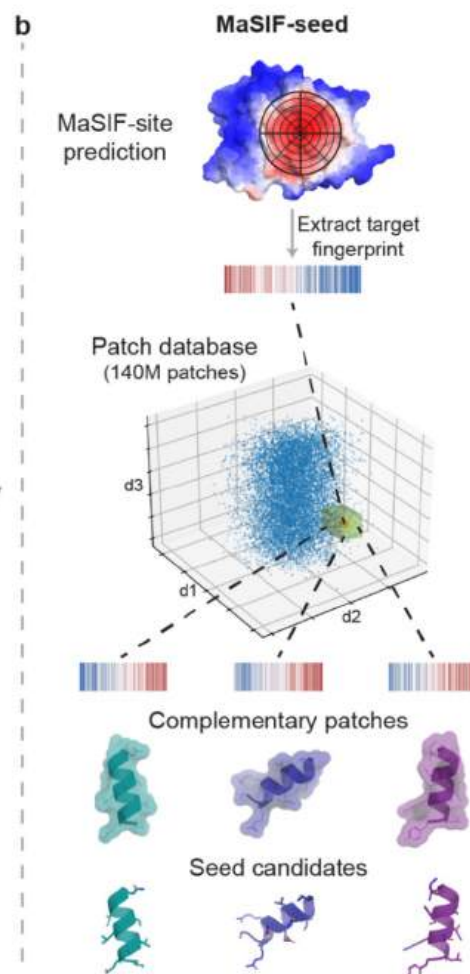
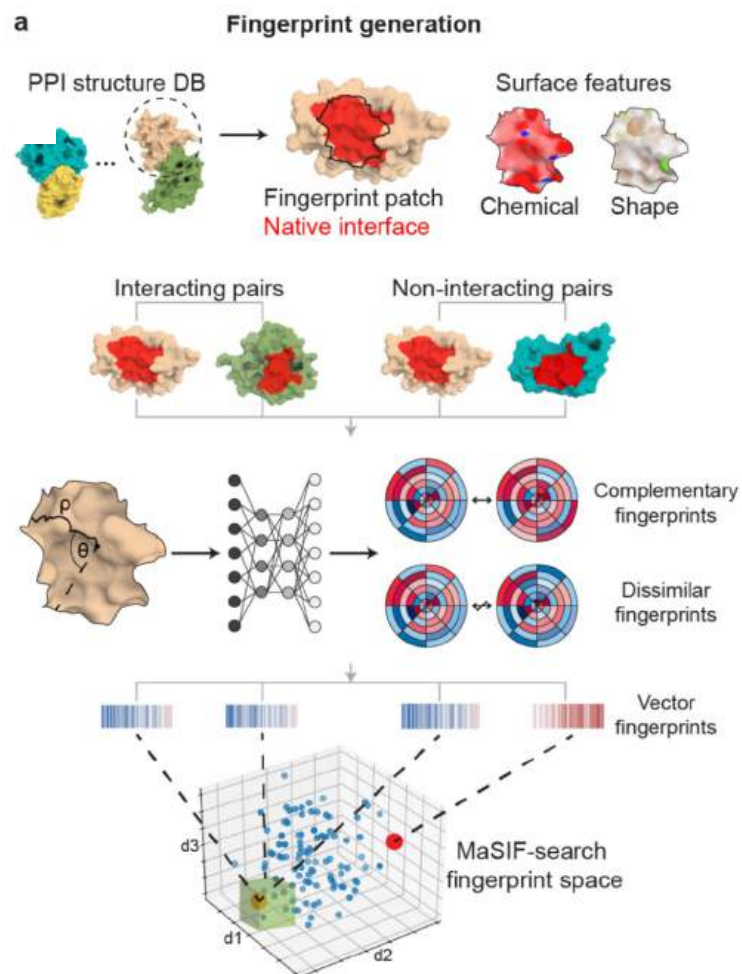
## *Surface-based Protein Representation*

**Abstract out internal structure** that is irrelevant for interactions + allow some **conformation changes**

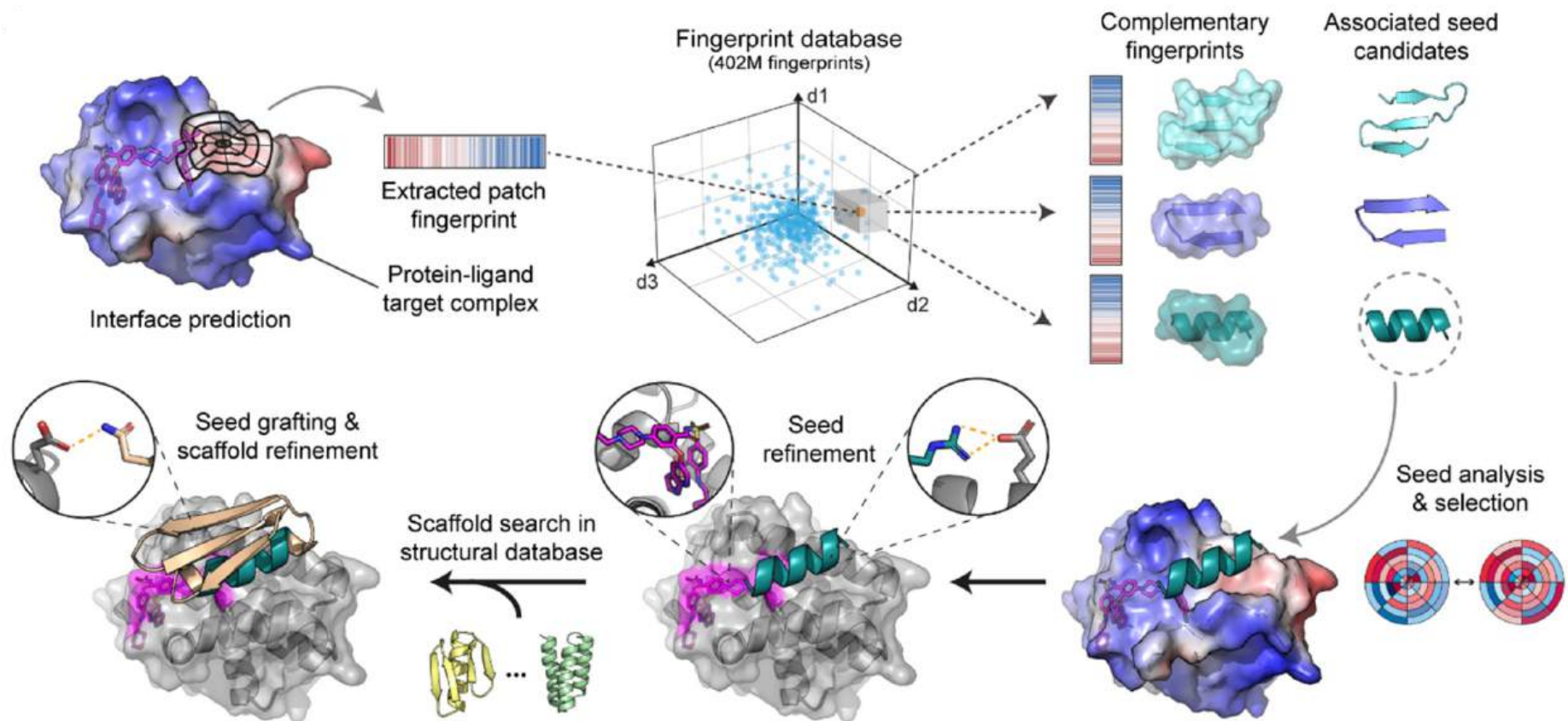


# *MaSIF: Geometric ML for Protein Function Prediction & Design*





# Switchable interactions



## Article

# De novo design of protein interactions via learned surface fingerprints

<https://doi.org/10.1038/s41586-023-05993-4>

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Physical interactions between proteins are essential for most biological governing life<sup>1</sup>. However, the molecular determinants of such interactions are challenging to understand, even as genomic, proteomic and structural data expand. This knowledge gap has been a major obstacle for the comprehensive design of cellular protein–protein interaction networks and for the design of protein binders that are crucial for synthetic biology and translational applications. Here we use a geometric deep-learning framework operating on protein surfaces to generate fingerprints to describe geometric and chemical features that drive protein–protein interactions<sup>2,3</sup>. We hypothesized that these fingerprints capture the key aspects of molecular recognition that represent a new paradigm for computational design of novel protein interactions. As a proof of principle, we computationally designed several de novo protein binders to engage targets: SARS-CoV-2 spike, PD-1, PD-L1 and CTLA-4. Several designs were experimentally optimized, whereas others were generated purely in silico, achieving nanomolar affinity with structural and mutational characterization and accurate predictions. Overall, our surface-centric approach captures chemical determinants of molecular recognition, enabling an approach to design de novo protein interactions and, more broadly, of artificial proteins.

Designing novel protein–protein interactions (PPIs) remains a fundamental challenge in computational protein design, with broad basic and translational applications in biology. The challenge consists of generating amino acid sequences that engage a target site and form a quaternary complex with a given protein. This represents a stringent test of our understanding of the physicochemical determinants that drive biomolecular interactions<sup>4</sup>. Robust computational methods to design de novo PPIs could be used to rapidly engineer protein-based therapeutics such as antibodies and protein inhibitors or vaccines among others, and are therefore of considerable interest for biomedical and translational applications<sup>5–8</sup>.

Despite recent advances in rational PPI design<sup>9–12</sup> and prediction<sup>13</sup>, designing novel protein binders against specific targets is very challenging, particularly when no structural elements from pre-existing

binders are known. Current state-of-the-art methods<sup>14,15</sup>, such as hotspot-centric approaches<sup>16</sup> or machine learning<sup>17,18</sup>, rely on placing disembodied residues at the interface and then optimizing their presentation. Intrinsic limitations of these approaches relate to the lack of energetic signatures provided by scoring functions and placements, which is compounded in flat interface pockets. These methods also face the challenge of protein scaffolds to precisely display the generated residues. To circumvent these limitations, new approaches to design de novo binders to various surface types are needed. A long-standing model of molecular recognition<sup>19</sup> posits that PPIs form between protein molecular surfaces with complementary shapes<sup>20,21</sup>. The complementarity



## Designing protein–ligand neosurfaces with a scalable deep learning tool

Anthony Marchand<sup>1,2</sup>, Stephen Buckley<sup>1,2</sup>, Anne Schmeising<sup>1,2</sup>, Martin Poeschl<sup>1,2</sup>, Madalena Elia<sup>1</sup>, Pablo Gaiña<sup>1,2</sup>, Evgenia Elizarova<sup>1</sup>, Rebecca M. Neusser<sup>1,2</sup>, Pao-Wan Lee<sup>1</sup>, Luc Raymond<sup>1</sup>, Yangyang Miao<sup>1</sup>, Leo Schaller<sup>1</sup>, Sandrine Georgeon<sup>1</sup>, Joseph Schmidt<sup>1</sup>, Philippe Schwaller<sup>1</sup>, Sebastian J. Maurk<sup>1</sup>, Michael Bronstein<sup>2,3</sup> & Bruno E. Correia<sup>1,2,3,4</sup>

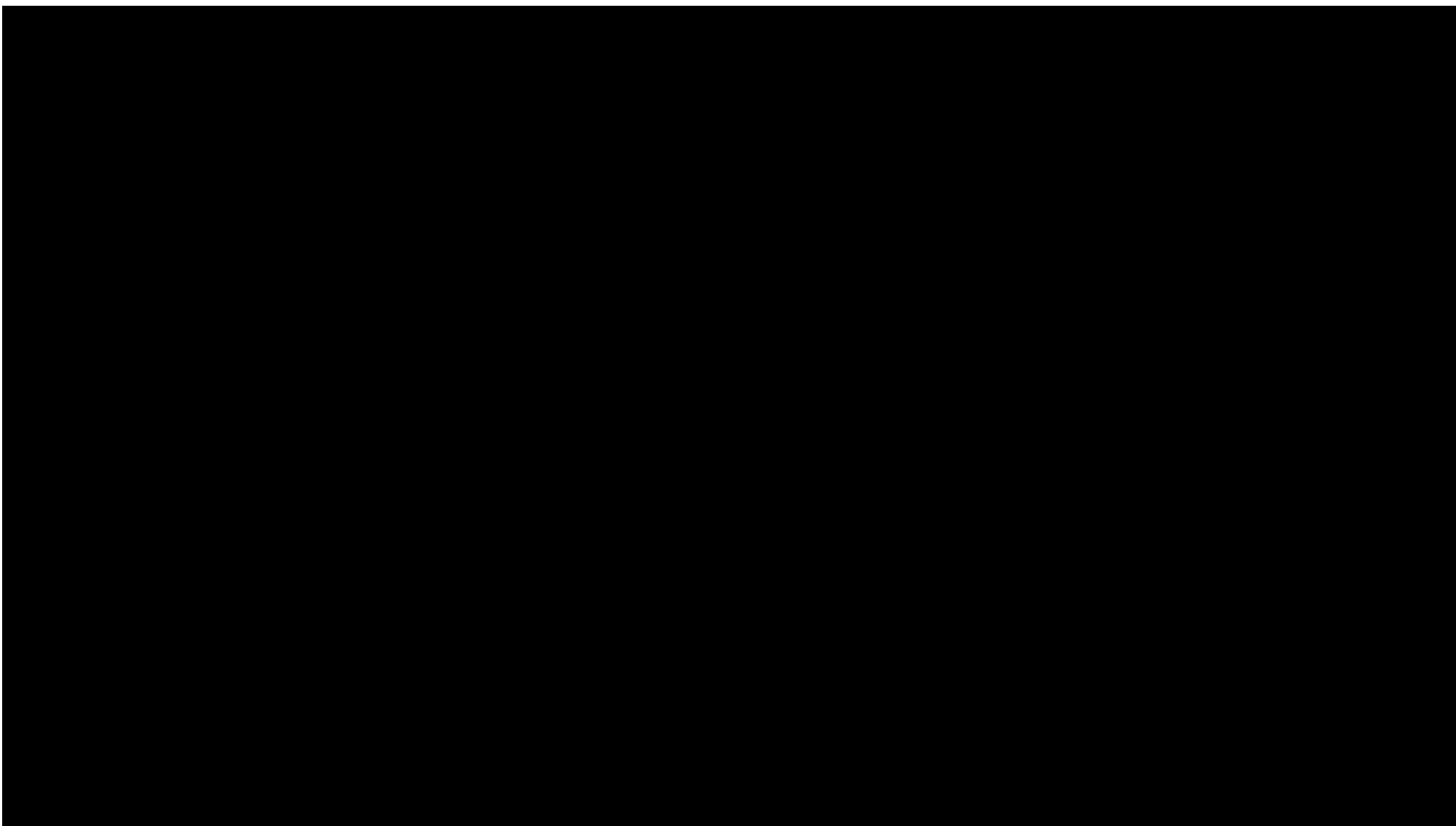
Molecular recognition events between proteins drive biological processes in living systems<sup>1</sup>. However, higher levels of mechanistic regulation have emerged, in which protein–protein interactions are conditioned to small molecules<sup>2–4</sup>. Despite recent advances, computational tools for the design of new chemically induced protein interactions have remained a challenging task for the field<sup>5</sup>. Here we present a computational strategy for the design of proteins that target neosurfaces, that is, surfaces arising from protein–ligand complexes. To develop this strategy, we leveraged a geometric deep learning approach based on learned molecular surface representations<sup>6,7</sup> and experimentally validated binders against three drug-bound protein complexes: Bcl-2–venetoclax, DB3–progesterone and PD-1–actinonin. All binders demonstrated high affinities and accurate specificities, as assessed by mutational and structural characterization. Remarkably, surface fingerprints previously trained only on proteins could be applied to neosurfaces induced by interactions with small molecules, providing a powerful demonstration of generalizability that is uncommon in other deep learning approaches. We anticipate that such designed chemically induced protein interactions will have the potential to expand the sensing repertoire and the assembly of new synthetic pathways in engineered cells for innovative drug-controlled cell-based therapies<sup>8</sup>.

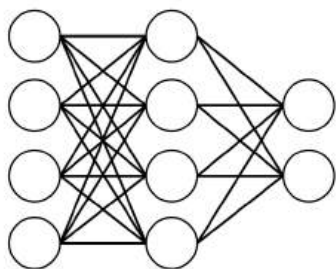
PPIs have essential roles in healthy cell function and in numerous diseases<sup>1,2</sup>. For this reason, PPIs have been developed over the years as tools for the design of new drugs<sup>3</sup> and for the design of new proteins<sup>4</sup>. The governing principles of proteins to form interactions with small molecules are complex, involving several contributions, such as electrostatics, dynamics and solvent interactions, which make it challenging to predict and design new proteins that interact with small molecules. Native PPIs are often highly specific, and their design is a complex task. Compound-bound neosurfaces, among the most fascinating recognition instances, are relatively easy to design and have a large impact on drug discovery. To circumvent these limitations, new approaches to design de novo binders to various surface types are needed. A long-standing model of molecular recognition<sup>19</sup> posits that PPIs form between protein molecular surfaces with complementary shapes<sup>20,21</sup>. The complementarity

In synthetic biology, molecular components that rely on small molecule-induced neosurfaces have been used to engineer chemically responsive systems with precise spatiotemporal control of cellular activities<sup>5</sup>. Small-molecule triggers have been used to both induce and disrupt PPIs, thereby functioning as ON or OFF switches for engineered cellular functions<sup>6–8</sup>. There are several practical advantages to using small molecules as triggers, including their simple administration, biocompatibility, safety, and high affinity and specificity to their target proteins. Protein-based switches controlled by small molecules have already been used to regulate transcription<sup>9</sup>, protein degradation<sup>10</sup> and protein localization<sup>11,12</sup>, among many other applications. In addition to their use in basic research, engineering molecular switches are increasingly used to control protein-based cellular therapeutics, the activity of which may need to be regulated to mitigate potentially dangerous side effects<sup>13,14</sup>. Although several chemically inducible heterodimer (OFF-switch) systems have been proposed<sup>15,16</sup>, computationally designed chemically induced dimerization (CID, ON-switch) systems remain challenging owing to the complexity of modelling neosurfaces. Previous attempts to design CID systems primarily relied on experimental methods<sup>17,18</sup> and, in some cases, on computational approaches<sup>19–21</sup>.

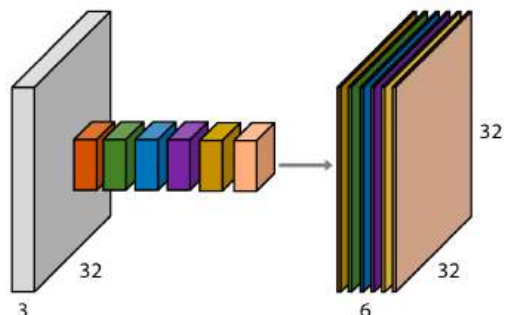
<sup>1</sup>Laboratory of Protein Design and Protein Engineering, Institute of Bioengineering, École Polytechnique Fédérale de Lausanne, Lausanne, Switzerland. <sup>2</sup>Thema Institute, Lausanne, Switzerland. <sup>3</sup>Laboratory of Biological Electron Microscopy, Institute of Physics, School of Basic Sciences, École Polytechnique Fédérale de Lausanne, Lausanne, Switzerland. <sup>4</sup>Department of Fundamental Microbiology, Faculty of Biology and Medicine, University of Lausanne, Lausanne, Switzerland. <sup>5</sup>IDS Key Laboratory of Protein Microscopy, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China. <sup>6</sup>Laboratory of Imaging and Genomics, School of Life Sciences, École Polytechnique Fédérale de Lausanne, Lausanne, Switzerland. <sup>7</sup>Laboratory of Biophysical Chemistry of Macromolecules, School of Basic Sciences, Institute of Chemical Sciences and Engineering (ICS), École Polytechnique Fédérale de Lausanne, Lausanne, Switzerland. <sup>8</sup>Thema Institute for Experimental Cancer Research, School of Life Sciences, École Polytechnique Fédérale de Lausanne, Lausanne, Switzerland. <sup>9</sup>Department of Computer Science, University of Oxford, Oxford, UK. <sup>10</sup>Present address: Merck Research, Basel, Switzerland. <sup>11</sup>Present address: Center for Biochemical Engineering, University of California, Berkeley, CA, USA. <sup>12</sup>Present address: Center for Biochemical Engineering, University of California, Berkeley, CA, USA. <sup>13</sup>Present address: Center for Biochemical Engineering, University of California, Berkeley, CA, USA. <sup>14</sup>Present address: Center for Biochemical Engineering, University of California, Berkeley, CA, USA. <sup>15</sup>Present address: Center for Biochemical Engineering, University of California, Berkeley, CA, USA. <sup>16</sup>Present address: Center for Biochemical Engineering, University of California, Berkeley, CA, USA. <sup>17</sup>Present address: Center for Biochemical Engineering, University of California, Berkeley, CA, USA. <sup>18</sup>Present address: Center for Biochemical Engineering, University of California, Berkeley, CA, USA. <sup>19</sup>Present address: Center for Biochemical Engineering, University of California, Berkeley, CA, USA. <sup>20</sup>Present address: Center for Biochemical Engineering, University of California, Berkeley, CA, USA. <sup>21</sup>Present address: Center for Biochemical Engineering, University of California, Berkeley, CA, USA.

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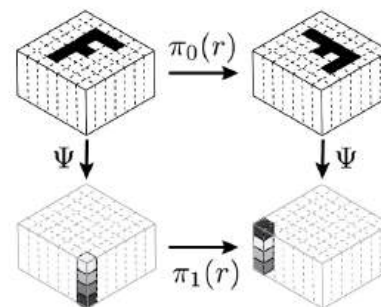




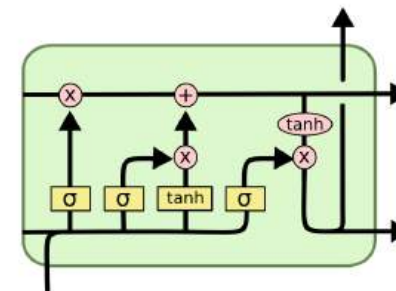
**Perceptrons**  
Function regularity



**CNNs**  
Translation



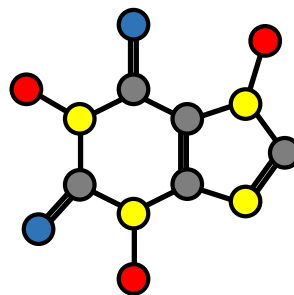
**Group-CNNs**  
Translation+Rotation,  
Global groups



**LSTMs**  
Time warping



**DeepSets / Transformers**  
Permutation



**GNNs**  
Permutation



**Intrinsic CNNs**  
Isometry / Gauge choice



Michael M. Bronstein, Joan Bruna, Yann LeCun,  
Arthur Szlam, and Pierre Vandergheynst

**M**any scientific fields study data with an underlying structure that is non-Euclidean. Some examples include social networks in computational social sciences, sensor networks in communications, functional networks in brain imaging, regulatory networks in genetics, and meshed surfaces in computer graphics. In many applications, such geometric data are large and complex (in the case of social networks, on the scale of billions) and are natural targets for machine-learning techniques. In particular, we would like to use deep neural networks, which have recently proven to be powerful tools for a broad range of problems from computer vision, natural-language processing, and audio analysis. However, these tools have been most successful on data with an underlying Euclidean or grid-like structure and in cases where the invariances of these structures are built into networks used to model them.

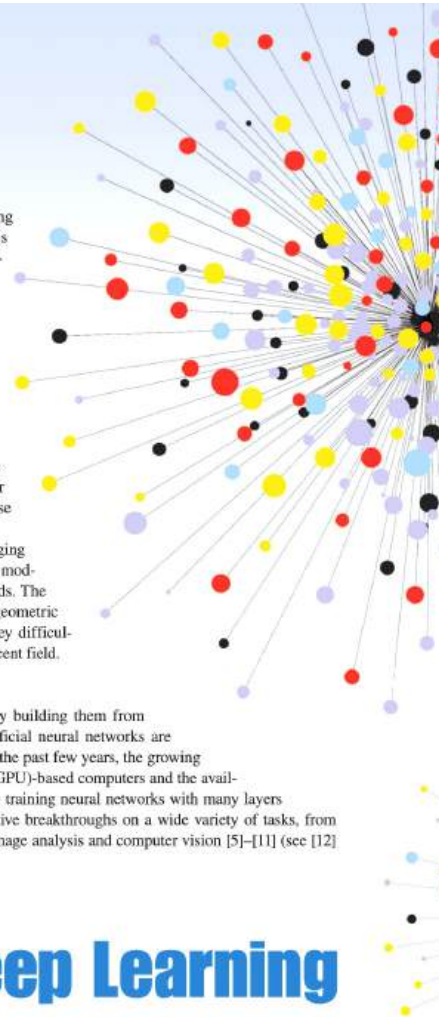
*Geometric deep learning* is an umbrella term for emerging techniques attempting to generalize (structured) deep neural models to non-Euclidean domains, such as graphs and manifolds. The purpose of this article is to overview different examples of geometric deep-learning problems and present available solutions, key difficulties, applications, and future research directions in this nascent field.

#### Overview of deep learning

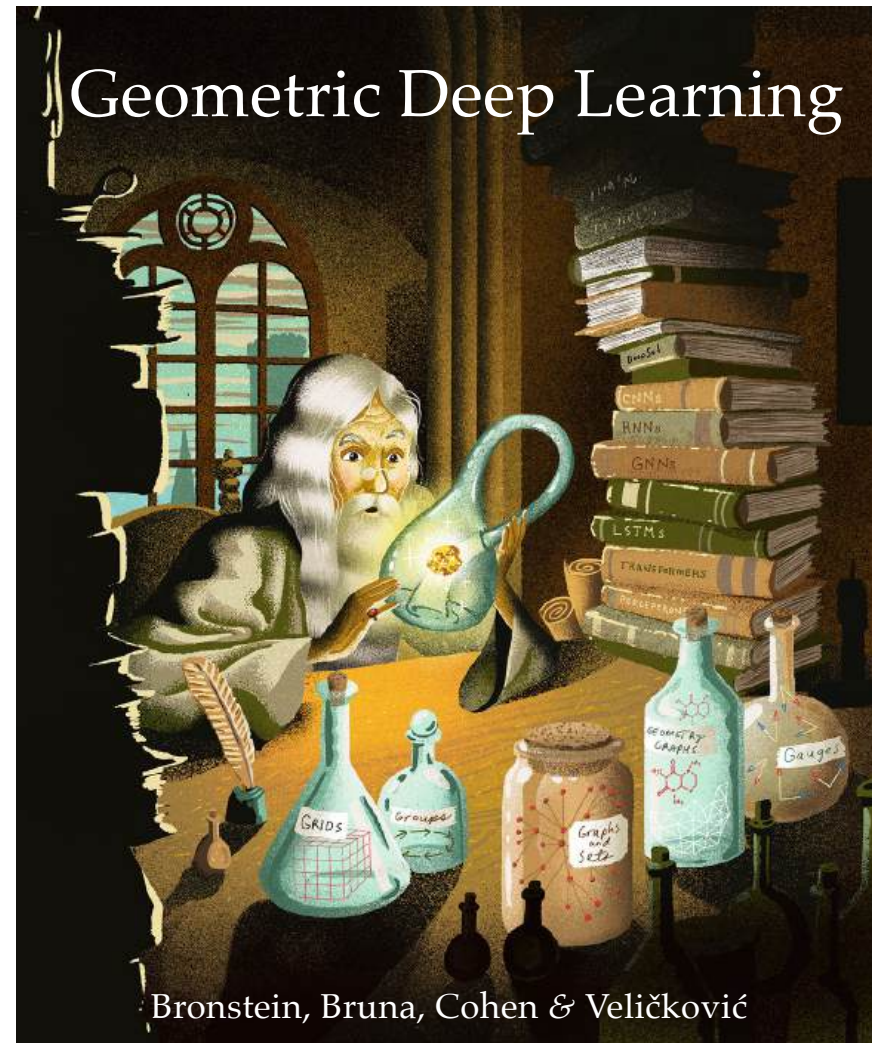
*Deep learning* refers to learning complicated concepts by building them from simpler ones in a hierarchical or multilayer manner. Artificial neural networks are popular realizations of such deep multilayer hierarchies. In the past few years, the growing computational power of modern graphics processing unit (GPU)-based computers and the availability of large training data sets have allowed successfully training neural networks with many layers and degrees of freedom (DoF) [1]. This has led to qualitative breakthroughs on a wide variety of tasks, from speech recognition [2], [3] and machine translation [4] to image analysis and computer vision [5]–[11] (see [12]

## Geometric Deep Learning

*Going beyond Euclidean data*

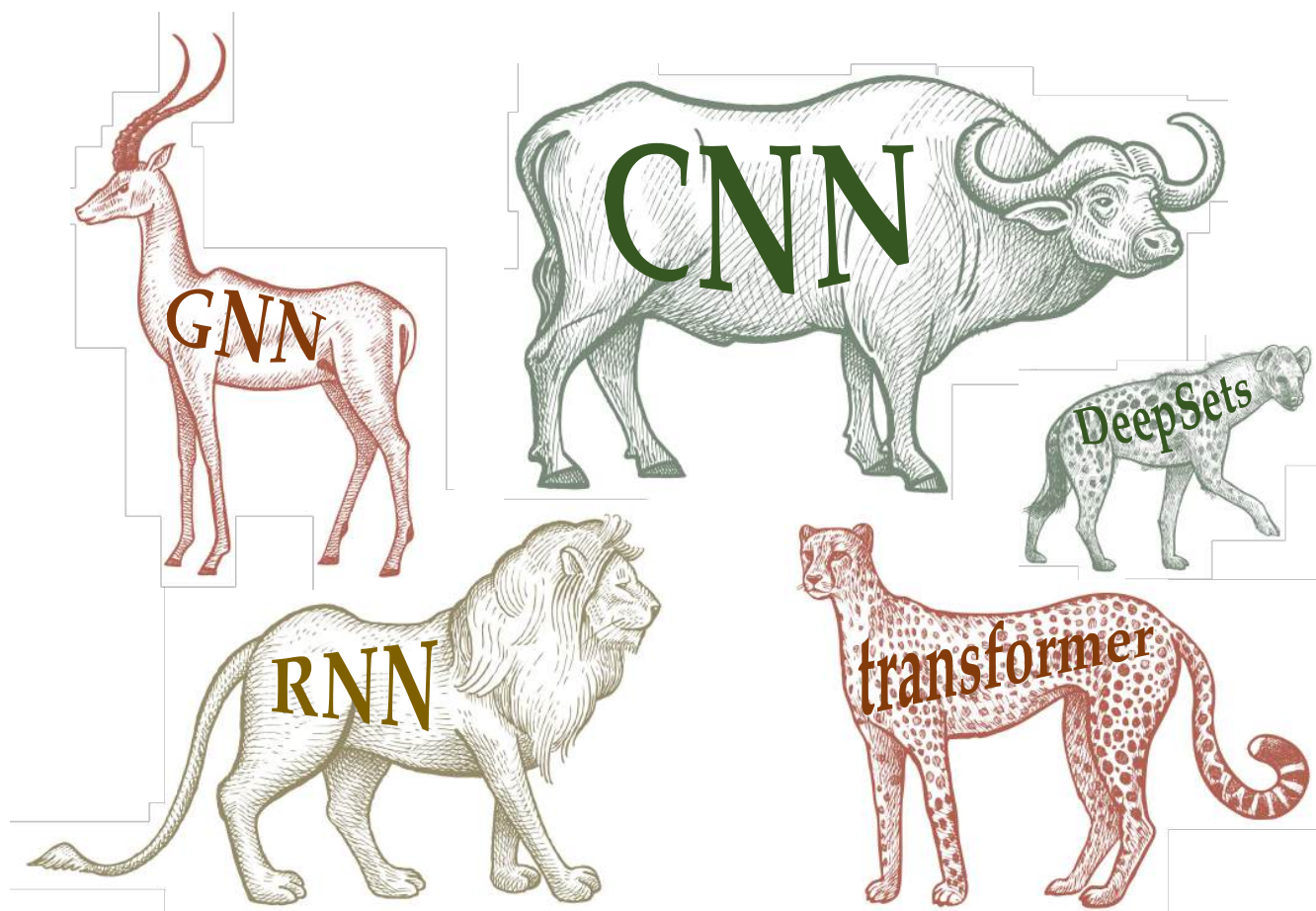


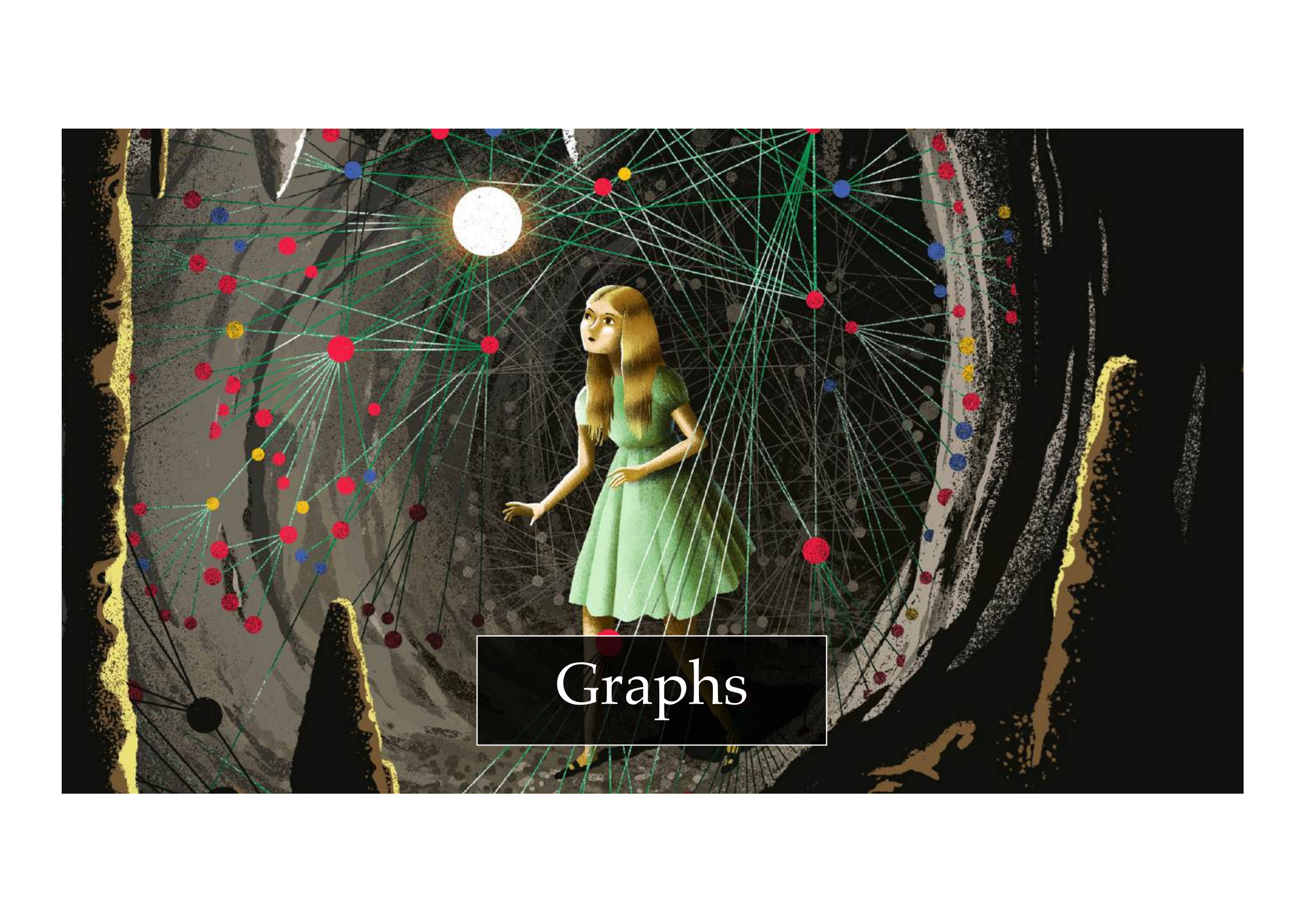
## Geometric Deep Learning



Bronstein, Bruna, Cohen & Veličković

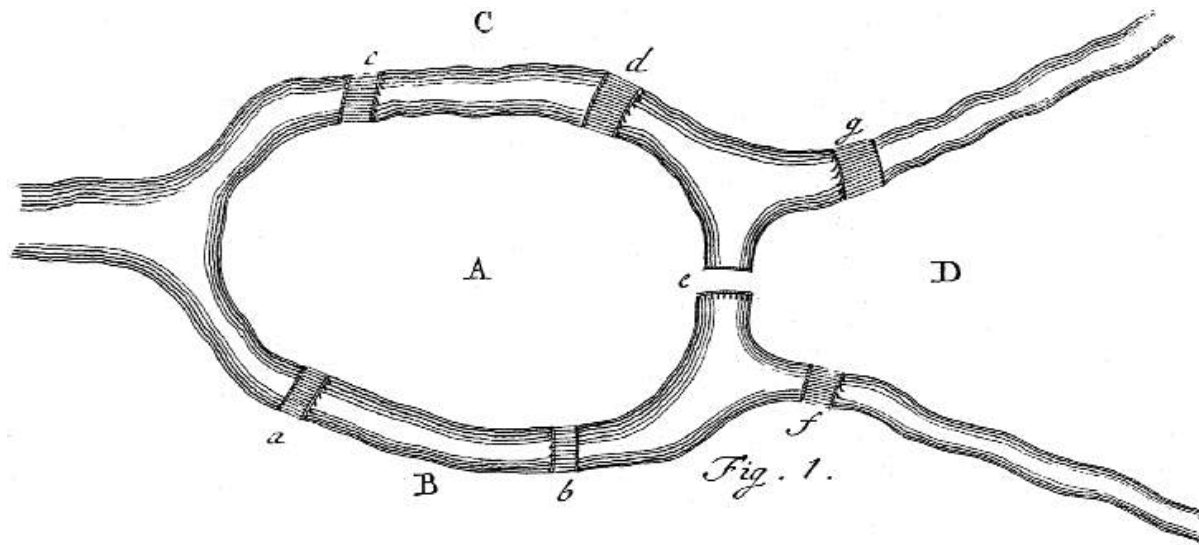
“The Erlangen Programme of ML”  
Geometric Deep Learning



A woman with long blonde hair, wearing a green dress, stands in a dark, textured space. She is looking up at a complex network of green lines and colored dots (red, blue, yellow) that form a web-like structure. A bright white sphere is visible in the background, surrounded by the network. The scene is framed by dark, jagged edges, suggesting a cave or a digital environment. The word "Graphs" is written in white serif font on a black rectangular background at the bottom center.

# Graphs

# Origins of Graph Theory



L. Euler

1741

The solution of the classical problem of the “Bridges of Königsberg” by Euler in 1736 first showed the power of graphs to abstract out the geometry (“*geometria situs*”)

# Origins of Topology

Poincaré's "*analysis situs*."  
His famous Conjecture  
appeared in a supplement  
published in 1904.



H. Poincaré

1895

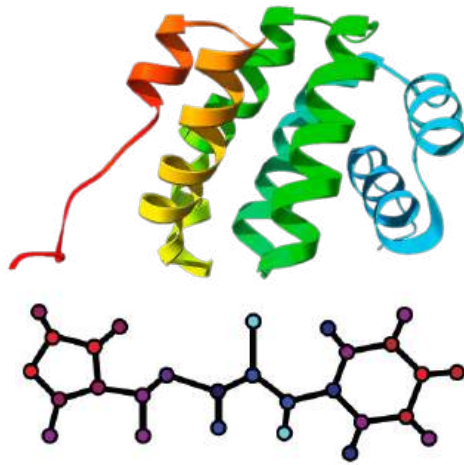


L. Euler

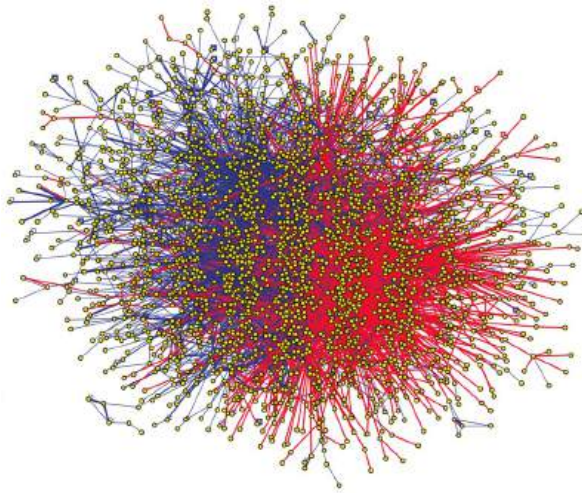
1741

Euler 1741; Poincaré 1895

*Graphs = Systems of Relations and Interactions*



**Molecules**

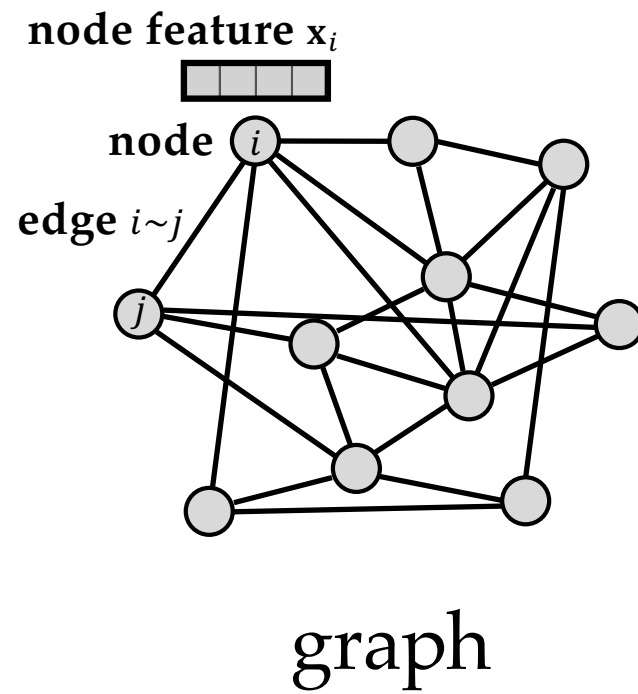


**Interactomes**

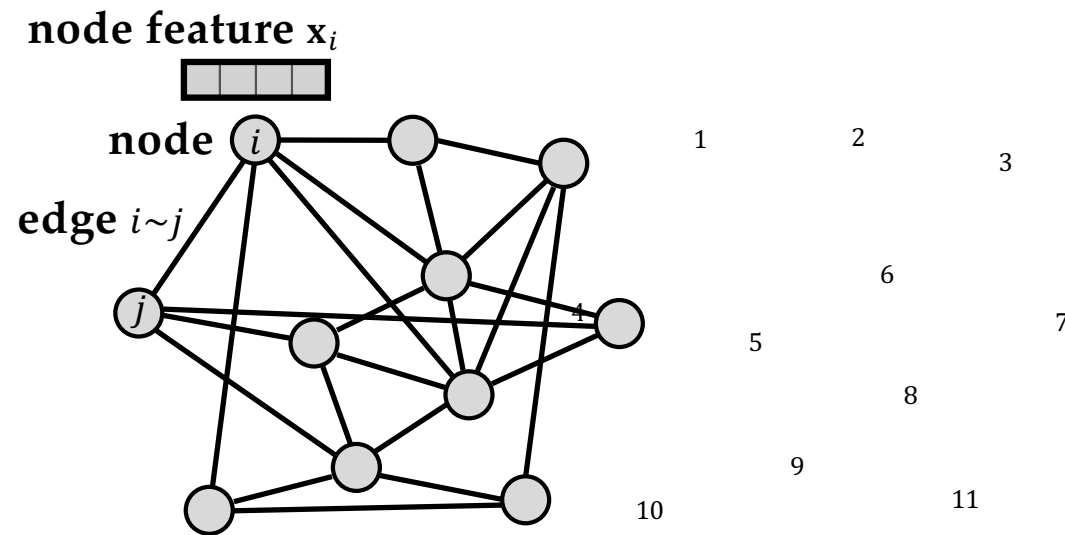


**Social networks**

# *Graphs: The Basics*



## Key Structural Properties of Graphs



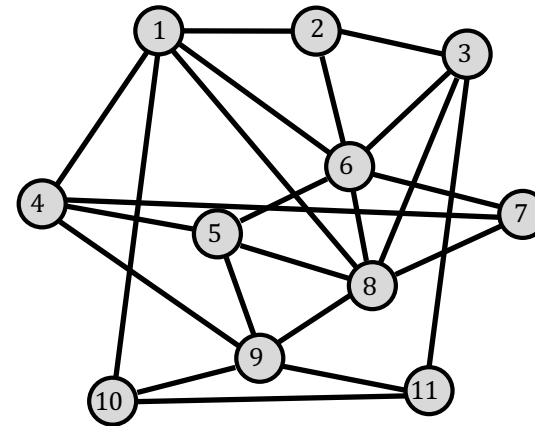
arbitrary ordering of nodes

## *Key Structural Properties of Graphs*

**Feature  
matrix  $n \times d$**

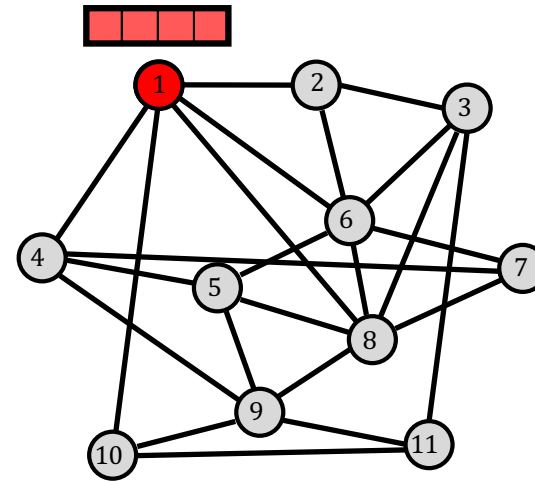
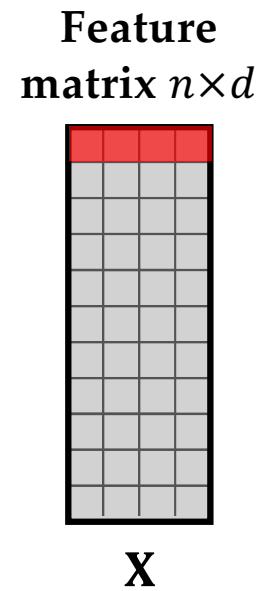
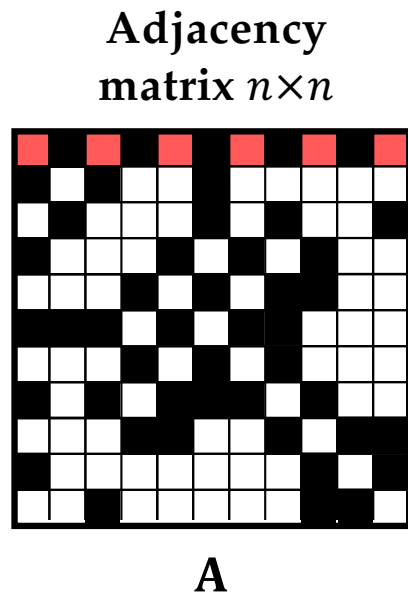
|    |  |  |  |  |
|----|--|--|--|--|
| 1  |  |  |  |  |
| 2  |  |  |  |  |
| 3  |  |  |  |  |
| 4  |  |  |  |  |
| 5  |  |  |  |  |
| 6  |  |  |  |  |
| 7  |  |  |  |  |
| 8  |  |  |  |  |
| 9  |  |  |  |  |
| 10 |  |  |  |  |
| 11 |  |  |  |  |

**X**



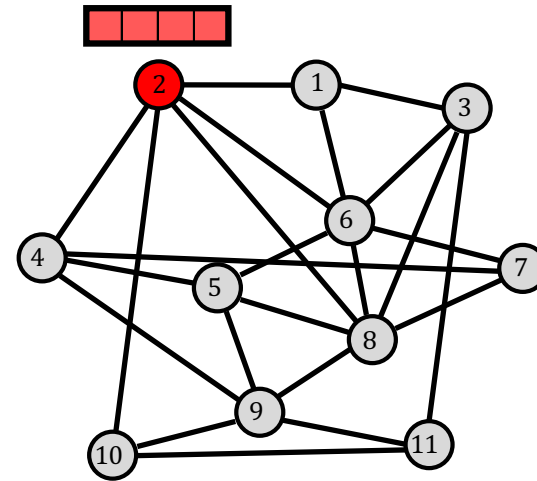
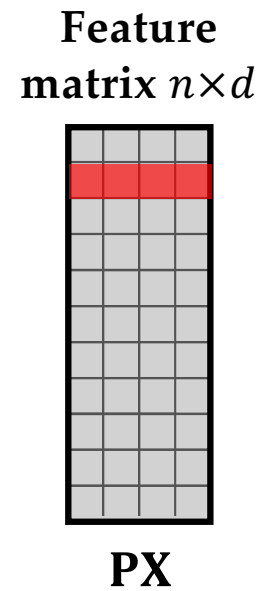
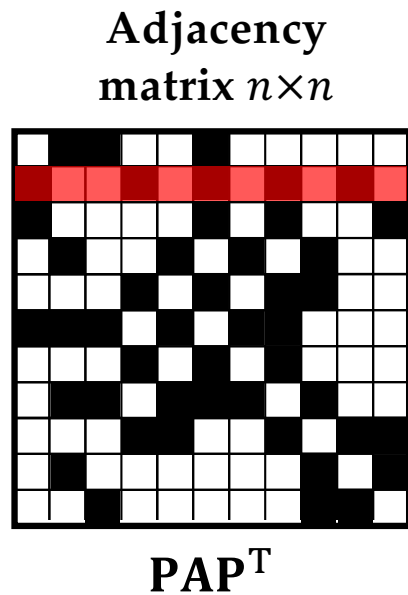
arbitrary ordering of nodes

## *Key Structural Properties of Graphs*



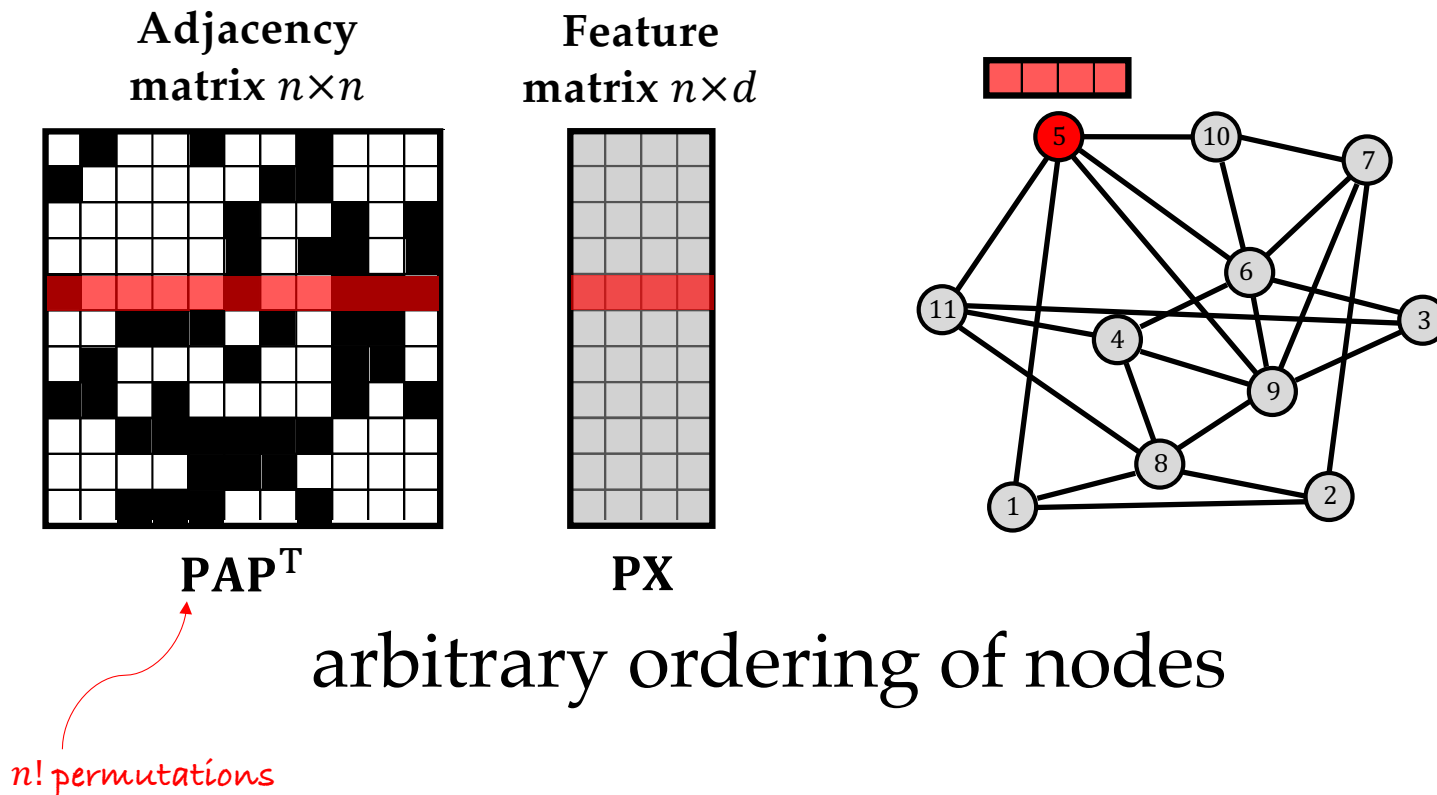
arbitrary ordering of nodes

## *Key Structural Properties of Graphs*

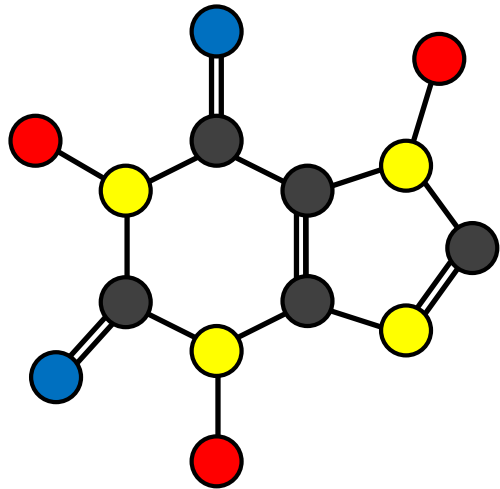


arbitrary ordering of nodes

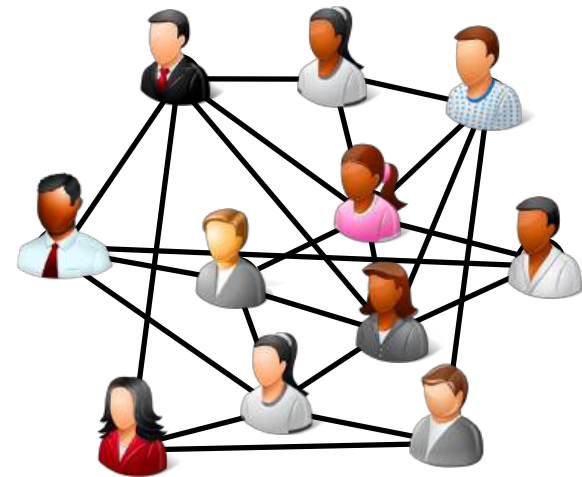
# Key Structural Properties of Graphs



## *Invariant vs Equivariant tasks*



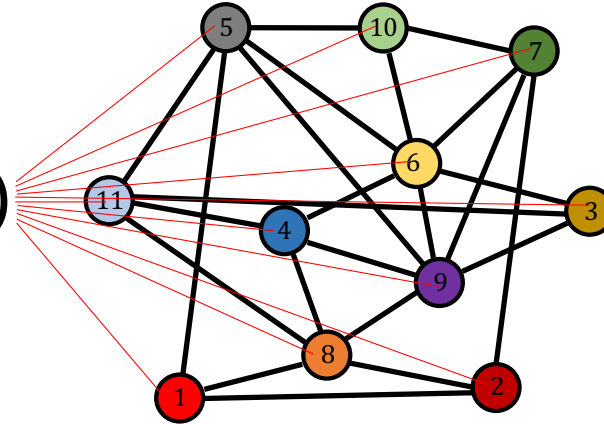
water solubility?



who is a spammer?

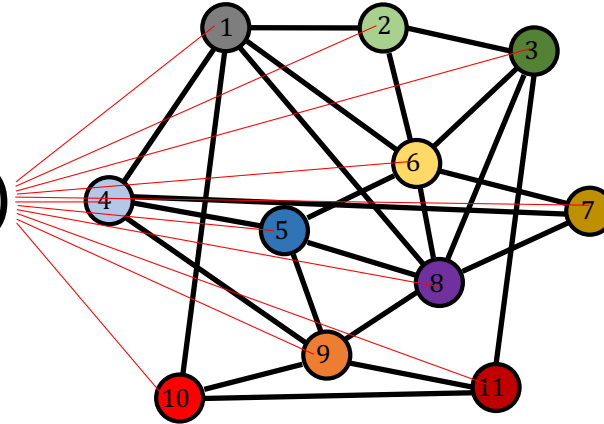
## *Invariant Graph Functions*

graph function  $f(\mathbf{X}, \mathbf{A})$



## *Invariant Graph Functions*

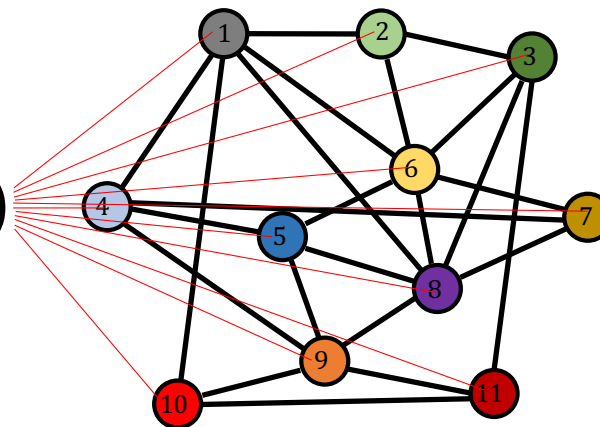
graph function  $f(\mathbf{X}, \mathbf{A})$



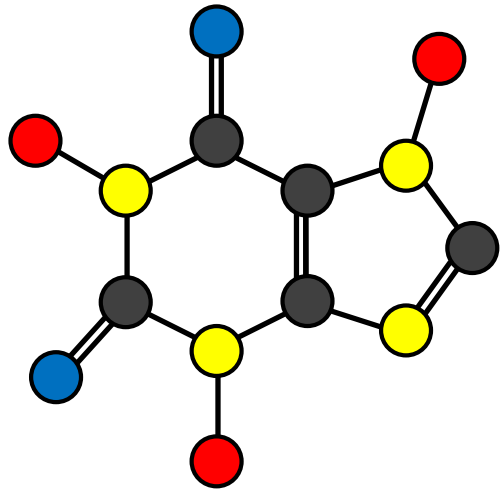
## *Invariant Graph Functions*

permutation-invariant

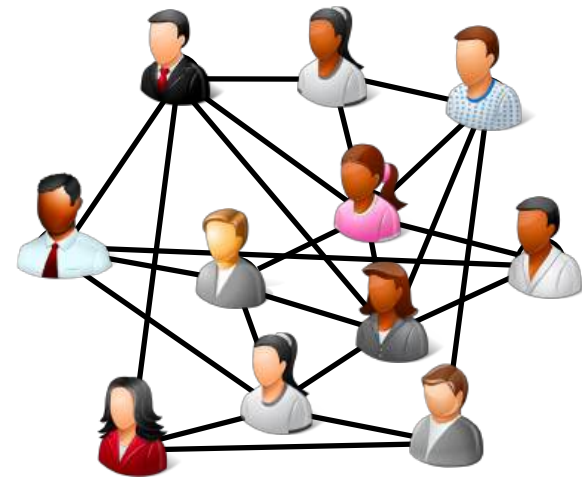
$$f(\mathbf{PX}, \mathbf{PA}\mathbf{P}^\top) = f(\mathbf{X}, \mathbf{A})$$



## *Invariant vs Equivariant tasks*



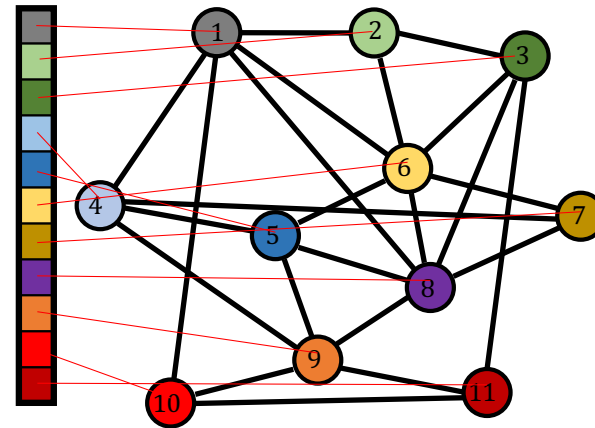
water solubility?



who is a spammer?

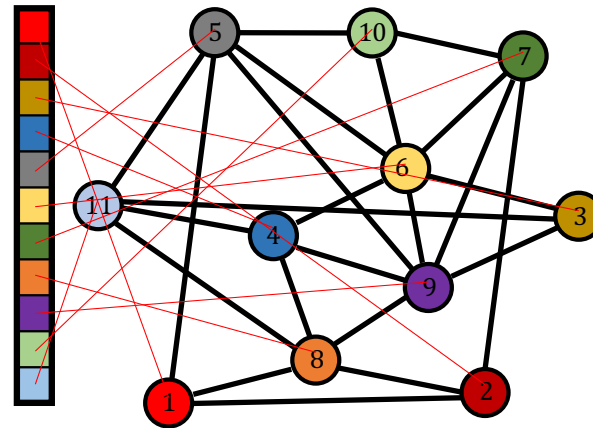
# *Equivariant Graph Functions*

node function  $\mathbf{F}(\mathbf{X}, \mathbf{A})$



# *Equivariant Graph Functions*

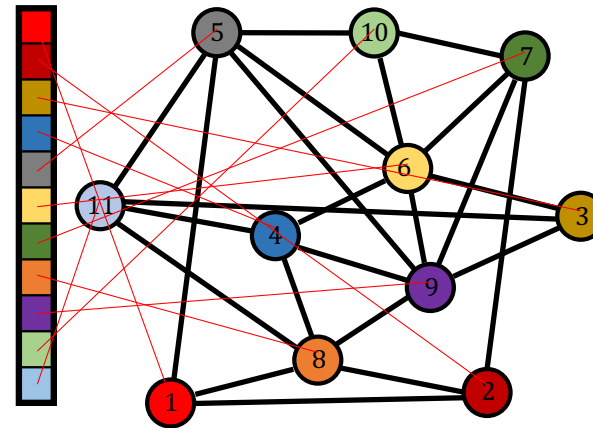
node function  $\mathbf{F}(\mathbf{X}, \mathbf{A})$



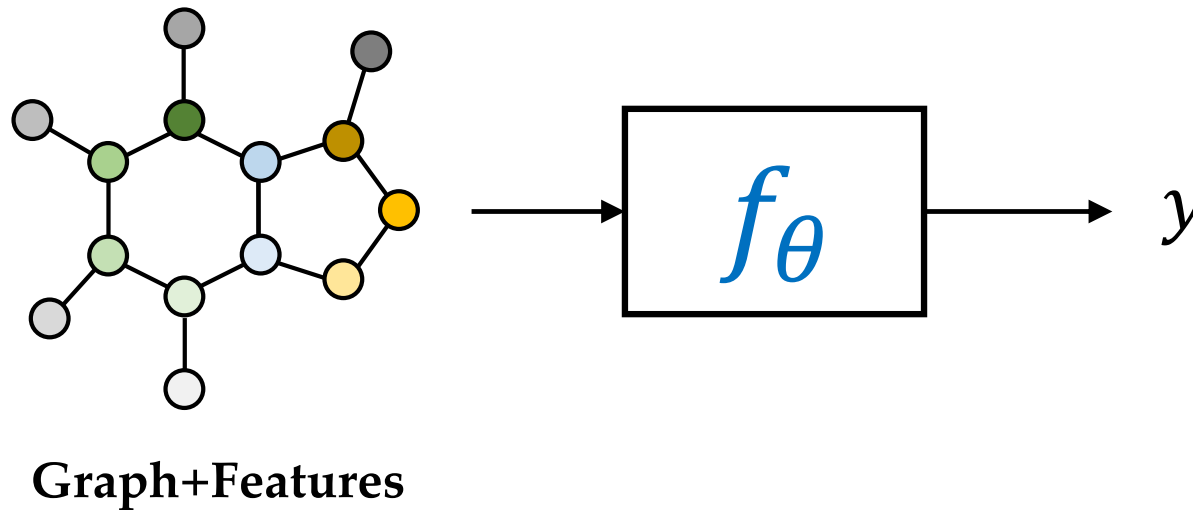
## *Equivariant Graph Functions*

permutation-equivariant

$$\mathbf{F}(\mathbf{P}\mathbf{X}, \mathbf{P}\mathbf{A}\mathbf{P}^\top) = \mathbf{P}\mathbf{F}(\mathbf{X}, \mathbf{A})$$

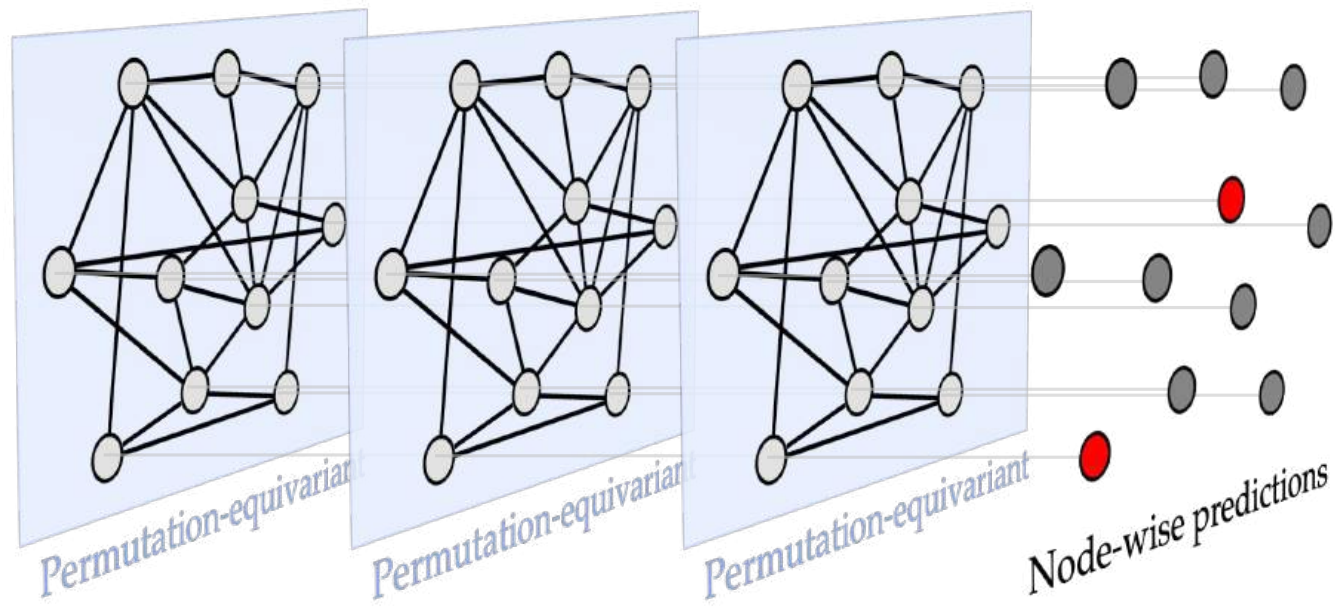


$GNNs = \text{Parametric graph functions}$

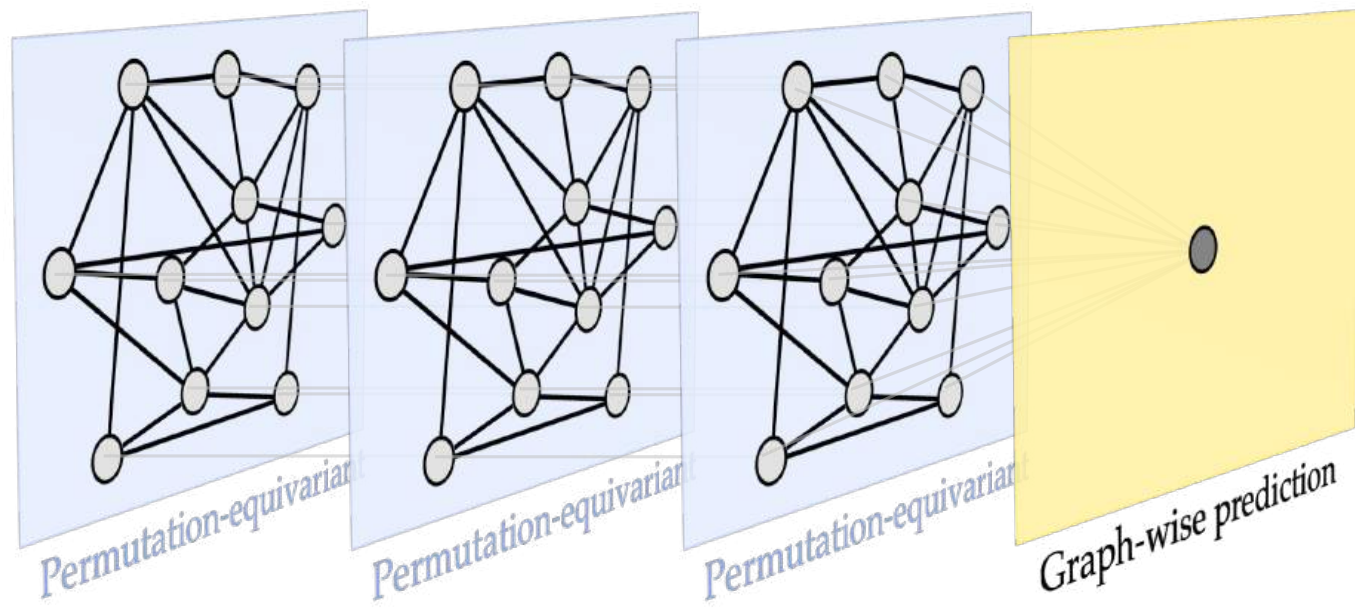


**Note:** we use the term “GNN” to refer to general parametric graph functions. The particular class of GNNs we consider are Message Passing Neural Networks (MPNNs). Petar Veličković argues that “it’s all message passing”

## *Graph Neural Networks: Node tasks*

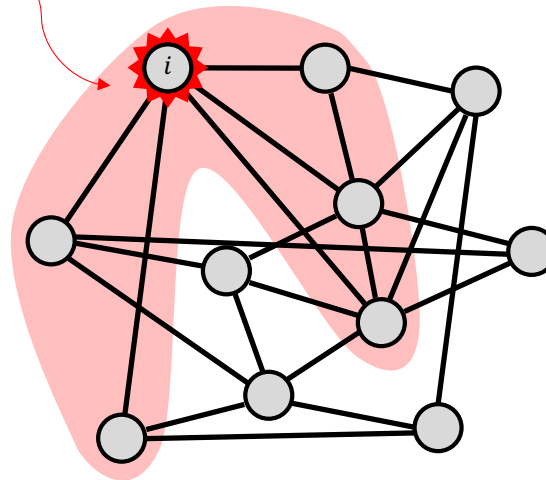


## *Graph Neural Networks: Graph tasks*



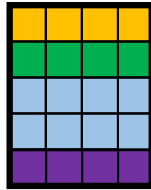
# Neighbour Aggregation

neighbourhood  
 $\mathcal{N}_i = \{j: i \sim j\}$



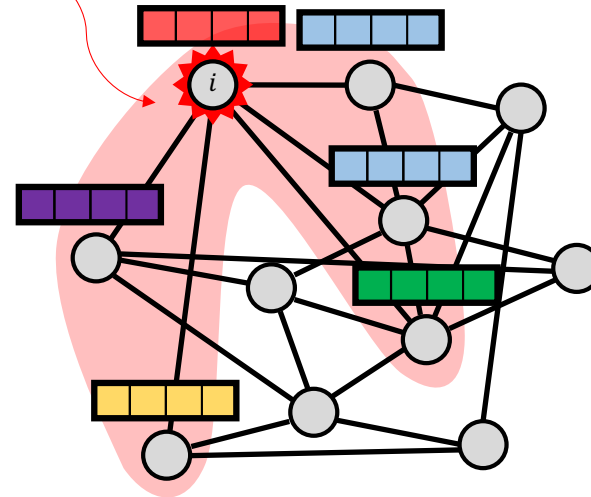
# Neighbour Aggregation

multiset of  
neighbour features

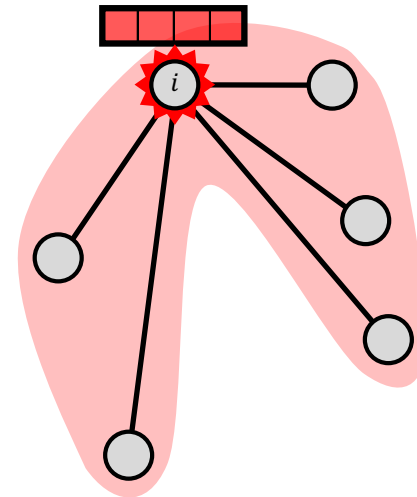
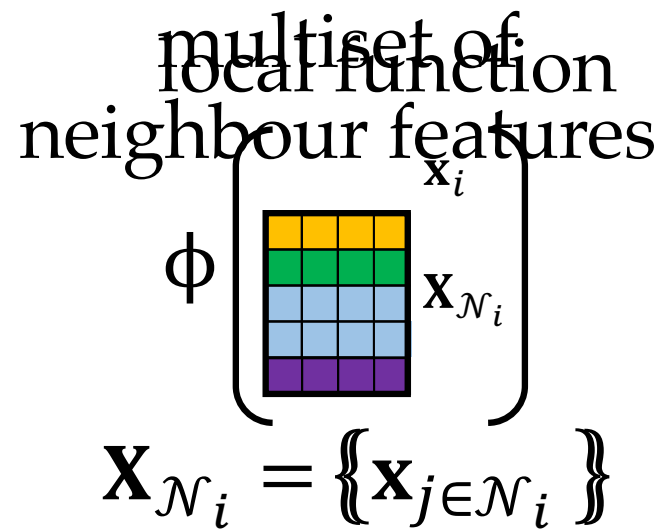


$$\mathbf{X}_{\mathcal{N}_i} = \{ \mathbf{x}_{j \in \mathcal{N}_i} \}$$

neighbourhood  
 $\mathcal{N}_i = \{j: i \sim j\}$



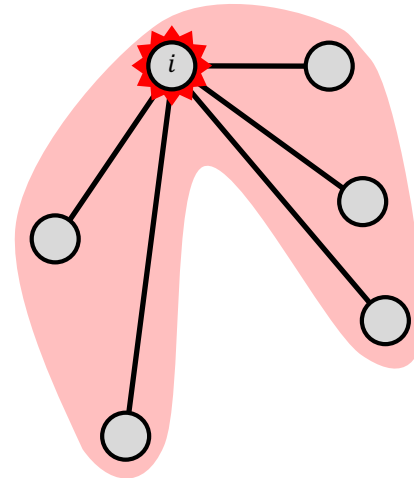
## Neighbour Aggregation



## *Neighbour Aggregation*

local function

$$\phi \left( \begin{array}{c} \text{red row} \\ \text{blue grid} \\ \text{purple grid} \\ \text{yellow grid} \\ \text{green grid} \\ \text{blue grid} \end{array} \right) \begin{array}{l} \mathbf{x}_i \\ \mathbf{X}_{\mathcal{N}_i} \end{array}$$

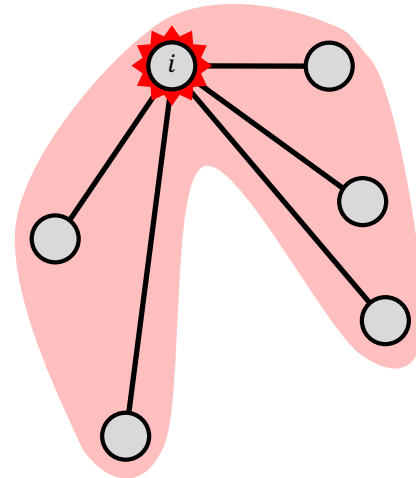


## *Neighbour Aggregation*

local function

$$\phi \left( \begin{array}{c} \text{red row} \\ \text{green row} \\ \text{yellow row} \\ \text{purple row} \\ \text{blue row} \end{array} \right) \begin{array}{l} \mathbf{x}_i \\ \mathbf{x}_{\mathcal{N}_i} \end{array}$$

permutation invariant

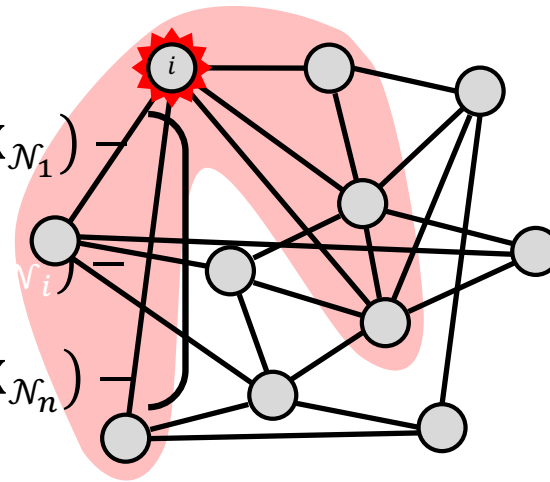


# Neighbour Aggregation

local function

$$\mathbf{f}(\mathbf{X}, \mathbf{A}) = \begin{pmatrix} \mathbf{x}_i \\ \mathbf{X}_{\mathcal{N}_i} \end{pmatrix} \begin{pmatrix} -\phi(\mathbf{x}_1, \mathbf{X}_{\mathcal{N}_1}) \\ \vdots \\ -\phi(\mathbf{x}_i, \mathbf{X}_{\mathcal{N}_i}) \\ \vdots \\ -\phi(\mathbf{x}_n, \mathbf{X}_{\mathcal{N}_n}) \end{pmatrix}$$

permutation invariant

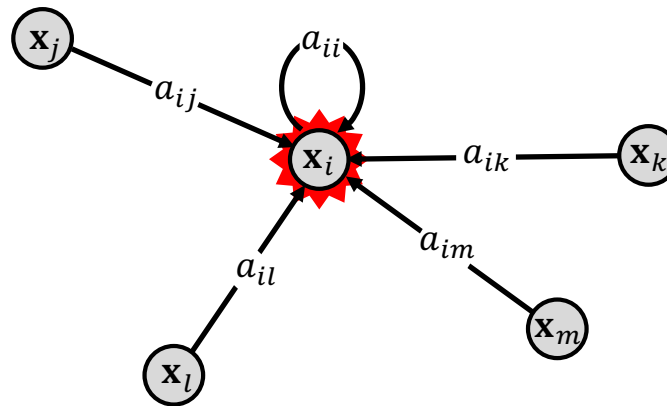


*GNN Layer*

$$\mathbf{F}(\mathbf{X}, \mathbf{A}) = \begin{pmatrix} -\phi(\mathbf{x}_1, \mathbf{X}_{\mathcal{N}_1}) - \\ \vdots \\ -\phi(\mathbf{x}_i, \mathbf{X}_{\mathcal{N}_i}) - \\ \vdots \\ -\phi(\mathbf{x}_n, \mathbf{X}_{\mathcal{N}_n}) - \end{pmatrix}$$

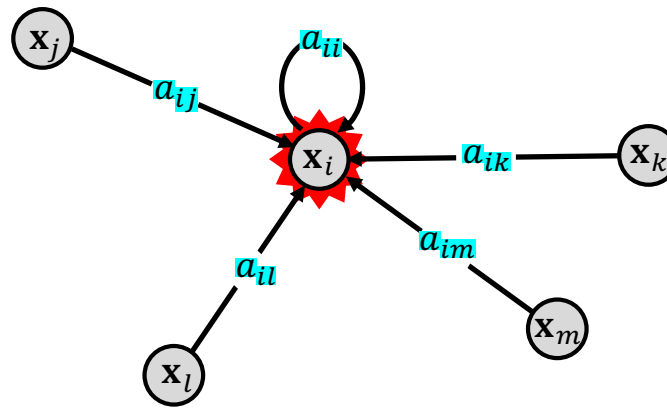
permutation equivariant

## Convolutional GNNs



$$\mathbf{x}_i \leftarrow \sigma \left( \sum_{j \in \mathcal{N}_i \cup \{i\}} a_{ij} \psi(\mathbf{x}_j) \right)$$

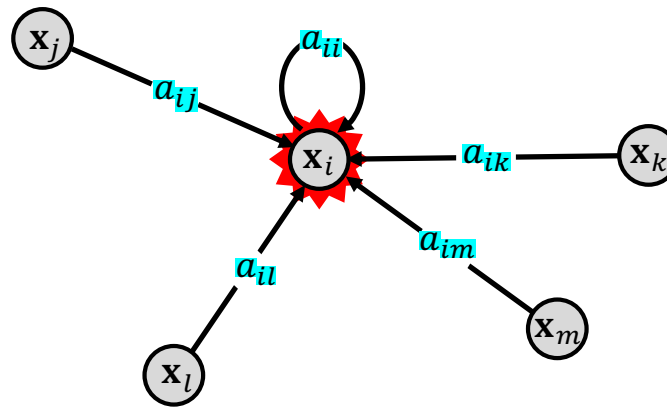
# Convolutional GNNs



$$\mathbf{x}_i \leftarrow \sigma \left( \sum_{j \in \mathcal{N}_i \cup \{i\}} a_{ij} \psi(\mathbf{x}_j) \right)$$

graph adjacency

# Convolutional GNNs



$$\mathbf{x}_i \leftarrow \sigma \left( \sum_{j \in \mathcal{N}_i \cup \{i\}} a_{ij} \psi(\mathbf{x}_j) \right)$$

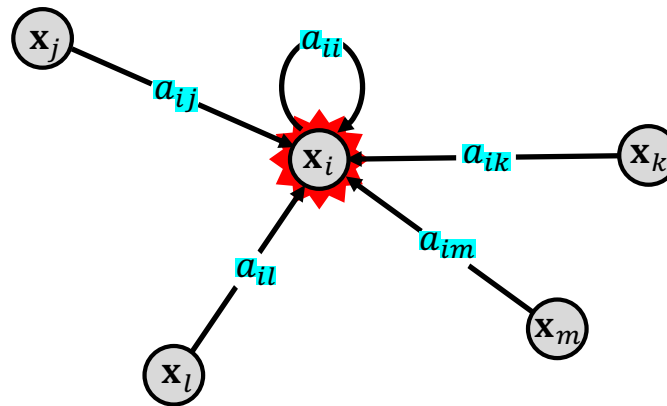
nonlinear activation

graph adjacency

node-wise transformation

Defferrard et al. 2016; Kipf, Welling 2016 (GCN)

# Convolutional GNNs



$$\mathbf{x}_i \leftarrow \sigma \left( \sum_{j \in \mathcal{N}_i \cup \{i\}} a_{ij} \mathbf{W} \mathbf{x}_j \right)$$

nonlinear activation

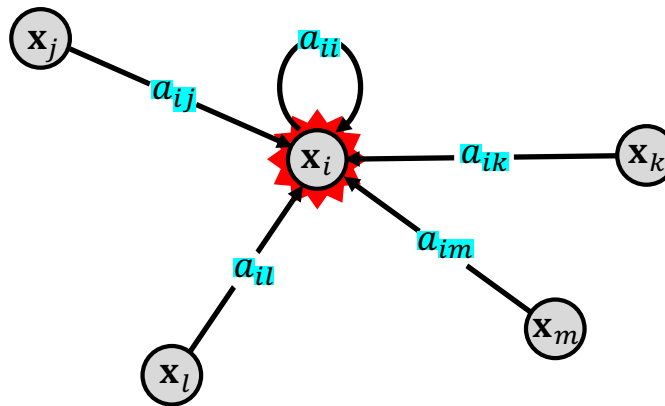
graph adjacency

node-wise linear transformation

Defferrard et al. 2016; Kipf, Welling 2016 (GCN)

# Convolutional GNNs

- Simplest GNN
- Highly scalable
- Industrial use cases
- Folklore: works only on **homophilic graphs**



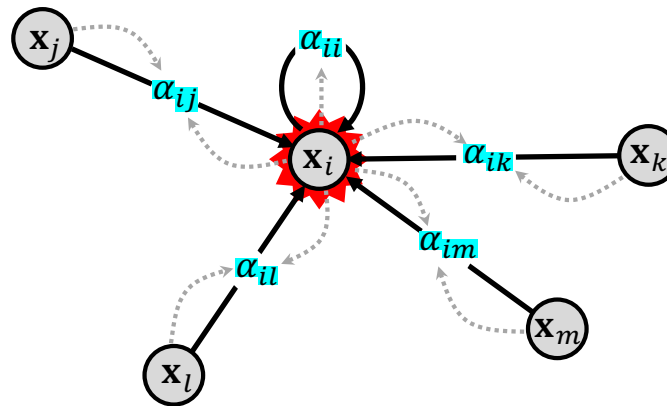
$$\mathbf{X} \leftarrow \sigma(\mathbf{A}\mathbf{X}\mathbf{W})$$

diffusion  
 $n \times n$

channel mixing  
 $d \times d$

Defferd et al. 2016; Kipf, Welling 2016 (GCN)  
Rossi, Frasca et al. 2020 (SIGN); Ying et al. 2018 (PinSAGE)

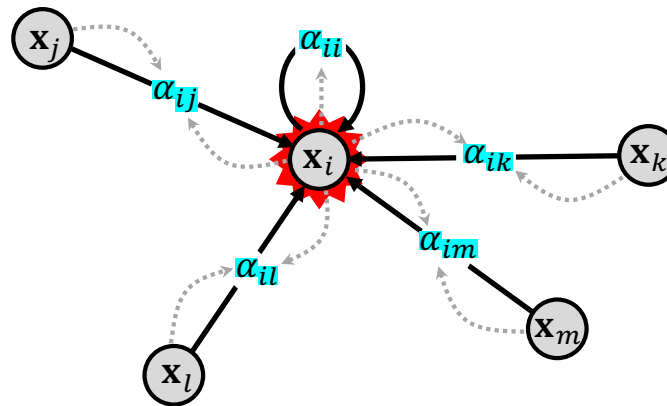
# Attentional GNNs



$$\mathbf{x}_i \leftarrow \sigma \left( \sum_{j \in \mathcal{N}_i \cup \{i\}} \alpha_{ij}(\mathbf{x}_i, \mathbf{x}_j) \psi(\mathbf{x}_j) \right)$$

learnable attention  
weights

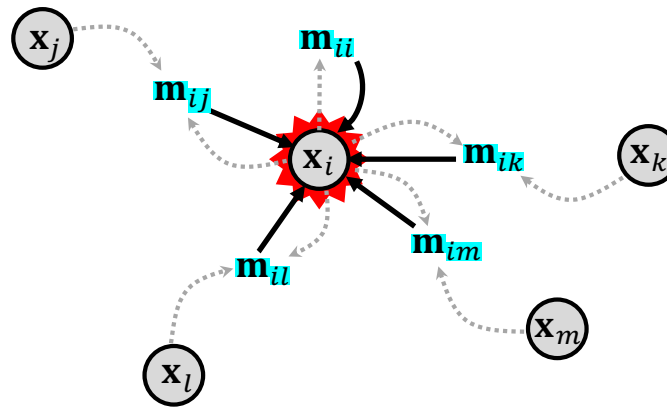
# Attentional GNNs



$$\mathbf{X} \leftarrow \sigma(\mathbf{A}(\mathbf{X})\mathbf{X})$$

Monti et al. 2017; Veličković et al. 2018 (GAT)

# Message-Passing GNNs



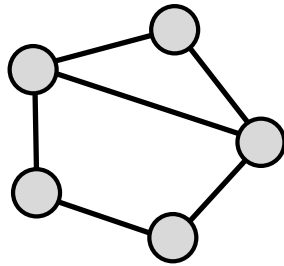
$$\mathbf{x}_i \leftarrow \sigma \left( \sum_{j \in \mathcal{N}_i \cup \{i\}} \psi(\mathbf{x}_i, \mathbf{x}_j) \right)$$

message from  
node  $j$  to node  $i$

Gilmer et al. 2017 (MPNN); Battaglia et al 2018 (Graph Networks)  
Wang et B, Solomon 2018 (edgeconv)

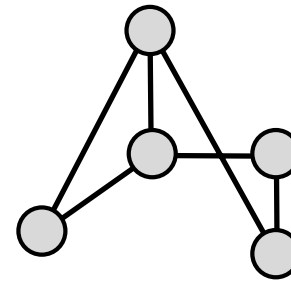
# EXPRESSIVE POWER OF GNNS & WEISFEILER-LEHMAN TEST

## *Graph isomorphism*



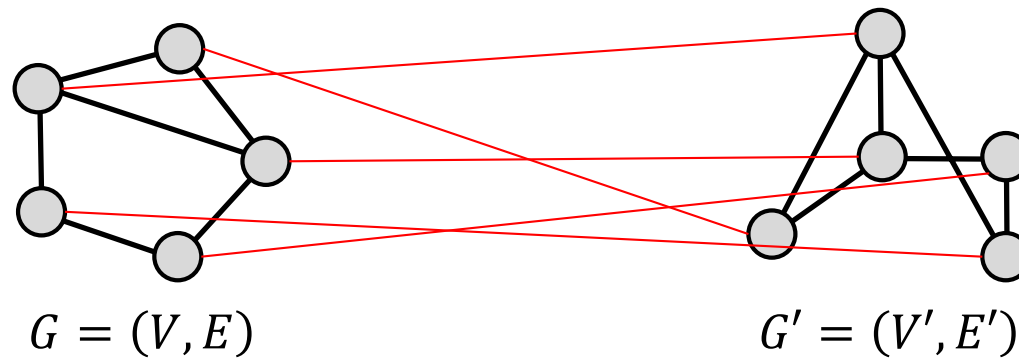
$$G = (V, E)$$

***“=”***



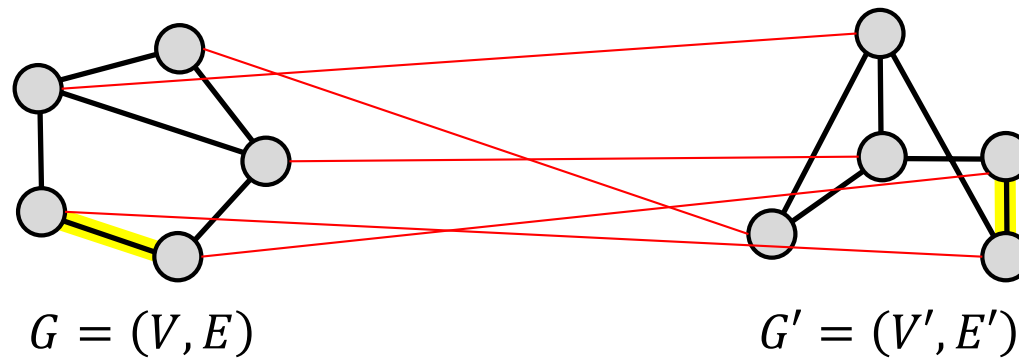
$$G' = (V', E')$$

## Graph isomorphism



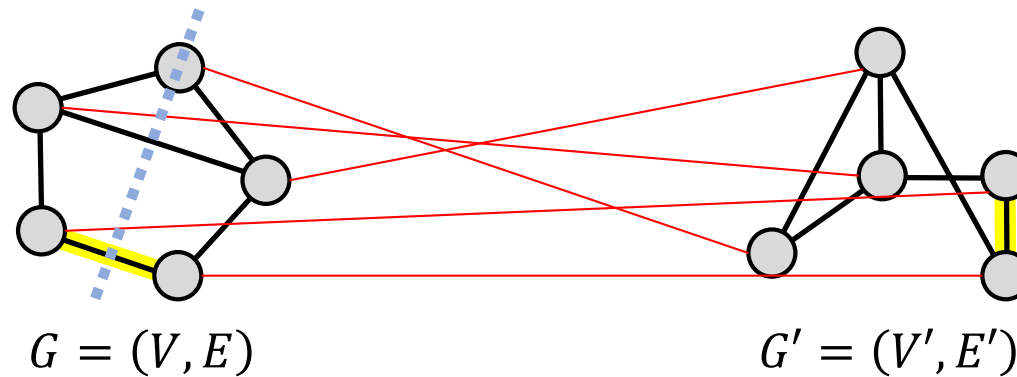
- Two graphs  $G = (V, E)$  and  $G' = (V', E')$  are **isomorphic** if there exists an *edge-preserving bijection*  $\varphi: V \rightarrow V'$  s.t.  $u \sim v$  in  $G$  iff  $\varphi(u) \sim \varphi(v)$  in  $G'$

## Graph isomorphism



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## Graph isomorphism



- Two graphs  $G = (V, E)$  and  $G' = (V', E')$  are **isomorphic** if there exists an *edge-preserving bijection*  $\varphi: V \rightarrow V'$  s.t.  $u \sim v$  in  $G$  iff  $\varphi(u) \sim \varphi(v)$  in  $G'$

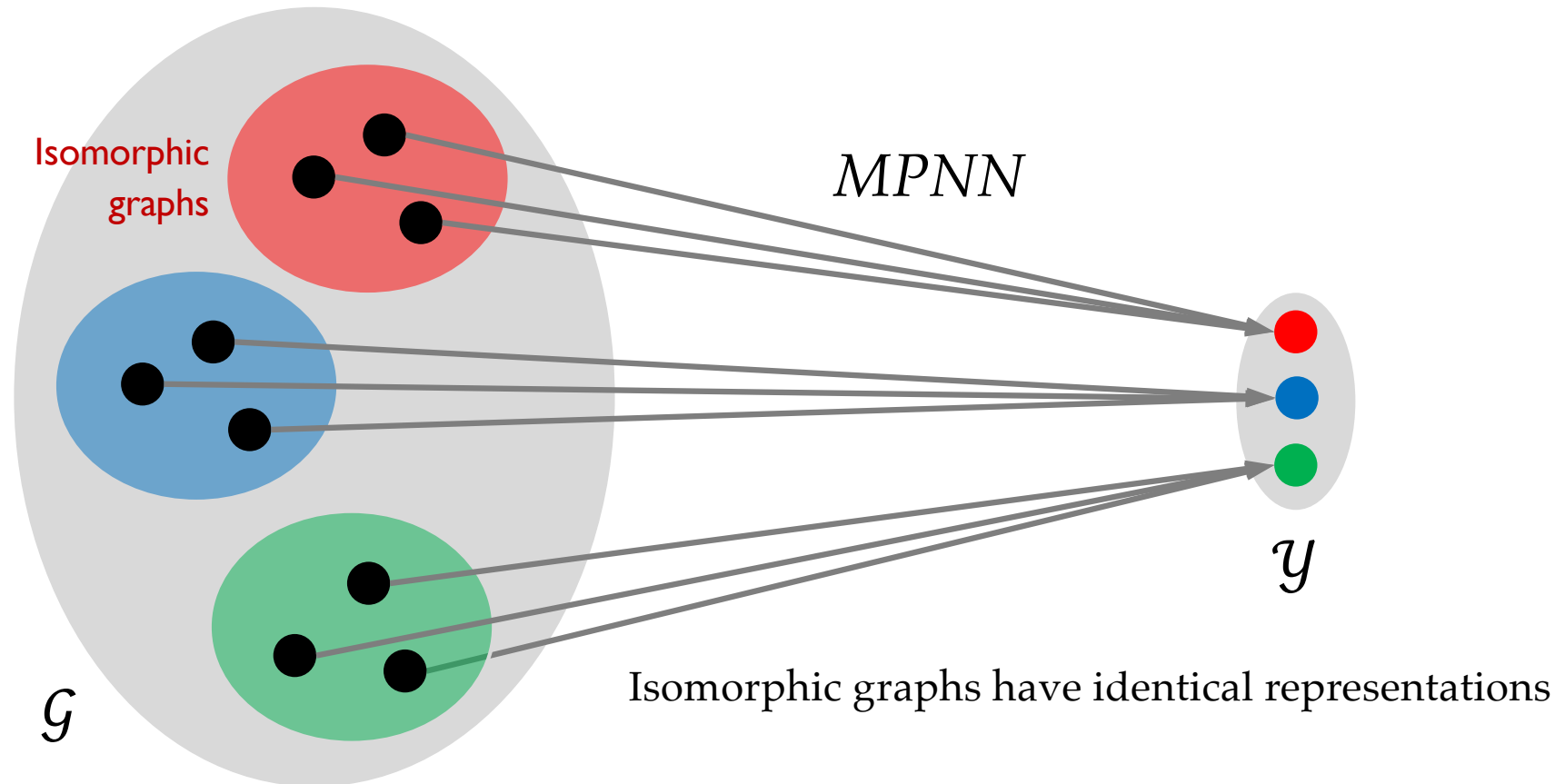
**Note:**  $\varphi$  is not unique where the graph has symmetries (edge-preserving automorphism)

## *Universal Approximation on Graphs*

**Theorem:** A class of functions is universally approximating permutation-invariant functions on graphs with finite node features iff it can discriminate graph isomorphisms.

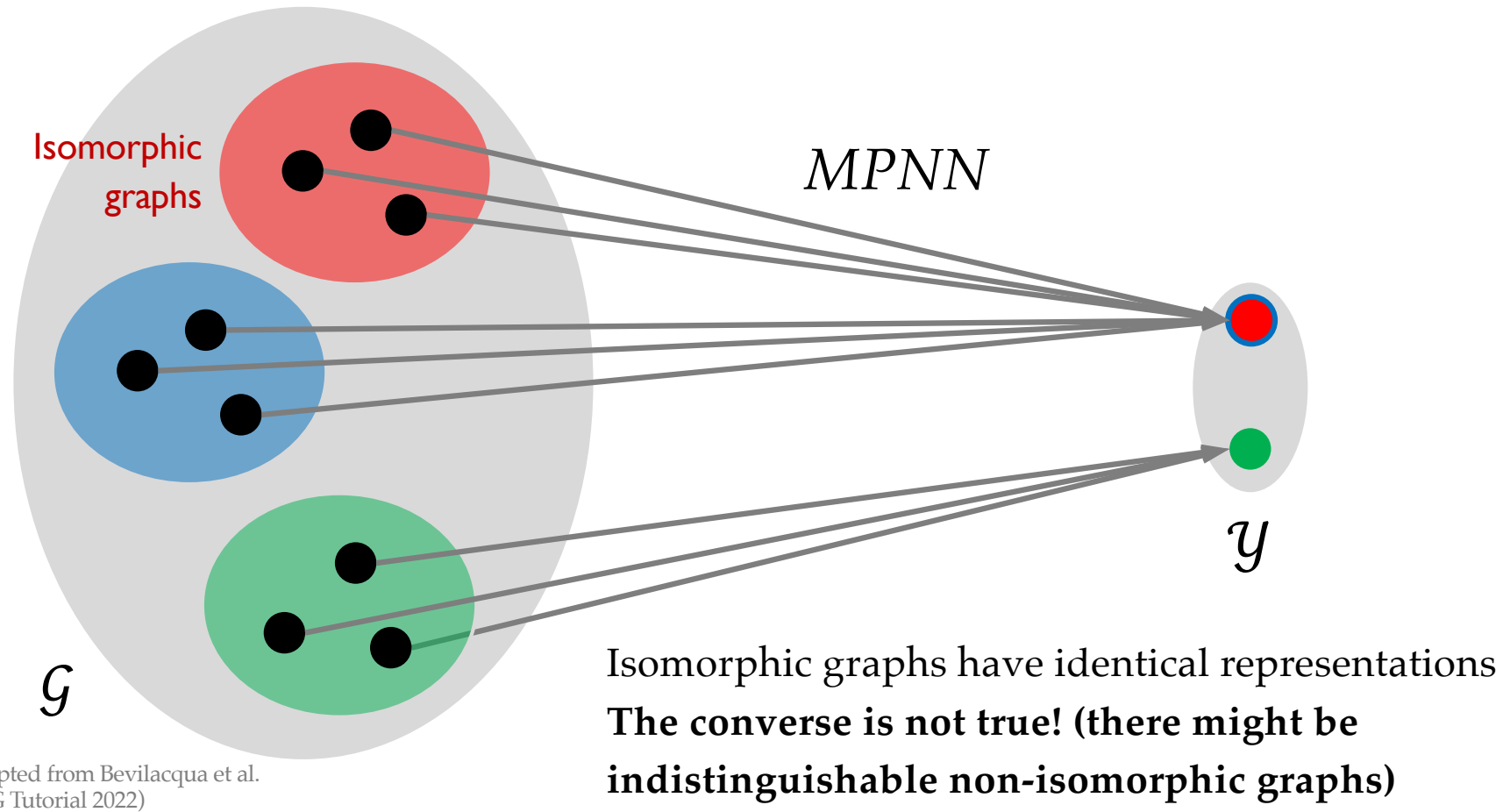
**Universal approximation on graphs is  
equivalent to graph isomorphism testing**

*What graphs can MPNNs represent?*



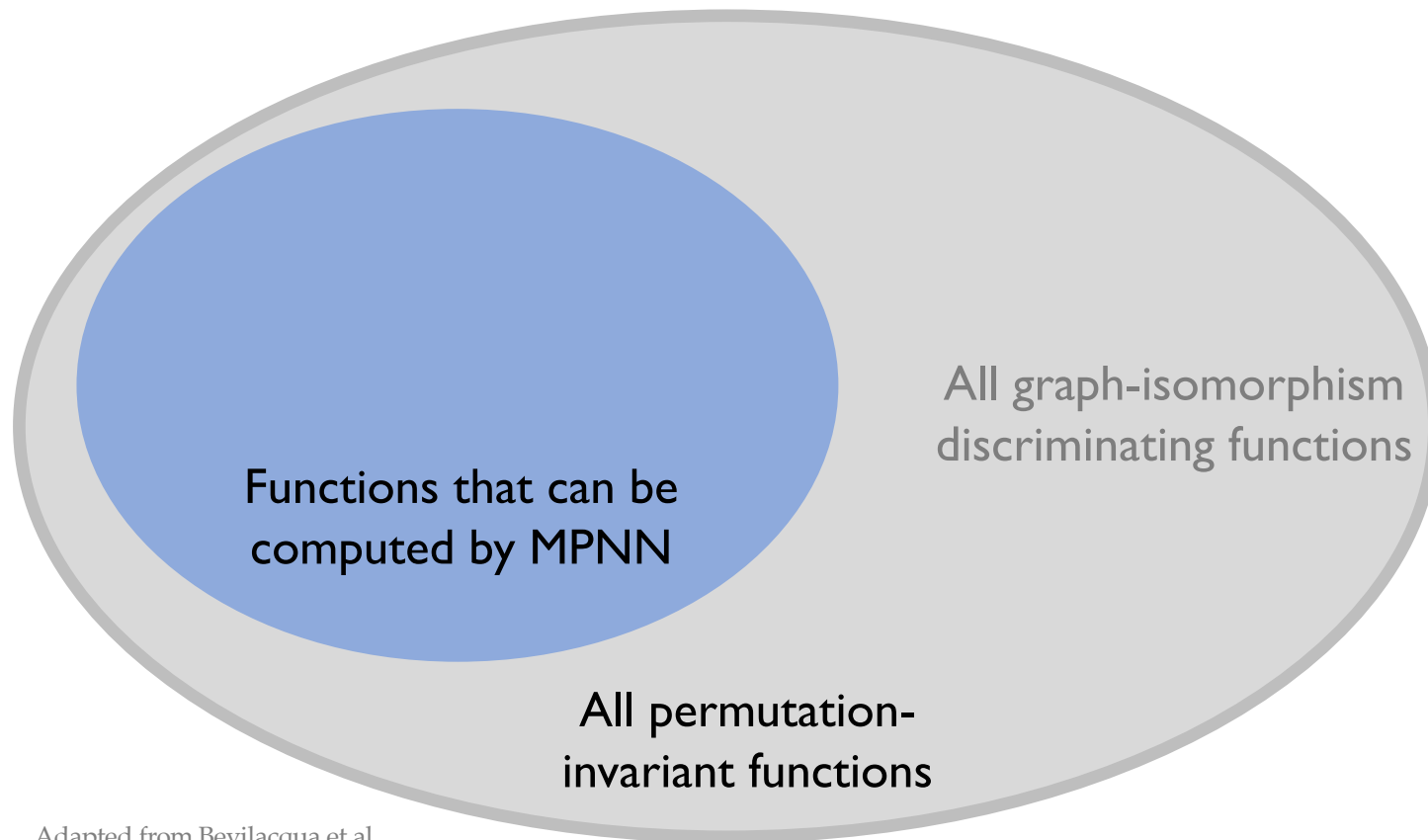
Adapted from Bevilacqua et al.  
(LoG Tutorial 2022)

*What graphs can MPNNs represent?*



Adapted from Bevilacqua et al.  
(LoG Tutorial 2022)

## *Expressive power of MPNNs*

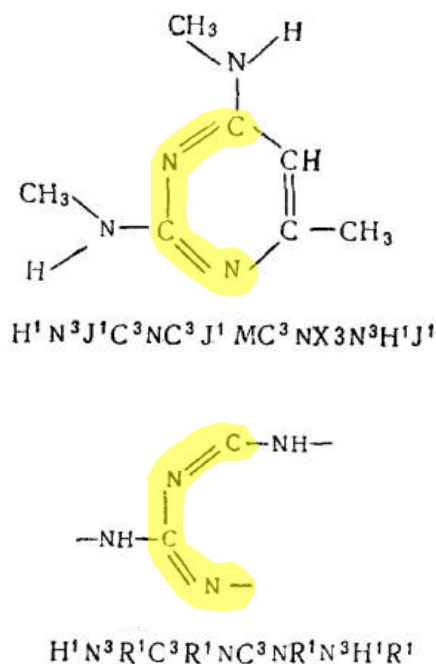


Adapted from Bevilacqua et al.  
(LoG Tutorial 2022)

# Weisfeiler-Lehman Test & Chemical precursors of GNNs



George Vlăduț



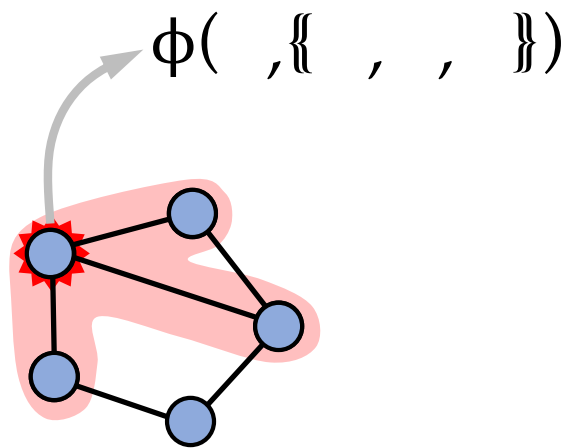
Andrey Lehman



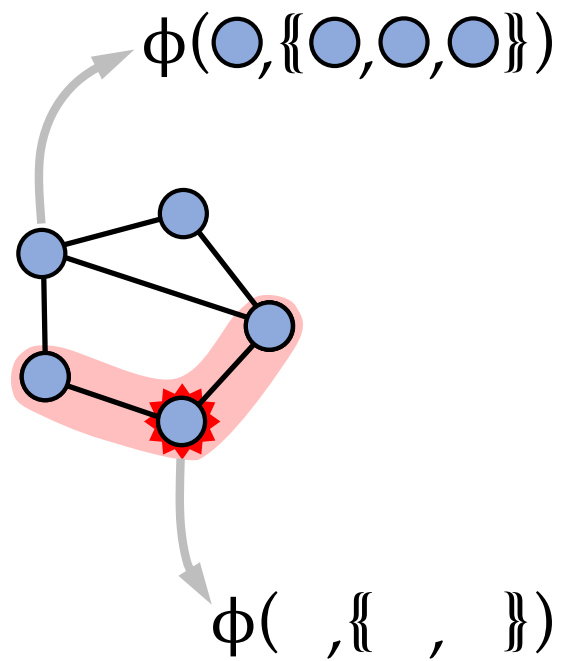
Boris Weisfeiler

Vlăduț et al. 1959; Weisfeiler, Lehman 1968

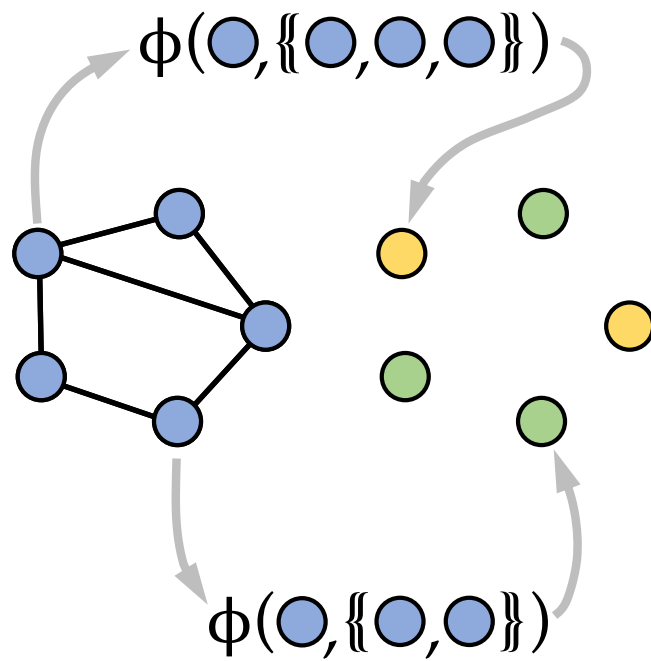
# Weisfeiler-Lehman Test



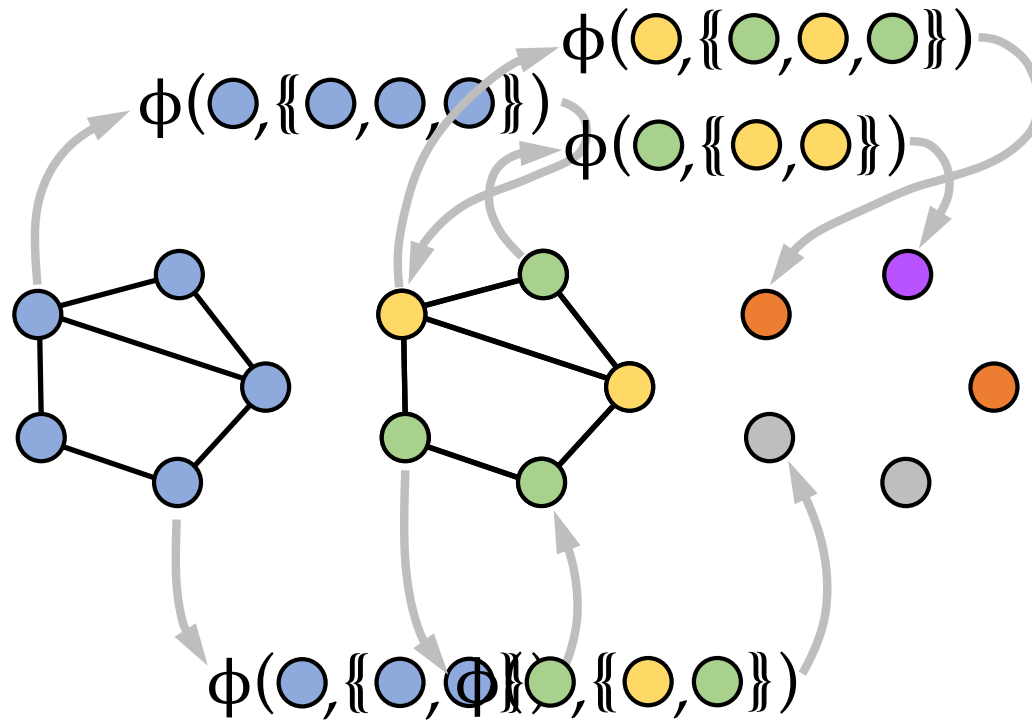
# Weisfeiler-Lehman Test



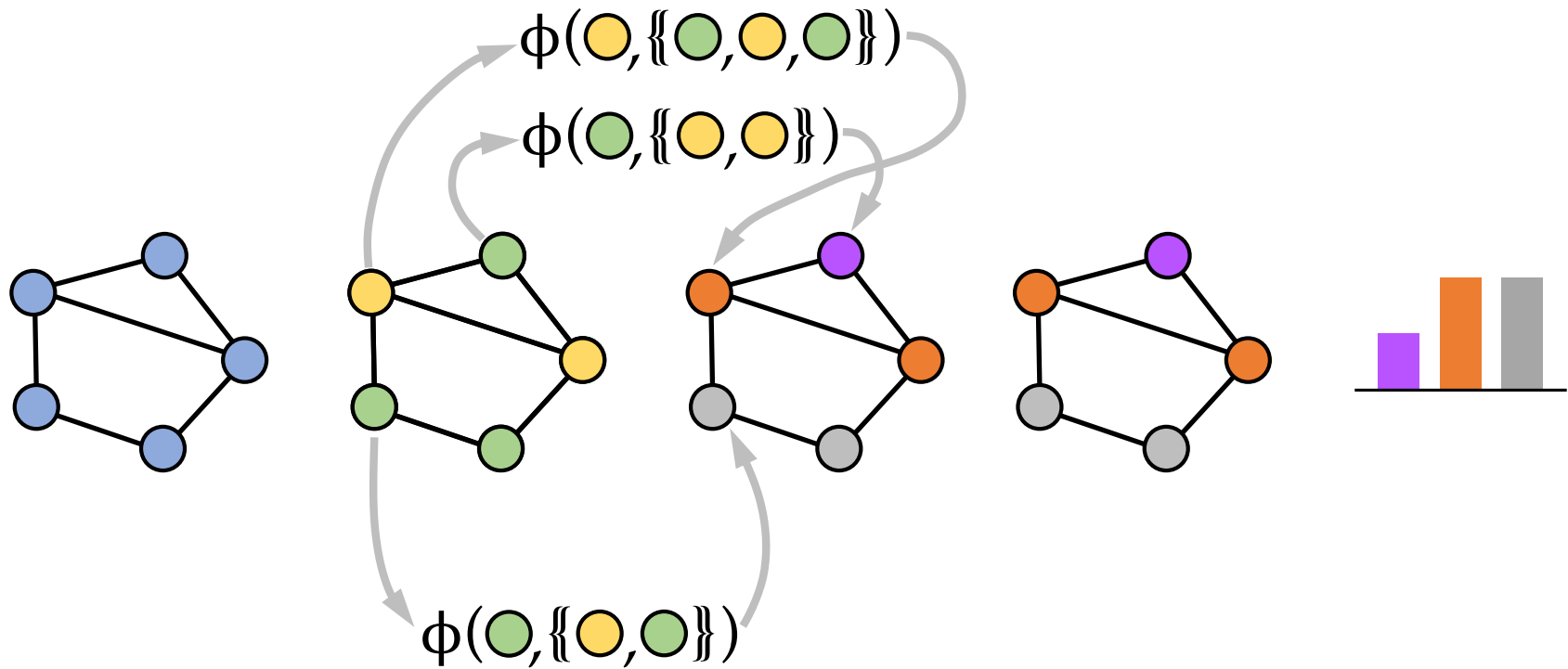
# Weisfeiler-Lehman Test



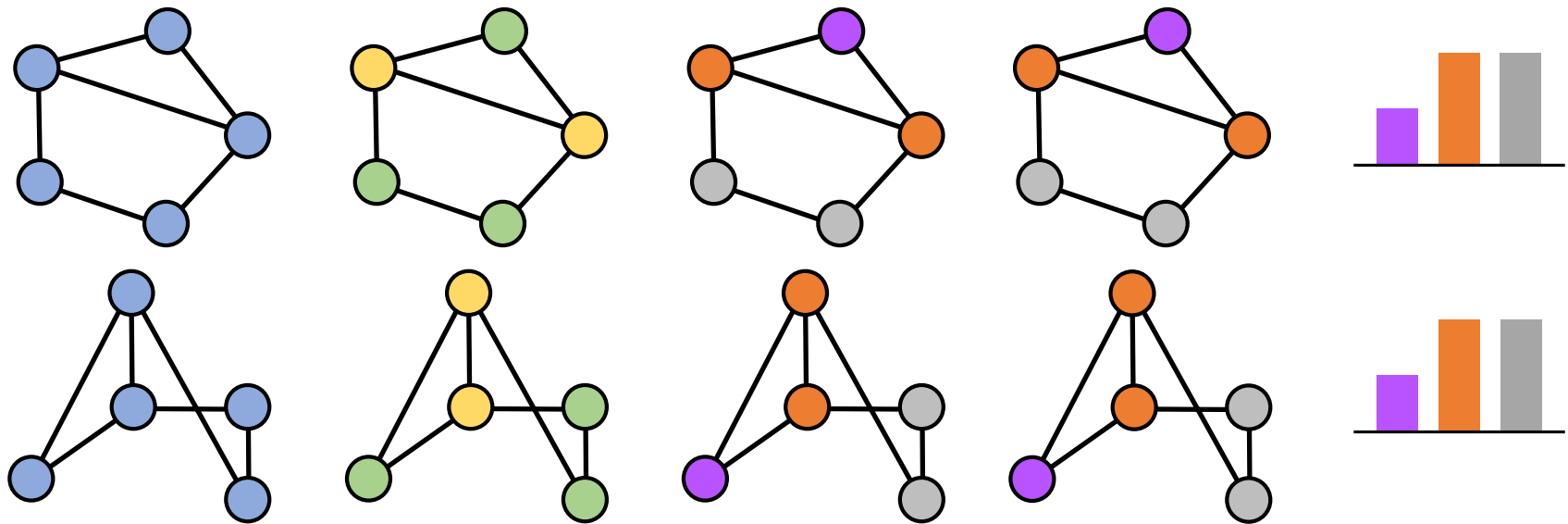
# Weisfeiler-Lehman Test



# Weisfeiler-Lehman Test



# Weisfeiler-Lehman Test

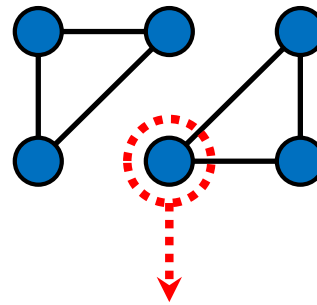
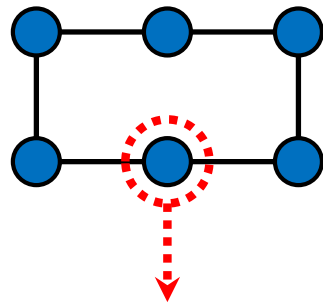




non-isomorphic graphs that are WL-equivalent

**Necessary but *insufficient* condition for  
graph isomorphism!**

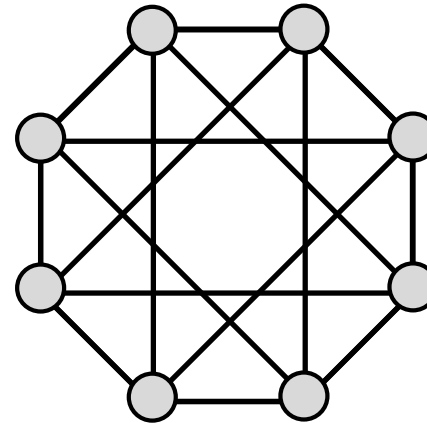
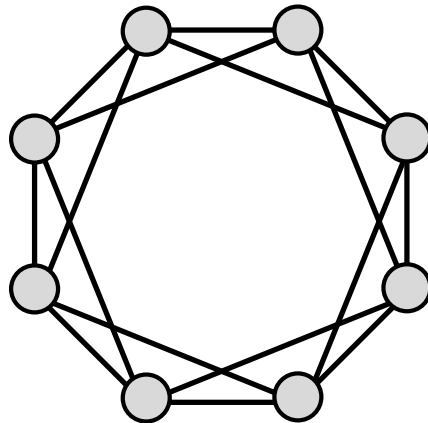
*What does WL test see?*



=

## *What WL cannot test?*

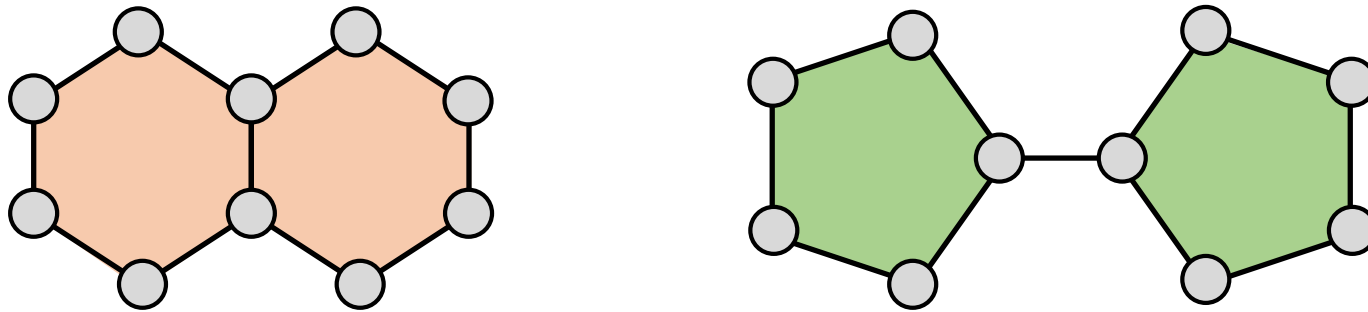
Example of non-isomorphic graphs that cannot be distinguished by Weisfeiler-Lehman test (outputs “possibly isomorphic”)



*r-regular graphs (deg=r at every node) with the same number of nodes*

## *What WL cannot test?*

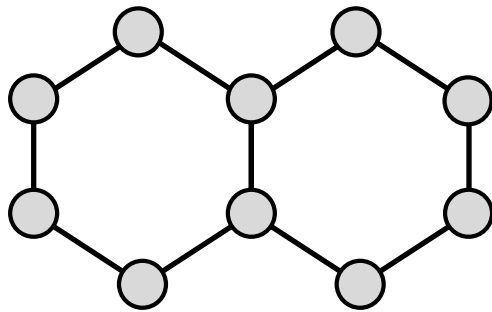
Example of non-isomorphic graphs that cannot be distinguished by Weisfeiler-Lehman test (outputs “possibly isomorphic”)



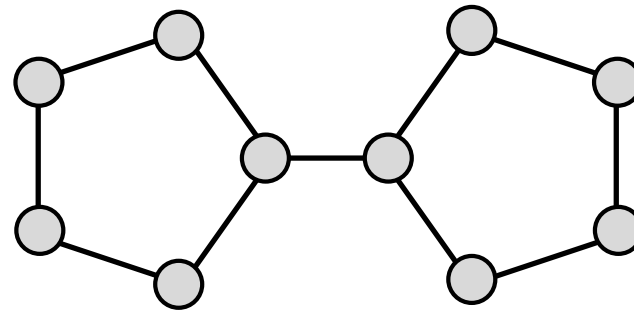
*Any induced connected pattern with  $\geq 3$  nodes (triangles, cycles, etc.)*

## *What WL cannot test?*

Example of non-isomorphic graphs that cannot be distinguished by Weisfeiler-Lehman test (outputs “possibly isomorphic”)



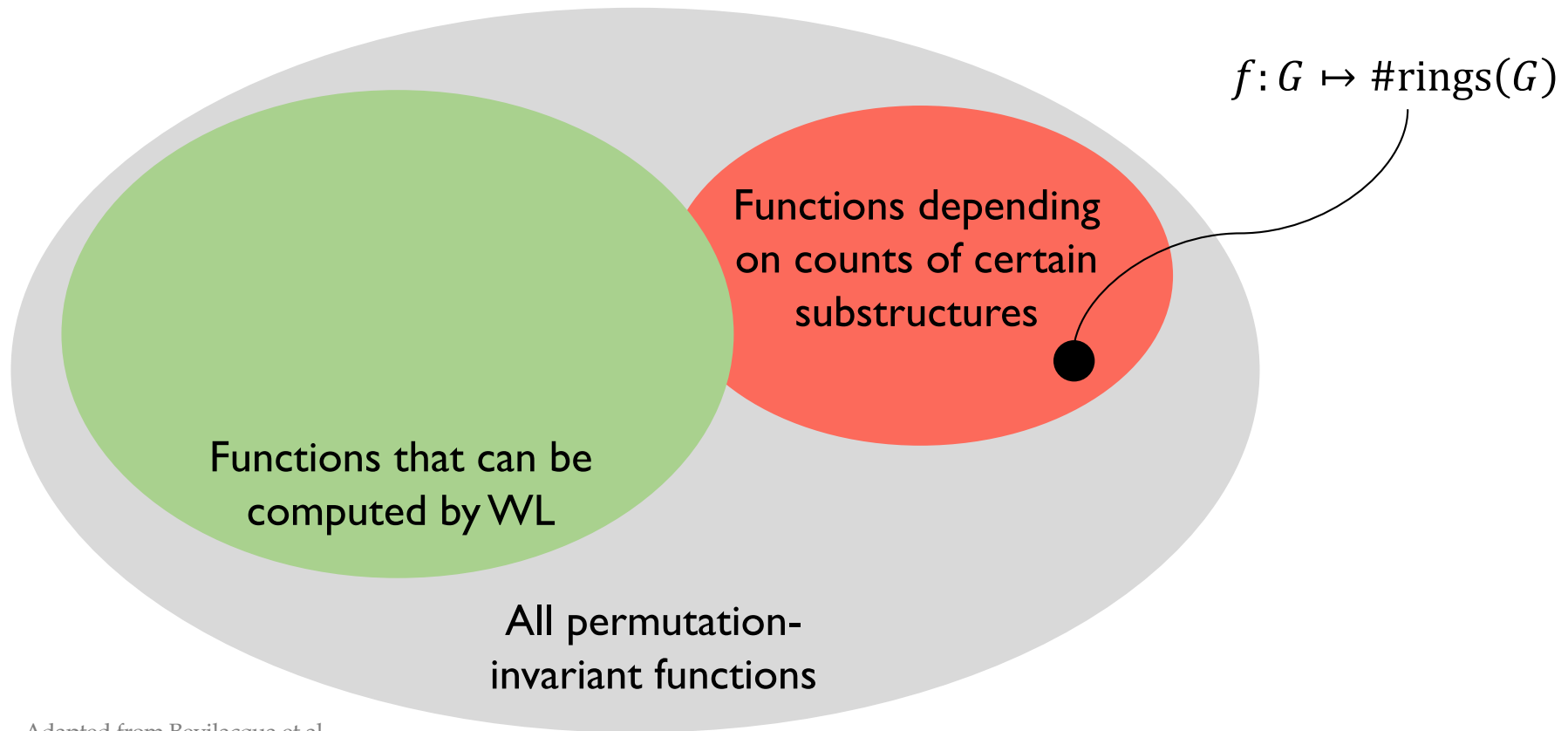
*decalin*



*bicyclo[4.4.0]dec-2-ene*

**Important implications e.g. in chemistry!**

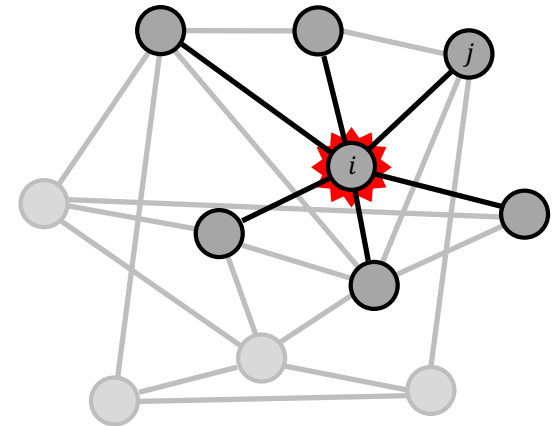
## *Expressive power of Weisfeiler-Lehman*



Adapted from Bevilacqua et al.  
(LoG Tutorial 2022)

## MPNNs vs WL

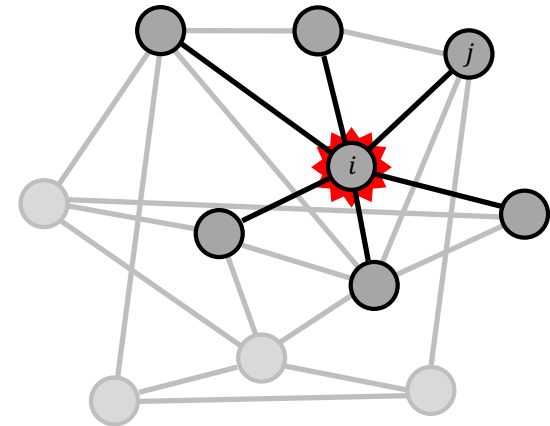
- **WL-test:**  $\mathbf{x}_i \leftarrow \phi(\mathbf{x}_i, \{\{\mathbf{x}_j : j \in \mathcal{N}_i\}\})$   
where  $\phi$  is *injective* (hash function)
- **MPNN:**  $\mathbf{x}_i \leftarrow \phi\left(\mathbf{x}_i, \bigoplus_{j \in \mathcal{N}_i} \psi(\mathbf{x}_i, \mathbf{x}_j)\right)$



**MPNN expressive power is upper-bounded  
by the Weisfeiler-Lehman test**

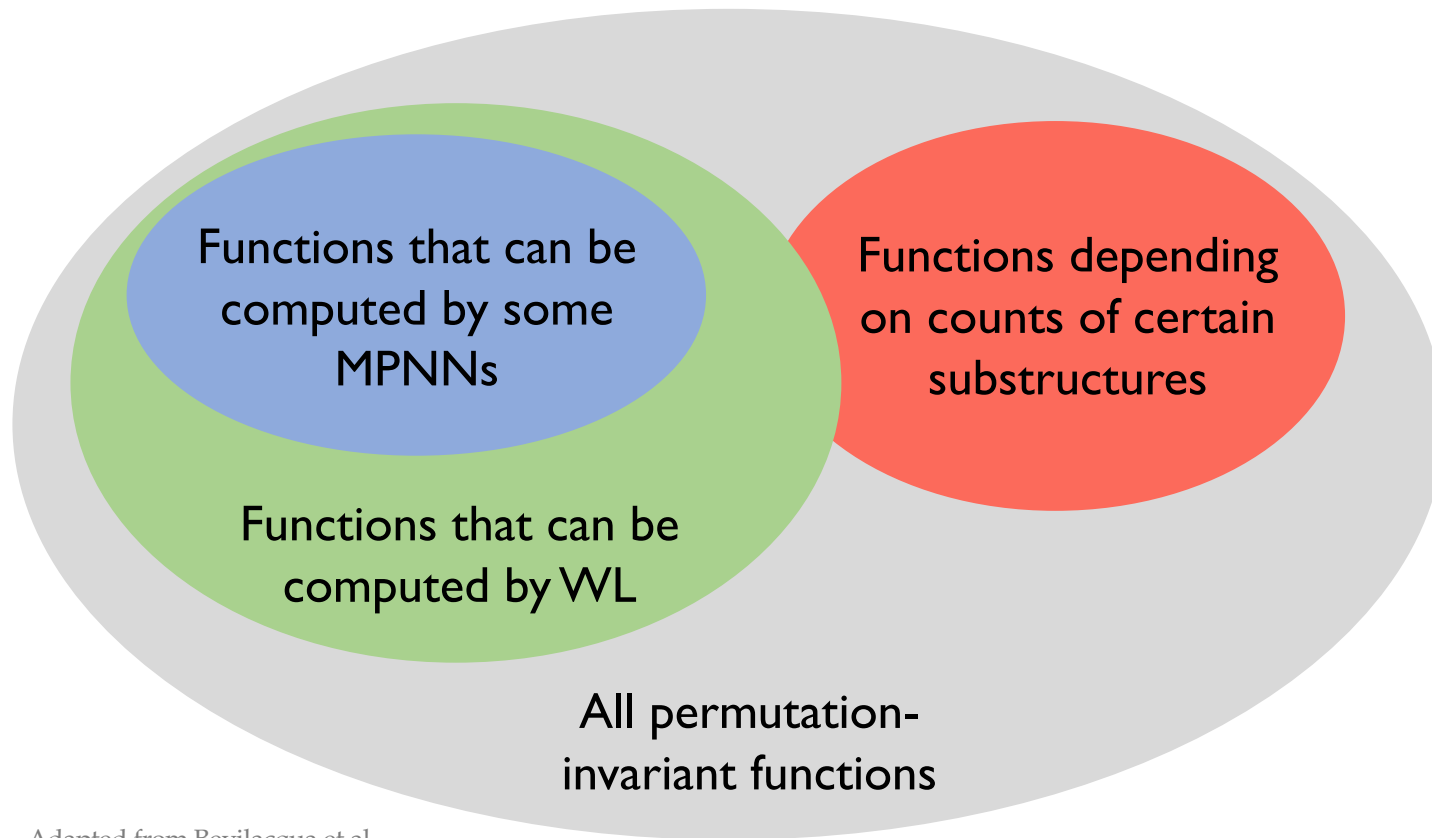
## MPNNs vs WL

- **WL-test:**  $\mathbf{x}_i \leftarrow \phi(\mathbf{x}_i, \{\{\mathbf{x}_j : j \in \mathcal{N}_i\}\})$   
where  $\phi$  is *injective* (hash function)
- **MPNN:**  $\mathbf{x}_i \leftarrow \phi\left(\mathbf{x}_i, \bigoplus_{j \in \mathcal{N}_i} \psi(\mathbf{x}_i, \mathbf{x}_j)\right)$



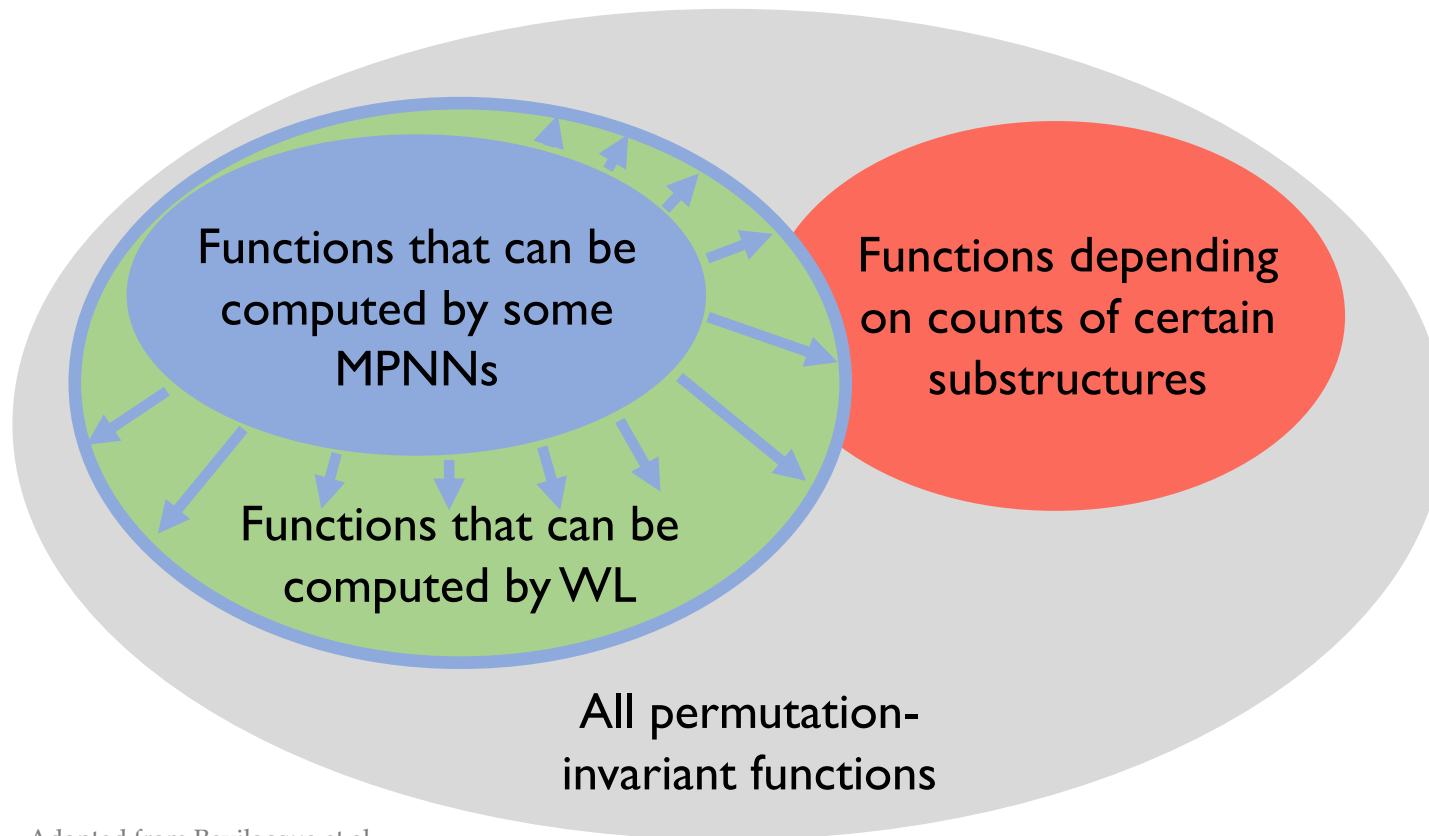
**When is MPNN as expressive as the Weisfeiler-Lehman test?**

## *Expressive power of MPNNs*



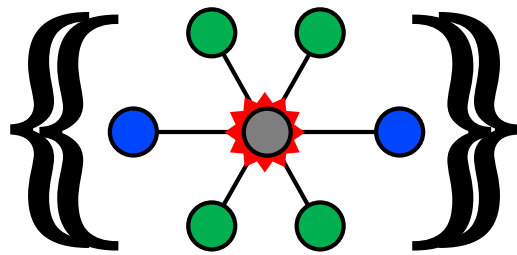
Adapted from Bevilacqua et al.  
(LoG Tutorial 2022)

## *Expressive power of MPNNs*

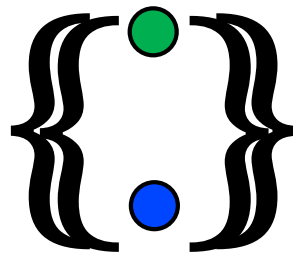


Adapted from Bevilacqua et al.  
(LoG Tutorial 2022)

*Are all Aggregators the same?*

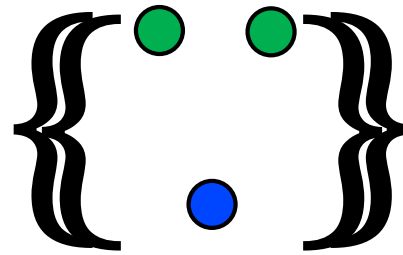


Input



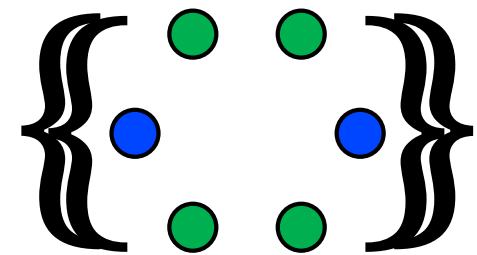
max

“skeleton”  
of the multiset



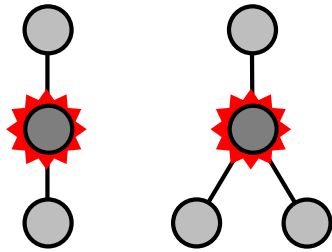
mean

Distribution  
of the multiset

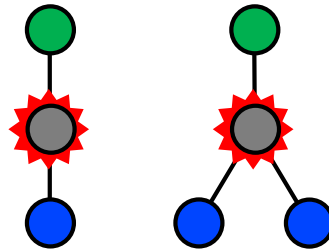


sum

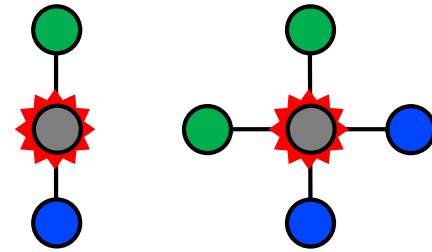
*Are all Aggregators the same?*



**mean** and **max**  
fail to distinguish



**max**  
fails to distinguish



**mean** and **max**  
fail to distinguish

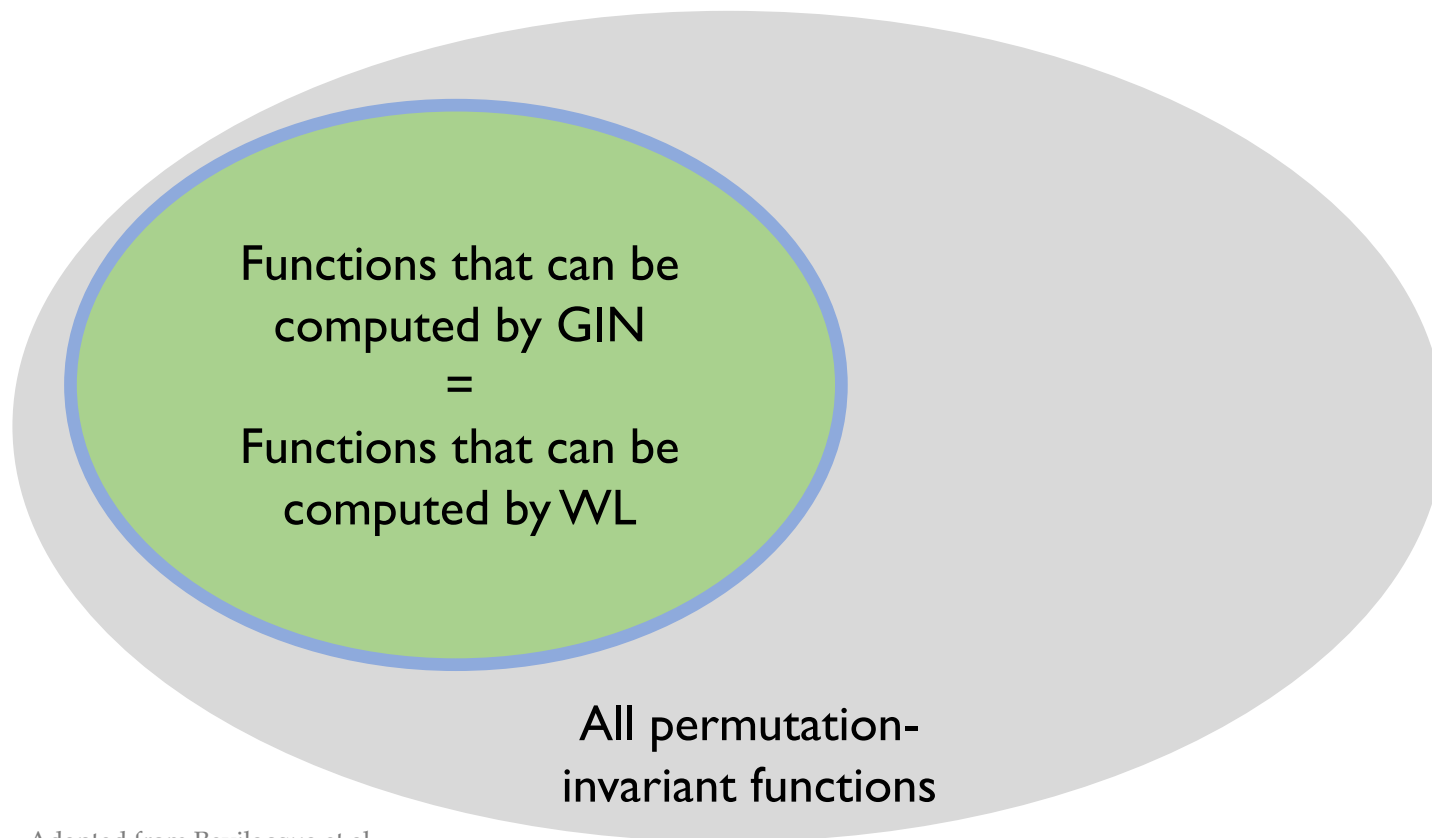
## Graph Isomorphism Network (GIN)

**Theorem:** Assume graph node features are from a countable set. Then, an MPNN with injective aggregator  $\square$ , update function  $\phi$ , and graph-wise readout function, is as powerful as the Weisfeiler-Lehman test.

- Assumption of **discrete countable features** (often not the case in practice)
- GIN: uses an injective multiset function of the form

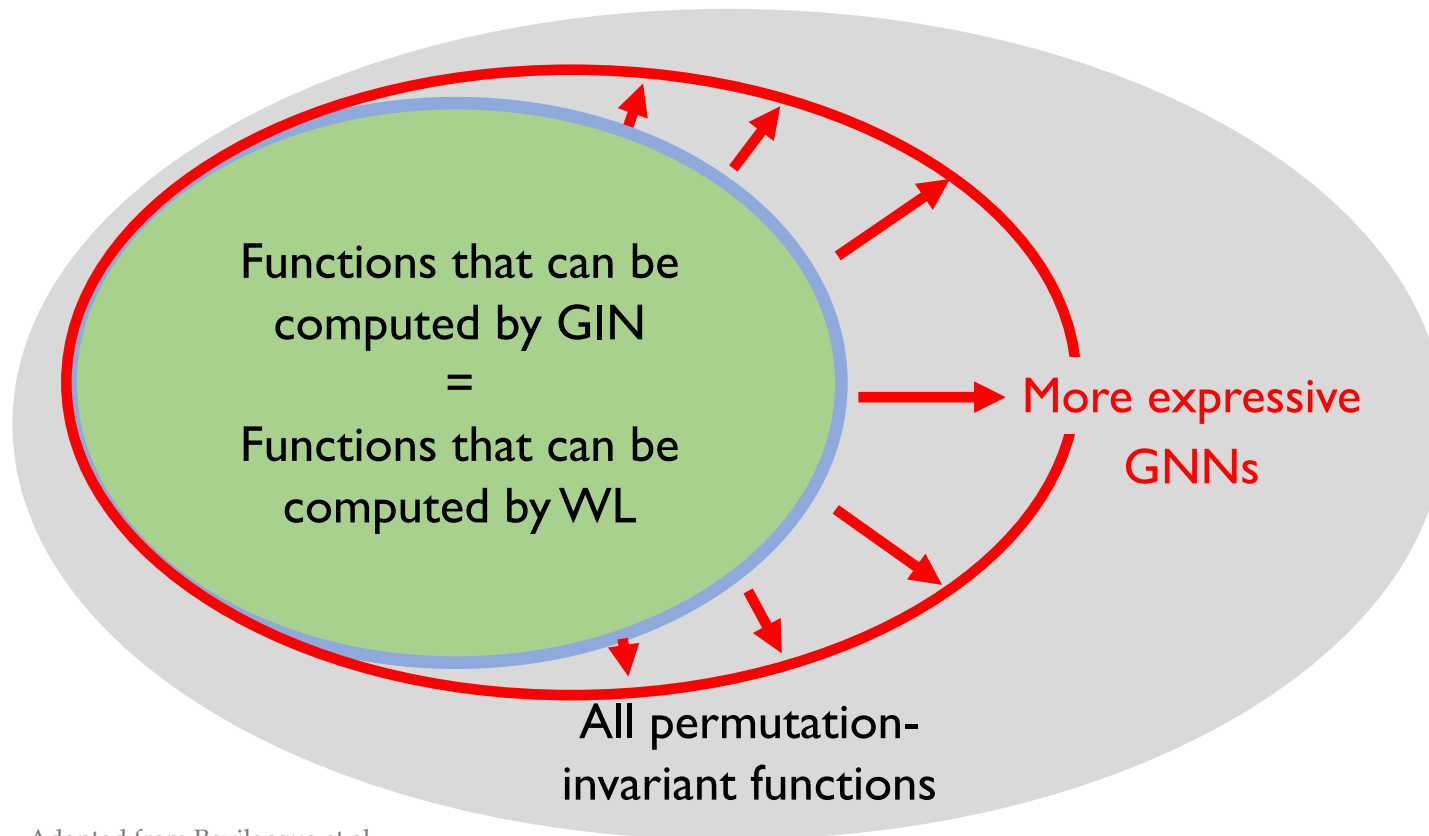
$$\text{MLP} \left( (1 + \epsilon) \mathbf{x}_i + \sum_{j \in \mathcal{N}_i} \mathbf{x}_j \right)$$

## *Expressive power of GIN (“best MPNN”)*



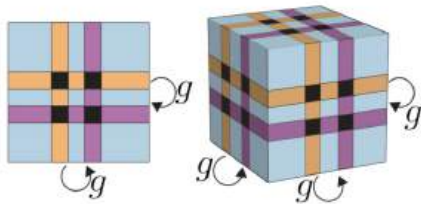
Adapted from Bevilacqua et al.  
(LoG Tutorial 2022)

## *Expressive power of GIN (“best MPNN”)*



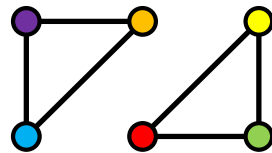
Adapted from Bevilacqua et al.  
(LoG Tutorial 2022)

# *Towards More Expressive GNNs*



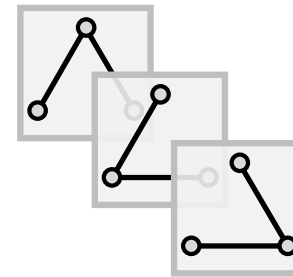
Higher-order  
WL tests

Maron et al. 2019  
Morris et al. 2019



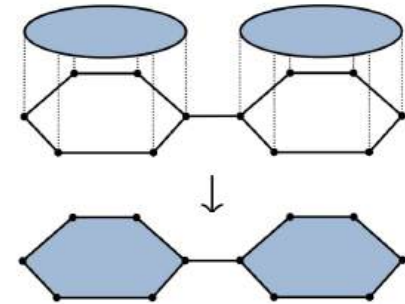
Positional &  
Structural encoding

Monti, Otness et B 2018  
Sato 2020  
Dwivedi et al. 2020  
Bouritsas, Frasca et B 2020  
...many more



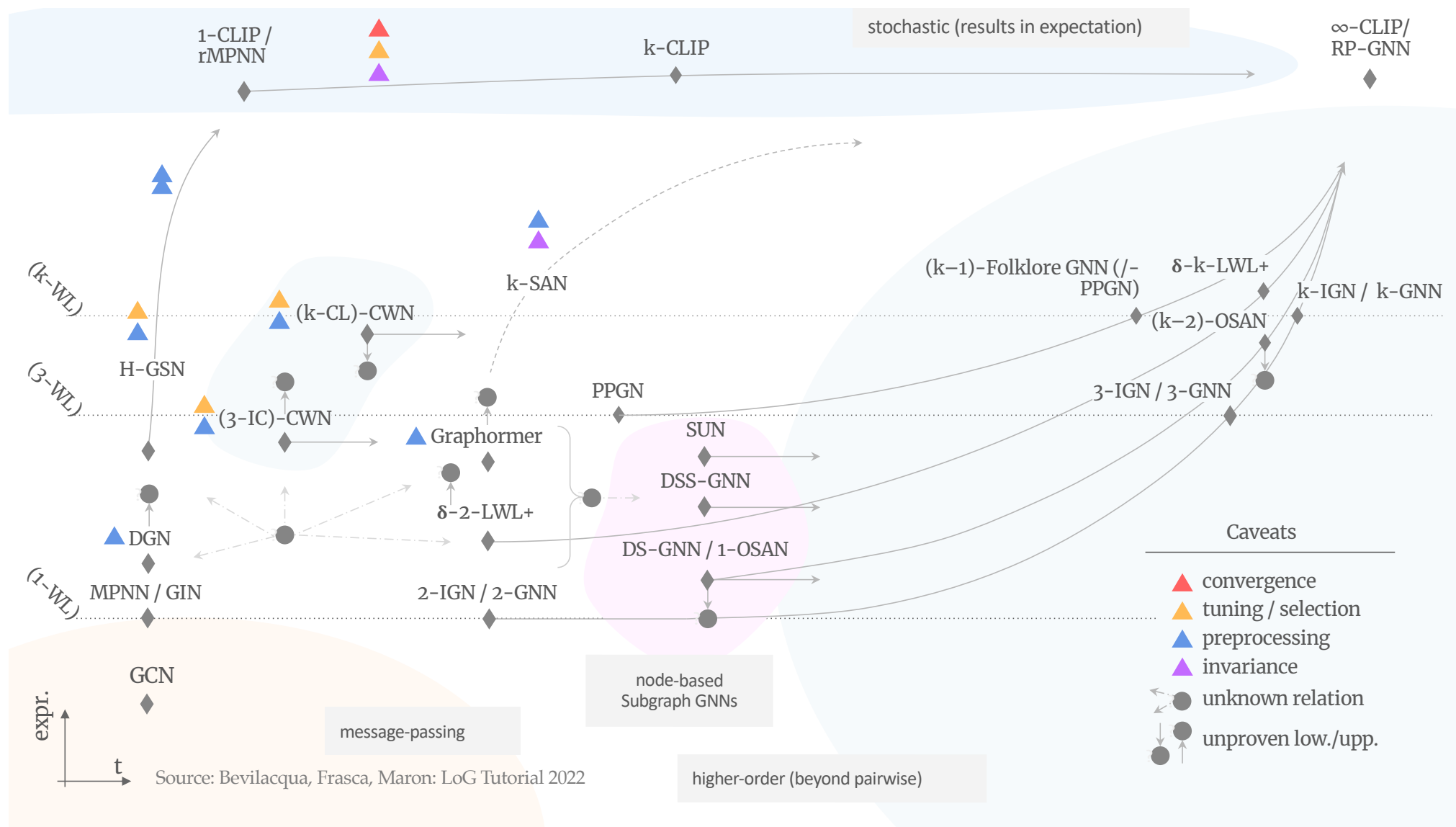
Subgraph  
GNNs

Papp et al. 2021  
Cotta et al. 2021  
Zhao et al. 2021  
Bevilacqua, Frasca et B, Maron 2021  
Frasca et B, Maron 2022



Topological  
message passing

Bodnar, Frasca et B 2021

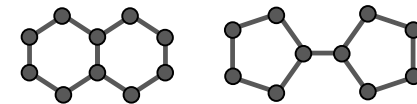


## Theory

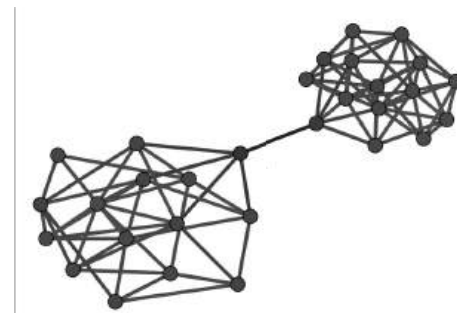


WL test = expressive power

## Practice

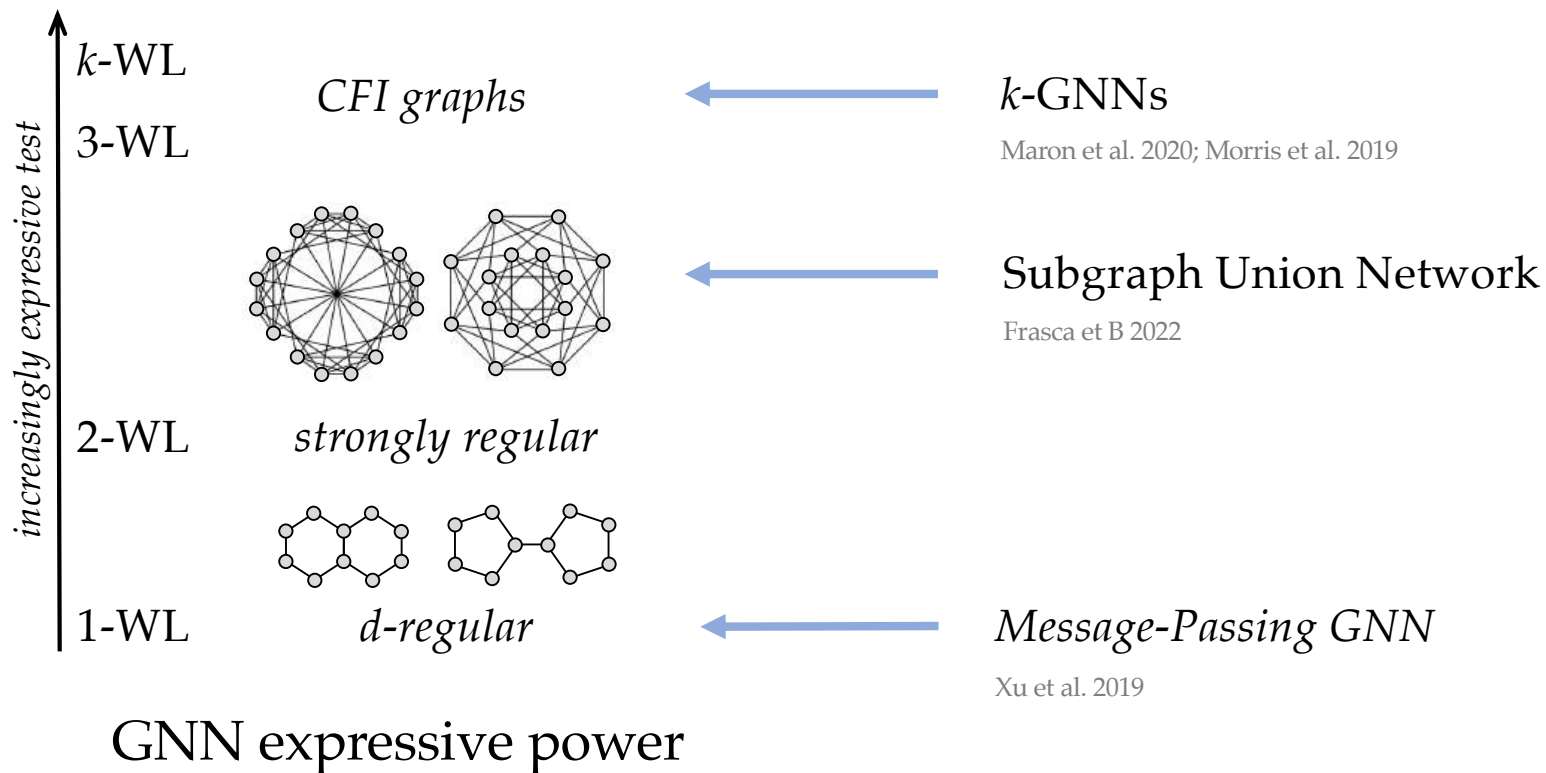


Some non-isomorphic graphs  
cannot be tested by WL



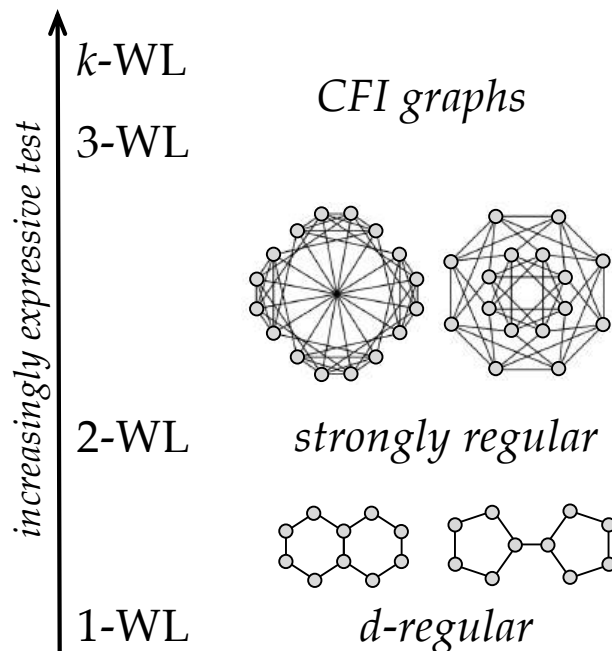
Some graphs may be  
unfriendly for message passing

## More expressive isomorphism tests ( $k$ -WL hierarchy)



Weisfeiler, Lehman 1968 (2-WL); Babai, Mathon 1979 ( $k$ -WL);  
Cai, Furer, Immerman 1992 (CFI graphs)

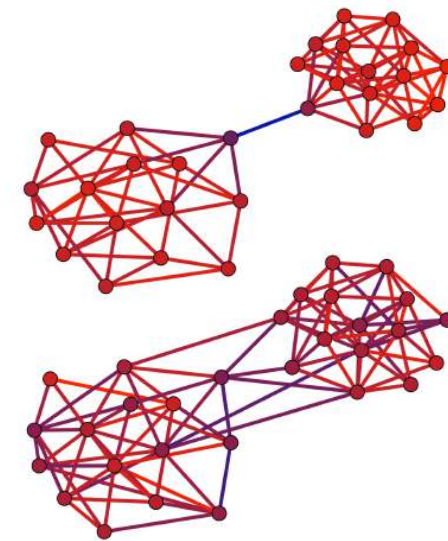
More expressive isomorphism tests ( $k$ -WL hierarchy)



GNN expressive power

Weisfeiler, Lehman 1968 (2-WL); Babai, Mathon 1979 ( $k$ -WL);  
Cai, Fürer, Immerman 1992 (CFI graphs)

Decouple input graph from the computational graph

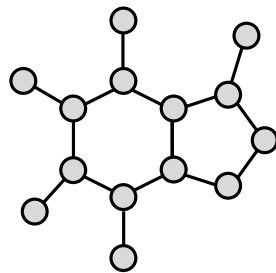


Graph rewiring

Alon, Yahav 2020 (bottlenecks); Hamilton et al. 2017 (neighbour sampling);  
Klicpera et al. 2019 (diffusion); Topping, Di Giovanni et al. 2022 (Ricci flow);  
Deac et al. 2022 (expanders); Barbero et al. 2024 (LASER)

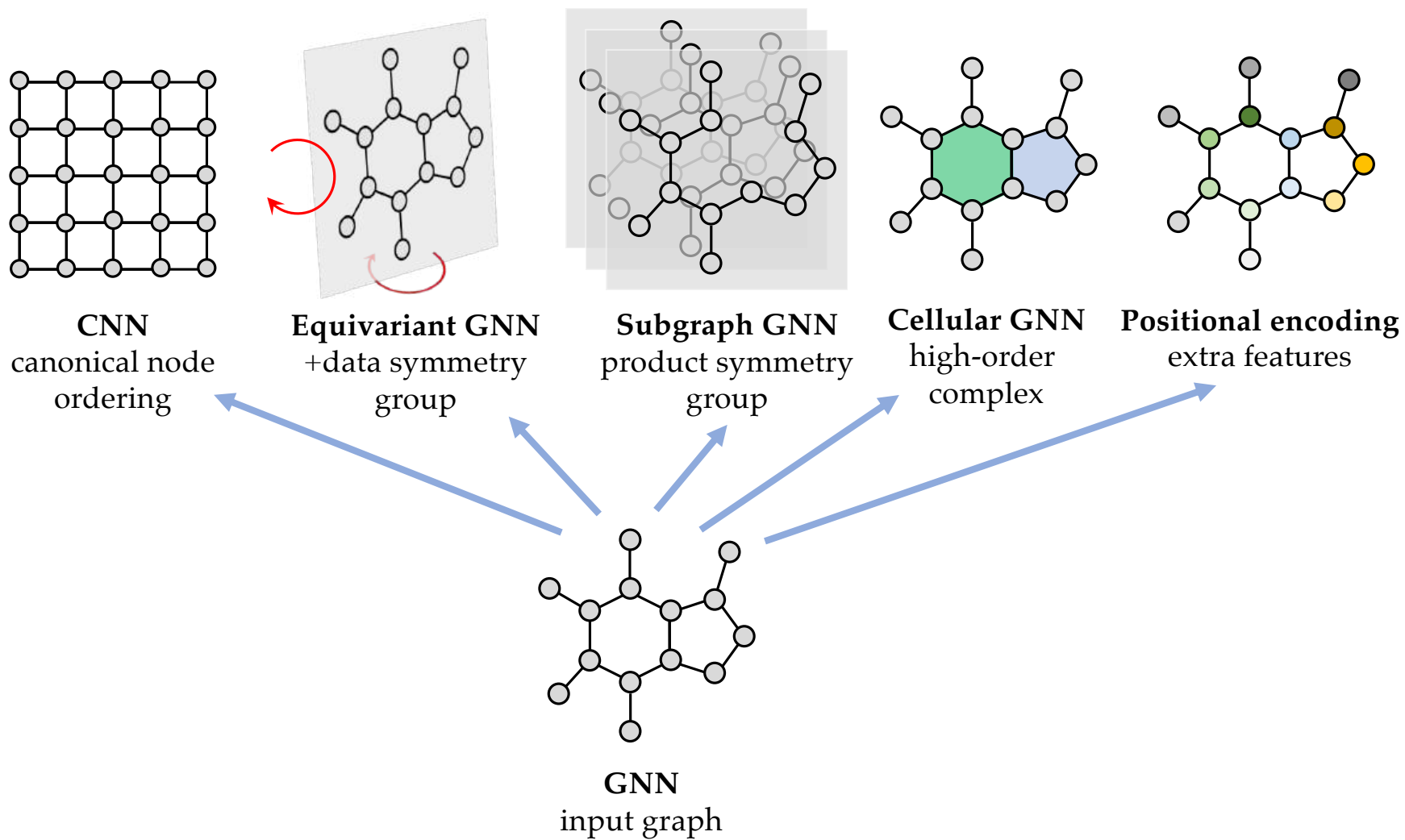
Gap between  
Theory & Practice

# Classical GNNs: propagate information on the input graph

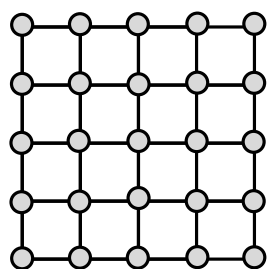


**GNN**  
input graph

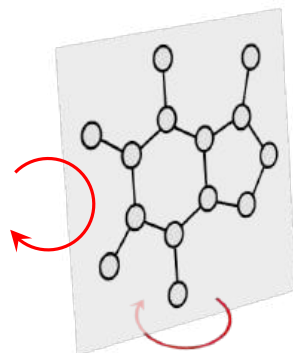
## MORE STRUCTURE



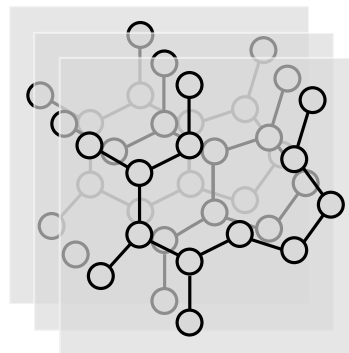
## MORE STRUCTURE



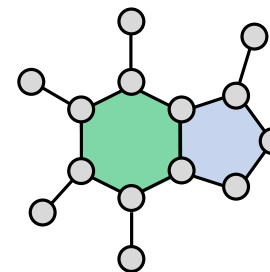
**CNN**  
canonical node  
ordering



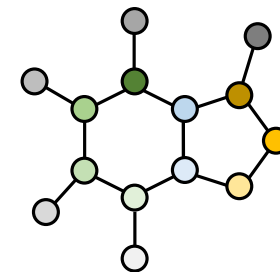
**Equivariant GNN**  
+data symmetry  
group



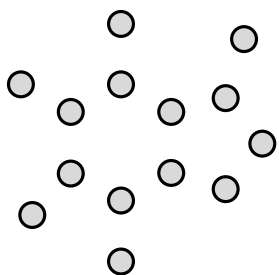
**Subgraph GNN**  
product symmetry  
group



**Cellular GNN**  
high-order  
complex

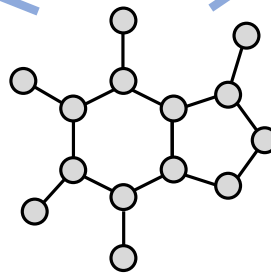


**Positional encoding**  
extra features



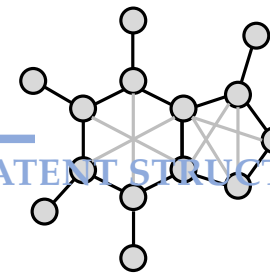
**DeepSet/PointNet**  
no graph

LESS STRUCTURE

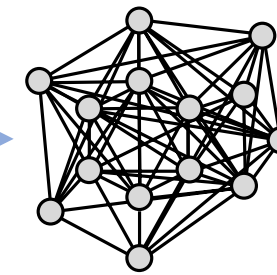


**GNN**  
input graph

LATEX STRUCTURE

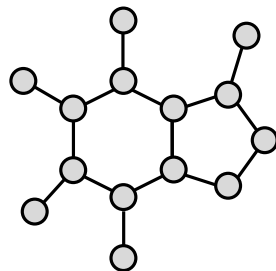


**Graph rewiring**  
modified graph

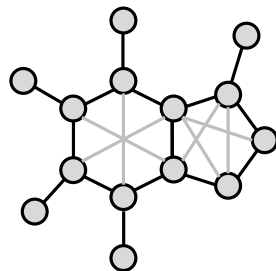


**Transformer**  
learnable graph

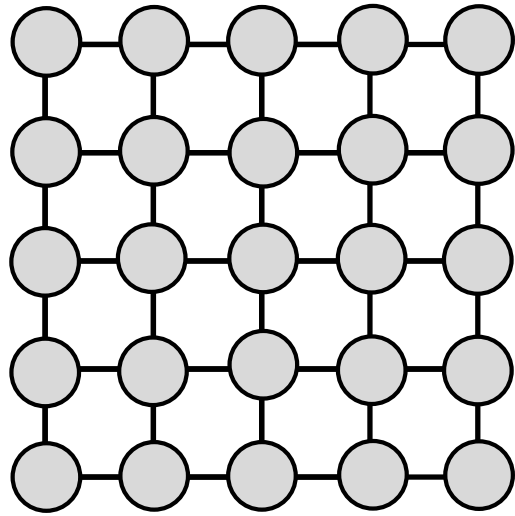
Classical GNNs: propagate information on  
the input graph



“Modern” GNNs: propagate information on  
some other “better” graph



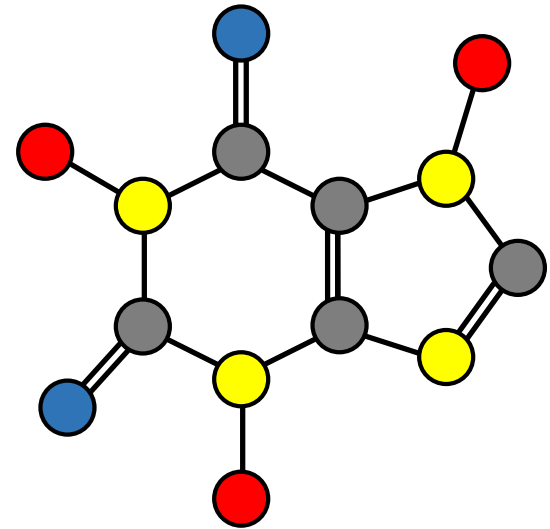
## *Graphs vs Meshes vs Grids*



**Grid**

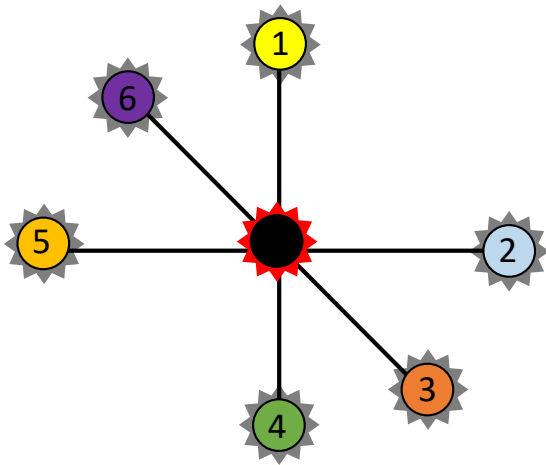


**Mesh**

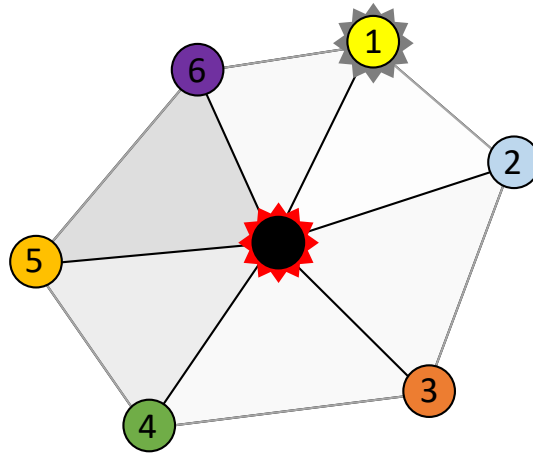


**Graph**

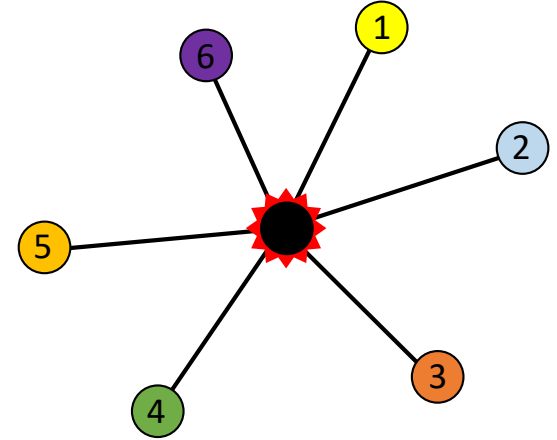
## *Graphs vs Meshes vs Grids*



**Grid**  
Fixed

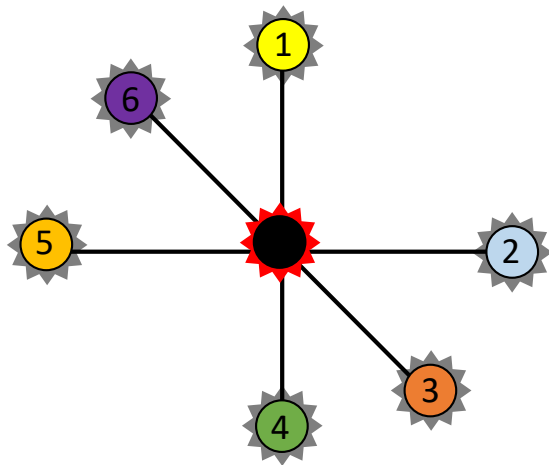


**Mesh**

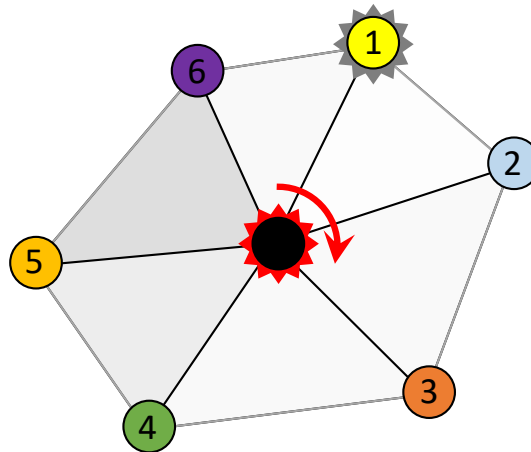


**Graph**

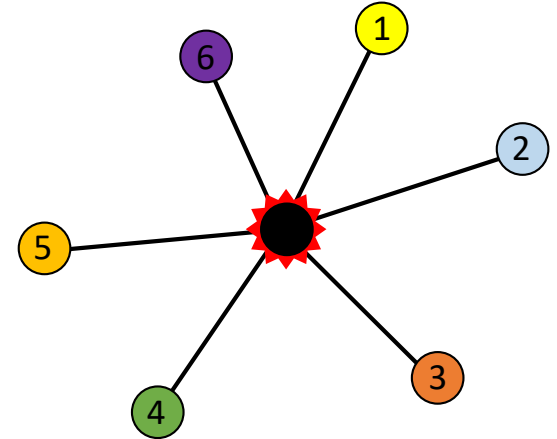
## *Graphs vs Meshes vs Grids*



**Grid**  
Fixed

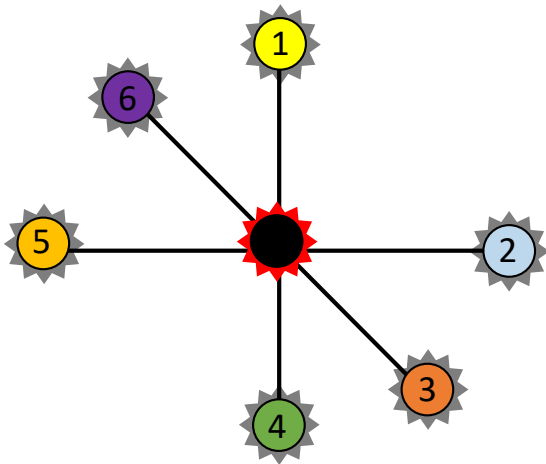


**Mesh**  
Rotation

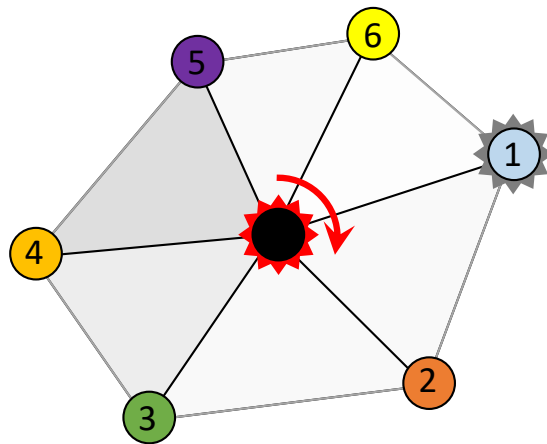


**Graph**

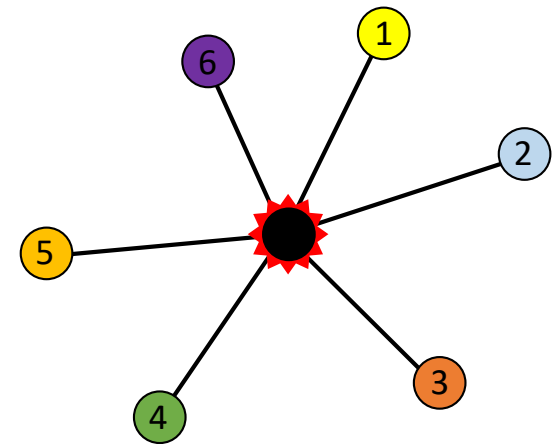
## *Graphs vs Meshes vs Grids*



**Grid**  
Fixed



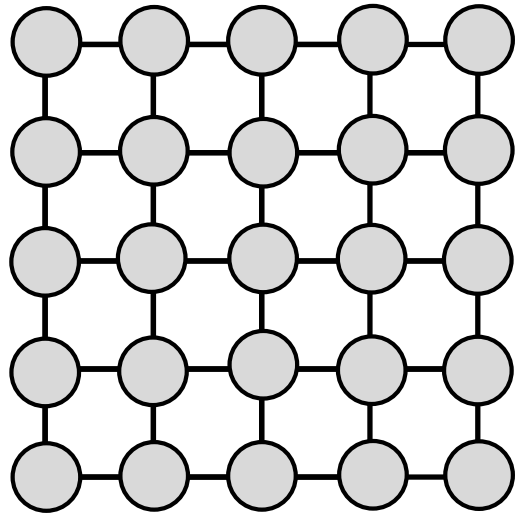
**Mesh**  
Rotation



**Graph**  
Permutation

Graphs have the least structure

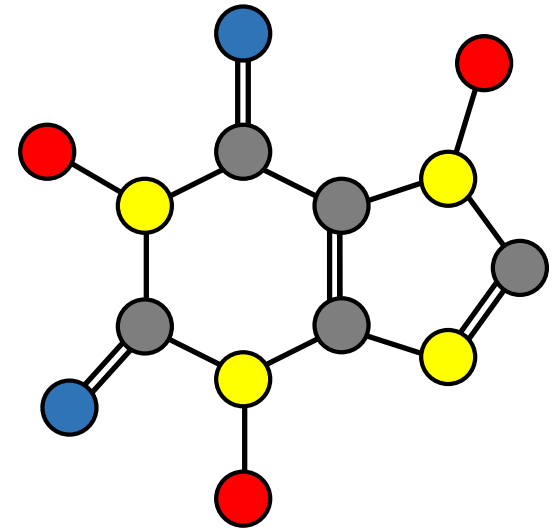
## *Graphs vs Meshes vs Grids*



**Grid**

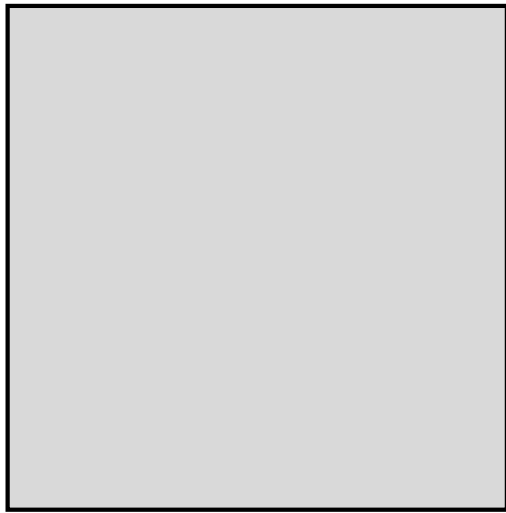


**Mesh**



**Graph**

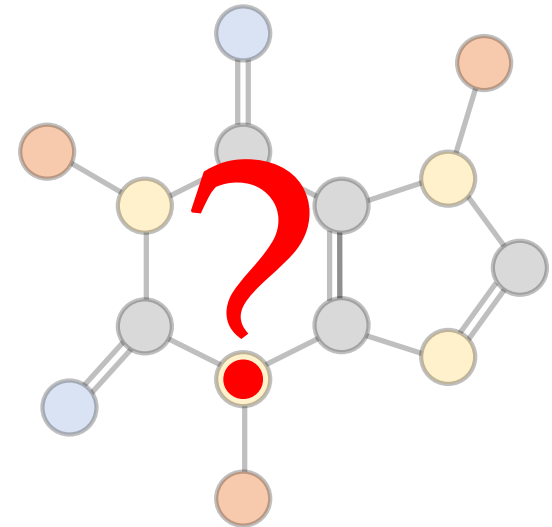
## *Graphs vs Meshes vs Grids*



**Grid**

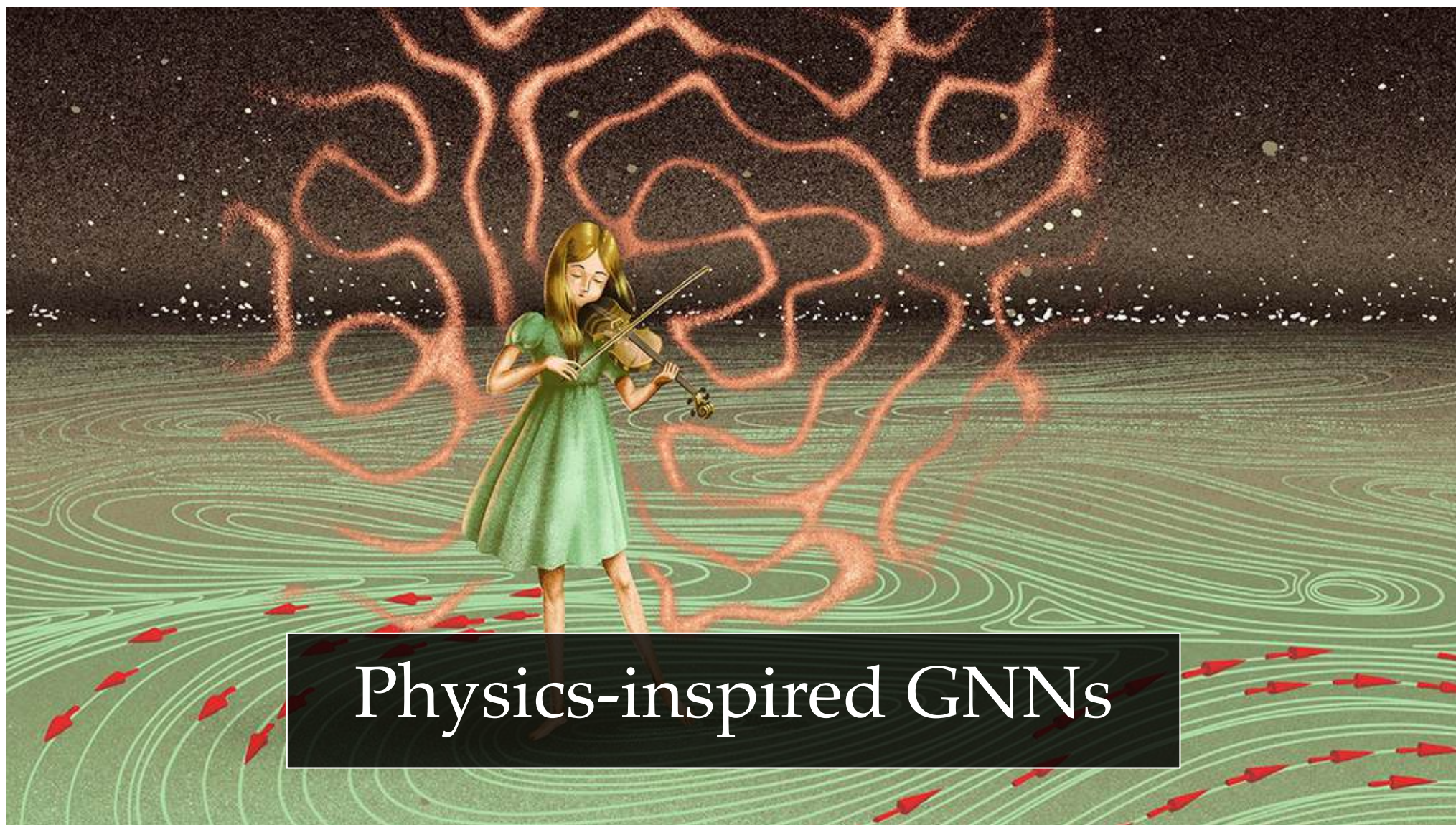


**Mesh**



**Graph**

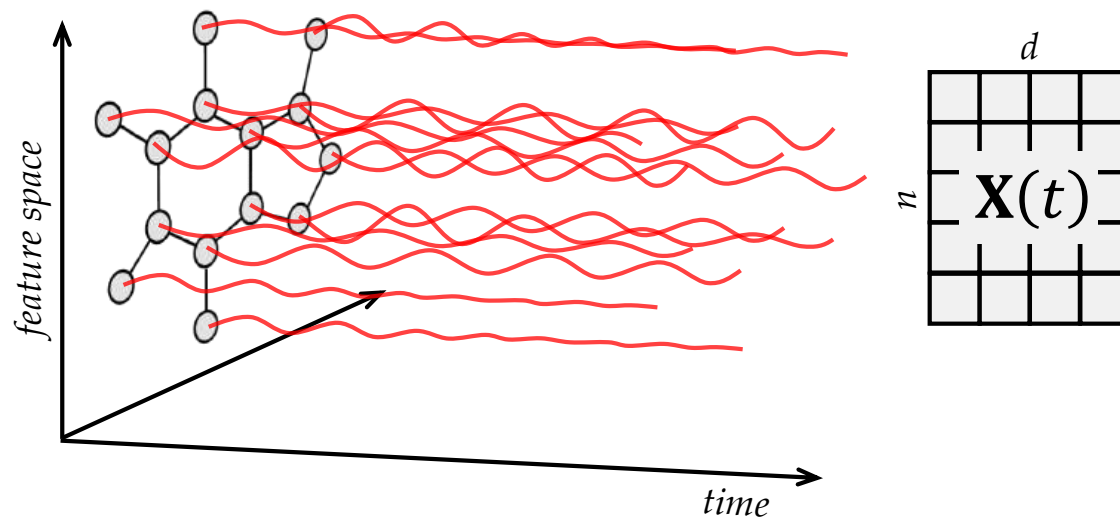
Continuous models for GNNs?



Physics-inspired GNNs

# Physical metaphor of Graph ML

- GNN = dynamic system

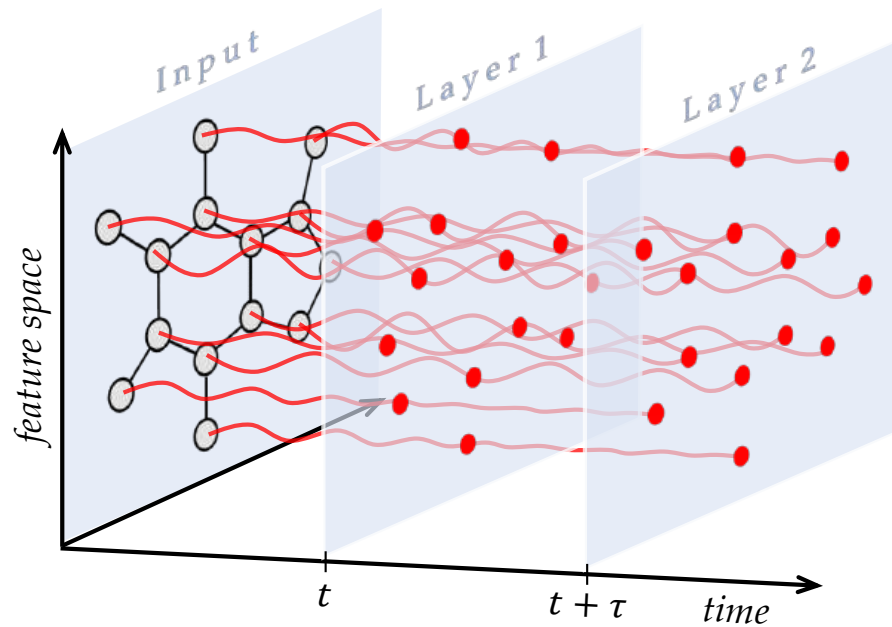


$$\begin{matrix} & d \\ n & \begin{bmatrix} & & & \\ & & & \\ & & & \\ & & & \\ & & & \end{bmatrix} \\ & \mathbf{X}(t) \end{matrix}$$

$$\dot{\mathbf{X}}(t) = \mathbf{F}_{\boldsymbol{\theta}(t)}(\mathbf{X}(t), \mathcal{G})$$

Haber, Ruthotto 2017; Chen et al. 2019 (Neural ODEs); Xhonneau et al. 2020 (CGNN); Chamberlain et B. 2021 (GRAND, BLEND); Eliasof, Haber 2021 (PDE-GCN); Di Giovanni, Rowbottom et B 2022 (GRAFF), Rusch et B 2022 (GraphCON); Wu et B, Yan 2023; Eliasof et al. 2023; 2024 (TDE-GNN)

# Physical metaphor of Graph ML



- GNN = dynamic system
- layers = discretisation of time
- graph = coupling function  
(discretisation of space)

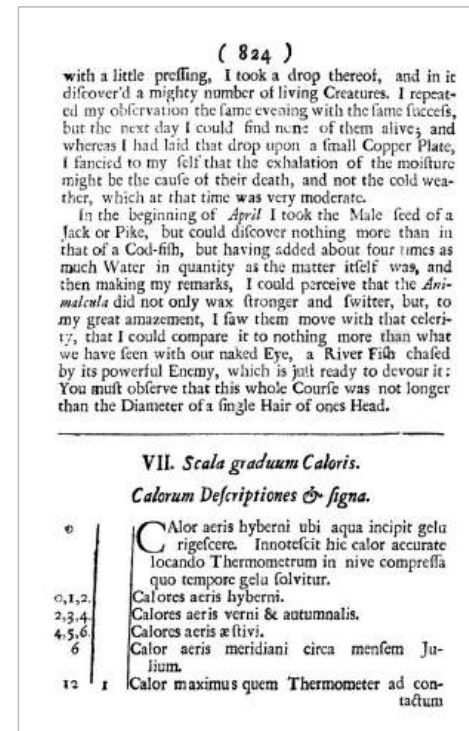
$$\mathbf{X}(t + \tau) = \mathbf{X}(t) + \tau \mathbf{F}_{\boldsymbol{\theta}(t)}(\mathbf{X}(t), \mathcal{G})$$

Haber, Ruthotto 2017; Chen et al. 2019 (Neural ODEs); Xhonneau et al. 2020 (CGNN); Chamberlain et B. 2021 (GRAND, BLEND); Eliasof, Haber 2021 (PDE-GCN); Di Giovanni, Rowbottom et B 2022 (GRAFF), Rusch et B 2022 (GraphCON); Wu et B, Yan 2023; Eliasof et al. 2023; 2024 (TDE-GNN)

# Heat Diffusion

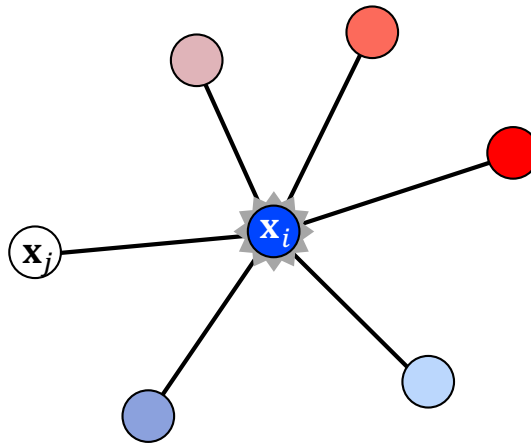
**Newton Law of Cooling:**  
“the [temperature] a hot  
body loses in a given time  
is proportional to the  
temperature difference  
between the object and the  
environment”

Anonymous 1701



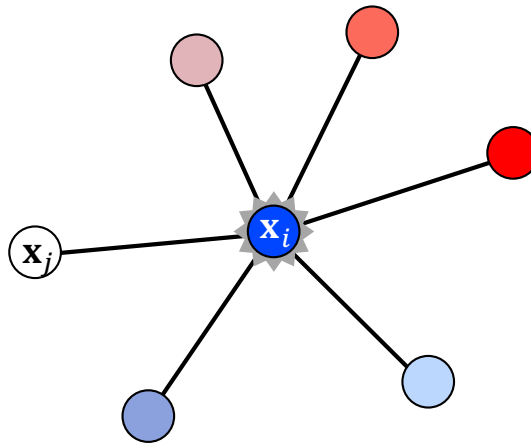
I. Newton

## *Heat Diffusion Equation on Graphs*



$$\dot{\mathbf{x}}_i(t) = \mathbf{x}_i(t) - \frac{1}{d_i} \sum_{j \in \mathcal{N}_i} a_{ij} \mathbf{x}_j(t)$$

# Heat Diffusion Equation on Graphs



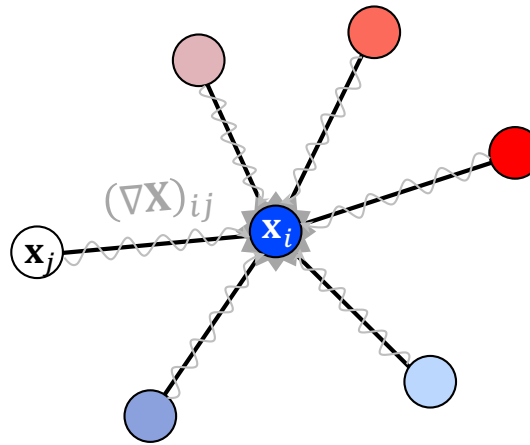
$$\dot{\mathbf{x}}_i(t) = \mathbf{x}_i(t) - \frac{1}{d_i} \sum_{j \in \mathcal{N}_i} a_{ij} \mathbf{x}_j(t)$$

rate of temperature change

self temperature

temperature of the environment

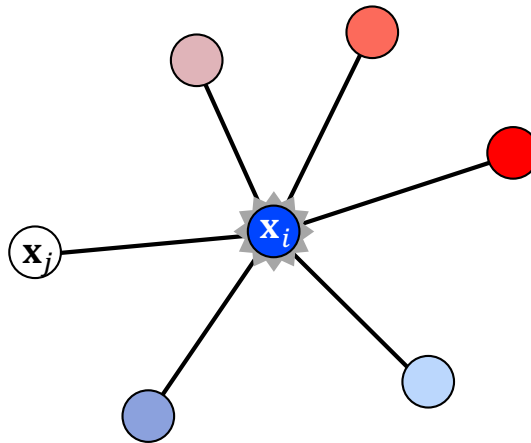
## Heat Diffusion Equation on Graphs



$$\dot{\mathbf{x}}_i(t) = \frac{1}{d_i} \sum_{j \in \mathcal{N}_i} a_{ij} \underbrace{(\mathbf{x}_i(t) - \mathbf{x}_j(t))}_{\text{gradient} - (\nabla \mathbf{X})_{ij}}$$

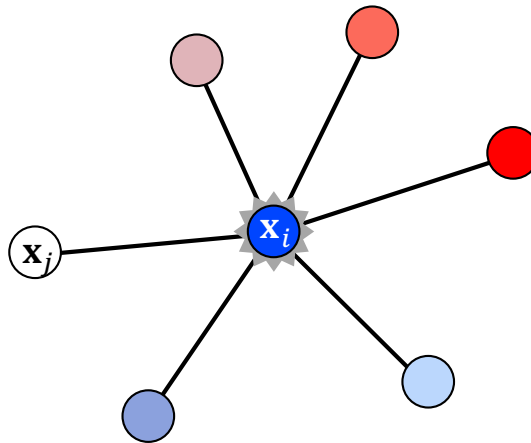
divergence  
div

## *Heat Diffusion Equation on Graphs*



$$\dot{\mathbf{X}}(t) = -\text{div}(\nabla \mathbf{X}(t))$$

## *Heat Diffusion Equation on Graphs*



$$\dot{\mathbf{X}}(t) = \Delta \mathbf{X}(t)$$

## Heat Diffusion Equation as a prototypical Gradient Flow

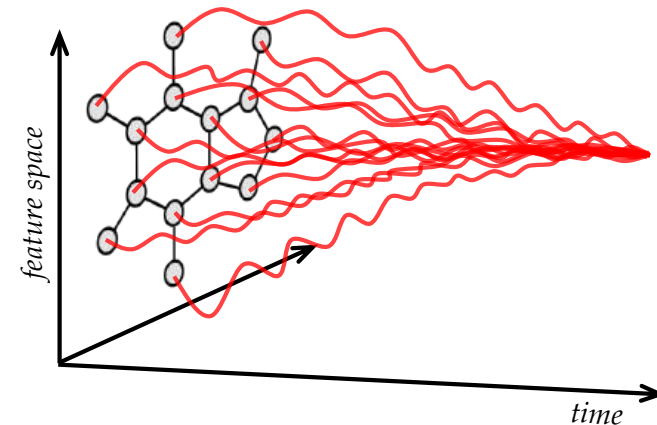
$$\dot{\mathbf{X}}(t) = -\nabla \mathcal{E}(\mathbf{X}(t))$$

$$\mathcal{E}_{\text{DIR}}(\mathbf{X}) = \frac{1}{2} \sum_{j \in \mathcal{N}_i} \|(\nabla \mathbf{X})_{ij}\|^2 = \frac{1}{2} \text{trace}(\mathbf{X}^T \Delta \mathbf{X})$$



**G. Dirichlet**

- Heat equation is the gradient flow of the Dirichlet energy
- “Smoothness” of the node features
- Dirichlet energy **decreases along the flow**
- In the limit  $t \rightarrow \infty$  results in “oversmoothing”



## Heat Diffusion Equation as a prototypical Gradient Flow

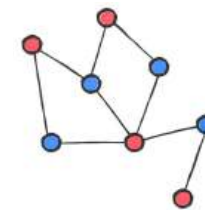
$$\dot{\mathbf{X}}(t) = -\nabla \mathcal{E}(\mathbf{X}(t))$$

$$\mathcal{E}_{\text{DIR}}(\mathbf{X}) = \frac{1}{2} \sum_{j \in \mathcal{N}_i} \|(\nabla \mathbf{X})_{ij}\|^2 = \frac{1}{2} \text{trace}(\mathbf{X}^T \Delta \mathbf{X})$$

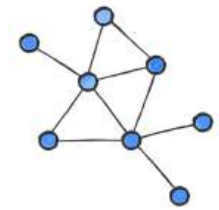


**G. Dirichlet**

- Heat equation is the gradient flow of the Dirichlet energy
- “Smoothness” of the node features
- Dirichlet energy **decreases along the flow**
- In the limit  $t \rightarrow \infty$  results in “oversmoothing”
- Not very expressive: works only in homophilic graphs (“similar neighbours”)

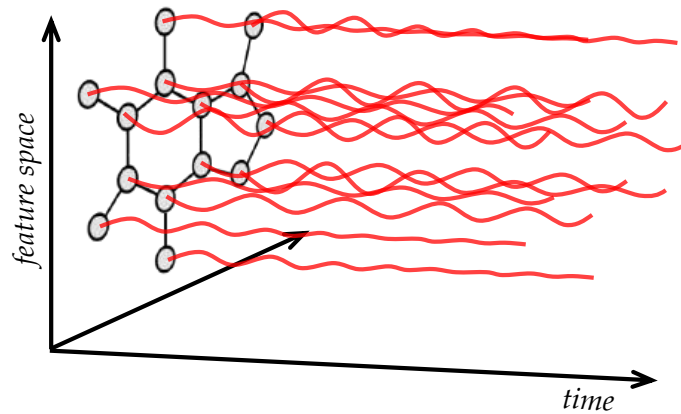


*heterophilic*



*homophilic*

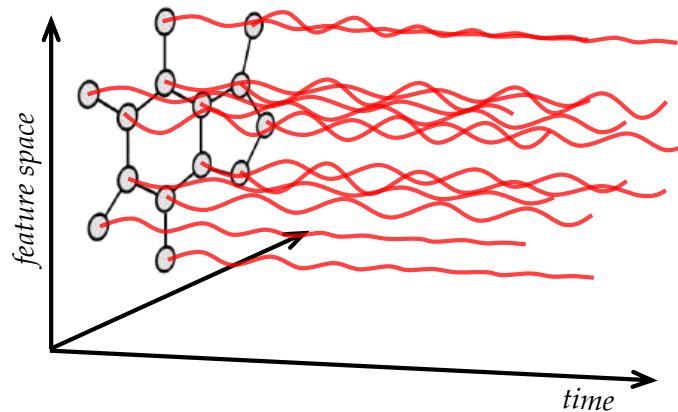
## *Gradient Flow Framework (GRAFF)*



**Traditional GNNs**

$$\dot{\mathbf{X}}(t) = \mathbf{F}_{\boldsymbol{\theta}(t)}(\mathbf{X}(t), \mathcal{G})$$

## Gradient Flow Framework (GRAFF)



**Traditional GNNs**

$$\mathbf{X}(k + 1) = \mathbf{X}(k) + \tau \mathbf{F}_{\boldsymbol{\theta}(k)}(\mathbf{X}(k), \mathcal{G})$$

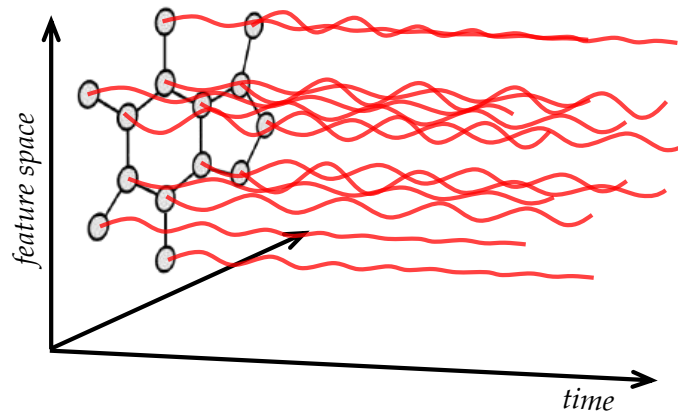
- Parametrize **evolution equations**

**GRAFF**

$$\mathcal{E}_{\boldsymbol{\theta}(t)}(\mathbf{X}(t), \mathcal{G})$$

- Parametrize **energy**

## Gradient Flow Framework (GRAFF)



**Traditional GNNs**

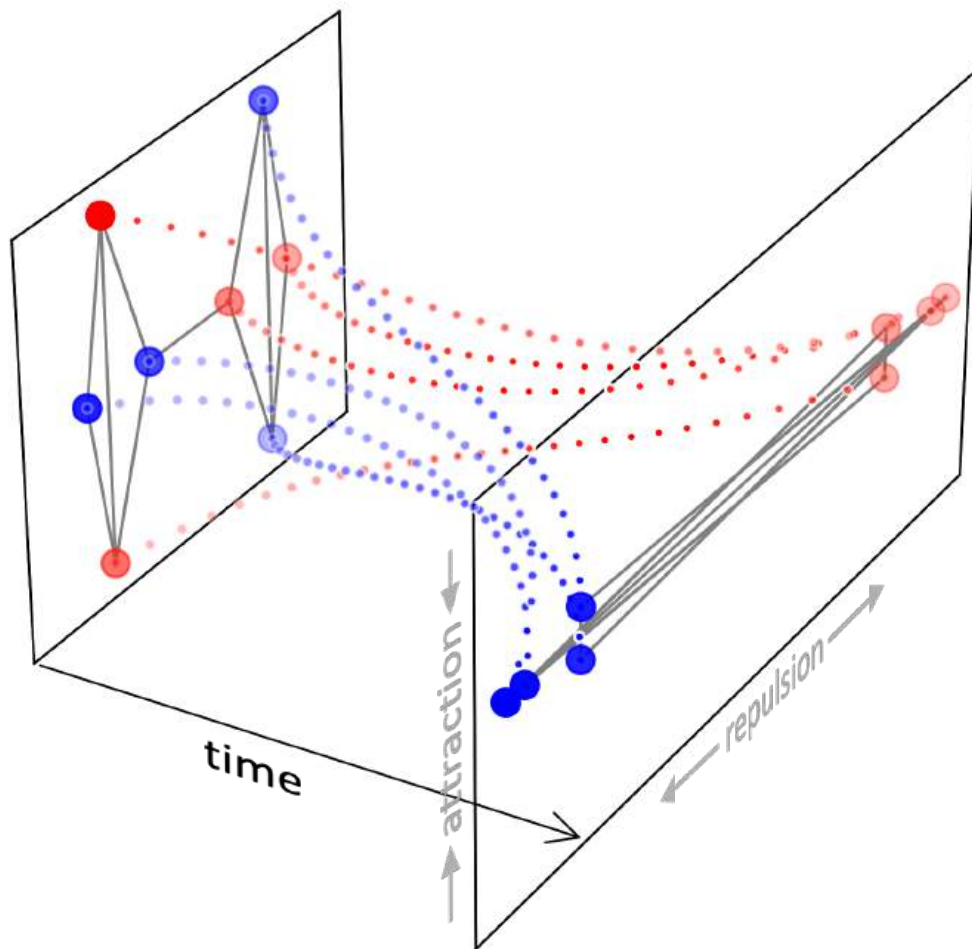
$$\mathbf{X}(k + 1) = \mathbf{X}(k) + \tau \mathbf{F}_{\boldsymbol{\theta}(k)}(\mathbf{X}(k), \mathcal{G})$$

- Parametrize **evolution equations**

**GRAFF**

$$\dot{\mathbf{X}}(t) = -\nabla \mathcal{E}_{\boldsymbol{\theta}(t)}(\mathbf{X}(t), \mathcal{G})$$

- Parametrize **energy**
- Derive evolution equation as GF
- Better “interpretability”

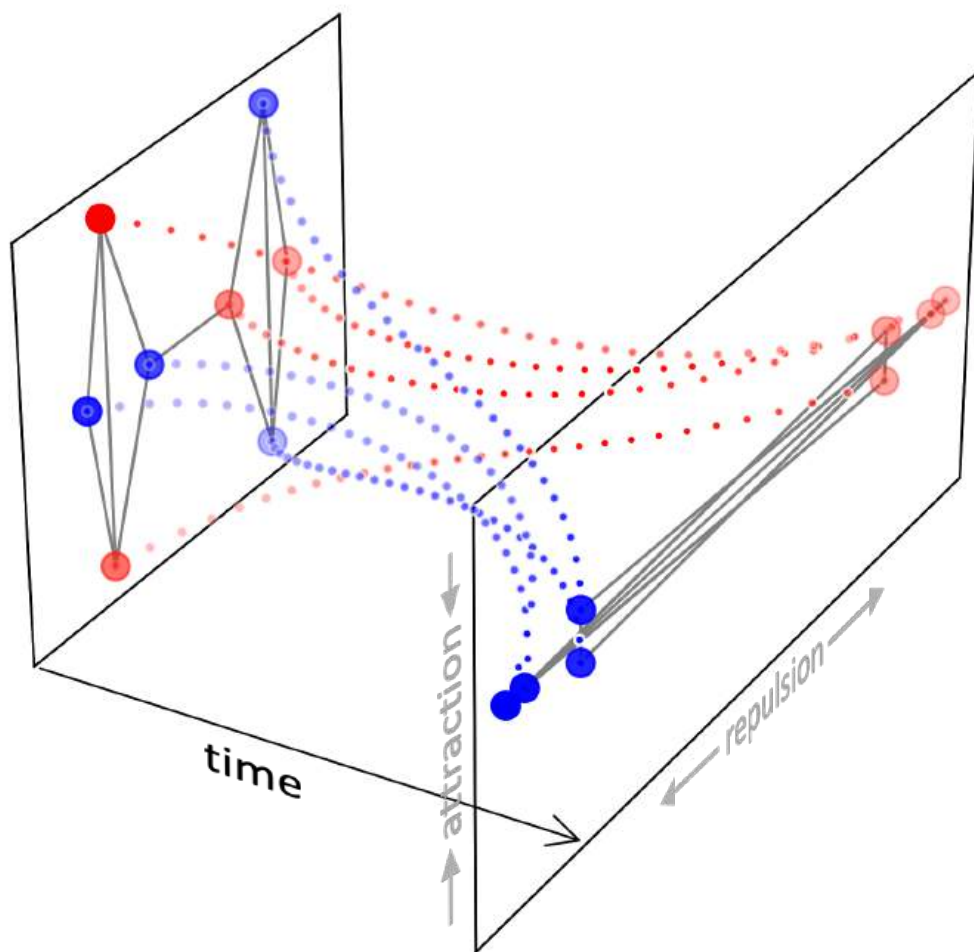


$$\varepsilon_{\theta}(\mathbf{X}) = -\frac{1}{2} \sum_{j \in \mathcal{N}_i} \bar{a}_{ij} \langle \mathbf{x}_i, \mathbf{W} \mathbf{x}_j \rangle$$

- **Attraction** along positive eigenvectors of  $\mathbf{W}$
- **Repulsion** along negative eigenvectors of  $\mathbf{W}$

$$\dot{\mathbf{X}}(t) = \bar{\mathbf{A}} \mathbf{X}(t) \mathbf{W}$$

**Theorem:** Linear graph diffusion (“convolutional GNN”) with appropriately designed channel mixing matrix  $\mathbf{W}$  (symmetric & with sufficiently large negative eigenvalues) can provably avoid oversmoothing.



$$\varepsilon_{\theta}(\mathbf{X}) = -\frac{1}{2} \sum_{j \in \mathcal{N}_i} \bar{a}_{ij} \langle \mathbf{x}_i, \mathbf{W} \mathbf{x}_j \rangle$$

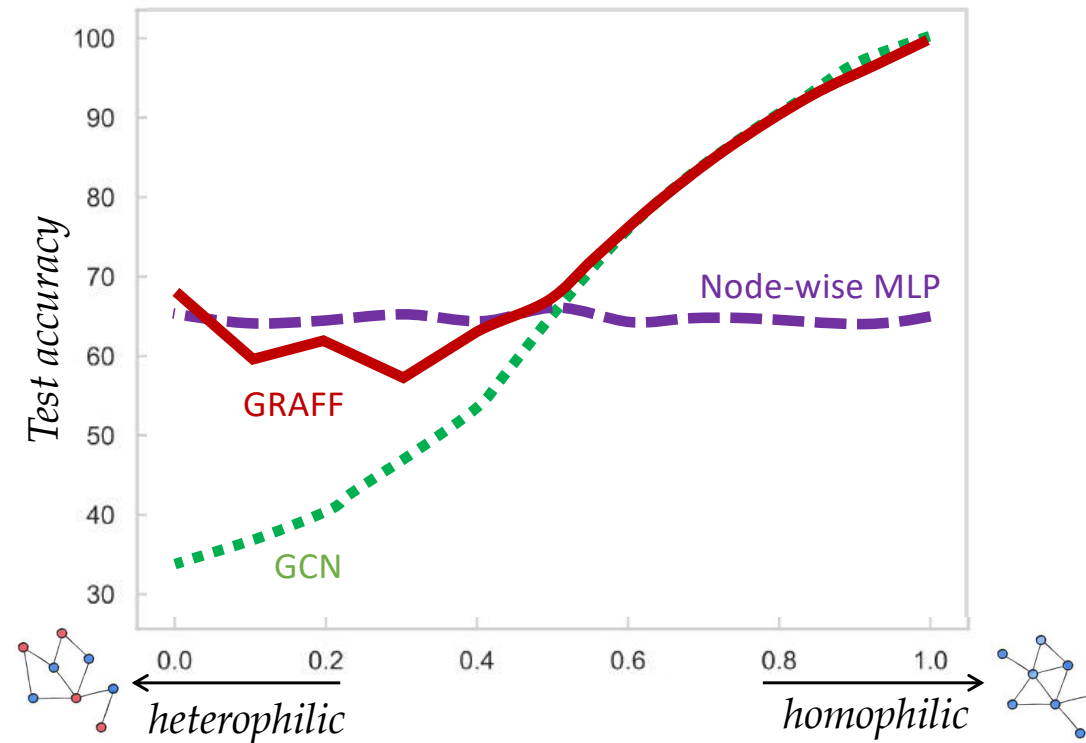
- **Attraction** along positive eigenvectors of  $\mathbf{W}$
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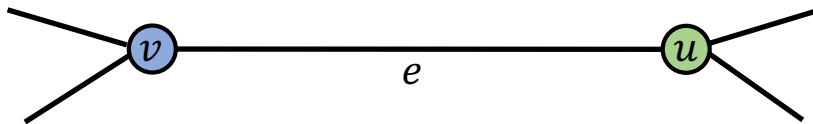
**Contradicts GNN “folklore”!**

# Homophily vs Heterophily

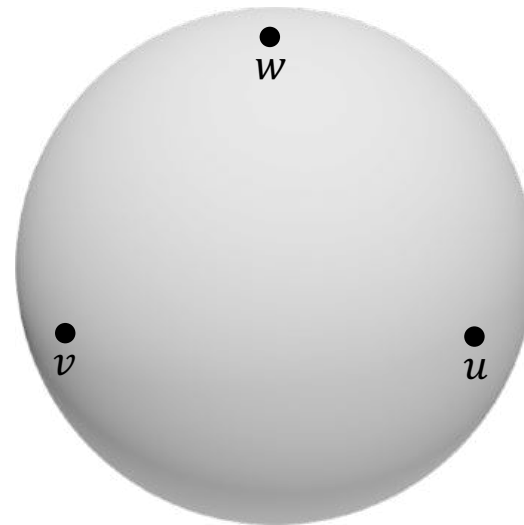


Synthetic Cora node classification task

# *Cellular Sheaves*

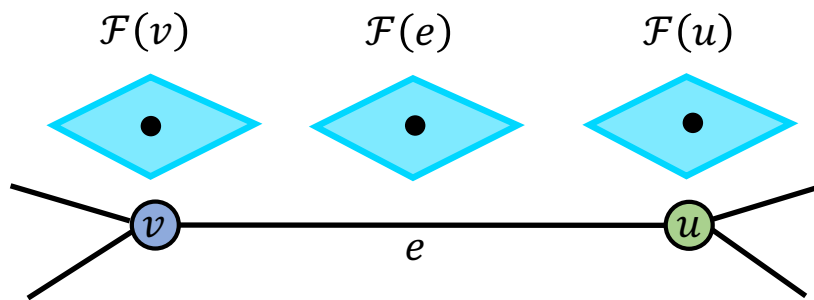


Graph

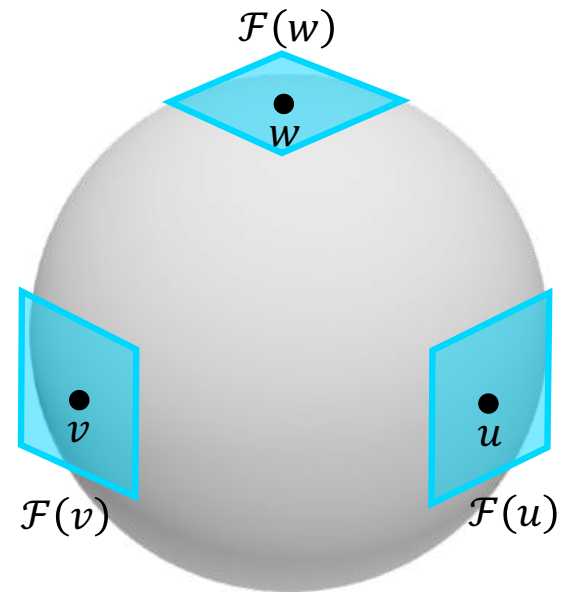


Manifold

# Cellular Sheaves

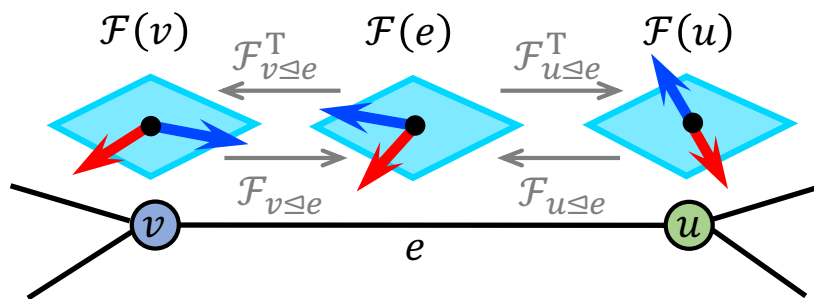


Cellular sheaf  $\mathcal{F}$

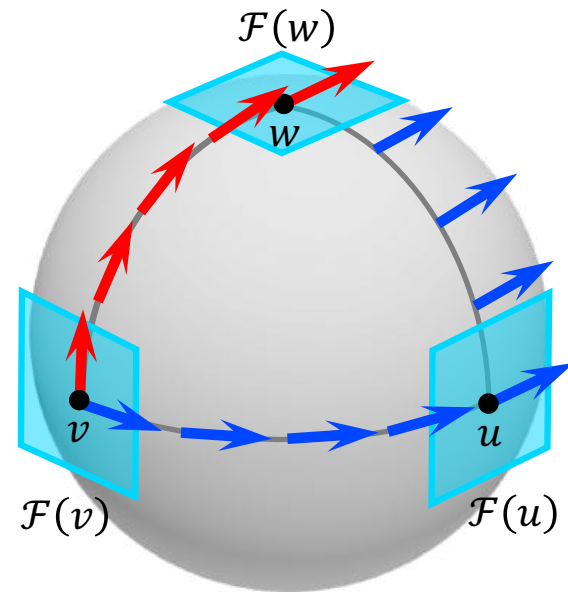


Manifold + Connection

# Cellular Sheaves

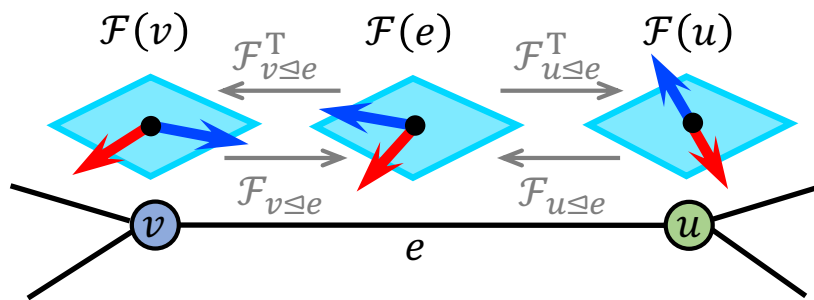


Cellular sheaf  $\mathcal{F}$

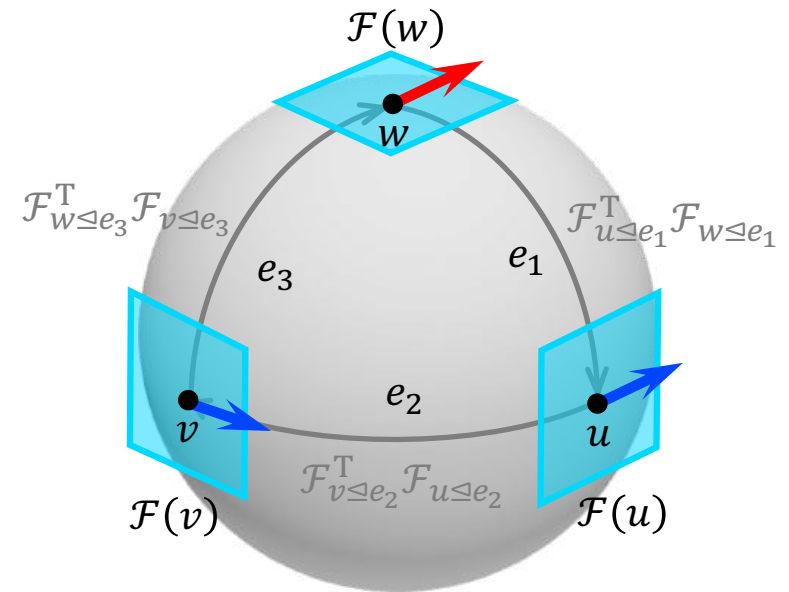


Manifold + Connection

# Cellular Sheaves

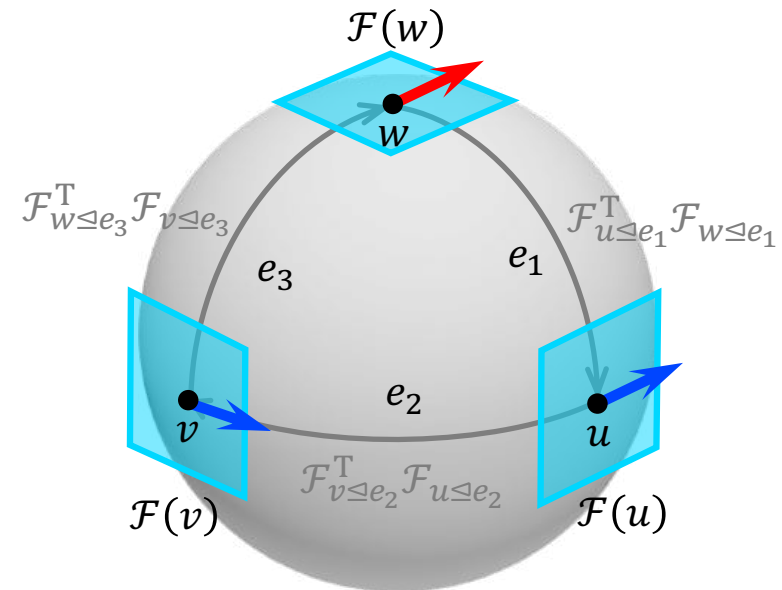
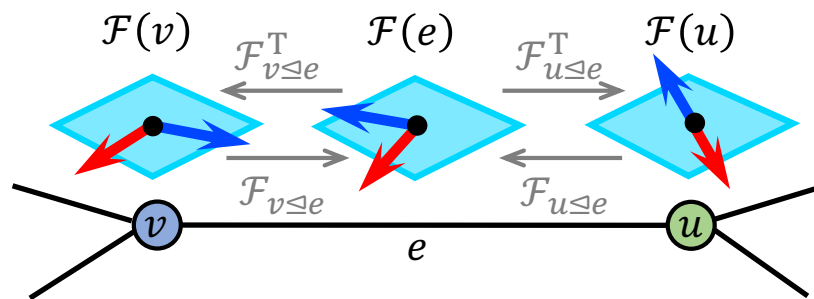


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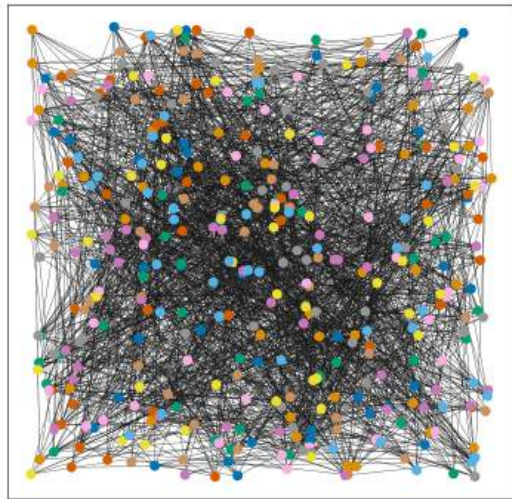
Analogy to parallel transport  
on manifolds

# Cellular Sheaves



Endow graph with "geometry" leading to richer diffusion  
with better separation, ability to cope with heterophily,  
and no oversmoothing

## Diffusion on Cellular Sheaves



| Graph type   | # Classes | Sheaf class $\mathcal{F}$ , $\dim=d$ |   |
|--------------|-----------|--------------------------------------|---|
| Homophilic   | 2         | Symmetric $d=1$                      | ✓ |
| Heterophilic | 2         | Symmetric $d=1$                      | ✗ |
|              | 2         | Non-symmetric $d=1$                  | ✓ |
|              | $\geq 3$  | Non-symmetric $d=1$                  | ✗ |
|              | $\leq 2d$ | Orthogonal, $d=\{2,4\}$              | ✓ |

$$\dot{\mathbf{X}}(t) = \Delta_{\mathcal{F}} \mathbf{X}(t)$$

Node classification = limit of sheaf diffusion equation  
with an appropriate sheaf class



Michael Galkin

## *Homogeneous Diffusion in Image Processing*

$$\dot{\mathbf{X}}(t) = -\text{div}(c\nabla\mathbf{X}(t))$$



$\mathbf{X}(0)$

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$$\dot{\mathbf{X}}(t) = -\text{div}(c\nabla\mathbf{X}(t))$$



$\mathbf{X}(0)$



$\mathbf{X}(t) = \mathbf{X}(0) \star \mathbf{G}_{\sigma\sqrt{t}}$

# Non-homogeneous Diffusion in Image Processing

$$\dot{\mathbf{X}}(t) = -\text{div} \left( \frac{\nabla \mathbf{X}(t)}{1 + c \underbrace{\|\nabla \mathbf{X}(t)\|^2}_{\text{edge indicator}}} \right)$$



$\mathbf{X}(0)$



“Do not diffuse across edges”



$$\mathbf{X}(t) = \mathbf{X}(0) \star \mathbf{G}_{\sigma\alpha t}$$

## *Non-homogeneous Diffusion in Image Processing*

$$\dot{\mathbf{X}}(t) = -\text{div} \left( \frac{\nabla \mathbf{X}(t)}{1 + c \underbrace{\|\nabla \mathbf{X}(t)\|^2}_{\text{edge indicator}}} \right)$$

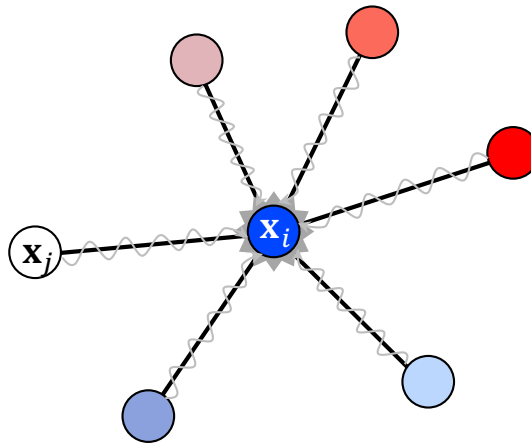


Non-homogeneous



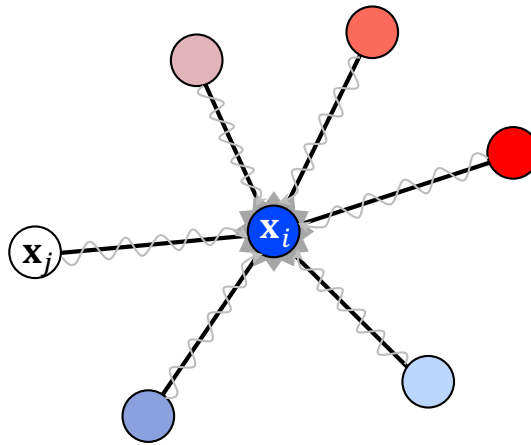
Homogeneous

## *Non-homogeneous Diffusion on Graphs*



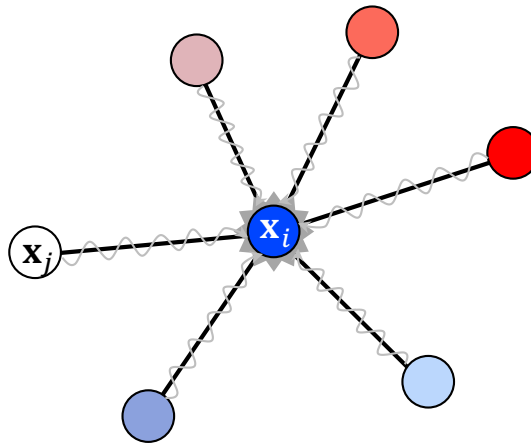
$$\dot{\mathbf{x}}_i(t) = \sum_{j \in \mathcal{N}_i} a(\mathbf{x}_i(t), \mathbf{x}_j(t)) (\mathbf{x}_j(t) - \mathbf{x}_i(t))$$

## *Non-homogeneous Diffusion on Graphs*



$$\dot{\mathbf{x}}_i(t) = \sum_{j \in \mathcal{N}_i} \underbrace{a(\mathbf{x}_i(t), \mathbf{x}_j(t))}_{\text{learnable diffusivity}} (\mathbf{x}_j(t) - \mathbf{x}_i(t))$$

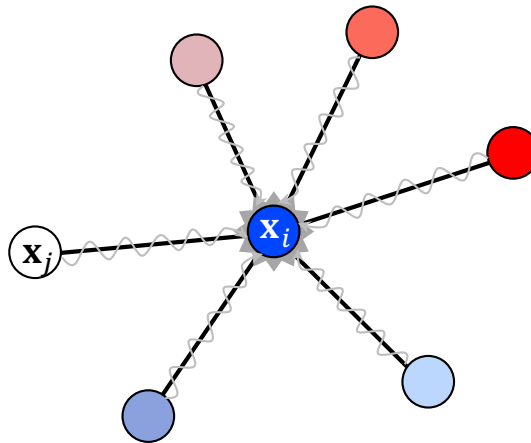
## Non-homogeneous Diffusion on Graphs



$$\mathbf{x}_i(t + \tau) = \mathbf{x}_i(t) + \underbrace{\tau}_{\substack{\text{time} \\ \text{step}}} \sum_{j \in \mathcal{N}_i} \underbrace{a(\mathbf{x}_i(t), \mathbf{x}_j(t))}_{\text{learnable diffusivity}} (\mathbf{x}_j(t) - \mathbf{x}_i(t))$$

Explicit (Forward Euler) discretization

## Non-homogeneous Diffusion on Graphs



$$\mathbf{x}_i(t + \tau) = \sum_{j \in \mathcal{N}_i} a(\mathbf{x}_i(t), \mathbf{x}_j(t)) \mathbf{x}_j(t)$$

normalised  $\sum_j a_{ij} = 1$   
unit step  $\tau = 1$

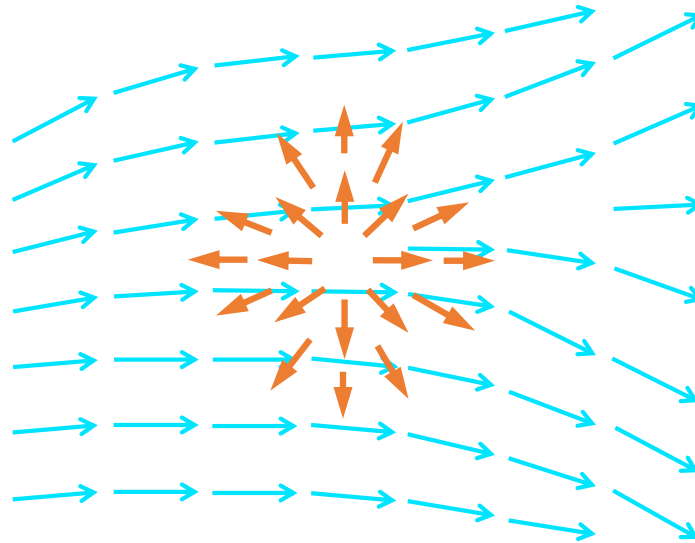
GAT!

## *Advective Diffusion Transformer*

$$\dot{\mathbf{X}}(t) = \operatorname{div}(\mathbf{S}(t)\nabla\mathbf{X}(t)) + \beta\operatorname{div}(\mathbf{V}(t)\mathbf{X}(t))$$

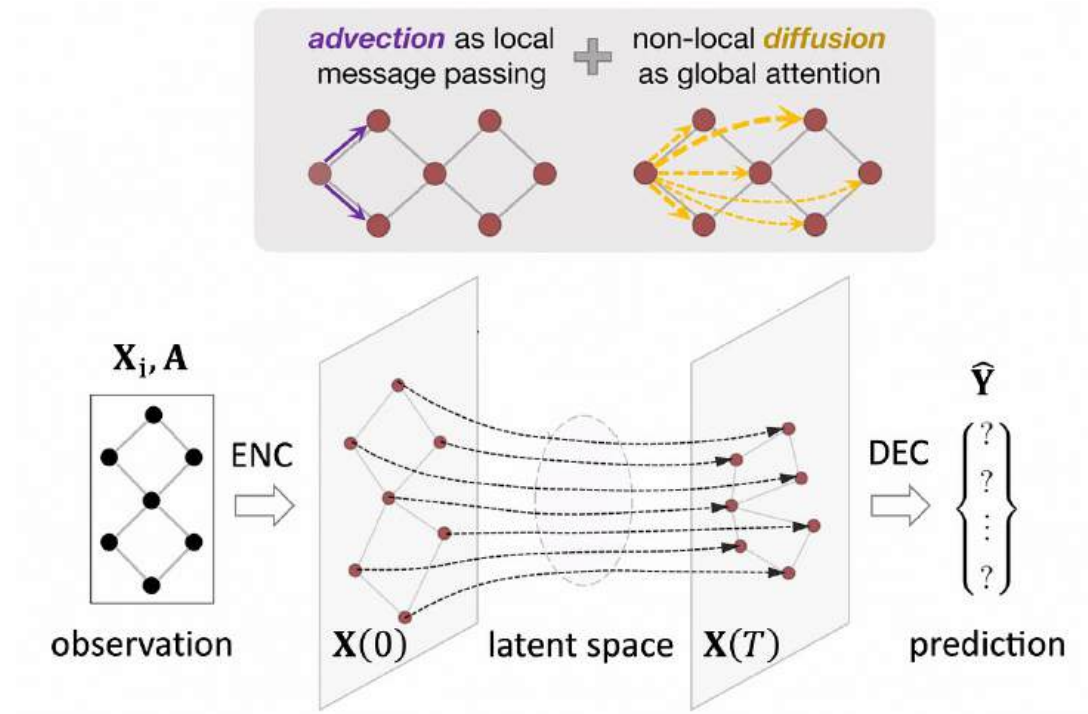
# Advective Diffusion Transformer

$$\dot{\mathbf{X}}(t) = \underbrace{\text{div}(\mathbf{S}(t)\nabla\mathbf{X}(t))}_{\text{diffusion}} + \underbrace{\beta\text{div}(\mathbf{V}(t)\mathbf{X}(t))}_{\text{advection}}$$



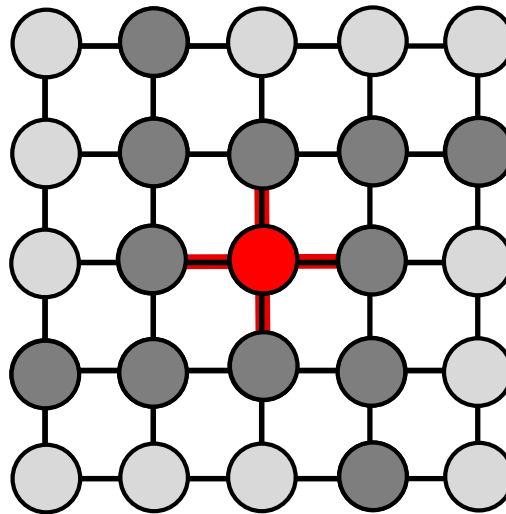
# Advection Diffusion Transformer

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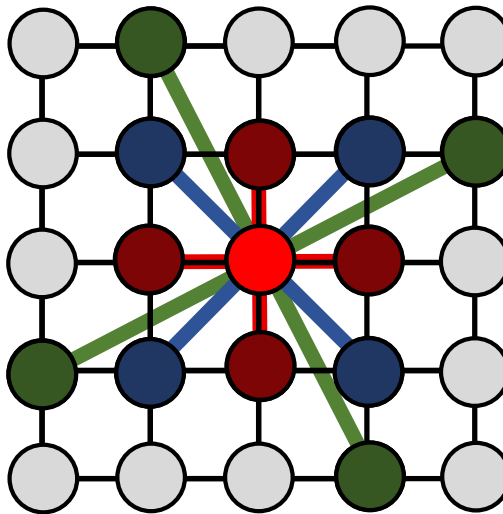
*Spatial Derivative: Graph Rewiring?*

$$\dot{x}(t) = \Delta x(t)$$



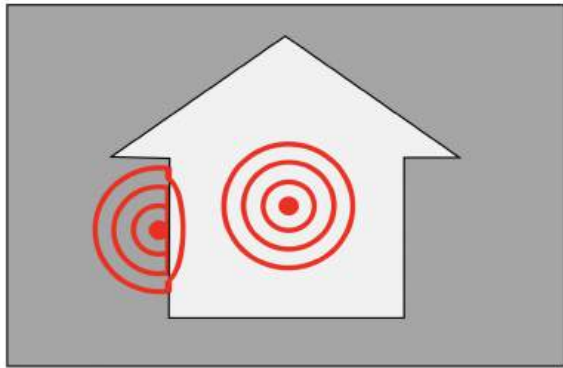
## *Spatial Derivative: Graph Rewiring?*

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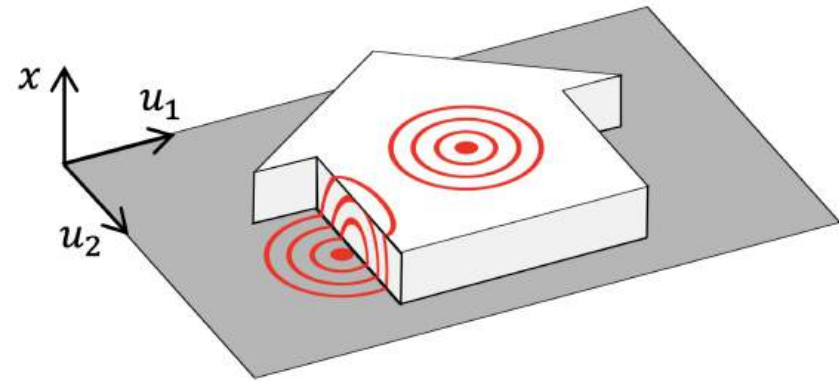
Different discretisations of 2D Laplacian

## *Images as embedded manifolds*



$$\dot{\mathbf{X}} = -\text{div}(a(\mathbf{X})\nabla\mathbf{X})$$

**Non-linear diffusion**



$$\dot{\mathbf{Z}} = \Delta_{\mathbf{G}}\mathbf{Z}$$

**Non-Euclidean diffusion**

## Beltrami flow

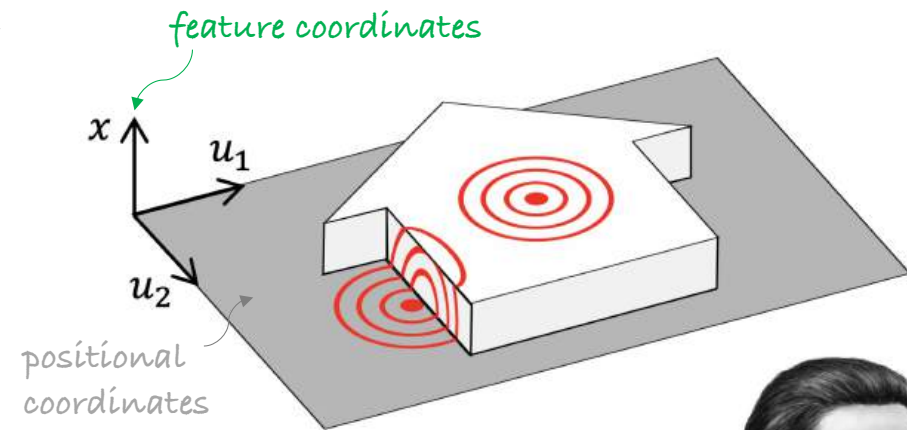
- Consider image as embedded 2-manifold

$$\mathbf{Z}(\mathbf{u}) = (\mathbf{u}, \alpha \mathbf{X}(\mathbf{u}))$$

- Pullback metric:  $2 \times 2$  matrix

$$\mathbf{G} = \mathbf{I} + \alpha^2 (\nabla_{\mathbf{u}} \mathbf{X}(\mathbf{u}))^T \nabla_{\mathbf{u}} \mathbf{X}(\mathbf{u})$$

- Beltrami flow = gradient flow of the Polyakov energy (harmonic energy of the embedding used in string theory)



$$\dot{\mathbf{Z}} = \Delta_{\mathbf{G}} \mathbf{Z}$$

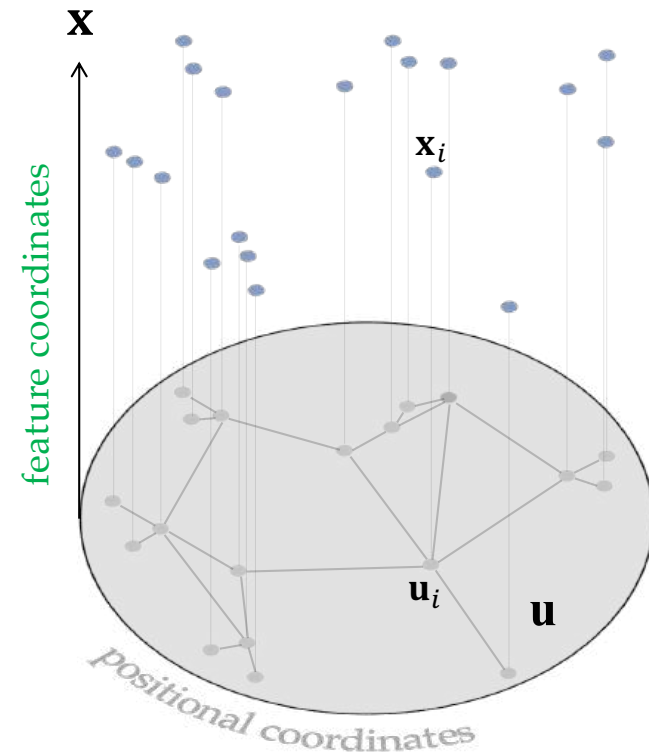


E. Beltrami

## Graph Beltrami flow

- Graph with positional and feature node coordinates  $\mathbf{z}_i = (\mathbf{u}_i, \mathbf{x}_i)$
- **Graph Beltrami flow**

$$\dot{\mathbf{z}}_i(t) = \sum_{j \in \mathcal{N}_i} a(\mathbf{z}_i(t), \mathbf{z}_j(t)) (\mathbf{z}_j(t) - \mathbf{z}_i(t))$$

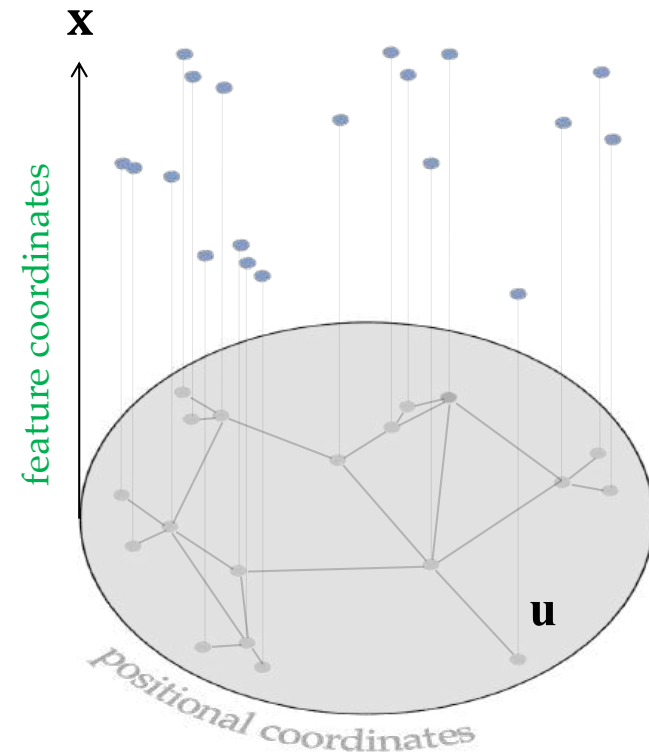


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- Evolution of  $\mathbf{x}$  = feature diffusion

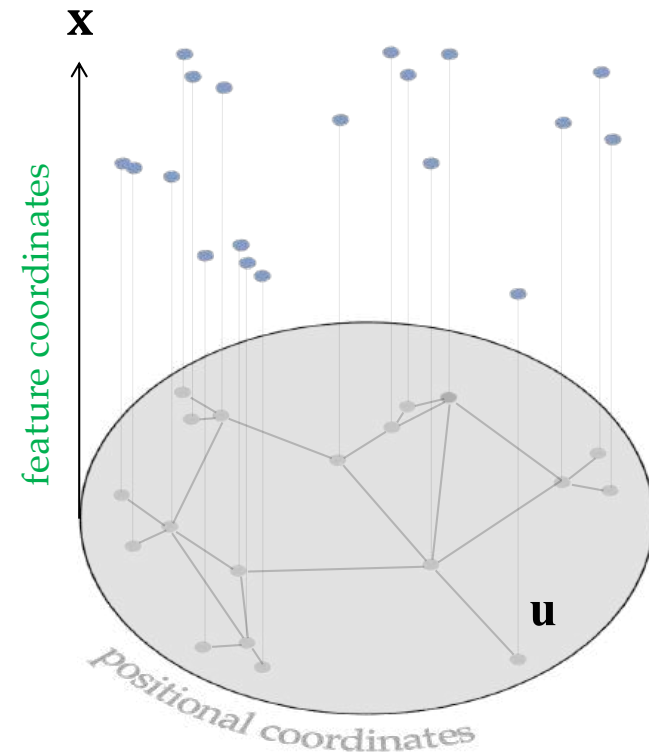


# Graph Beltrami flow

- Graph with positional and feature node coordinates  $\mathbf{z}_i = (\mathbf{u}_i, \mathbf{x}_i)$
- **Graph Beltrami flow**

$$\dot{\mathbf{z}}_i(t) = \sum_{j \in \mathcal{N}_i} a(\mathbf{z}_i(t), \mathbf{z}_j(t)) (\mathbf{z}_j(t) - \mathbf{z}_i(t))$$

- Evolution of  $\mathbf{x}$  = feature diffusion
- Evolution of  $\mathbf{u}$  = graph rewiring



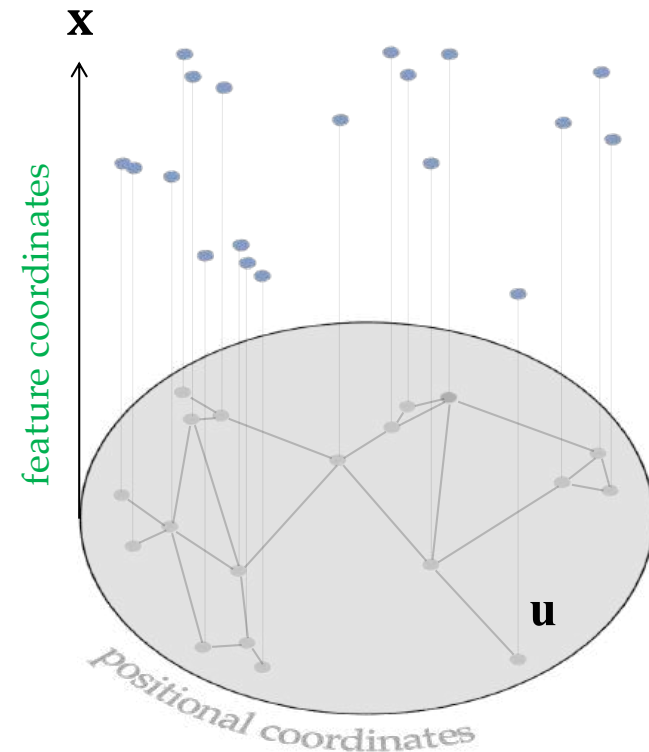
# Graph Beltrami flow

- Graph with positional and feature node coordinates  $\mathbf{z}_i = (\mathbf{u}_i, \mathbf{x}_i)$
- **Graph Beltrami flow**

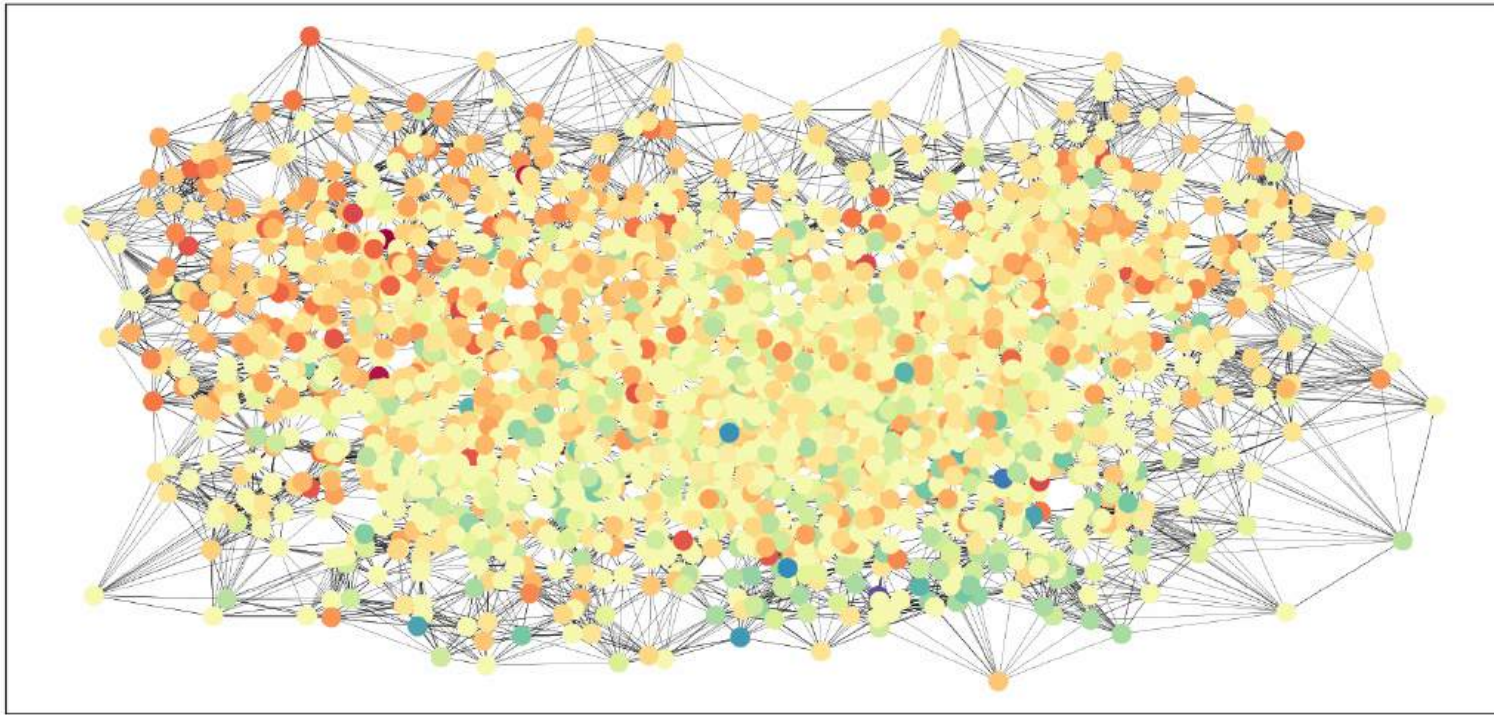
$$\dot{\mathbf{z}}_i(t) = \sum_{j \in \mathcal{N}'_i} a(\mathbf{z}_i(t), \mathbf{z}_j(t)) (\mathbf{z}_j(t) - \mathbf{z}_i(t))$$

*rewired graph*

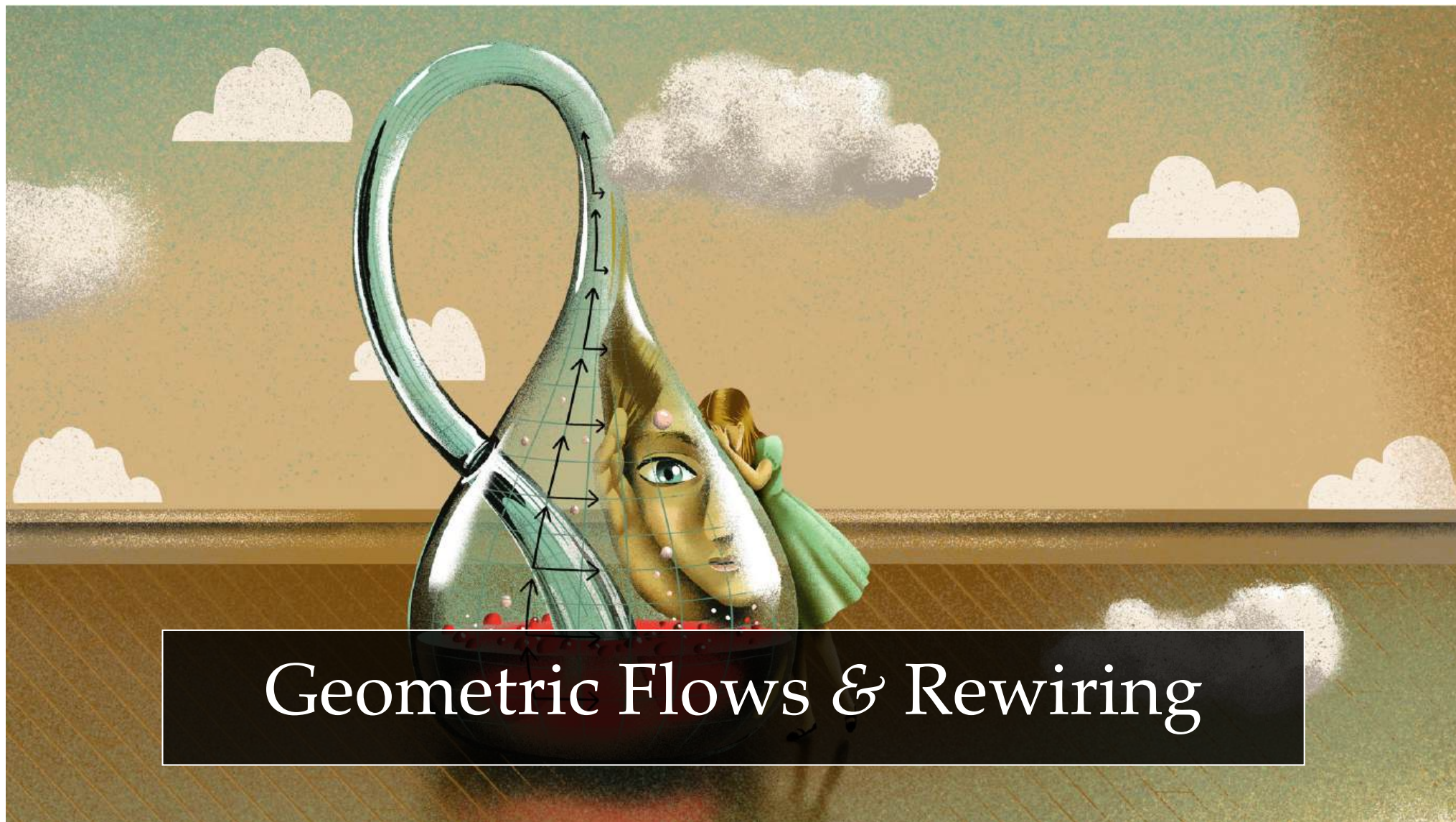
- Evolution of  $\mathbf{x}$  = feature diffusion
- Evolution of  $\mathbf{u}$  = graph rewiring



## *Graph Beltrami flow*



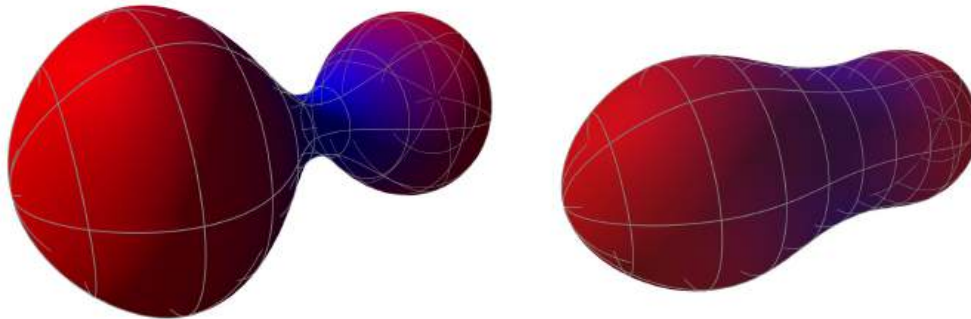
Evolution of positional/feature components + rewiring of the Cora graph



## *Ricci flow*

- **Ricci flow:** “diffusion of the Riemannian metric”

$$\frac{\partial g_{ij}}{\partial t} = R_{ij}$$



Evolution of a manifold under Ricci flow



**G. Ricci-  
Curbastro**

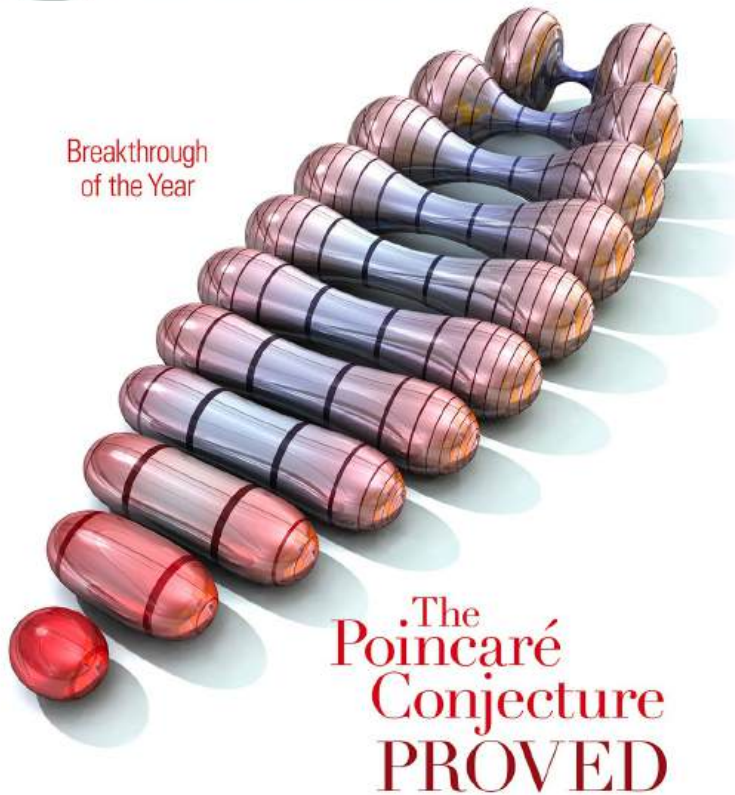


**R. Hamilton**

# Science

22 December 2006 | \$10

Breakthrough  
of the Year



**G. Perelman**



**G. Ricci-  
Curbastro**

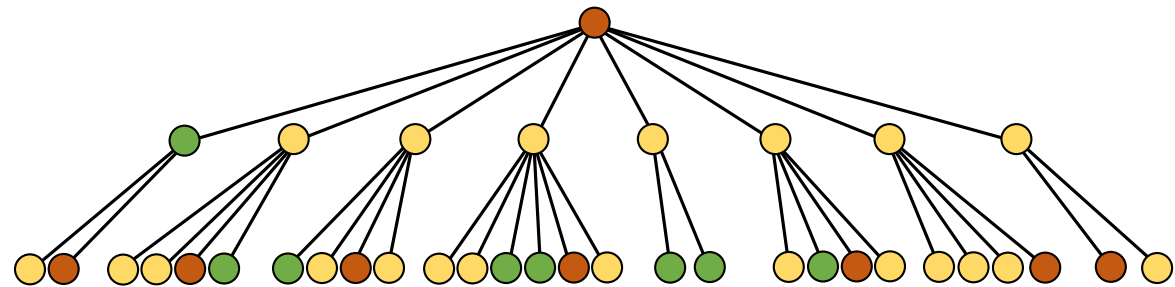
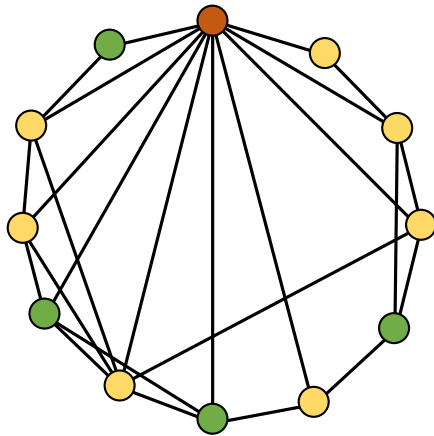


**R. Hamilton**

Ricci 1903; Hamilton 1988; Perelman 2003

**“Failure of Message Passing to propagate  
information on the graph”**

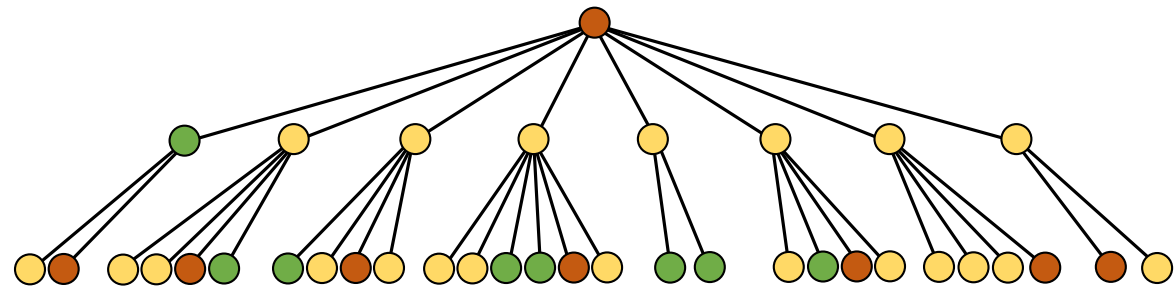
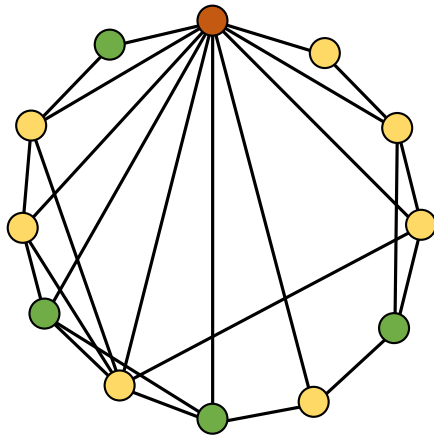
## *Over-squashing & Bottlenecks*



In some graphs metric ball volume grows exponentially  
with ball radius

Over-squashing = Fast volume growth  
+ Long-range interactions

## Over-squashing & Bottlenecks



In some graphs metric ball volume grows exponentially  
with ball radius

Over-squashing = <sup>graph topology</sup> Fast volume growth  
+ Long-range interactions<sub>task</sub>

# Over-squashing

- Consider an MPNN of the form

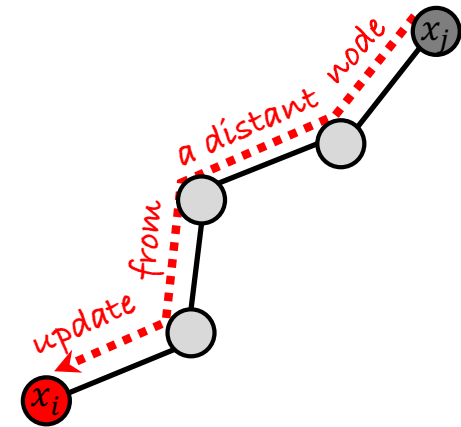
$$\mathbf{x}_i^{(k+1)} = \sigma \left( \mathbf{W}_1 \mathbf{x}_i^{(k)} + \sum_j a_{ij} \mathbf{W}_2 \mathbf{x}_j^{(k)} \right)$$

- $L = \text{depth}$  (number of layers)
- $p = \text{width}$  (hidden dimension)
- Nonlinearity  $\sigma$  is  $c_\sigma$ -Lipschitz-continuous
- $w = \text{maximum element of weight matrices } \mathbf{W}_1, \mathbf{W}_2$

**Theorem (Sensitivity bound):** For any  $i, j$

$$\left\| \frac{\partial \mathbf{x}_i^{(L)}}{\partial \mathbf{x}_j^{(0)}} \right\|_1 \leq (c_\sigma w p)^L (\mathbf{I} + \mathbf{A})_{ij}^L$$

Topping, Di Giovanni et B 2021; Di Giovanni et B 2023



**Over-squashing:** small Jacobian

$\left\| \partial \mathbf{x}_i^{(L)} / \partial \mathbf{x}_j^{(0)} \right\|$  indicates poor information propagation from input node

# Over-squashing

- Consider an MPNN of the form

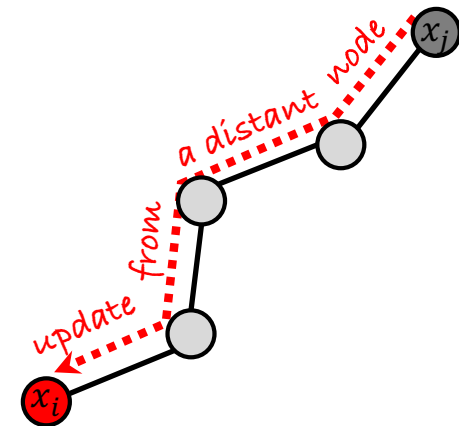
$$\mathbf{x}_i^{(k+1)} = \sigma \left( \mathbf{W}_1 \mathbf{x}_i^{(k)} + \sum_j a_{ij} \mathbf{W}_2 \mathbf{x}_j^{(k)} \right)$$

- $L$  = depth (number of layers)
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Topping, Di Giovanni et B 2021; Di Giovanni et B 2023

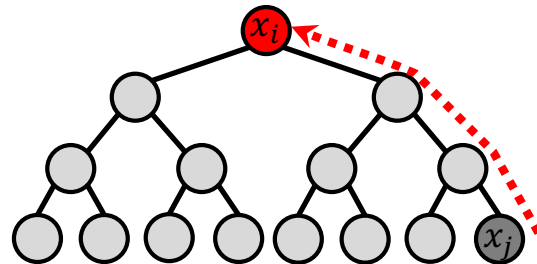
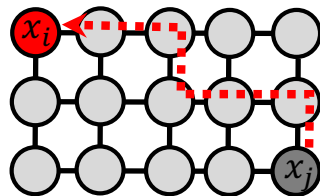


**Over-squashing:** small Jacobian

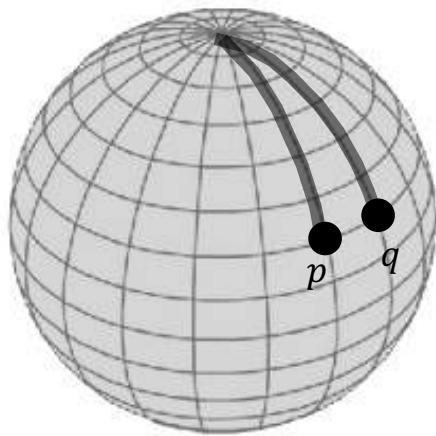
$\left\| \partial \mathbf{x}_i^{(L)} / \partial \mathbf{x}_j^{(0)} \right\|$  indicates poor information propagation from input node

## Preventing over-squashing

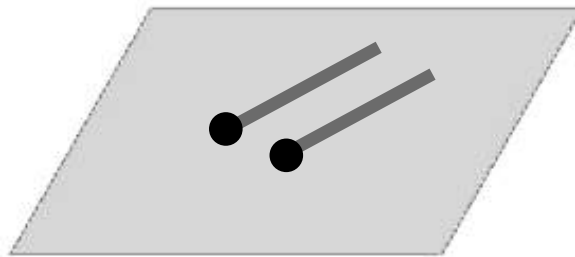
$$\left\| \frac{\partial \mathbf{x}_i^{(L)}}{\partial \mathbf{x}_j^{(0)}} \right\|_1 \leq (\underbrace{\mathbf{C}_\sigma \mathbf{W} \mathbf{P}}_{\text{model}})^L (\underbrace{\mathbf{I} + \mathbf{A}}_{\text{topology}})^L_{ij}$$



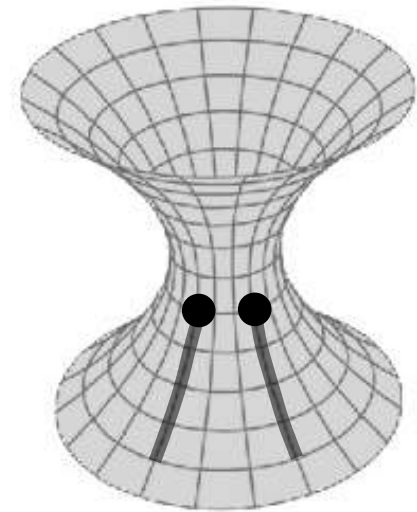
## *Ricci Curvature on Manifolds*



Spherical ( $>0$ )



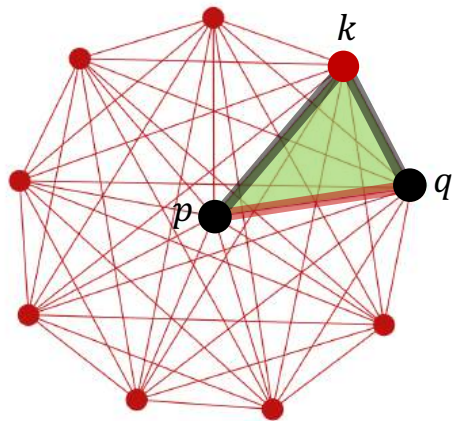
Euclidean ( $=0$ )



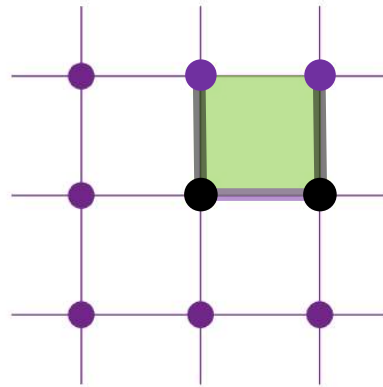
Hyperbolic ( $<0$ )

**“geodesic dispersion”**

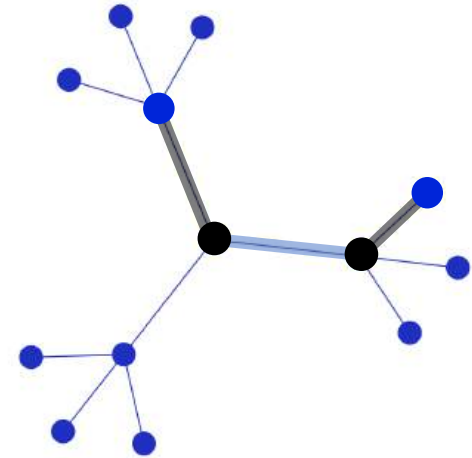
# *Discrete Ricci Curvature on Graphs*



Clique ( $>0$ )

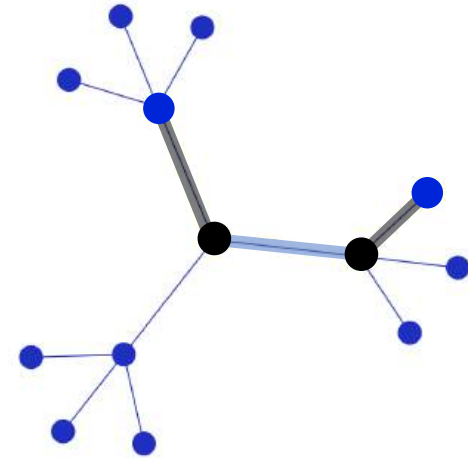
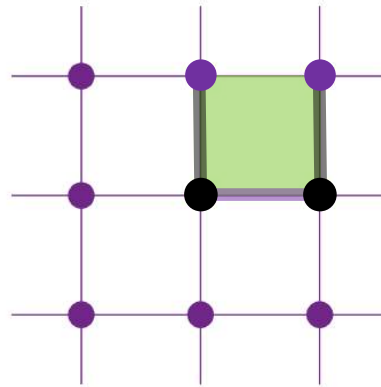
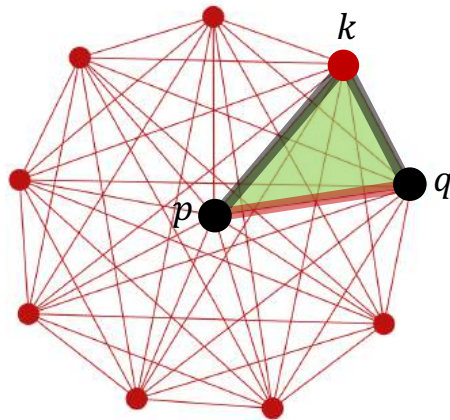


Grid ( $=0$ )



Tree ( $<0$ )

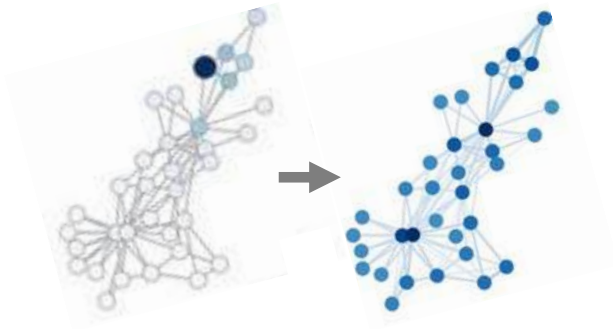
What contributes to over-squashing?



**Theorem:** (informal) *strong negatively-curved edges* contribute to over-squashing.

Clique ( $>0$ )      Grid ( $=0$ )      Tree ( $<0$ )

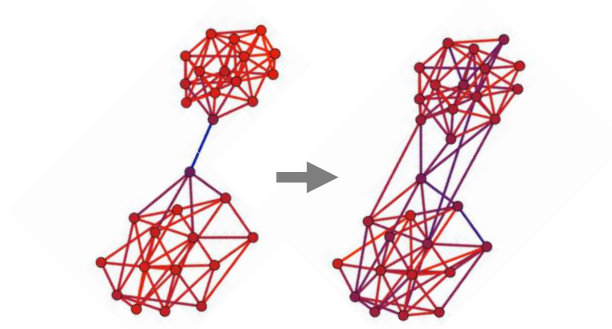
# Graph Rewiring Approaches



**Connectivity Diffusion  
(DIGL)**

Gasteiger et al. 2019

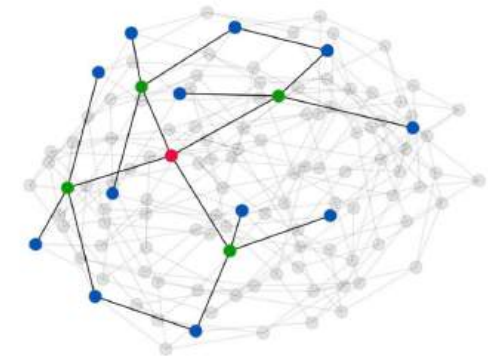
- KNN graph on PPR embedding
- + Good for homophilic graphs
- Bad for heterophilic graphs
- Drastically different graph



**Discrete Ricci flow  
(SDRF)**

Topping, Di Giovanni et B. 2022

- Remove negatively-curved edges
- + Good for both homophilic and heterophilic graphs
- + “Surgical” rewiring
- Curvature is computationally expensive



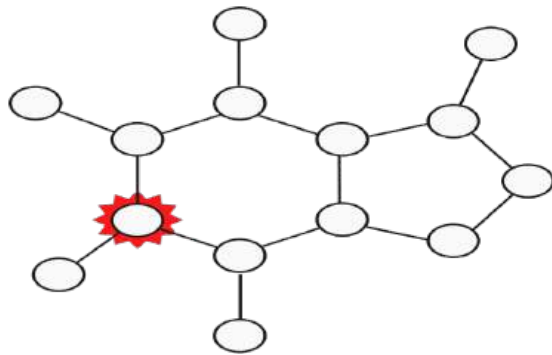
**Expander Propagation  
(EGP)**

Deac et al. 2022

- Fixed expander graph
- Alternate MP on original and new graph
- + Optimal graph for MP
- No relation to input graph
- No permutation equivariance

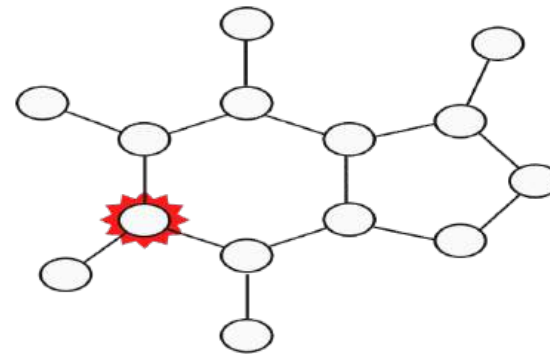
**No relation to the task!**

*Why it is important to consider the task?*



**Van der Waals interactions**

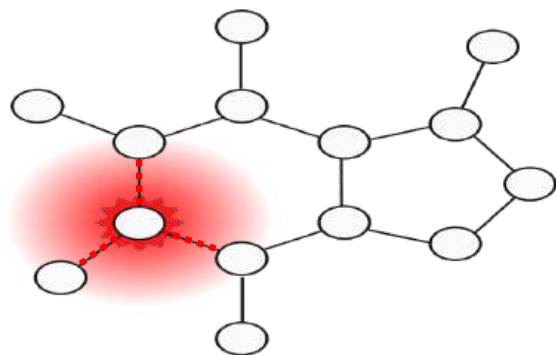
$$\propto r^{-12}$$



**Coulomb interactions**

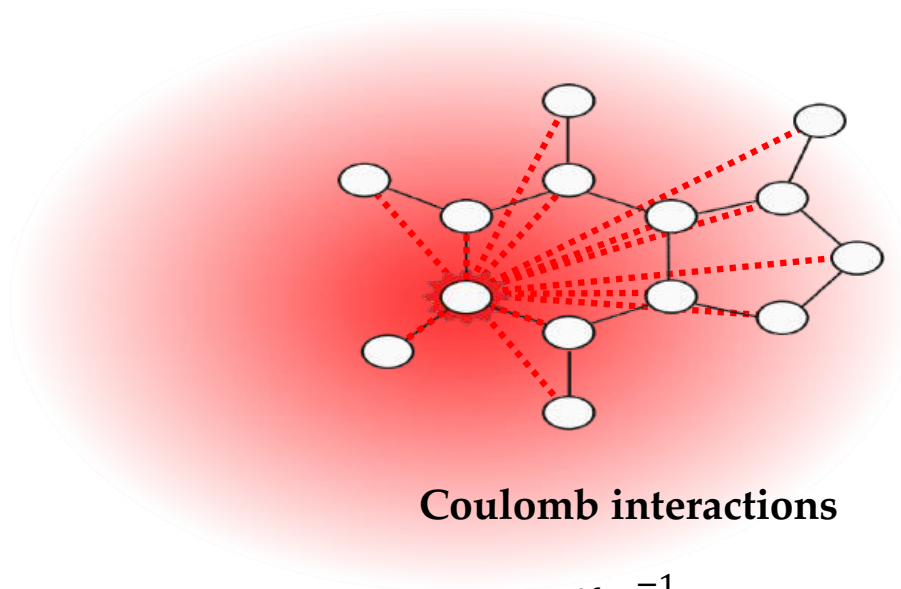
$$\propto r^{-1}$$

*Why it is important to consider the task?*



**Van der Waals interactions**

$$\propto r^{-12}$$



**Coulomb interactions**

$$\propto r^{-1}$$

**Same graph+features, different task**

**Whether the graph is good depends on the task!**



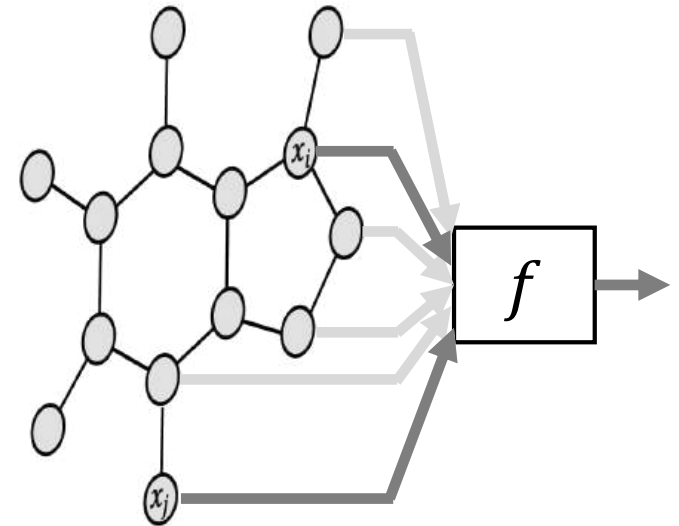
Long-range interactions & Expressivity

## Long-range interactions in graph tasks

- **Task** = a function  $f(\mathbf{X})$  on the node features of a graph  $G$
- The interaction between features in nodes  $i$  and  $j$  required for the task is given by

$$\text{Mixing of } f: \text{mix}_f(i, j) = \max_{\mathbf{X}} \max_{1 \leq \alpha, \beta \leq d} \left| \frac{\partial^2 f(\mathbf{X})}{\partial x_i^\alpha \partial x_j^\beta} \right|$$

- $f(\mathbf{X}) = \phi(\mathbf{x}_i) + \phi(\mathbf{x}_j)$  is fully separable, thus  $\text{mix}_f(i, j) = 0$

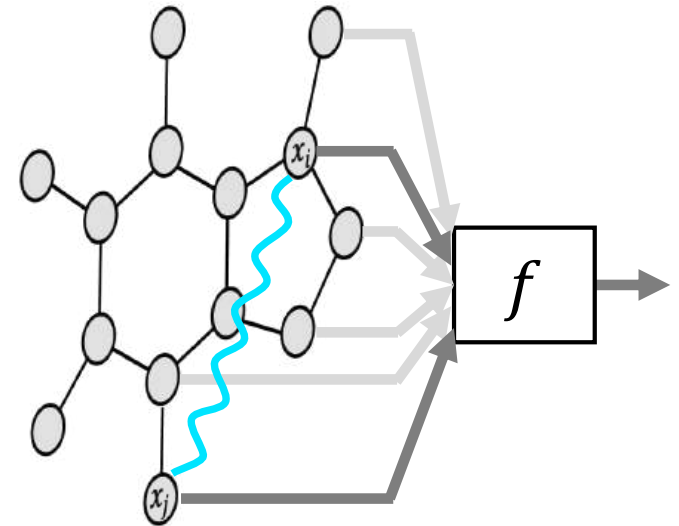


## Long-range interactions in graph tasks

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- $f(\mathbf{X}) = \phi(\mathbf{x}_i) + \phi(\mathbf{x}_j)$  is fully separable, thus  $\text{mix}_f(i, j) = 0$
- $f(\mathbf{X}) = \phi(\langle \mathbf{x}_i, \mathbf{x}_j \rangle)$  mixing depends on how non-linear  $\phi$  is



## Capacity bounds

$$\underset{\text{task}}{\text{mix}_f}(i, j) \leq \sum_{k=1}^{L-1} (\underset{\text{model}}{c_\sigma w})^{2^{L-k}-1} \left( \underset{\text{topology}}{w} (\mathbf{s}^{L-k})^T \text{diag}(\mathbf{1}^T \mathbf{s}^k) \mathbf{s}^{L-k} + \mathbf{c} \mathbf{Q}_k \right)_{ij}$$

**What is the capacity of MPNN required for a given task?**

## Capacity bounds

$$\text{mix}_f(i, j) \leq \sum_{k=1}^{L-1} (\underbrace{c_o w}_{\text{model}})^{2^{L-k}-1} \left( \underbrace{w (\mathbf{s}^{L-k})^T \text{diag}(\mathbf{1}^T \mathbf{s}^k) \mathbf{s}^{L-k}}_{\text{topology}} + \underbrace{c \mathbf{Q}_k}_{\text{mixing}} \right)_{ij}$$

What is the **capacity of MPNN** required for a **given task**?

*model + topology* *mixing*

## Capacity bounds

$$\text{mix}_f(i, j) \leq \sum_{k=1}^{L-1} (c_\sigma w)^{2L-k-1} \left( w(\mathbf{s}^{L-k})^T \text{diag}(\mathbf{1}^T \mathbf{s}^k) \mathbf{s}^{L-k} + C \mathbf{Q}_k \right)_{ij}$$

### Bound on weights $w$

$$w \geq \frac{d_{\min}}{c_2} \left( \frac{\text{mix}_f(i, j)}{q} \right)^{1/d(i, j)}$$

- $d_{\min}$  = min node degree
- Fixed depth  $L = \lceil d(i, j)/2 \rceil$
- $q$  = number of paths of length  $d(i, j)$  between  $i$  and  $j$

### Bound on depth $L$

$$L \geq \frac{d(i, j)}{4c_2} + \frac{|E|}{\sqrt{d_i d_j}} (\alpha \text{mix}_f(i, j) - \beta)$$

- $d_i$  = degree of node  $i$
- $\alpha, \beta$  = model-related constants
- $|E|$  = number of edges
- Bounded weights

## Capacity bounds

$$\text{mix}_f(i, j) \leq \sum_{k=1}^{L-1} (c_\sigma w)^{2L-k-1} \left( w(\mathbf{s}^{L-k})^\top \text{diag}(\mathbf{1}^\top \mathbf{s}^k) \mathbf{s}^{L-k} + C \mathbf{Q}_k \right)_{ij}$$

### Bound on weights $w$

$$w \geq \frac{d_{\min}}{c_2} \left( \frac{\text{mix}_f(i, j)}{q} \right)^{1/d(i, j)}$$

*“weights need to be large enough to allow mixing”*

### Bound on depth $L$

$$L \geq \frac{\tau(i, j)}{4c_2} + \frac{|E|}{\sqrt{d_i d_j}} (\alpha \text{mix}_f(i, j) - \beta)$$

- Depth must be  $\sim$ commute time  $\tau(i, j)$
- Rewiring tries to improve  $\tau$
- $\tau$  can be as large as  $O(n^3)$ , which implies **impossibility statements**

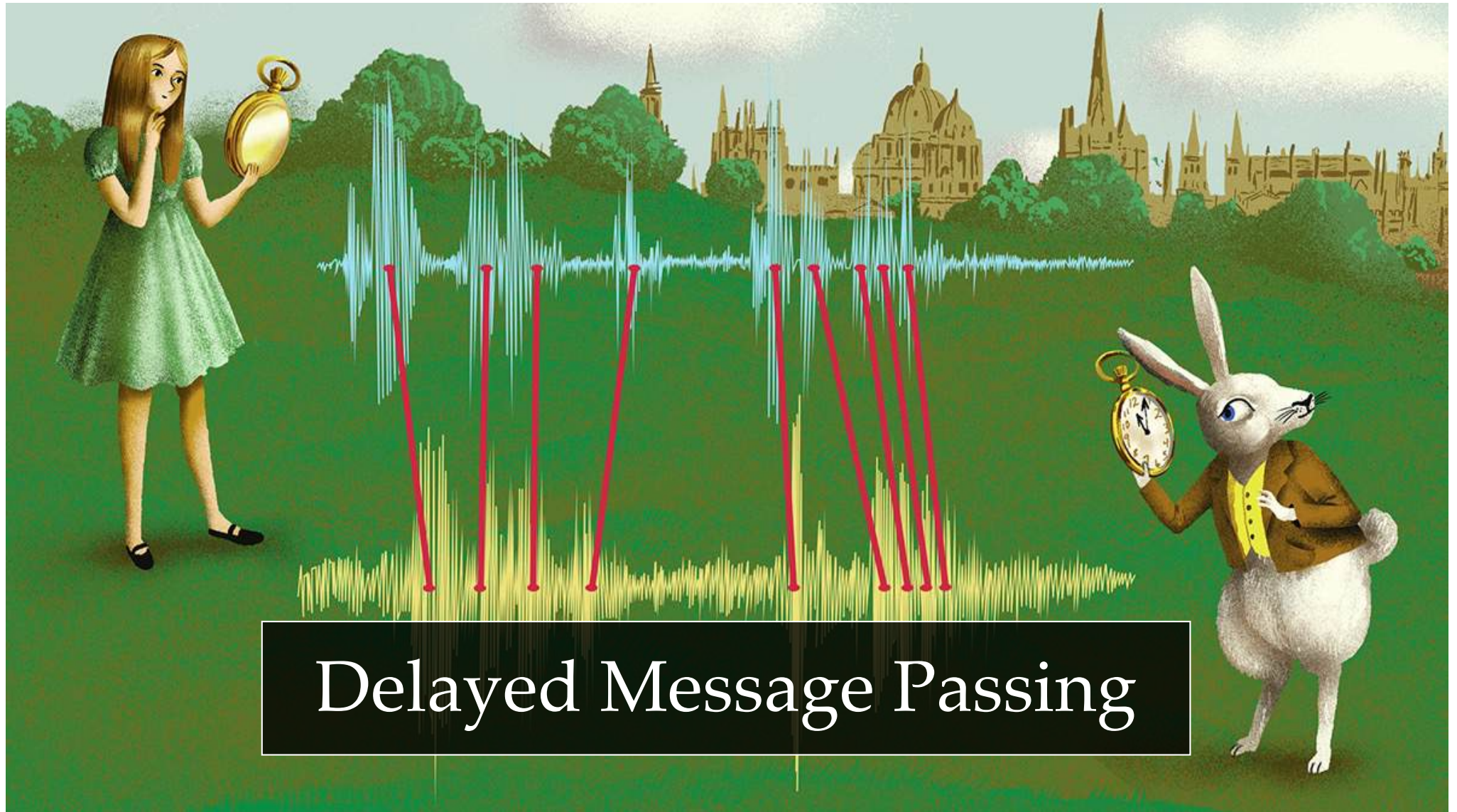
## *Expressive power without Weisfeiler-Lehman*

**Expressive power (informal):** MPNN with  $L \leq n$  layers cannot learn tasks that require high mixing among features at nodes with large commute time.



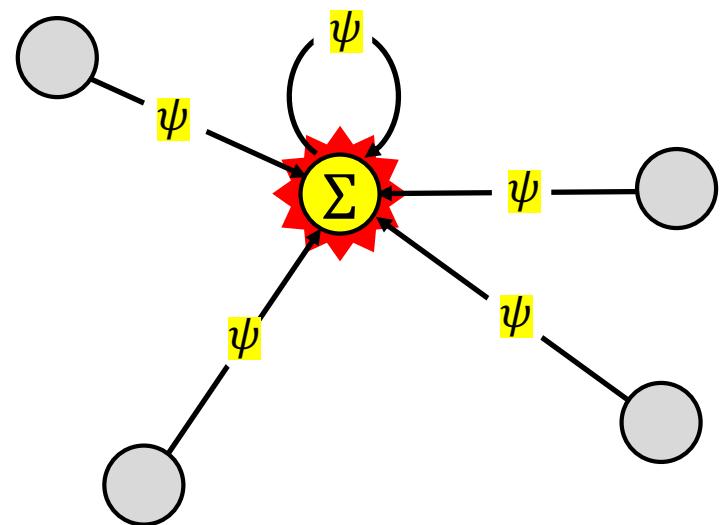
A. Lehman

B. Weisfeiler

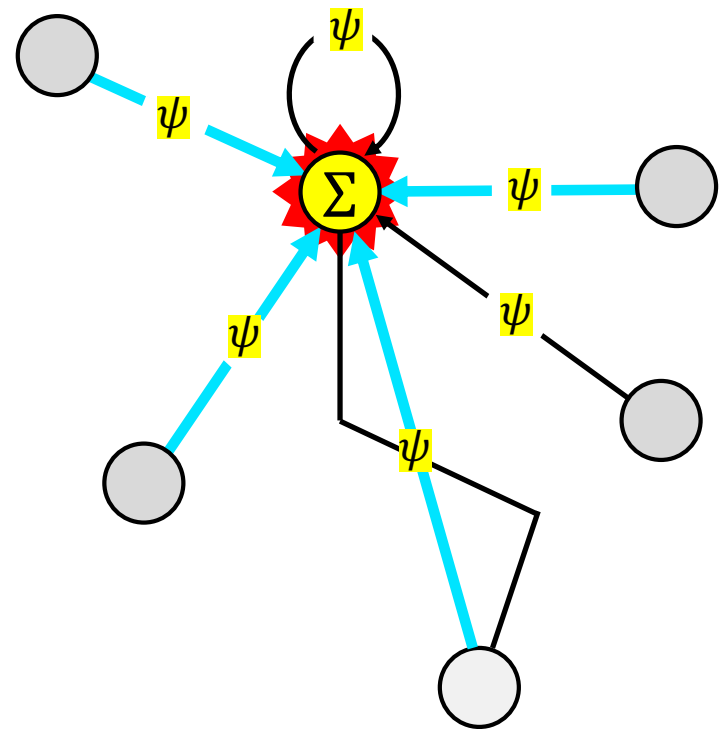


Delayed Message Passing

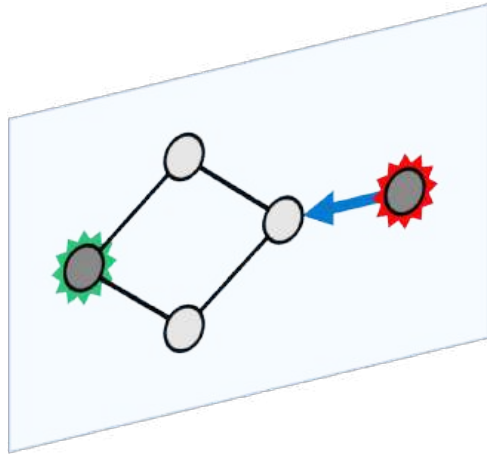
What



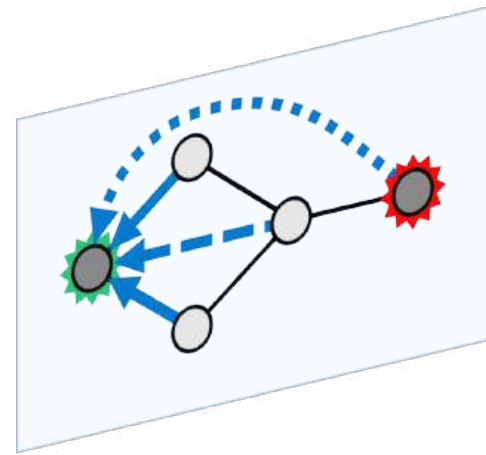
What + Where



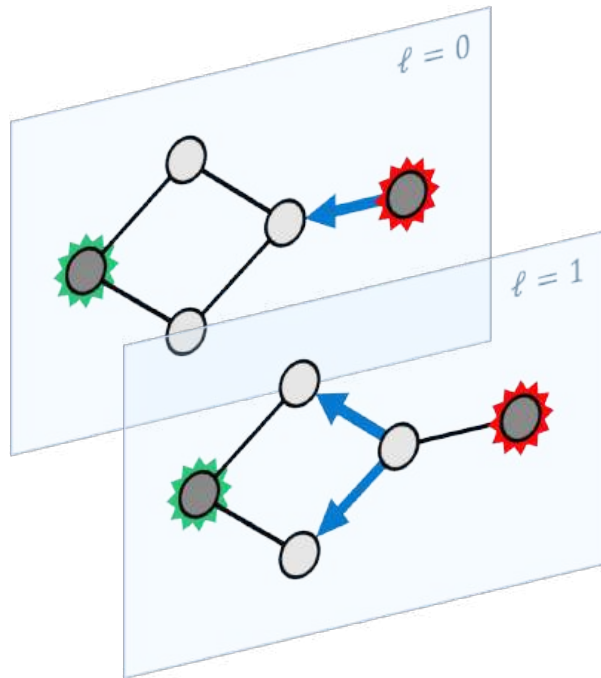
What + Where + When



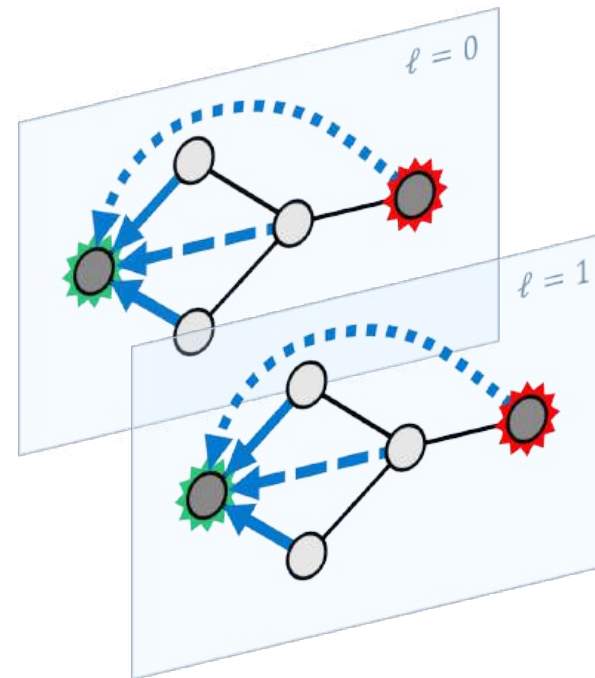
Classical MPNN



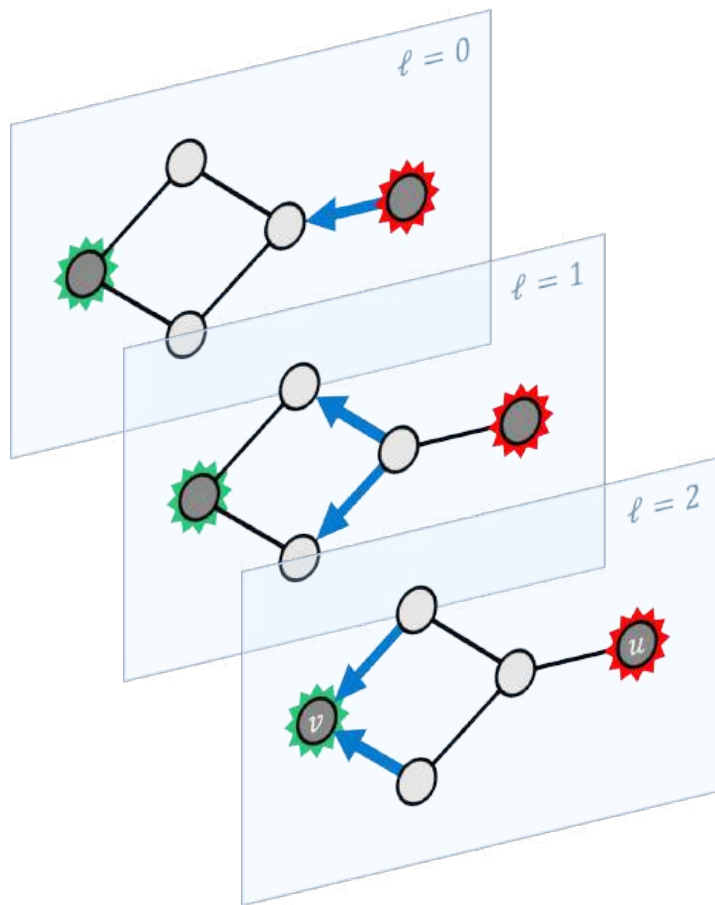
Graph Transformer



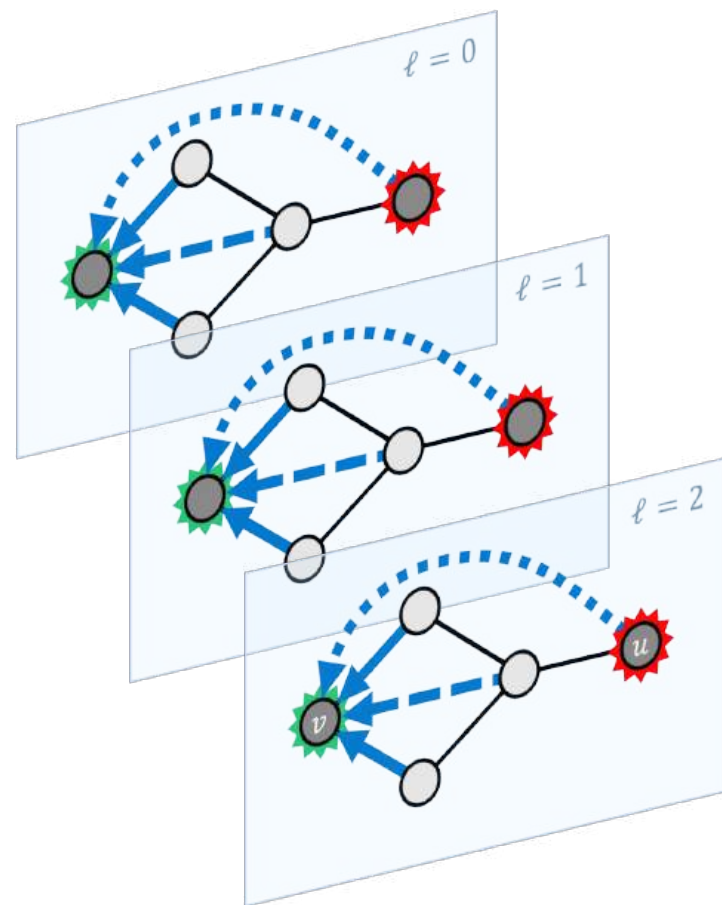
Classical MPNN



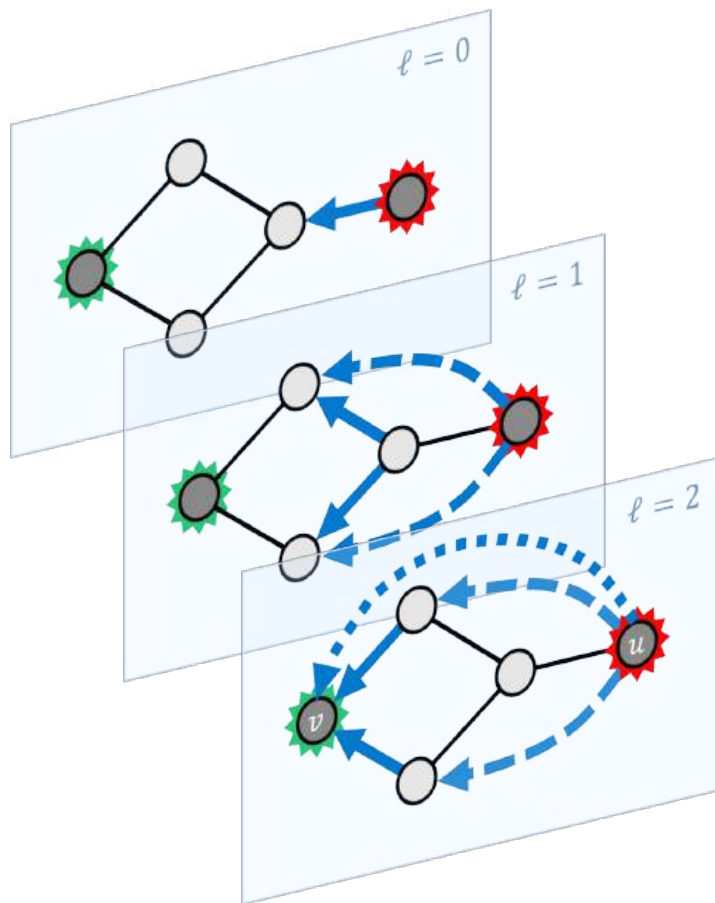
Graph Transformer



Classical MPNN

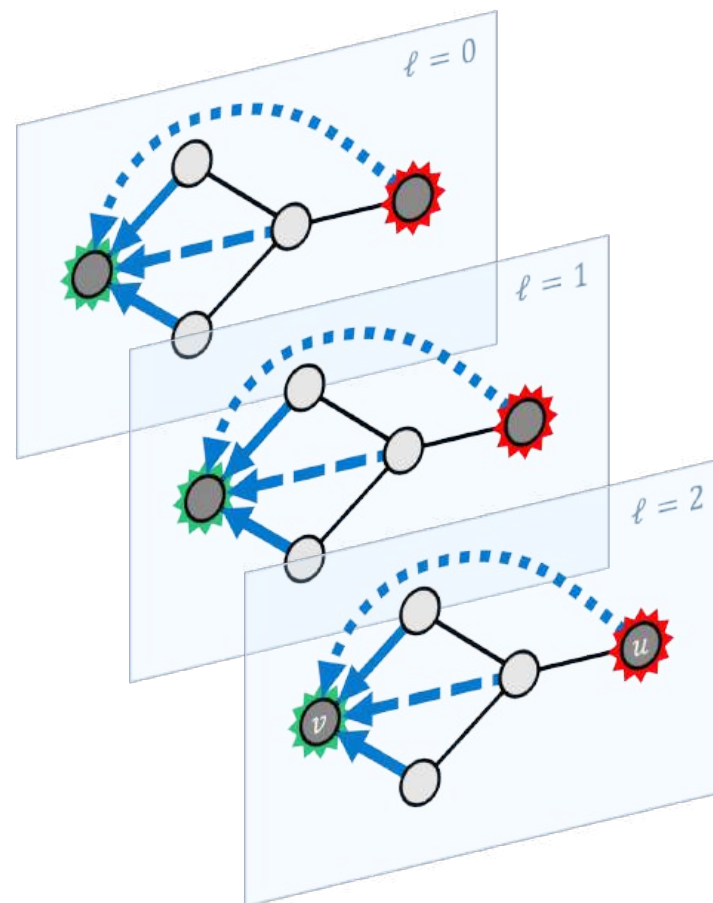


Graph Transformer

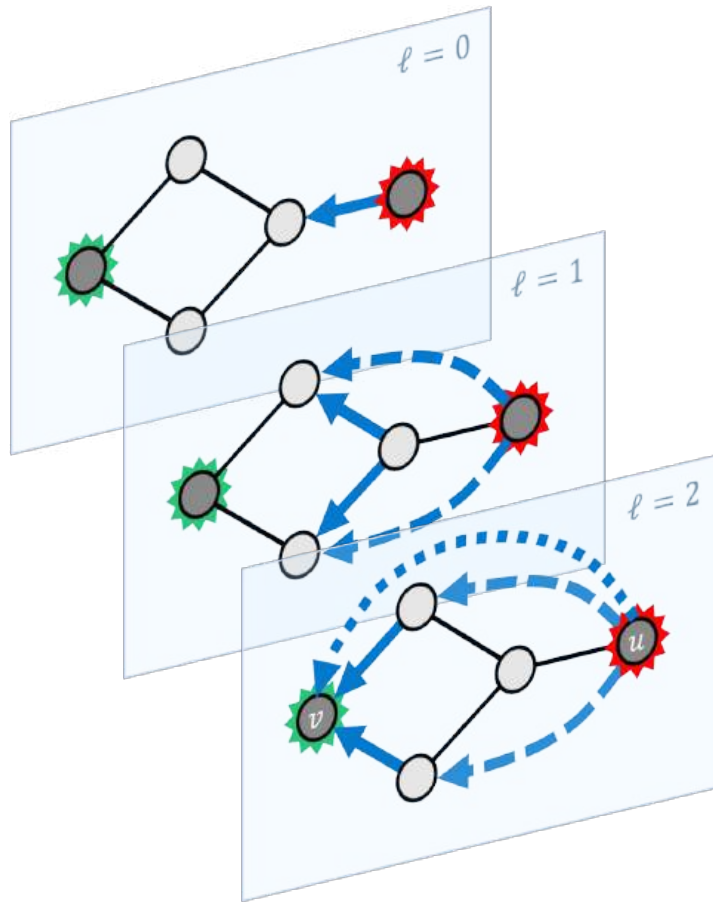


Dynamic Rewiring  
(DRew)

Gutteridge, Di Giovanni et B 2023

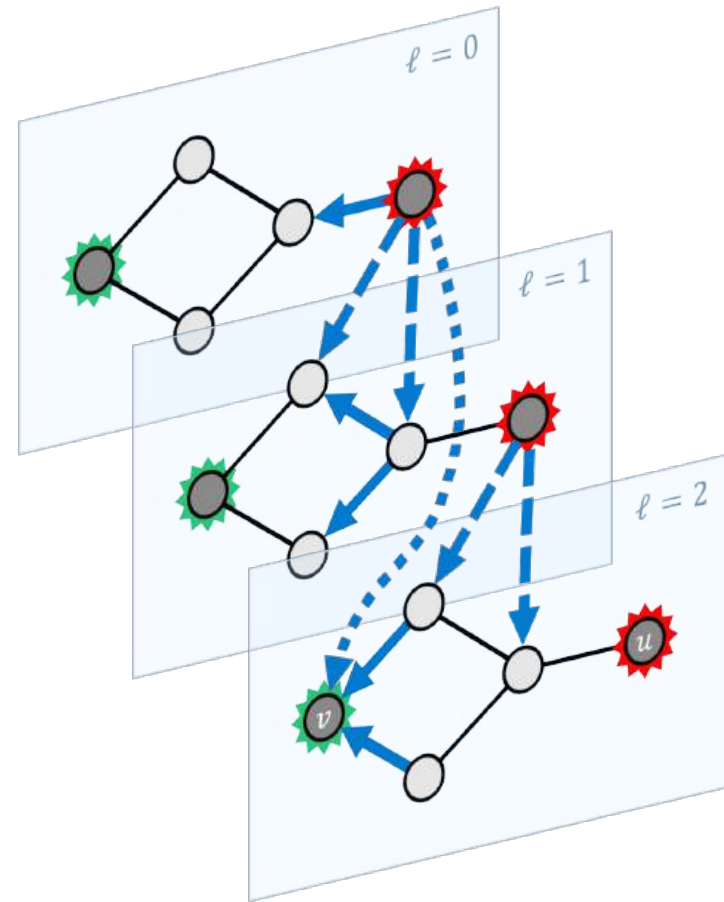


Graph Transformer



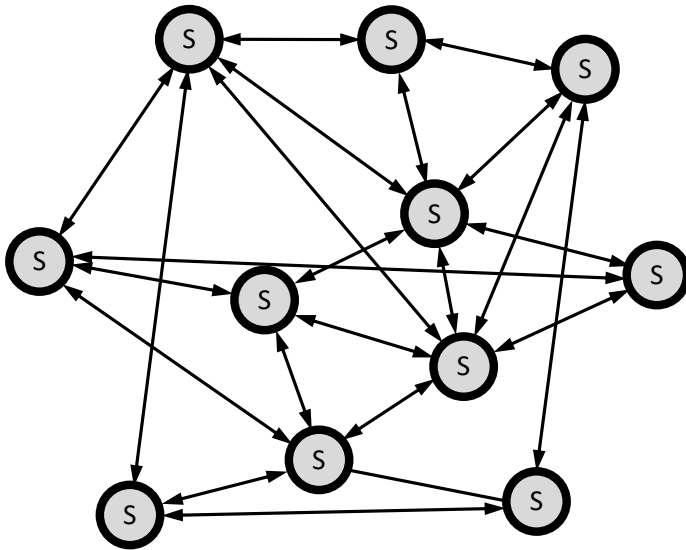
Dynamic Rewiring  
(DRew)

Gutteridge, Di Giovanni et B 2023



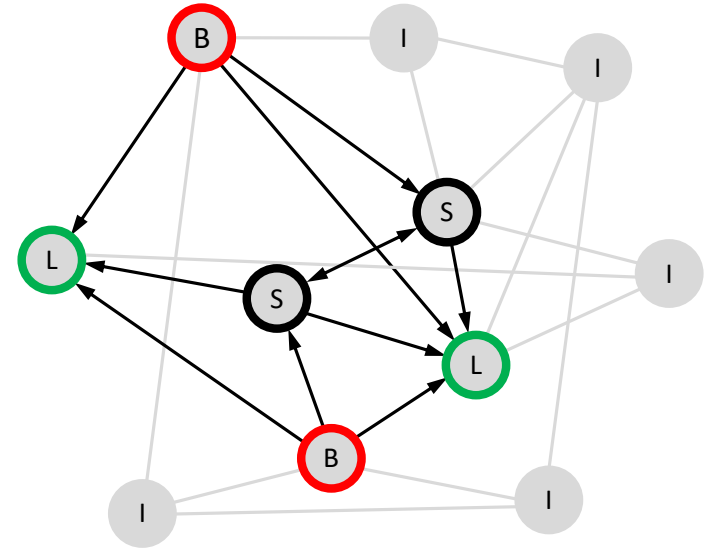
Dynamic Rewiring + delay  
(vDRew)

## Cooperative Message Passing



## Standard Message Passing

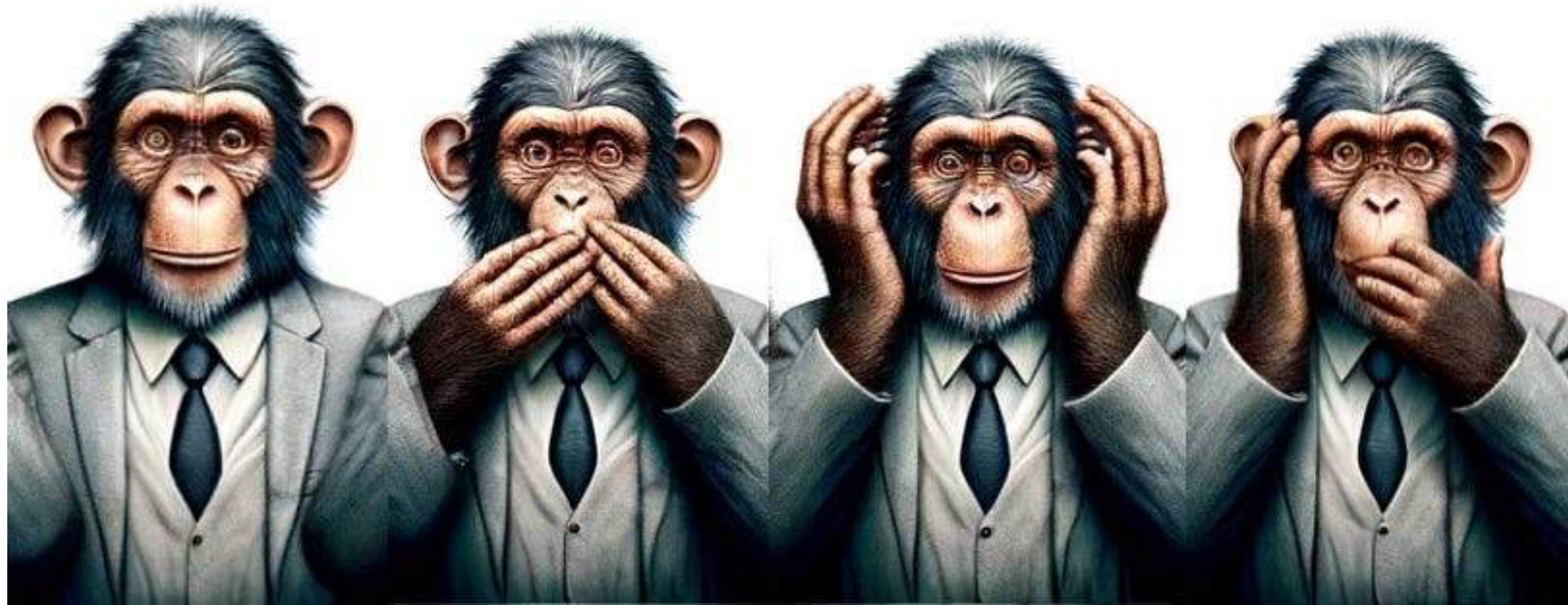
each node Broadcasts & Listens



## Cooperative Message Passing

each node individually decides

## *Cooperative Message Passing*



**Broadcast &  
Listen**

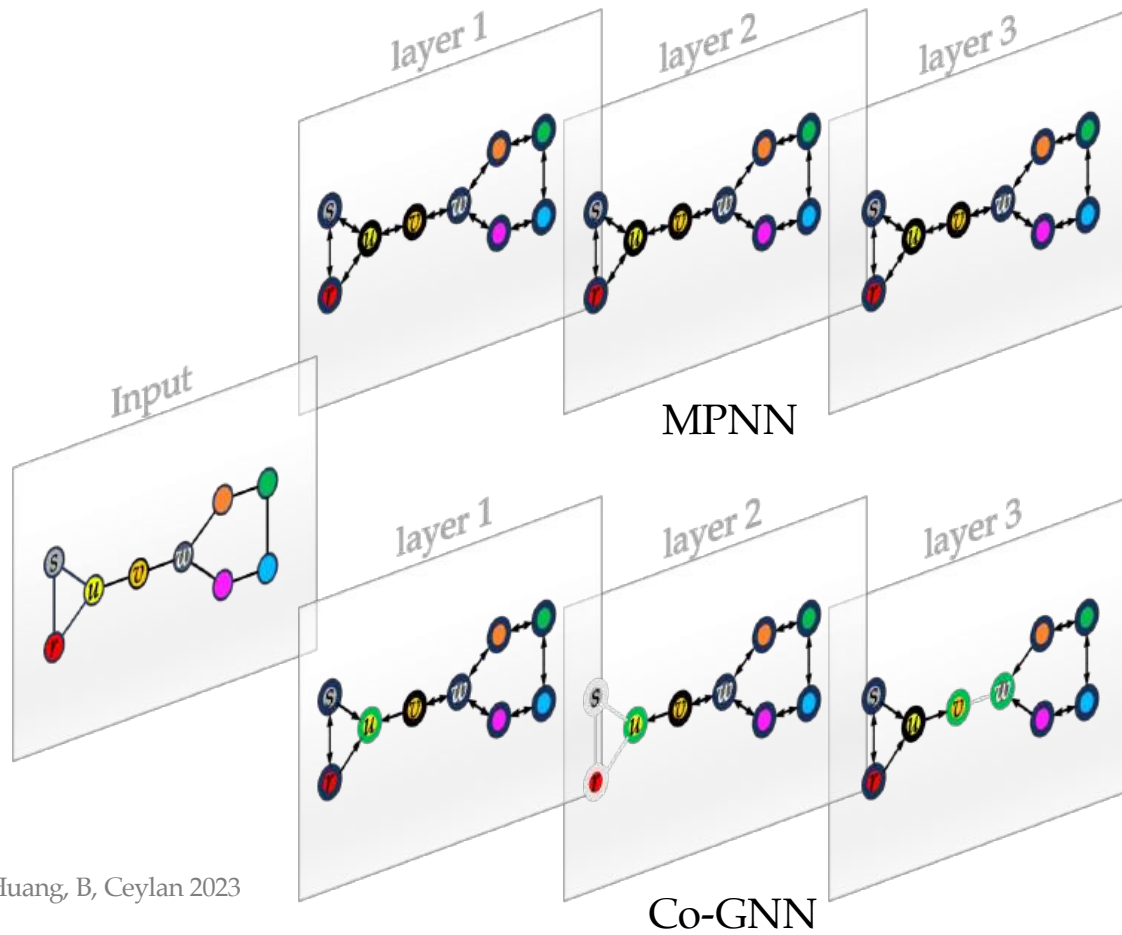
**Listen**

**Broadcast**

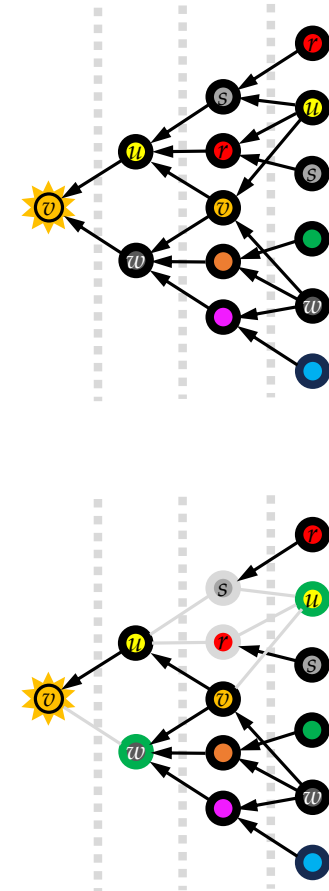
**Isolate**

Finkelshtein, Huang, B, Ceylan 2023; Illustration: DALL-E 3 (after a lot of effort)

# Cooperative Message Passing

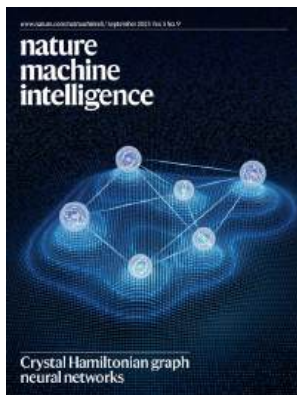


Finkelshtein, Huang, B, Ceylan 2023

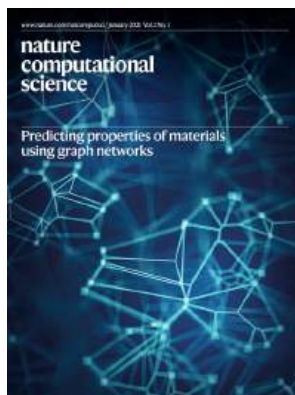


## *What do we gain from physics-inspired GNNs?*

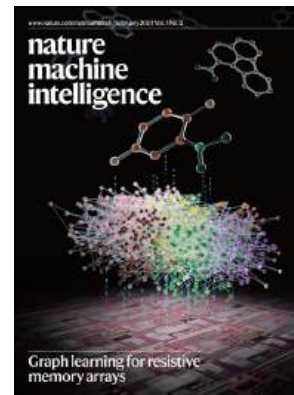
- New perspectives on old problems (e.g. oversmoothing, bottlenecks, etc.)
- Explains old architectures & gives rise to new ones
- Principled architectural choices (residual connection, shared symmetric weights)
- Theoretical guarantees (e.g. stability, convergence, expressive power, etc.)
- Deep links to other fields less known in GNN literature (e.g. differential geometry & algebraic topology)
- In GNNs, the graph is both *input* and *computational device* – not all graphs are good!
- Rewiring tells *what* messages to send *where*
- Dynamic rewiring+delay adds control also *when*



Physics



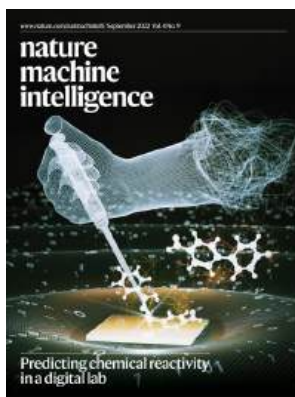
New materials



Chip design



Biology



Chemistry



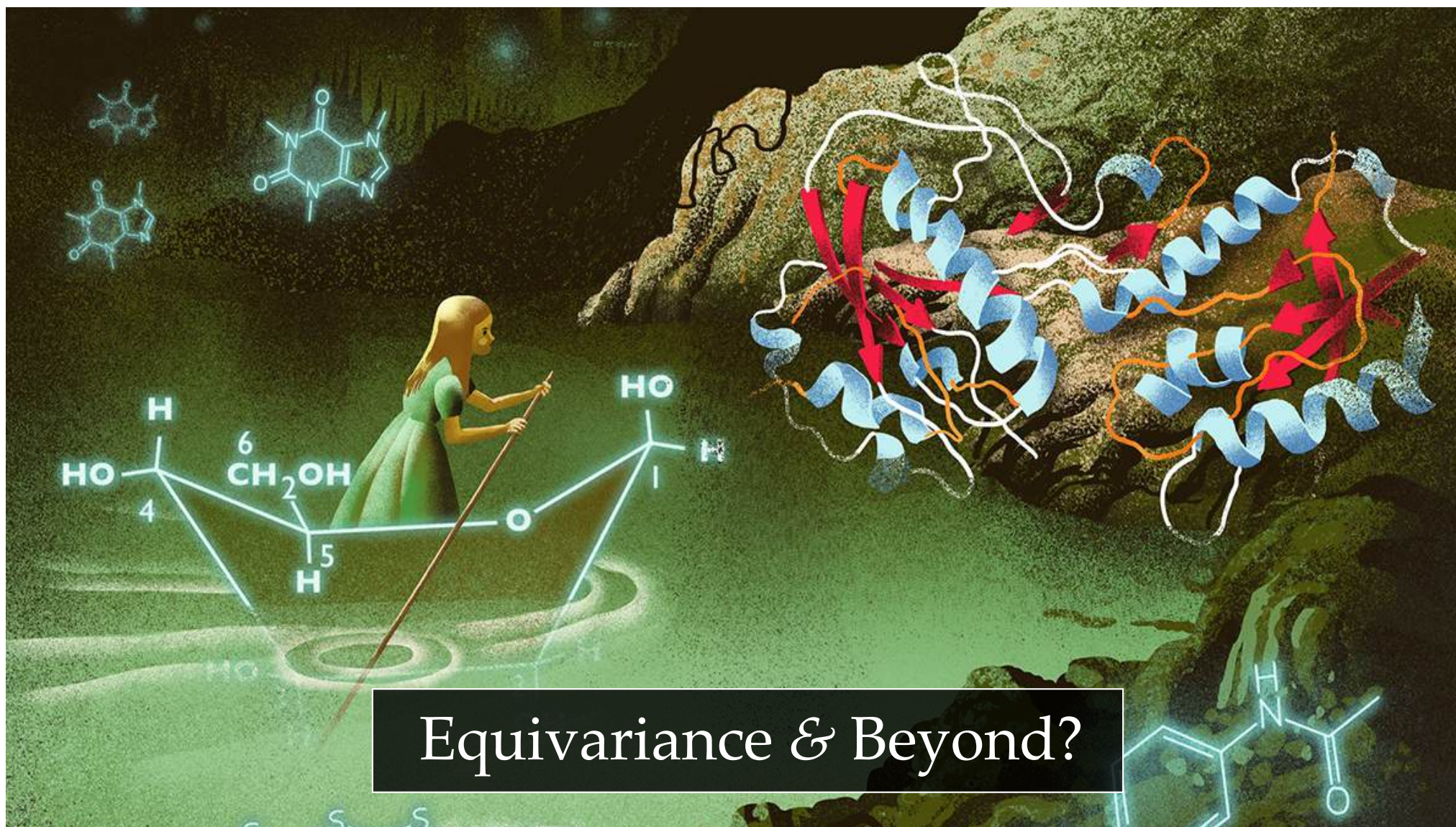
Urban planning



Pure math

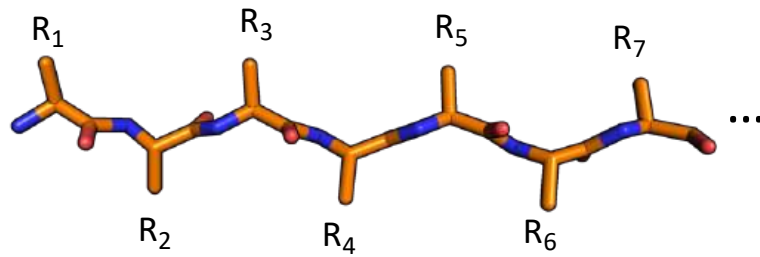


Weather

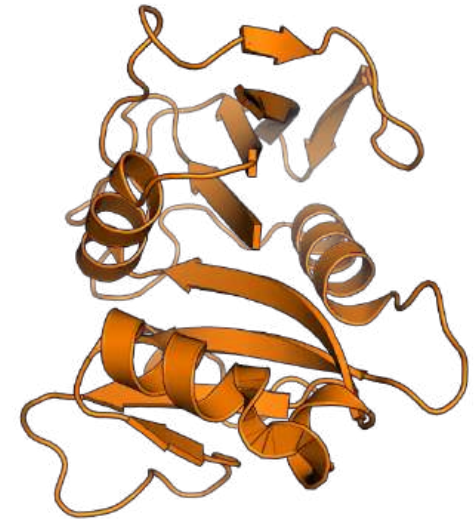


# *Protein Folding*

Protein folding



Sequence of  
amino acids



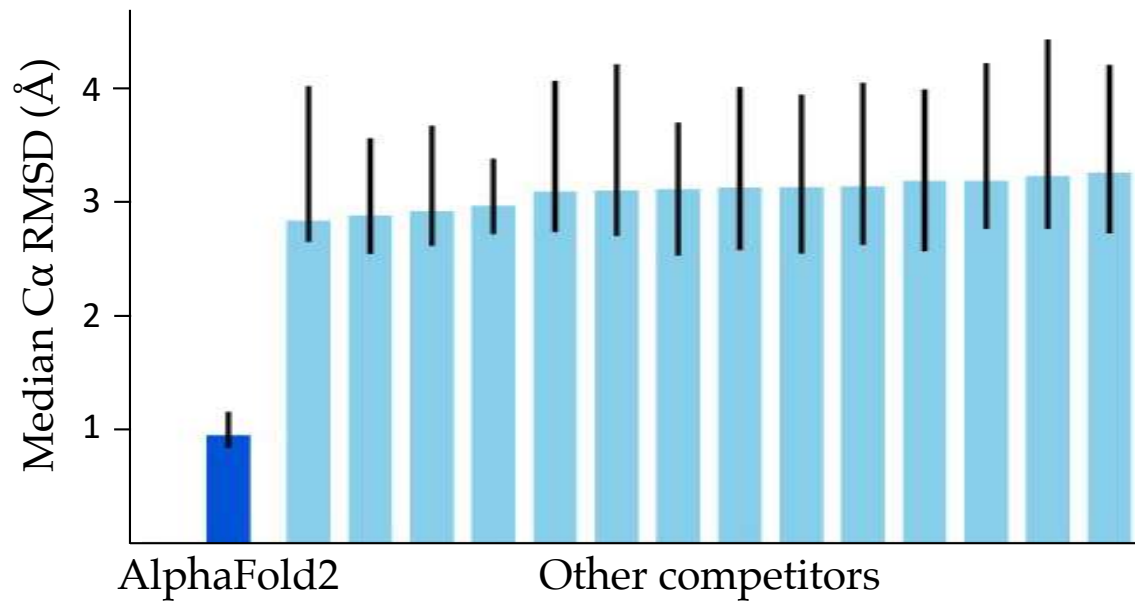
3D structure

“[protein] conformation is determined by the totality of interatomic interactions and hence by the amino acid sequence”

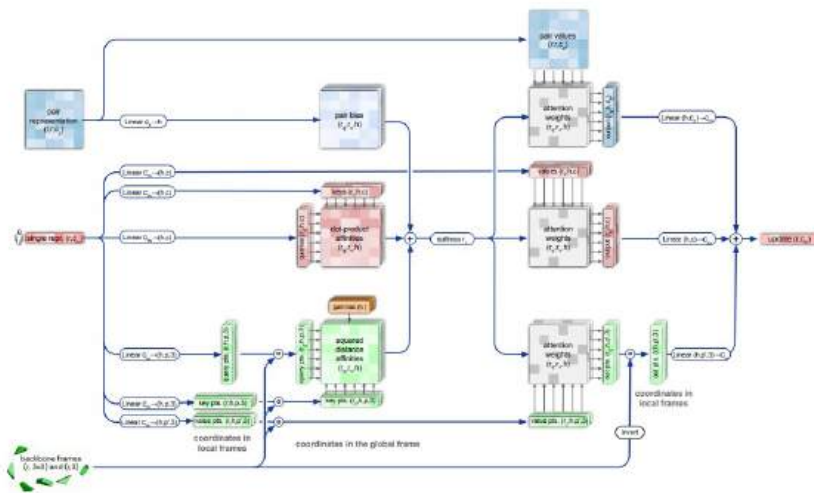


**C. Anfinsen**

# AlphaFold2: the “ImageNet moment” of Structural Biology



# Revolution in Structural Biology



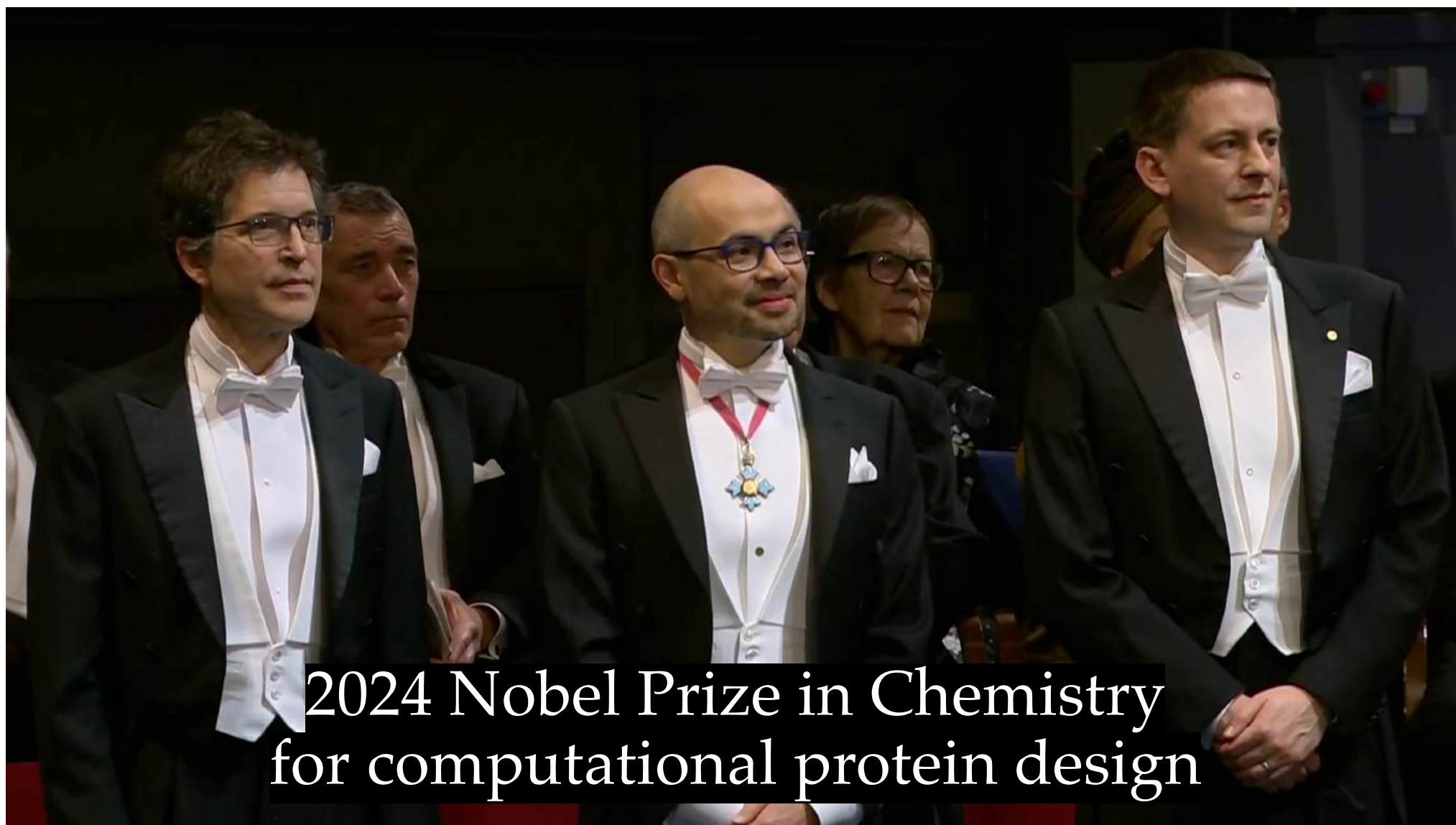
Jumper et al. 2021

**AlphaFold 2**  
“Invariant point  
attention”



Baek et al. 2021

**RosettaFold**  
SE(3)-equivariant  
Transformer



2024 Nobel Prize in Chemistry  
for computational protein design

AND THEY LIVED

HAPPILY EVER AFTER



## The Bitter Lesson: Equivariance is dead...long live equivariance!

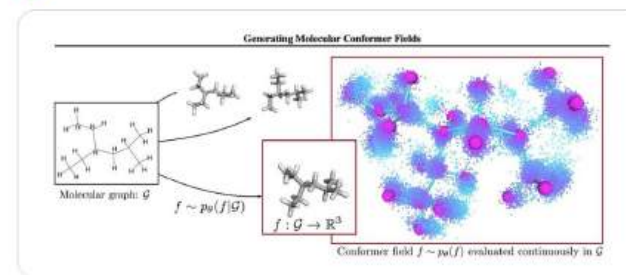
► **Equivariance is the idea of giving a model the inductive biases to natively handle rotations, translations and (sometimes) reflections. It has been at the core of Geometric Deep Learning and biomolecular modelling research since AlphaFold 2. However, recent works by top labs have questioned the existing mantra.**

- **The first shots were fired by Apple**, with a paper that obtained SOTA results on predicting the 3D structures of small molecules using a non-equivariant diffusion model with a transformer encoder.
- Remarkably, the authors showed that using the domain-agnostic model did not deleteriously impact generalization and was consistently able to outperform specialist models (assuming sufficient scale was used).
- **Next was AlphaFold 3, which infamously dropped all the equivariance** and frames constraints from the previous model in favour of another diffusion process coupled with augmentations and, of course, scale.
- Regardless, the greatly improved training efficiency of equivariant models means the practice is likely to stay for a while (at least for academic groups working on large systems such as proteins).



"We [...] empirically show that explicitly enforcing roto-translation equivariance is not a strong requirement for generalization."

"Furthermore, we also show that approaches that do not explicitly enforce roto-translation equivariance (like ours) can match or outperform approaches that do."



**stateof.ai 2024**

# Swallowing the Bitter Pill: Simplified Scalable Conformer Generation

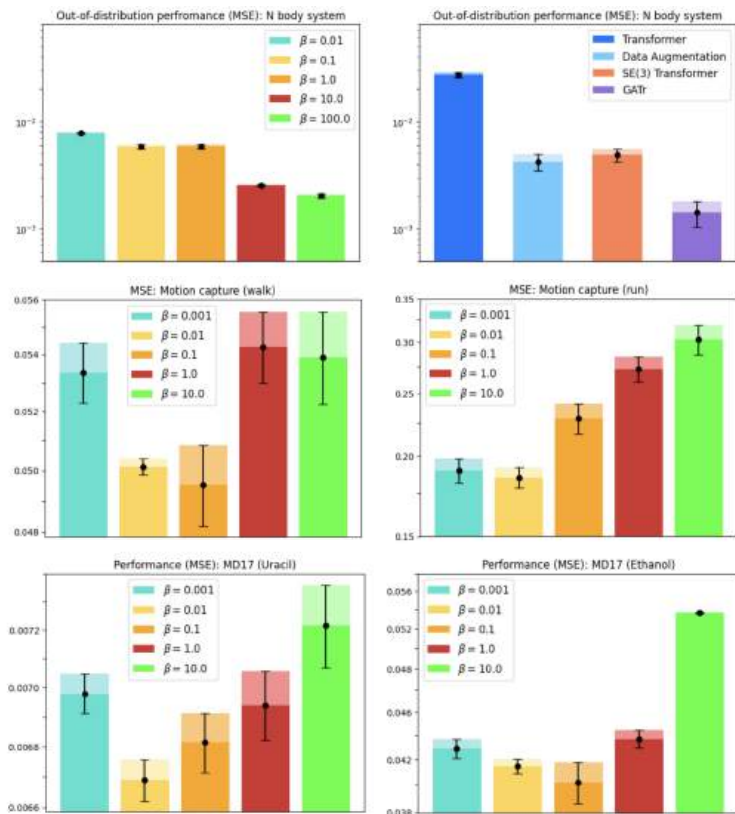
Yuyang Wang<sup>1</sup> Ahmed A. Elhag<sup>1,2</sup> Navdeep Jaitly<sup>1</sup> Joshua M. Susskind<sup>1</sup> Miguel Ángel Bautista<sup>1</sup>

## Abstract

We present a novel way to predict molecular conformers through a simple formulation that sidesteps many of the heuristics of prior works and achieves state of the art results by using the advantages of scale. By training a diffusion generative model directly on 3D atomic positions without making assumptions about the explicit structure of molecules (*e.g.* modeling torsional angles) we are able to radically simplify structure learning, and make it trivial to scale up the model sizes. This model, called Molecular Conformer Fields (MCF), works by parameterizing conformer structures as functions that map elements from a molecular graph directly to their 3D location in space. This formulation allows us to boil down the essence of structure prediction to learning a distribution over functions. Experimental results show that scaling up the model capacity leads to large gains in generalization performance *without enforcing inductive biases* like rotational equivariance. MCF represents an advance in extending diffusion models to handle complex scientific problems in a conceptually simple, scalable and effective manner.

is the vast complexity of the 3D structure space, encompassing factors such as bond lengths and torsional angles. Despite the molecular graph dictating potential 3D conformers through specific constraints, such as bond types and spatial arrangements determined by chiral centers, the conformational space experiences exponential growth with the expansion of the graph size and the number of rotatable bonds (Axelrod & Gomez-Bombarelli, 2022). This complicates brute force and exhaustive approaches, making them virtually unfeasible for even moderately small molecules.

Systematic methods, like OMEGA (Hawkins et al., 2010), offer rapid processing through rule-based generators and curated torsion templates. Despite their efficiency, these models typically fail on complex molecules, as they often overlook global interactions and are tricky to extend to inputs like transition states or open-shell molecules. Classic stochastic methods, like molecular dynamics (MD) and Markov chain Monte Carlo (MCMC), rely on extensively exploring the energy landscape to find low-energy conformers. Such techniques suffer from sampling inefficiency for large molecules and struggle to generate diverse representative conformers (Hawkins, 2017; Wilson et al., 1991; Grebner et al., 2011). In the domain of learning-based approaches, several works have looked at conformer generation problems through the lens of probabilistic modeling, using either





## The Bitter Lesson: Equivariance is dead...long live equivariance!

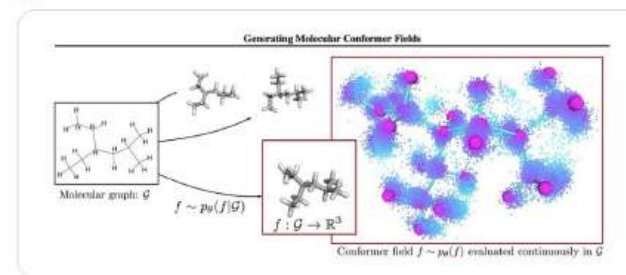
► **Equivariance is the idea of giving a model the inductive biases to natively handle rotations, translations and (sometimes) reflections. It has been at the core of Geometric Deep Learning and biomolecular modelling research since AlphaFold 2. However, recent works by top labs have questioned the existing mantra.**

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- Remarkably, the authors showed that using the domain-agnostic model did not deleteriously impact generalization and was consistently able to outperform specialist models (assuming sufficient scale was used).
- **Next was AlphaFold 3, which infamously dropped all the equivariance** and frames constraints from the previous model in favour of another diffusion process coupled with augmentations and, of course, scale.
- Regardless, the greatly improved training efficiency of equivariant models means the practice is likely to stay for a while (at least for academic groups working on large systems such as proteins).



"We [...] empirically show that explicitly enforcing roto-translation equivariance is not a strong requirement for generalization."

"Furthermore, we also show that approaches that do not explicitly enforce roto-translation equivariance (like ours) can match or outperform approaches that do."



**stateof.ai 2024**



# The Hardware Lottery

Sara Hooker

Google Research, Brain Team

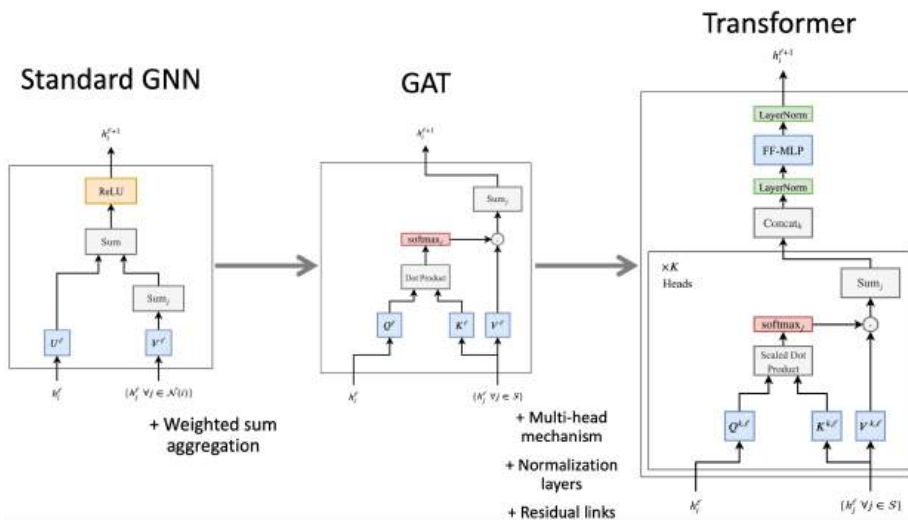
Hardware, systems and algorithms research communities have historically had different incentive structures and fluctuating motivation to engage with each other explicitly. This historical treatment is odd given that hardware and software have frequently determined which research ideas succeed (and fail). This essay introduces the term hardware lottery to describe when a research idea wins because it is suited to the available software and hardware and *not* because the idea is superior to alternative research directions. Examples from early computer science history illustrate how hardware lotteries can delay research progress by casting successful ideas as failures. These lessons are particularly salient given the advent of domain specialized hardware which make it increasingly costly to stray off of the beaten path of research ideas. This essay posits that the gains from progress in computing are likely to become even more uneven, with certain research directions moving into the fast-lane while progress on others is further obstructed.

# Transformers are Graph Neural Networks

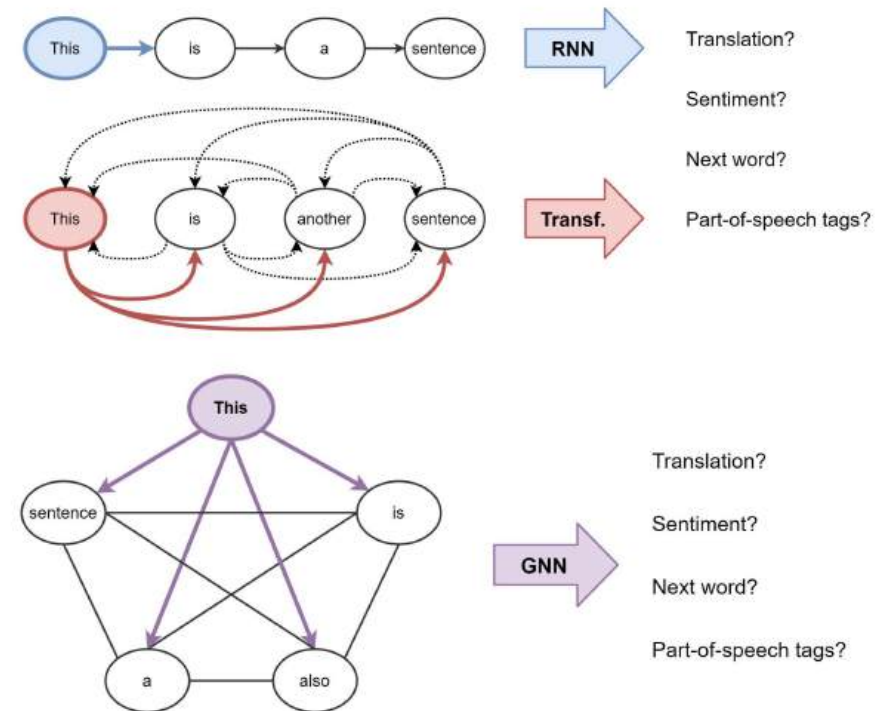
Exploring the connection between Transformer models such as GPT and BERT for Natural Language Processing, and Graph Neural Networks.

Chaitanya K. Joshi

Last updated on Jun 21, 2021 · 12 min read



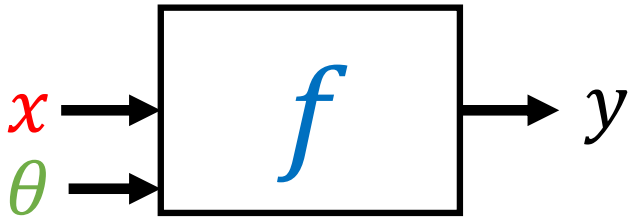
Joshi 2021





*“How  $f$  interacts with the group  $G$  acting on  $x$ ?”*

$$f(g \cdot x) = f(x)$$



*“How  $f$  interacts with the group  $G$  acting on  $x$ ?”*

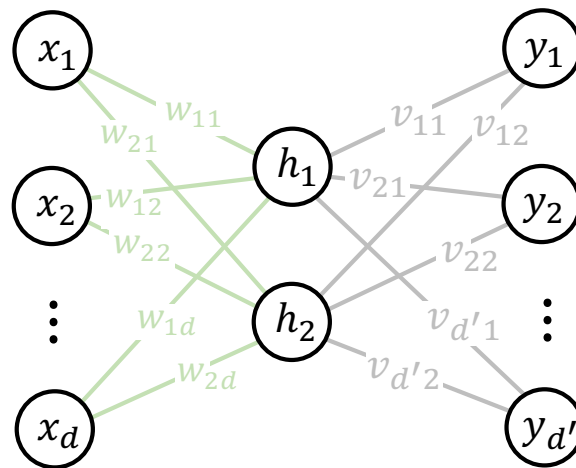
$$f(g \cdot x) = f(x)$$



*“How  $f$  interacts with the group  $G$  acting on  $x$  and  $H$  acting on  $\theta$ ?”*

$$f(g.x, h.\theta) = f(x, \theta)$$

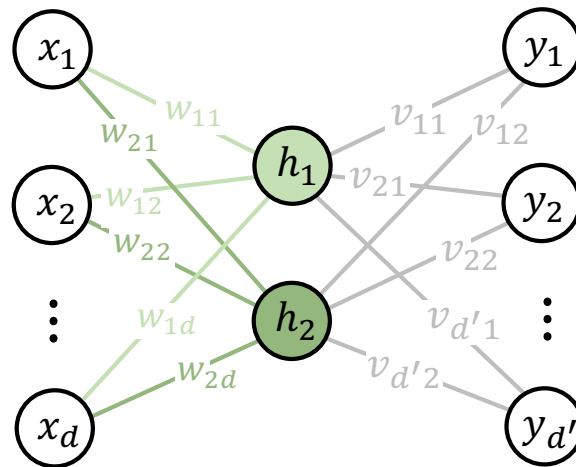
## *Symmetries of the Weights*



$$\mathbf{y} = \mathbf{V} \sigma \left( \mathbf{W} \mathbf{x} \right)$$

The equation shows the relationship between the output vector  $\mathbf{y}$ , the weight matrix  $\mathbf{W}$  (green grid), the input vector  $\mathbf{x}$  (red column), and the output weight matrix  $\mathbf{V}$  (grey grid). The activation function  $\sigma$  is applied to the product of  $\mathbf{W}$  and  $\mathbf{x}$ .

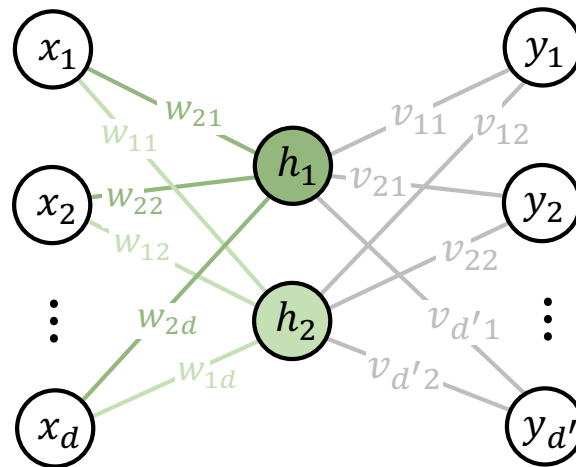
## *Symmetries of the Weights*



$$\mathbf{y} = \mathbf{V} \sigma \left( \mathbf{W} \mathbf{x} \right)$$

The equation shows the relationship between the output vector  $\mathbf{y}$ , the output matrix  $\mathbf{V}$ , the activation function  $\sigma$ , the weight matrix  $\mathbf{W}$ , and the input vector  $\mathbf{x}$ . The matrix  $\mathbf{W}$  is represented by a grid of green and light green squares, and the vector  $\mathbf{x}$  is represented by a column of red squares.

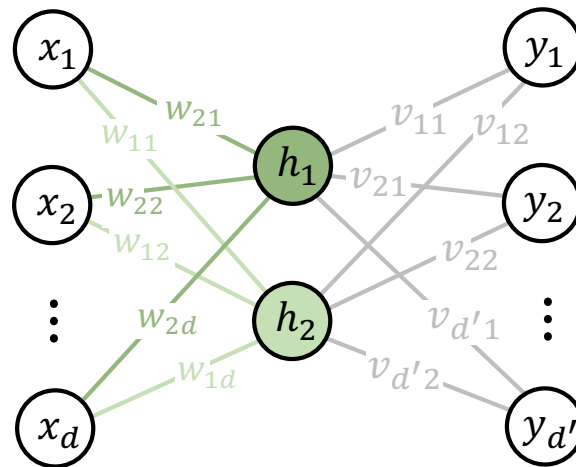
## *Symmetries of the Weights*



$$\mathbf{y} = \mathbf{V} \sigma \left( \mathbf{\Pi} \begin{bmatrix} \text{green grid} \\ \mathbf{w} \end{bmatrix} \begin{bmatrix} \text{red grid} \\ \mathbf{x} \end{bmatrix} \right)$$

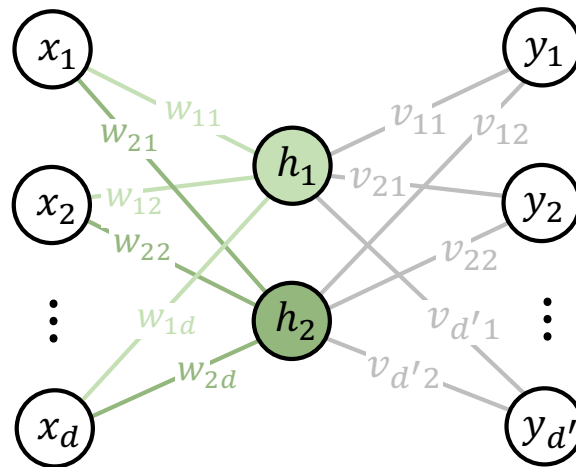
The diagram shows the matrix  $\mathbf{V}$  as a 3x3 grey grid,  $\mathbf{\Pi}$  as a 2x4 green grid,  $\mathbf{w}$  as a 2x4 green grid, and  $\mathbf{x}$  as a 4x1 red column vector.

## *Symmetries of the Weights*



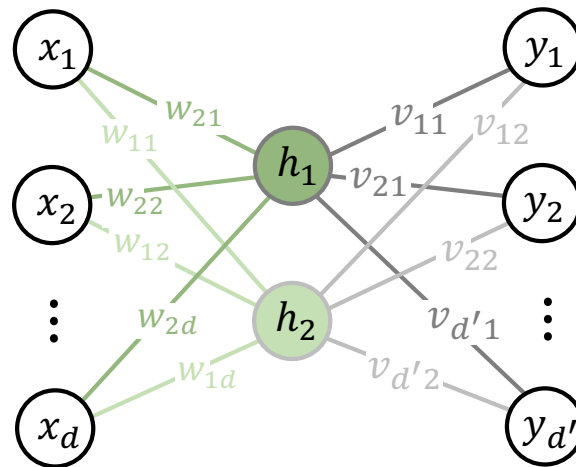
$$\mathbf{y} = \underset{\mathbf{V}}{\begin{bmatrix} \square & \square \\ \square & \square \\ \square & \square \end{bmatrix}} \Pi \sigma \left( \underset{\mathbf{W}}{\begin{bmatrix} \square & \square & \square \\ \square & \square & \square \end{bmatrix}} \underset{\mathbf{X}}{\begin{bmatrix} \square \\ \square \\ \square \end{bmatrix}} \right)$$

## *Symmetries of the Weights*



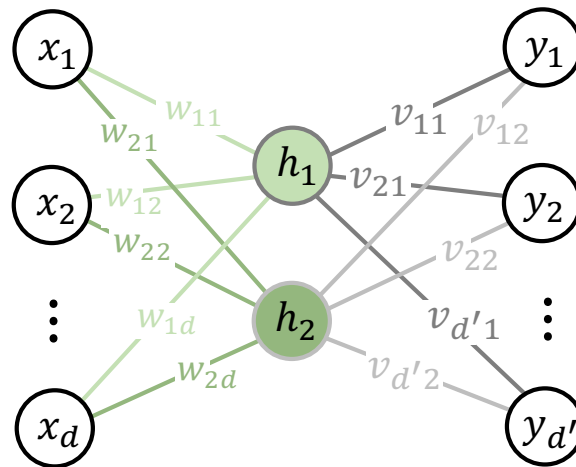
$$\mathbf{y} = \underset{\mathbf{V}}{\begin{bmatrix} \square & \square \\ \square & \square \\ \square & \square \end{bmatrix}} \Pi \sigma \left( \underset{\mathbf{W}}{\begin{bmatrix} \square & \square & \square & \square \\ \square & \square & \square & \square \end{bmatrix}} \underset{\mathbf{x}}{\begin{bmatrix} \square \\ \square \\ \square \\ \square \end{bmatrix}} \right)$$

## *Symmetries of the Weights*



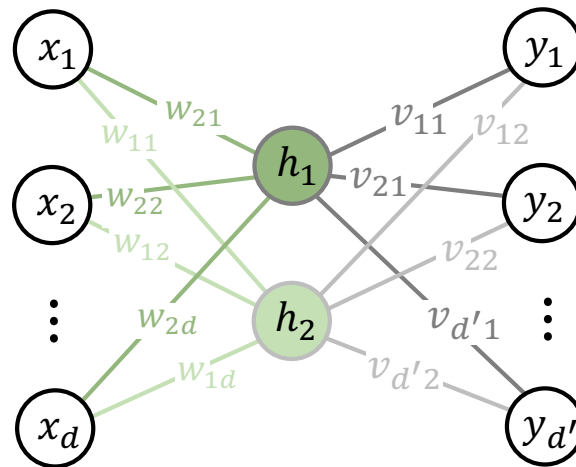
$$\mathbf{y} = \underset{\mathbf{V}}{\begin{bmatrix} \text{grey} & \text{grey} \\ \text{grey} & \text{grey} \\ \text{grey} & \text{grey} \end{bmatrix}} \Pi \sigma \left( \underset{\mathbf{W}}{\begin{bmatrix} \text{green} & \text{green} & \text{green} & \text{green} \\ \text{green} & \text{green} & \text{green} & \text{green} \end{bmatrix}} \underset{\mathbf{x}}{\begin{bmatrix} \text{red} \\ \text{red} \\ \text{red} \\ \text{red} \end{bmatrix}} \right)$$

# *Symmetries of the Weights*



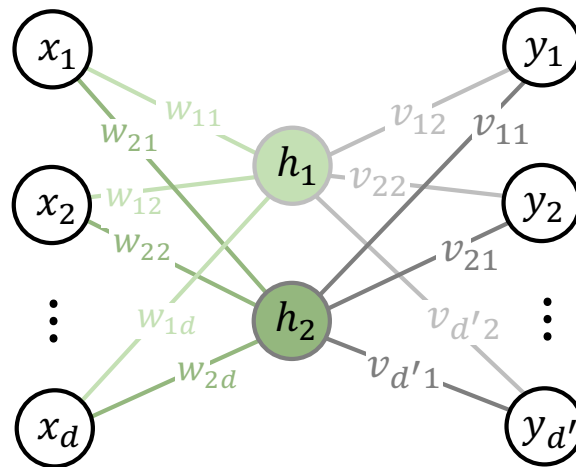
$$\mathbf{y} = \underset{\mathbf{V}}{\begin{bmatrix} \text{grey} & \text{grey} \\ \text{grey} & \text{grey} \\ \text{grey} & \text{grey} \end{bmatrix}} \Pi \sigma \left( \underset{\mathbf{W}}{\begin{bmatrix} \text{green} & \text{green} & \text{green} & \text{green} \\ \text{green} & \text{green} & \text{green} & \text{green} \end{bmatrix}} \underset{\mathbf{x}}{\begin{bmatrix} \text{pink} \\ \text{pink} \\ \text{pink} \\ \text{pink} \end{bmatrix}} \right)$$

## *Symmetries of the Weights*



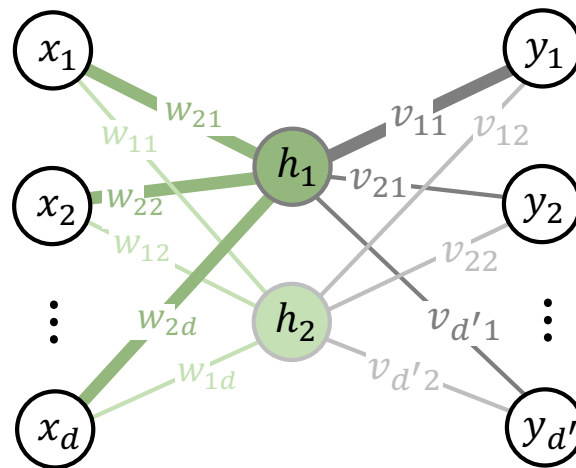
$$\mathbf{y} = \underset{\mathbf{V}}{\begin{bmatrix} \square & \square \\ \square & \square \\ \square & \square \end{bmatrix}} \mathbf{\Pi}^T \mathbf{\Pi} \sigma \left( \underset{\mathbf{W}}{\begin{bmatrix} \square & \square & \square & \square \\ \square & \square & \square & \square \end{bmatrix}} \underset{\mathbf{X}}{\begin{bmatrix} \square \\ \square \\ \square \\ \square \end{bmatrix}} \right)$$

# Symmetries of the Weights



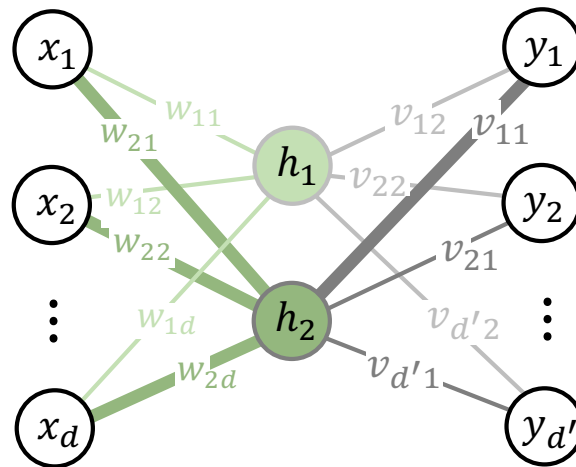
$$\mathbf{y} = \underset{\mathbf{V}}{\begin{bmatrix} \square & \square \\ \square & \square \\ \square & \square \end{bmatrix}} \mathbf{\Pi}^T \mathbf{\Pi} \sigma \left( \underset{\mathbf{W}}{\begin{bmatrix} \square & \square & \square & \square \\ \square & \square & \square & \square \end{bmatrix}} \underset{\mathbf{X}}{\begin{bmatrix} \square \\ \square \\ \square \\ \square \end{bmatrix}} \right)$$

## *Symmetries of the Weights*



$$\mathbf{y} = \underset{\mathbf{V}}{\begin{bmatrix} \square & \square & \square \\ \square & \square & \square \\ \square & \square & \square \end{bmatrix}} \mathbf{\Pi}^T \mathbf{\Pi} \sigma \left( \underset{\mathbf{W}}{\begin{bmatrix} \square & \square & \square & \square \\ \square & \square & \square & \square \end{bmatrix}} \underset{\mathbf{X}}{\begin{bmatrix} \square \\ \square \\ \square \\ \square \end{bmatrix}} \right)$$

# *Symmetries of the Weights*



$$\mathbf{y} = \underset{\mathbf{V}}{\begin{bmatrix} \square & \square \\ \square & \square \\ \square & \square \end{bmatrix}} \mathbf{\Pi}^T \mathbf{\Pi} \sigma \left( \underset{\mathbf{W}}{\begin{bmatrix} \square & \square & \square & \square \\ \square & \square & \square & \square \end{bmatrix}} \underset{\mathbf{X}}{\begin{bmatrix} \square \\ \square \\ \square \\ \square \end{bmatrix}} \right)$$

## *Symmetries of the Weights*

- $L$ -layer neural network with weights  $\boldsymbol{\theta} = (\mathbf{W}_1, \mathbf{b}_1, \dots, \mathbf{W}_L, \mathbf{b}_L)$
- Parameter space symmetry  $G = S_{d_1} \times \dots \times S_{d_L}$

$$\mathbf{W}'_1 = \boldsymbol{\Pi}_1^T \mathbf{W}_1$$

$$\mathbf{b}'_1 = \boldsymbol{\Pi}_1^T \mathbf{b}_1$$

$$\mathbf{W}'_l = \boldsymbol{\Pi}_l^T \mathbf{W}_l \boldsymbol{\Pi}_{l-1}$$

$$\mathbf{b}'_l = \boldsymbol{\Pi}_l^T \mathbf{b}_l$$

$$\vdots$$

$$\vdots$$

$$\mathbf{W}'_L = \mathbf{W}_L \boldsymbol{\Pi}_{L-1}$$

$$\mathbf{b}'_L = \mathbf{b}_L$$

such that  $f(\cdot, g\boldsymbol{\theta}) = f(\cdot, \boldsymbol{\theta})$

## *Symmetries in the Gradient Space*

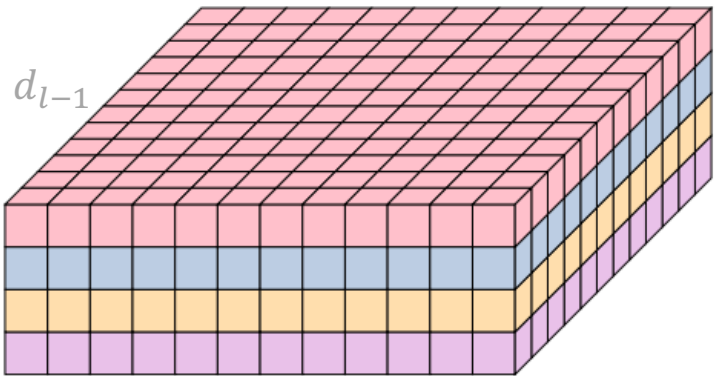
$$\mathcal{L}_{\mathcal{B}} = \frac{1}{|\mathcal{B}|} \sum_{(\mathbf{x}, \mathbf{y}) \in \mathcal{B}} \underbrace{\ell(f(\mathbf{x}, \boldsymbol{\theta}), \mathbf{y})}_{\mathcal{L}_{(\mathbf{x}, \mathbf{y})}}$$

$$\nabla_{\mathbf{b}_l} \mathcal{L}_{(\mathbf{x}, \mathbf{y})} = \mathbf{g}_l \quad \text{where} \quad \mathbf{g}_l = \frac{\partial \ell(f(\mathbf{x}, \boldsymbol{\theta}), \mathbf{y})}{\partial \mathbf{u}_l}$$

$$\nabla_{\mathbf{w}_l} \mathcal{L}_{(\mathbf{x}, \mathbf{y})} = \mathbf{g}_l \mathbf{a}_{l-1}^T$$

## *Symmetries in the Gradient Space*

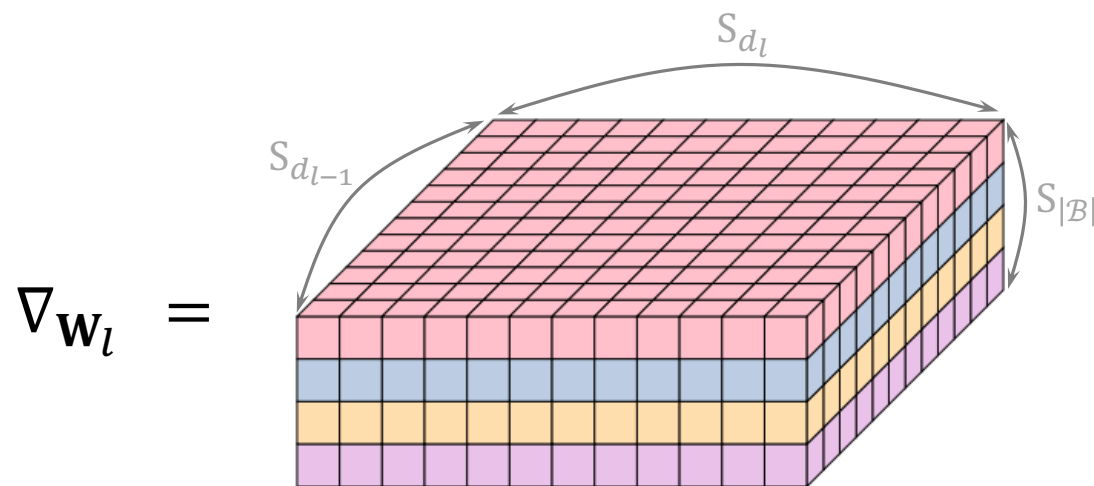
$$\mathcal{L}_{\mathcal{B}} = \frac{1}{|\mathcal{B}|} \sum_{(\mathbf{x}, \mathbf{y}) \in \mathcal{B}} \ell(f(\mathbf{x}, \boldsymbol{\theta}), \mathbf{y})$$

$$\nabla_{\mathbf{w}_l} =$$


A 3D grid representing the gradient space. The grid has dimensions  $d_{l-1}$  (width),  $d_l$  (depth), and  $|\mathcal{B}|$  (height). The grid is divided into four horizontal layers of different colors: pink (top), blue, yellow, and purple (bottom). The pink layer is the largest, followed by blue, yellow, and purple.

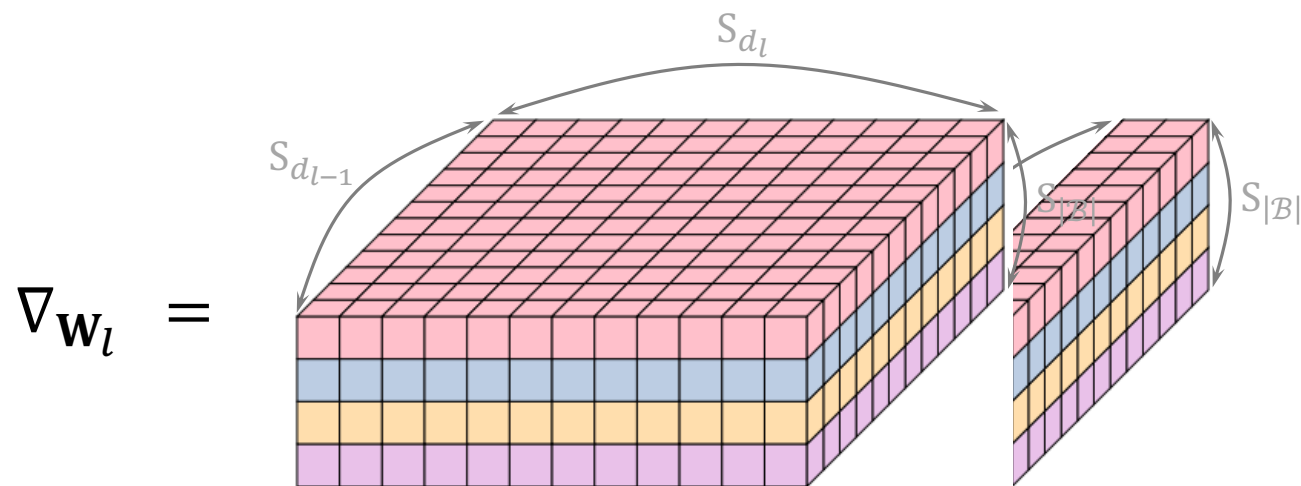
## *Symmetries in the Gradient Space*

$$\mathcal{L}_{\mathcal{B}} = \frac{1}{|\mathcal{B}|} \sum_{(\mathbf{x}, \mathbf{y}) \in \mathcal{B}} \ell(f(\mathbf{x}, \boldsymbol{\theta}), \mathbf{y})$$



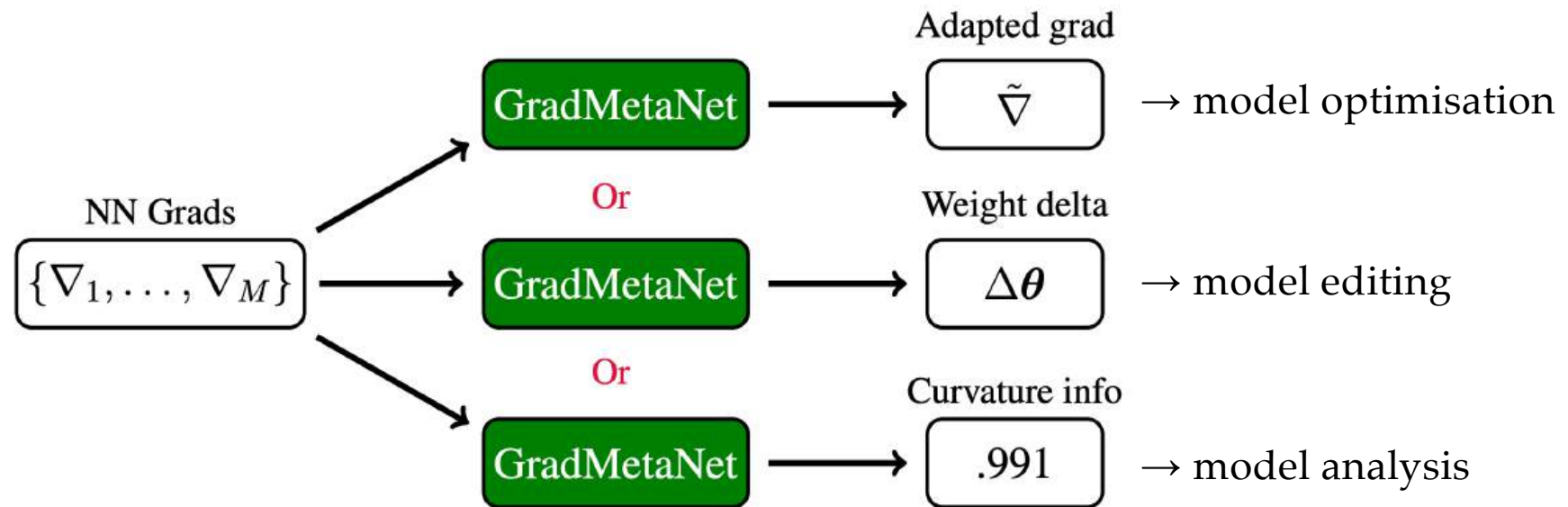
## Symmetries in the Gradient Space

$$\mathcal{L}_{\mathcal{B}} = \frac{1}{|\mathcal{B}|} \sum_{(\mathbf{x}, \mathbf{y}) \in \mathcal{B}} \ell(f(\mathbf{x}, \boldsymbol{\theta}), \mathbf{y})$$

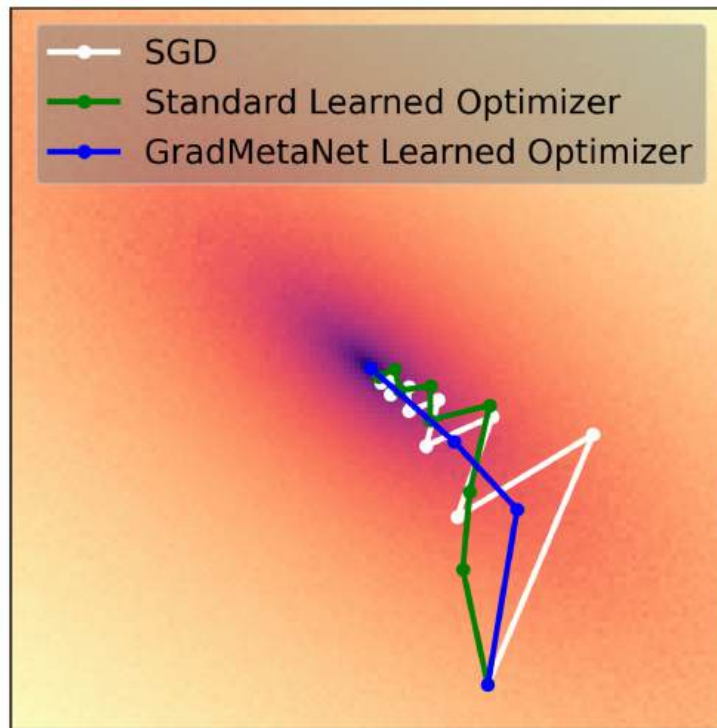


$$G_b = S_{|\mathcal{B}|} \times S_{d_1} \times \dots \times S_{d_L}$$

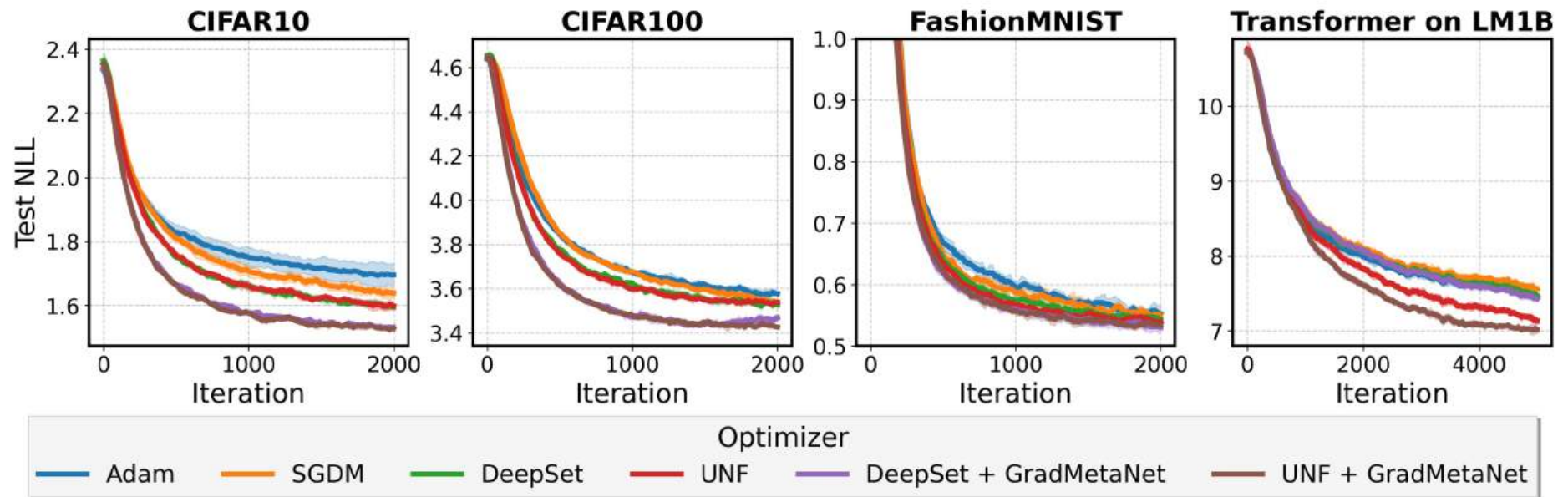
# GradMetaNet

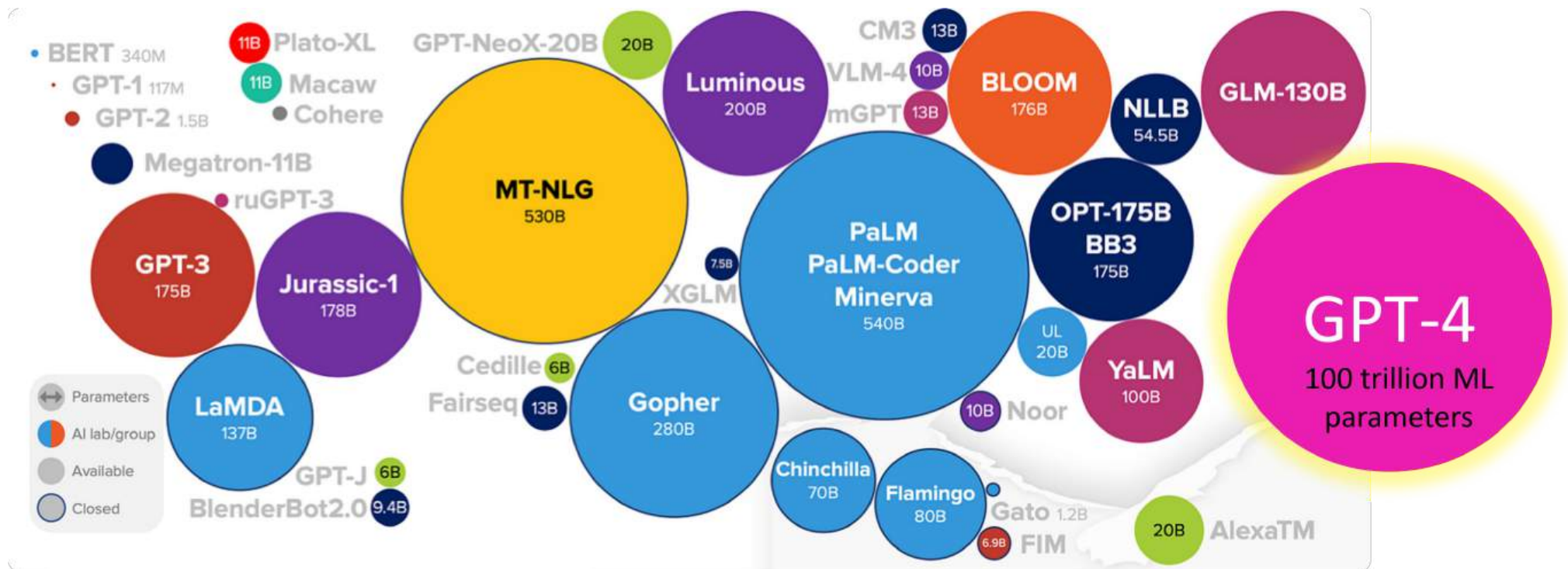


# *GradMetaNet: Learning Optimisation*

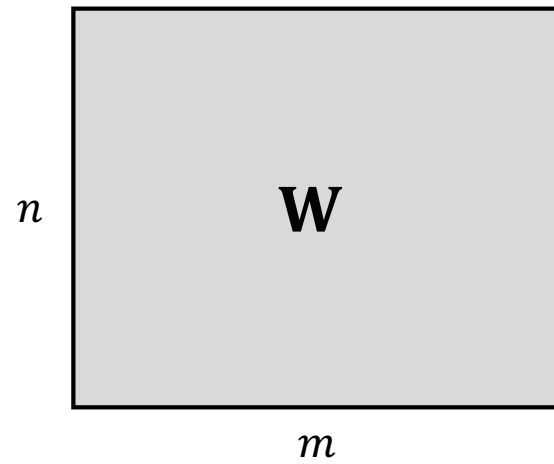


# *GradMetaNet: Learning Optimisation*

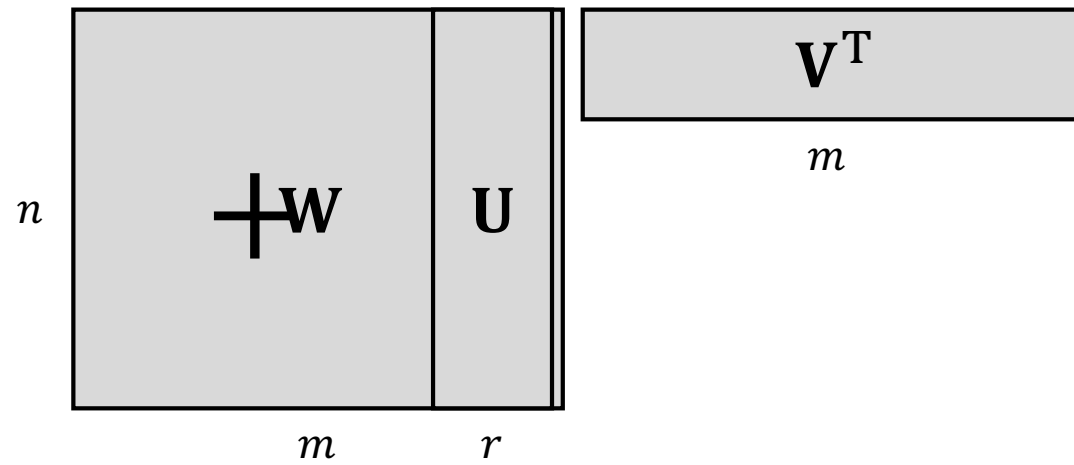




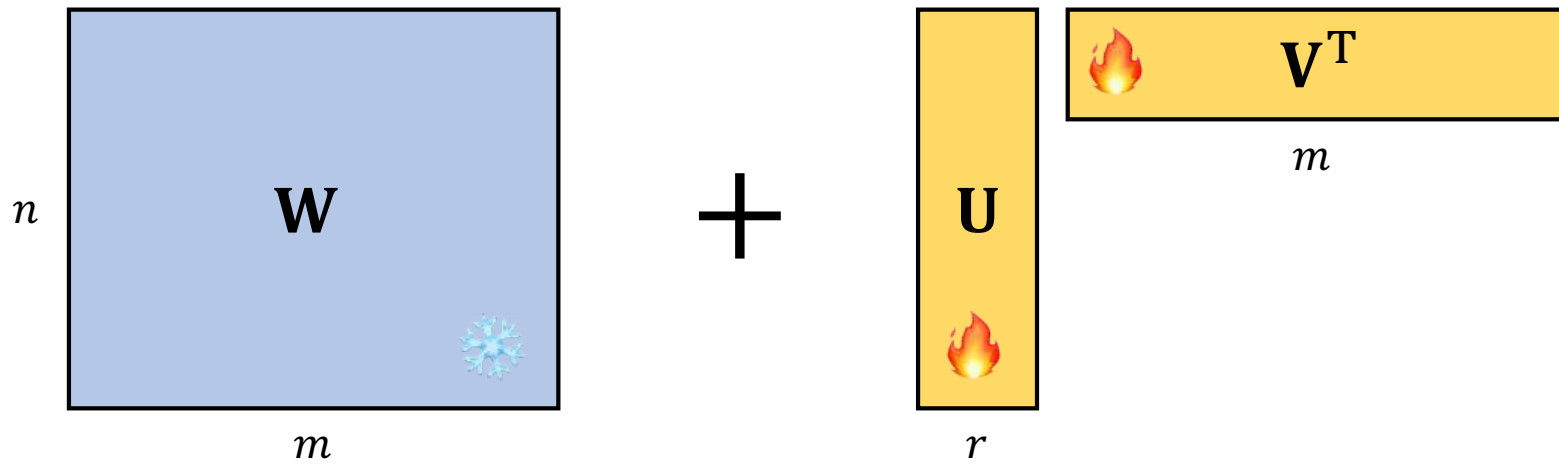
## *Low-Rank Adaptors (LoRA)*



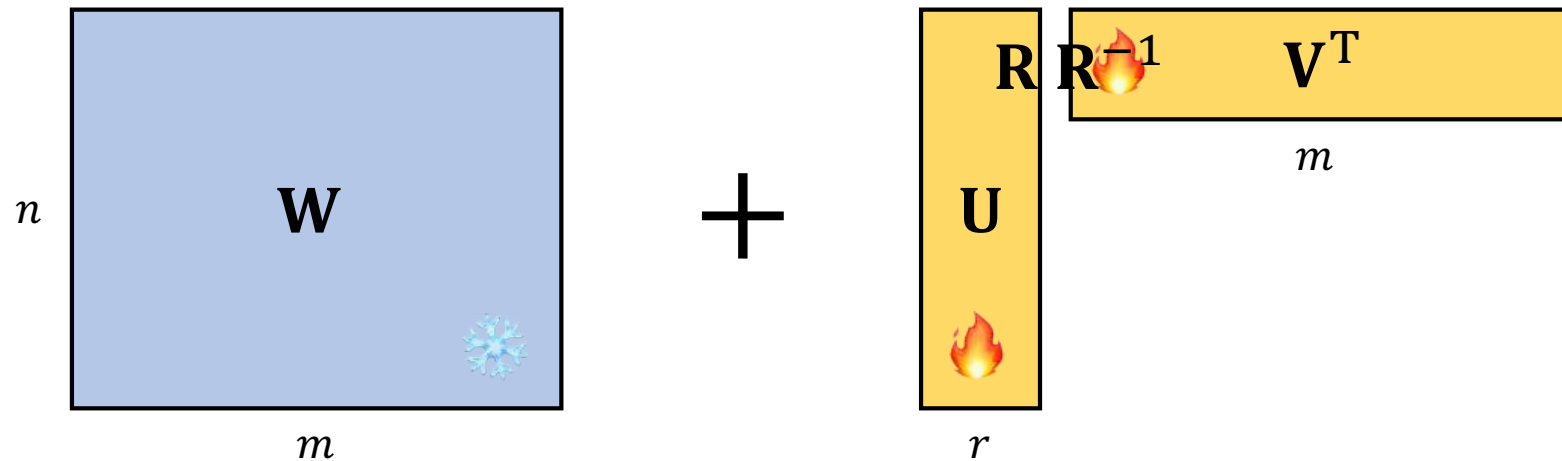
## *Low-Rank Adaptors (LoRA)*



## *Low-Rank Adaptors (LoRA)*

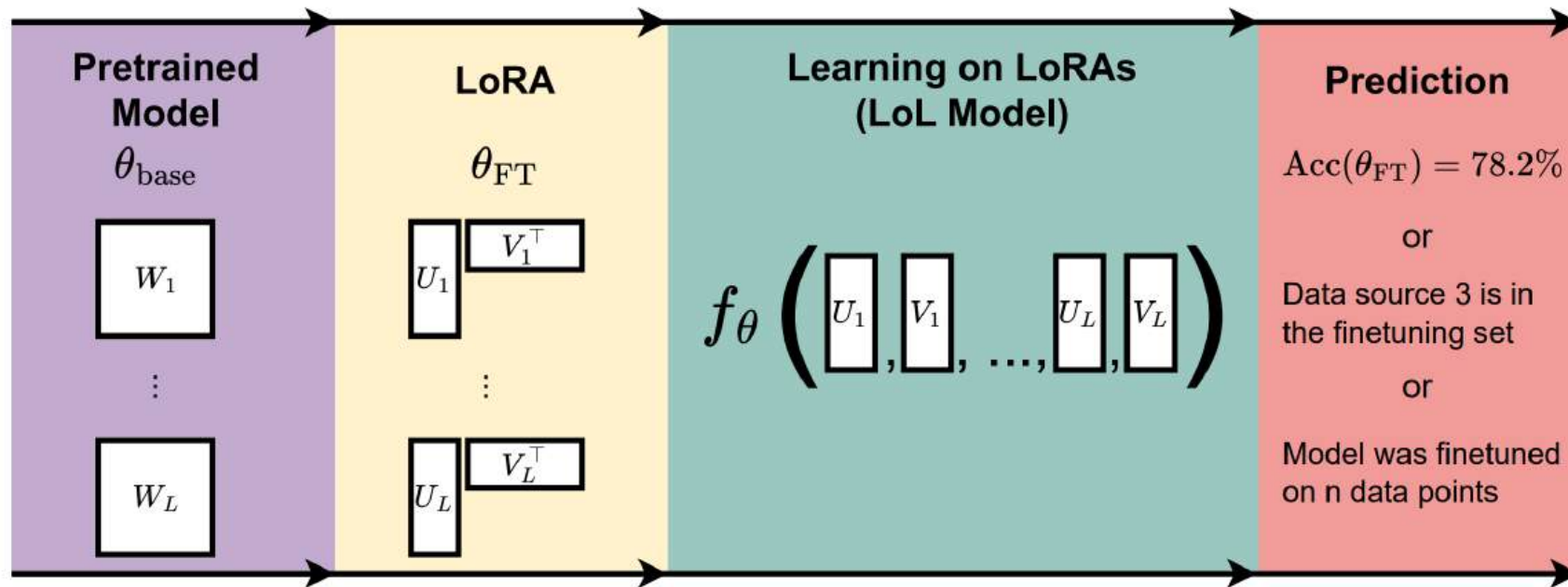


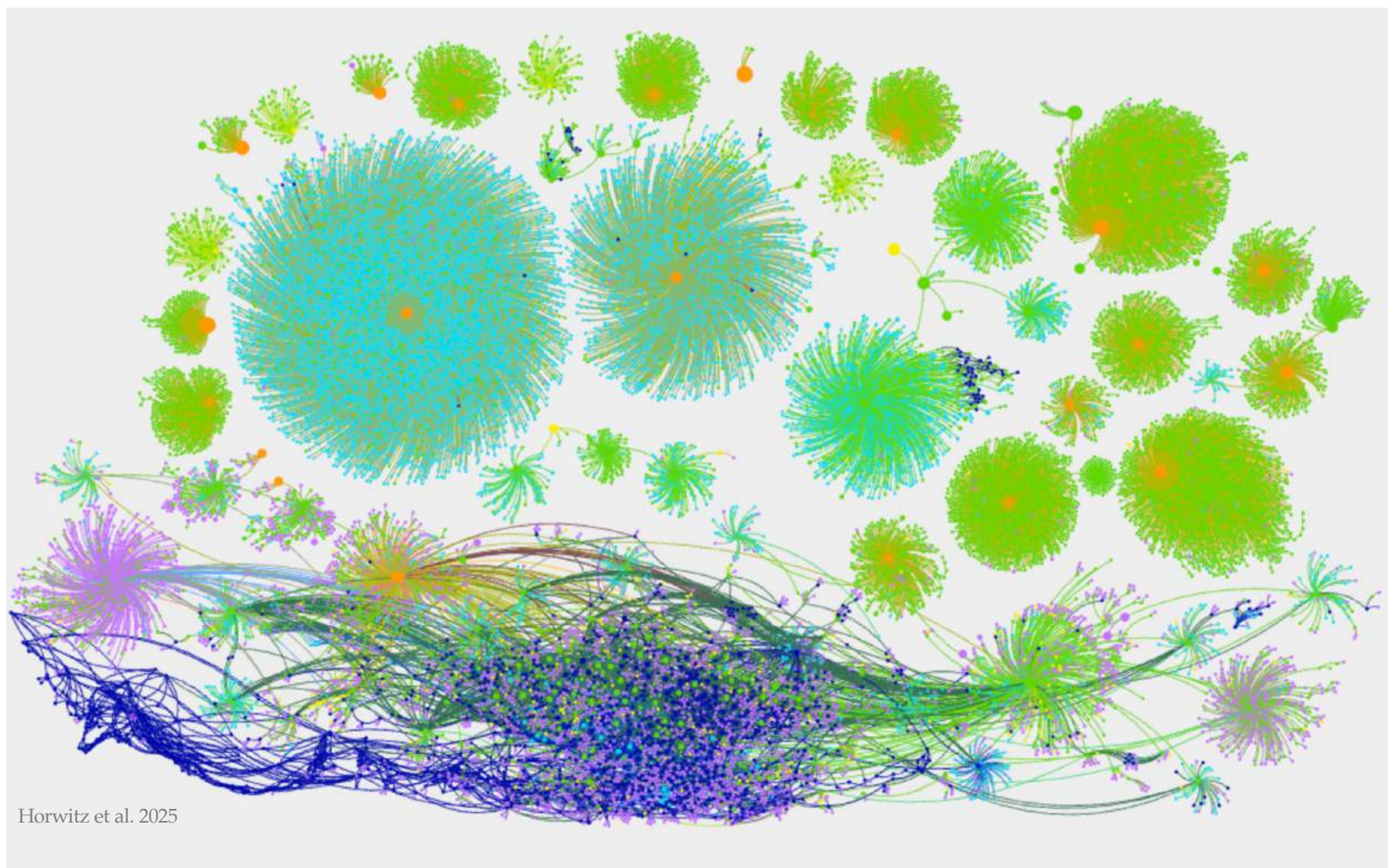
## *Low-Rank Adaptors (LoRA)*



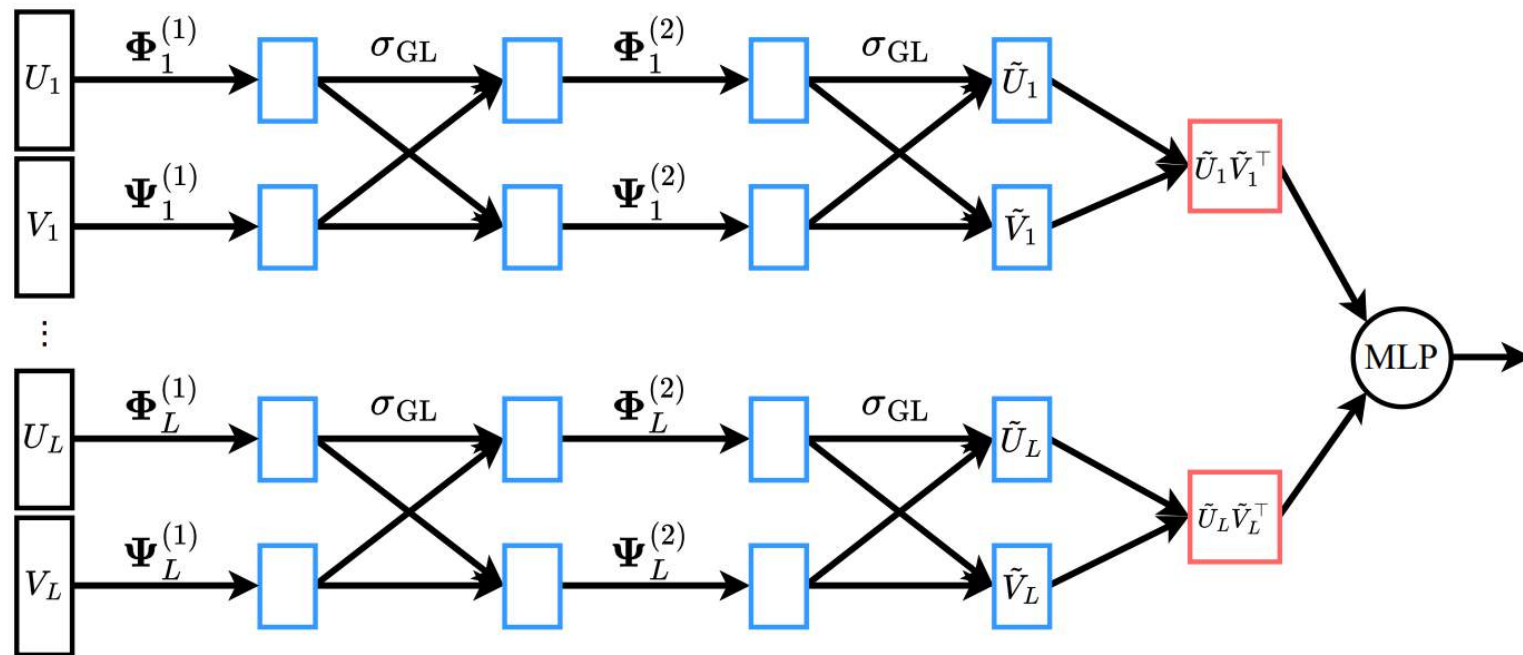
*LoRA ( $\mathbf{U}, \mathbf{V}$ ) defined up to  $GL(r)$*

## *Learning on LoRAs (LOL)*





# Learning on LoRAs (LOL)



# Learning on LoRAs (LOL)

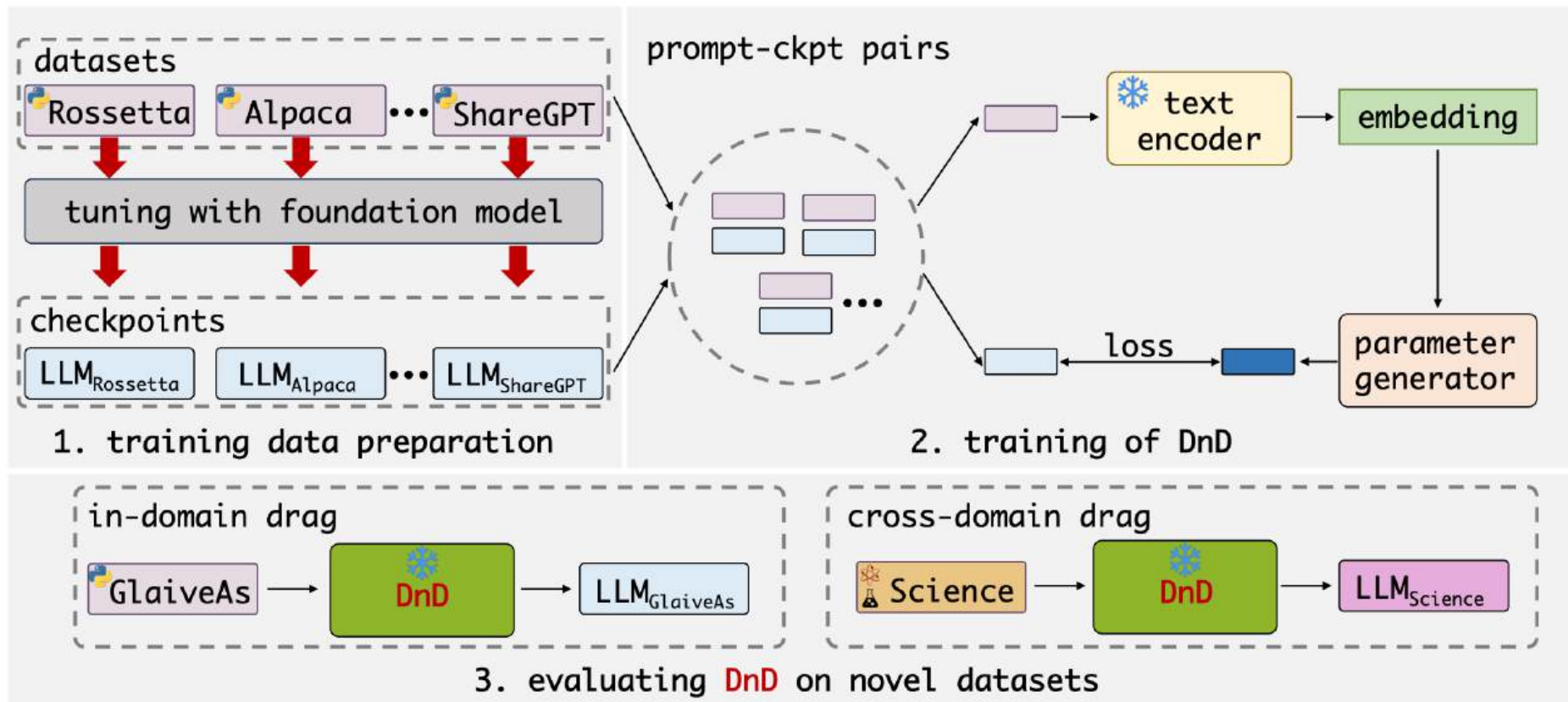
| LoL Model                                     | GL-Inv. | O-Inv. | Expressive | Preprocess Time | Forward Time |
|-----------------------------------------------|---------|--------|------------|-----------------|--------------|
| <b>Naive architectures</b>                    |         |        |            |                 |              |
| MLP( $[U, V]$ )                               | ✗       | ✗      | ✓          | $O((m+n)r)$     | $O((m+n)r)$  |
| Transformer( $[U, V]$ )                       | ✗       | ✗      | ✓          | $O((m+n)r)$     | $O((m+n)r)$  |
| MLP( $UV^\top$ )                              | ✓       | ✓      | ✓          | $O(mnr)$        | $O(mn)^2$    |
| <b>Efficient symmetry-aware architectures</b> |         |        |            |                 |              |
| MLP(O-Align( $[U, V]$ ))                      | ✗       | ✓      | ✓          | $O((m+n)r^2)$   | $O((m+n)r)$  |
| MLP( $\sigma(UV^\top)$ )                      | ✓       | ✓      | ✗          | $O((m+n)r^2)$   | $O((m+n)r)$  |
| GL-net                                        | ✓       | ✓      | ✓          | $O((m+n)r)$     | $O((m+n)r)$  |

## Learning on LoRAs (LOL)

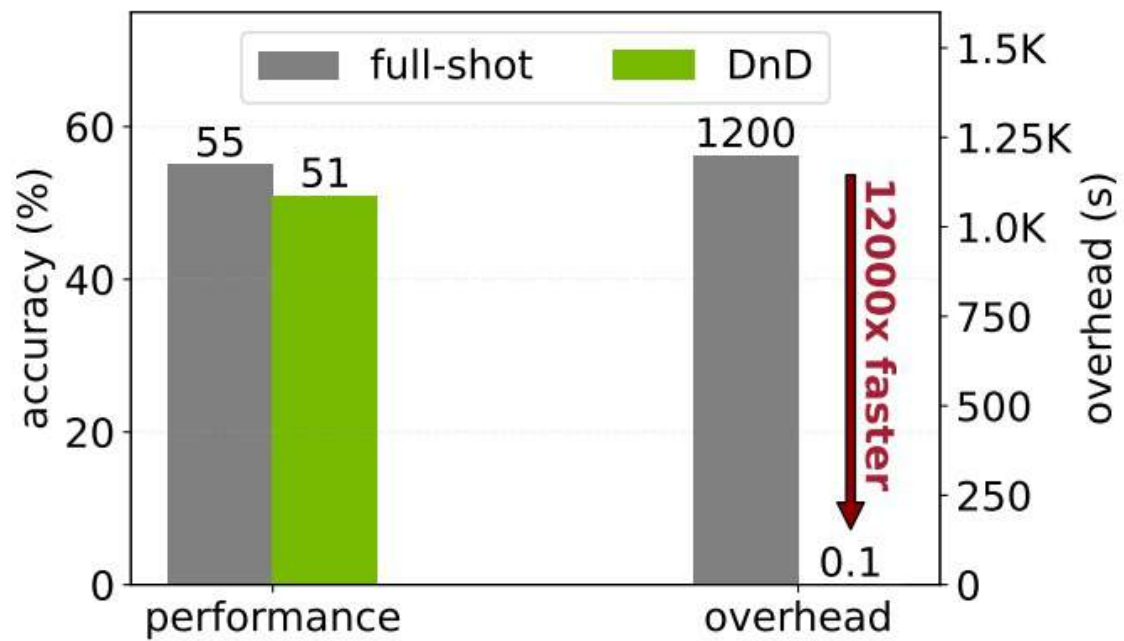
|                     |                          | CelebA Attributes                 |                                  | Imagenette Classes                |                                  |
|---------------------|--------------------------|-----------------------------------|----------------------------------|-----------------------------------|----------------------------------|
| LoL Model           |                          | Test Loss ( $\downarrow$ )        | Test Acc ( $\uparrow$ )          | Test Loss ( $\downarrow$ )        | Test Acc ( $\uparrow$ )          |
| Naive Models        | MLP( $[U, V]$ )          | $.554 \pm .000$                   | $72.4 \pm 0.0$                   | $.709 \pm .004$                   | $49.6 \pm 1.3$                   |
|                     | Transformer( $[U, V]$ )  | $.586 \pm .014$                   | $73.2 \pm 0.9$                   | $.695 \pm .001$                   | $50.0 \pm 1.3$                   |
|                     | MLP( $UV^\top$ )         | $.267 \pm .007$                   | $89.1 \pm 0.4$                   | $.264 \pm .011$                   | $88.9 \pm 0.6$                   |
| Efficient Invariant | MLP(O-Align( $[U, V]$ )) | $.333 \pm .008$                   | $87.2 \pm 0.5$                   | $.278 \pm .008$                   | $87.8 \pm 0.3$                   |
|                     | MLP( $\sigma(UV^\top)$ ) | $.509 \pm .013$                   | $77.3 \pm 1.3$                   | $.638 \pm .013$                   | $65.6 \pm 0.6$                   |
|                     | GL-net                   | <b><math>.232 \pm .007</math></b> | <b><math>91.3 \pm 0.1</math></b> | <b><math>.244 \pm .005</math></b> | <b><math>90.4 \pm 0.3</math></b> |

Using LoL models to predict *CelebA* attributes (left) and *Imagenette* classes (right) of the finetuning data of diffusion models, given only the LoRA weights.

# Drag-and-Drop LLMs



## *Drag-and-Drop LLMs*



THE STORY CONTINUES  
IN THE WEIGHT SPACE



**ICLR**  
International Conference On  
Learning Representations

# First Workshop on Weight Space Learning

<https://weight-space-learning.github.io/>

## Invited Speaker



Stella X. Yu

University of Michigan



Michael Mahoney

UC Berkeley, ICSI



Boris Knyazev

Samsung AI Lab (SAIT)



Naomi Saphra

Harvard University



Ludwig Schmit

Stanford University / Anthropic

## Organization



Konstantin  
Schürholt



Giorgos  
Bouritsas



Eliahu  
Horwitz



Derek  
Lim



Yoav  
Gelberg



Bo  
Zhao



Allan  
Zhou



Damian  
Borth



Stefanie  
Jegelka

## Steering



Michael  
Bronstein



Gal  
Chechik



Stella  
X. Yu



Haggai  
Maron

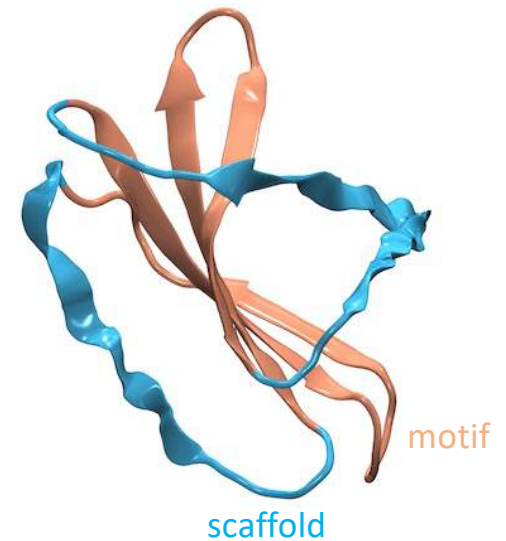
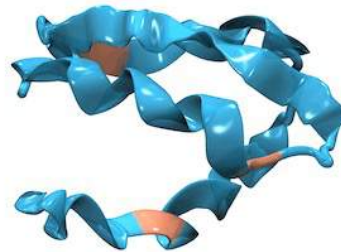
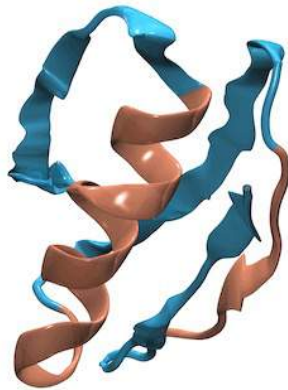


Yedid  
Hoshen



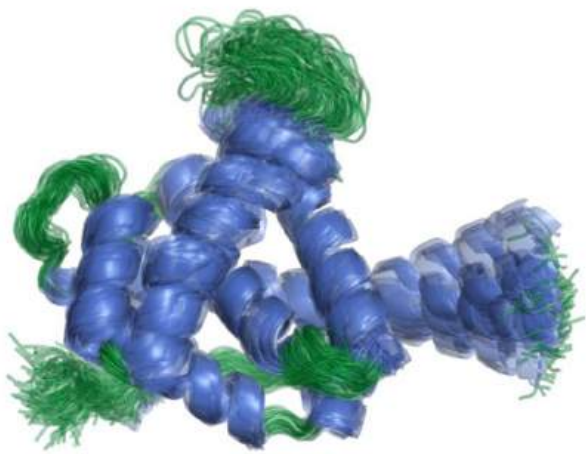
Thank you!

# *Motif-Scaffolding*

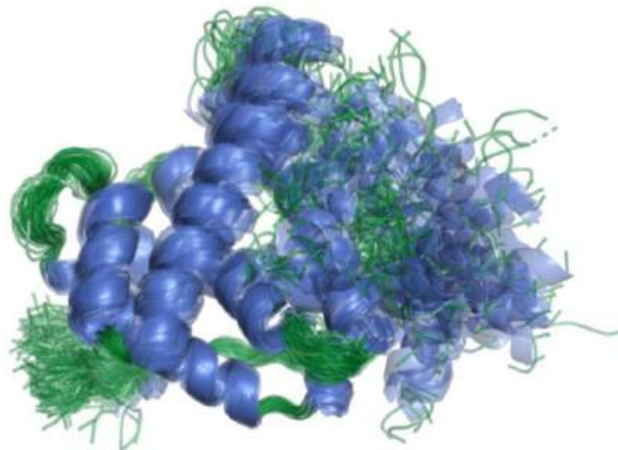


Designing novel proteins where functional part (**motif**) is known and the remaining part (**scaffold**) is generated

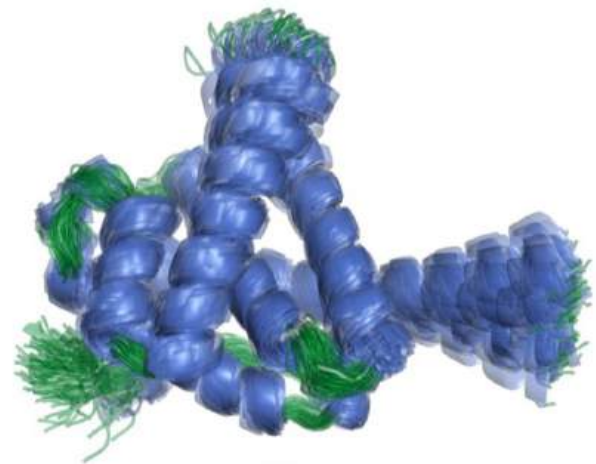
## *Zero-shot Molecular Dynamics*



**Groundtruth**



**ESMFlow-MD**

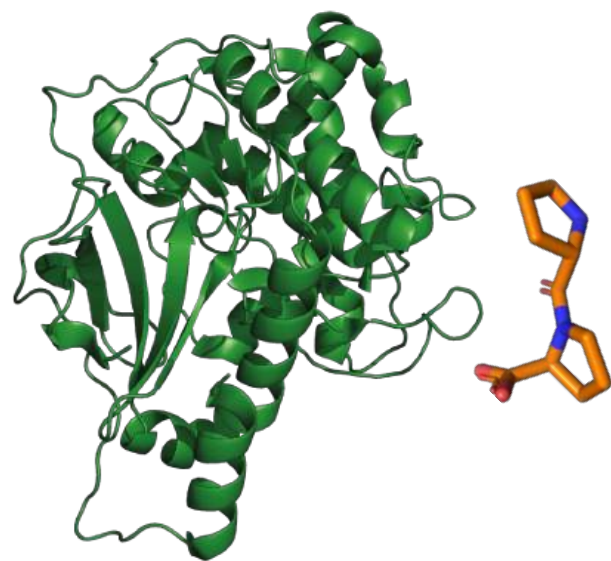


**FoldFlow++**

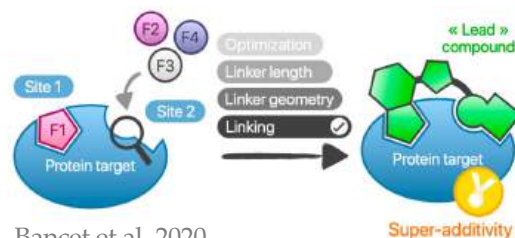
Protein conformations generated by different models

Jing et al. 2024 (ESMFlow); Huguet et Bose, Tong, B 2024 (FoldFlow++)





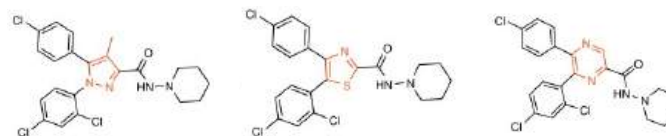
## Fragment-based



Bancet et al. 2020

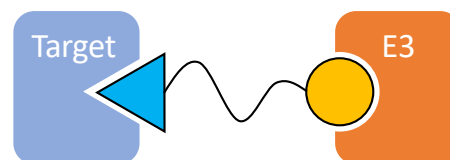
- Molecule growing
- Fragment merging
- Fragment linking

## Scaffold hopping



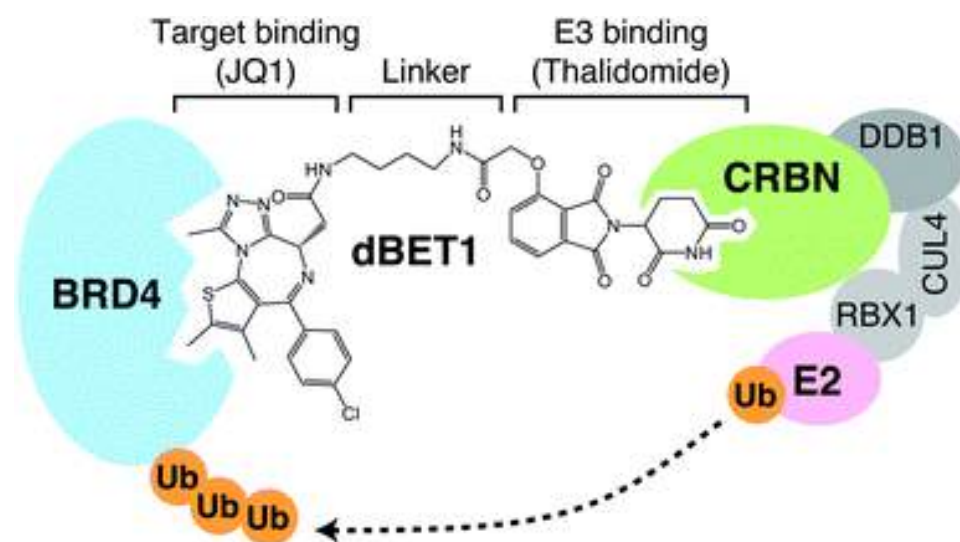
Sun et al. 2012

## Targeted protein degradation

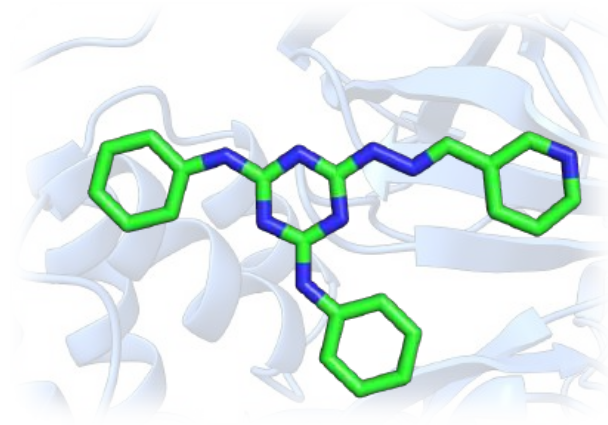
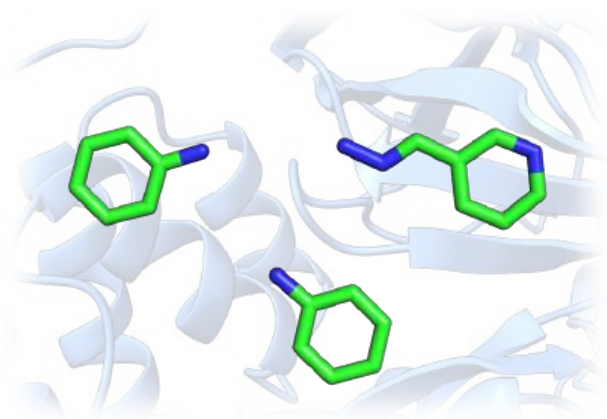


Békés et al. 2022

- PROTAC
- Molecular glue

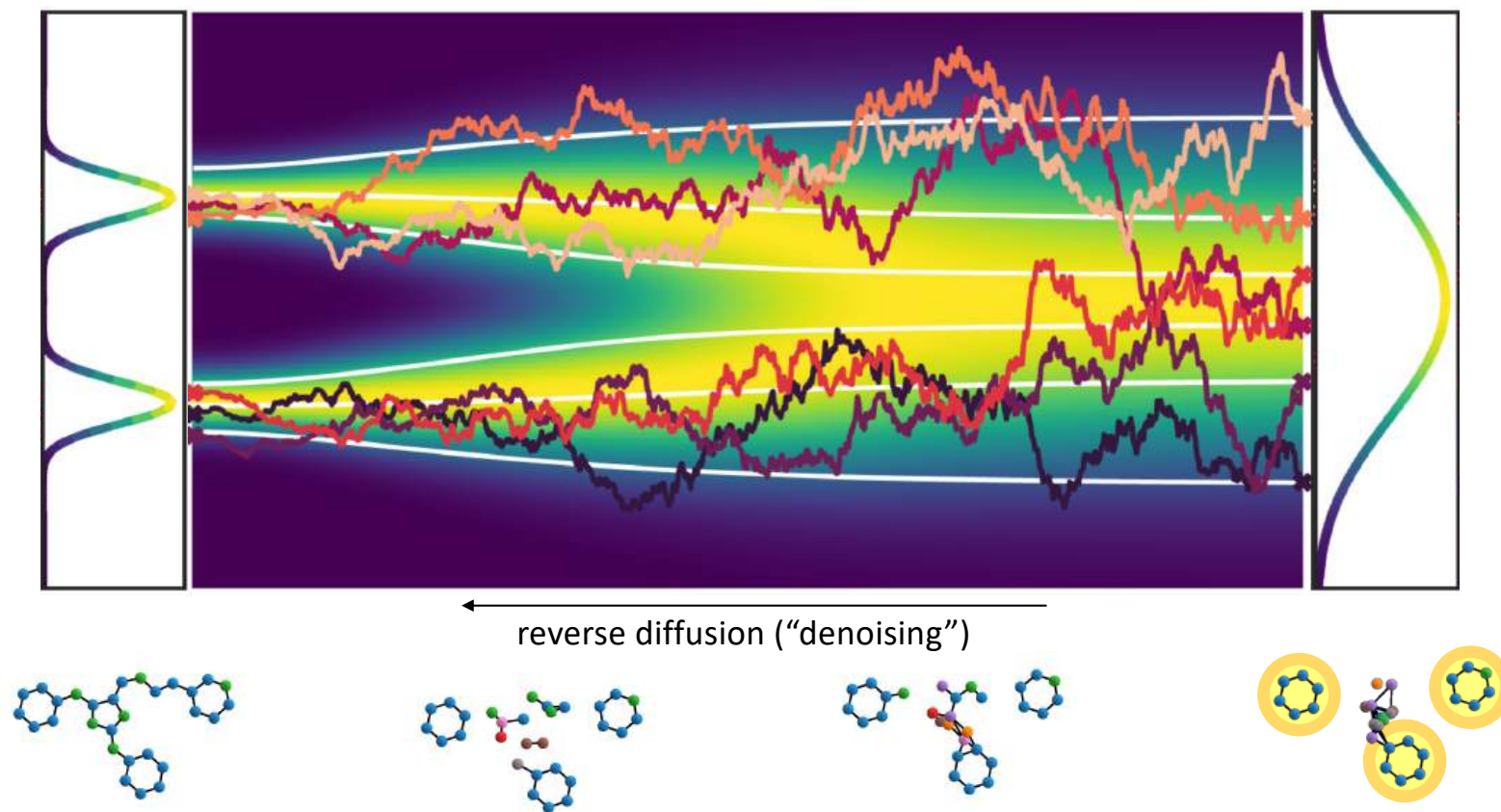


## *Problem setup: “molecular impainting”*



- Fragments placed in 3D space (known fixed orientation)
- Variable linker size
- Unknown attachment atoms (anchors)
- Variable number of fragments
- No clashes with protein pocket

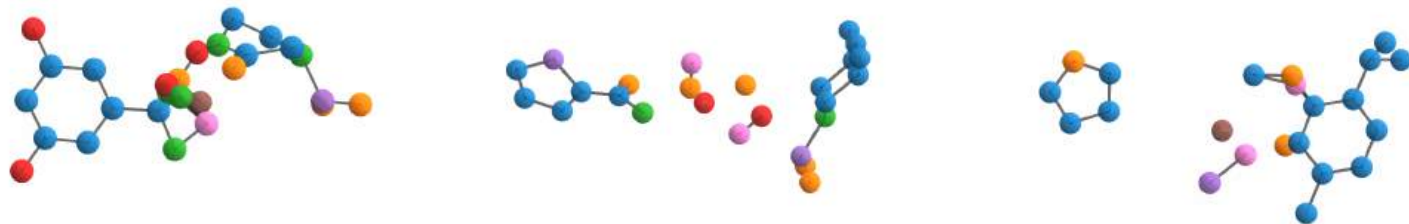
# DiffLinker



Igashov, Stärk, Vignac et Welling, B, Correia 2022

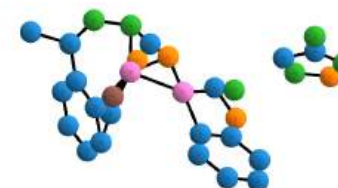
## Linking pairs of fragments

|      | Method                                   | QED $\uparrow$ | SA $\downarrow$ | # Rings $\uparrow$ | Valid, %    | Unique, %   | Novel, %    |
|------|------------------------------------------|----------------|-----------------|--------------------|-------------|-------------|-------------|
| ZINC | DeLinker + ConfVAE + MMFF                | 0.64           | 3.11            | 0.21               | <b>98.3</b> | 44.2        | <b>47.1</b> |
|      | 3DLinker (given anchors)                 | 0.65           | 3.11            | 0.23               | <b>99.3</b> | 29.0        | 41.2        |
|      | 3DLinker                                 | 0.65           | 3.14            | 0.24               | 71.5        | 29.2        | 41.9        |
|      | DiffLinker                               | <b>0.68</b>    | <b>3.01</b>     | 0.25               | 93.8        | 24.0        | 30.3        |
|      | DiffLinker (given anchors)               | <b>0.68</b>    | <b>3.03</b>     | 0.26               | 97.6        | 22.7        | 32.4        |
|      | DiffLinker (sampled size)                | 0.65           | 3.19            | <b>0.32</b>        | 90.6        | <b>51.4</b> | 42.9        |
|      | DiffLinker (given anchors, sampled size) | 0.65           | 3.24            | <b>0.36</b>        | 94.8        | <b>50.9</b> | <b>47.7</b> |
| CASF | DeLinker + ConfVAE + MMFF                | 0.35           | 4.05            | 0.35               | <b>95.7</b> | 51.6        | <b>55.6</b> |
|      | DiffLinker                               | <b>0.41</b>    | <b>4.00</b>     | 0.34               | 85.3        | 40.5        | 41.8        |
|      | DiffLinker (given anchors)               | 0.40           | <b>4.03</b>     | <b>0.38</b>        | <b>90.2</b> | 37.3        | 48.4        |
|      | DiffLinker (sampled size)                | <b>0.40</b>    | 4.06            | 0.30               | 63.7        | <b>60.0</b> | 49.3        |
|      | DiffLinker (given anchors, sampled size) | 0.40           | 4.10            | <b>0.38</b>        | 68.4        | <b>57.1</b> | <b>56.9</b> |



# Linking multiple fragments

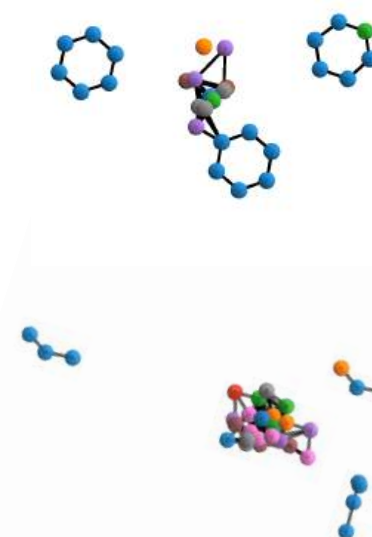
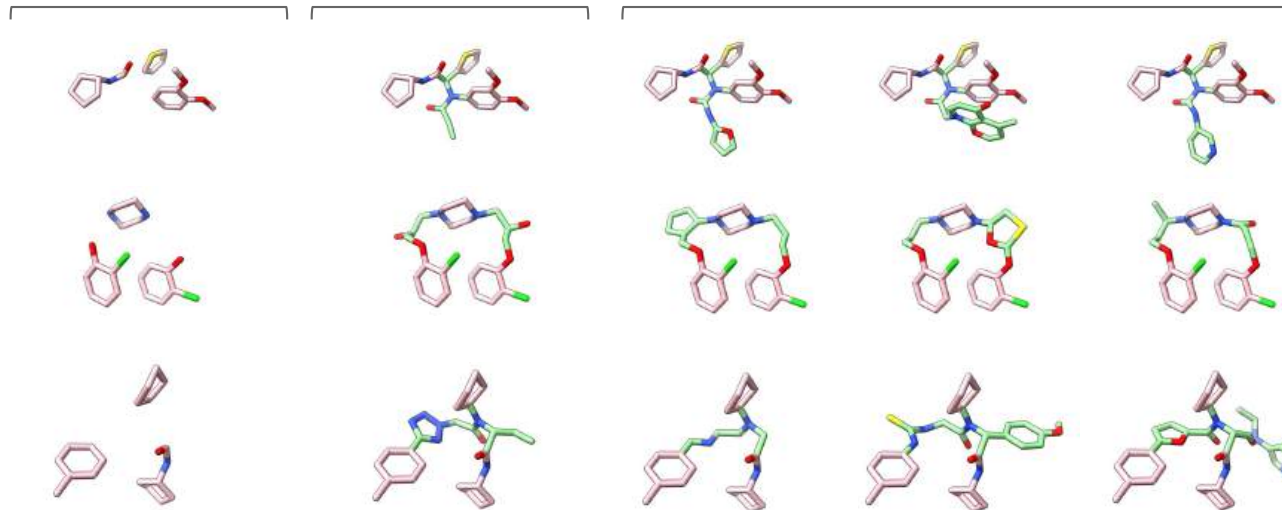
| Method |                                          | QED $\uparrow$ | SA $\downarrow$ | # Rings $\uparrow$ | Valid, %    | Unique, %   | Novel, %    |
|--------|------------------------------------------|----------------|-----------------|--------------------|-------------|-------------|-------------|
| GEOM   | 3DLinker                                 | 0.36           | 3.56            | 0.00               | 16.3        | <b>73.7</b> | —           |
|        | DiffLinker                               | <b>0.48</b>    | <b>2.99</b>     | 0.75               | <b>94.0</b> | 34.7        | 68.6        |
|        | DiffLinker (given anchors)               | <b>0.49</b>    | <b>3.01</b>     | <b>0.79</b>        | <b>94.0</b> | 35.0        | 68.4        |
|        | DiffLinker (sampled size)                | 0.45           | 3.27            | 0.75               | 87.2        | 62.4        | <b>76.0</b> |
|        | DiffLinker (given anchors, sampled size) | 0.46           | 3.33            | <b>0.83</b>        | 88.8        | <b>63.6</b> | <b>76.0</b> |



Input Fragments

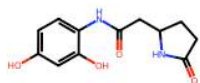
Groundtruth

DiffLinker samples

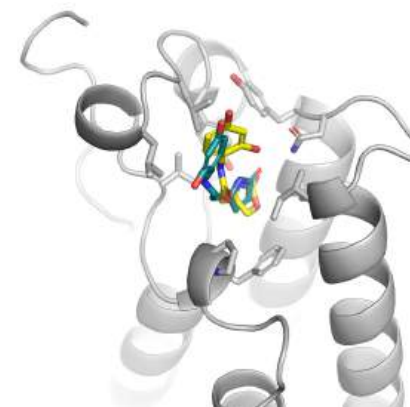
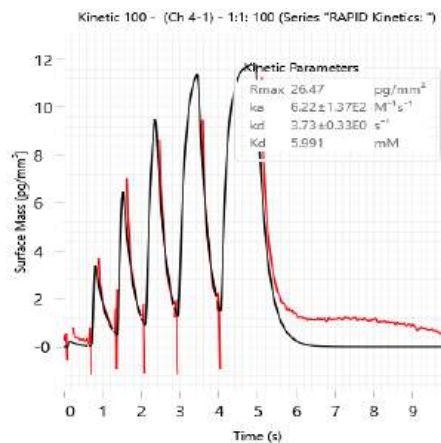


## Experimental results: Binders

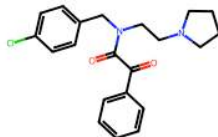
LogP 0.02



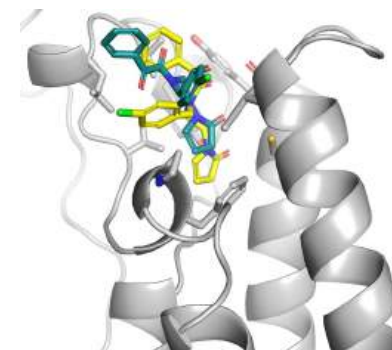
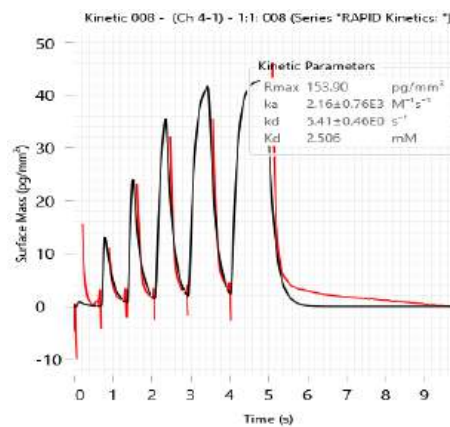
High solubility,  
up to 5 mM



LogP 3.88

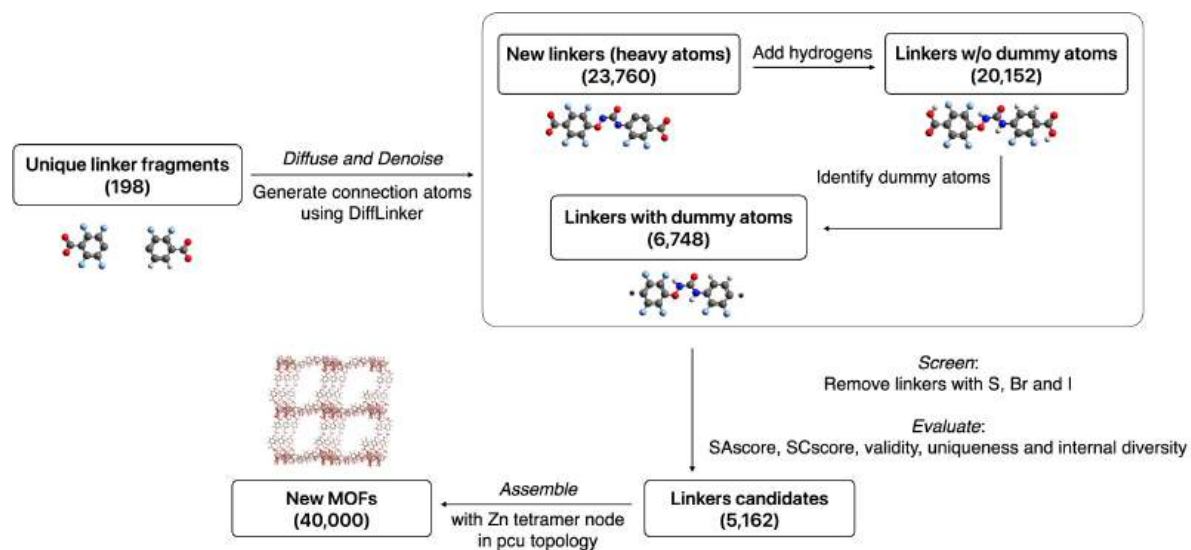


Soluble at 1 mM

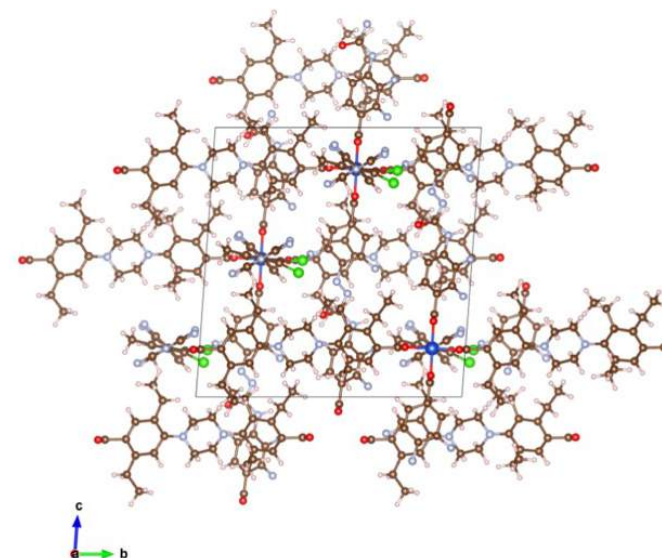


Bromodomain-containing protein 4  
(BrD4)

# Unexpected Application: Material Design for Carbon capture

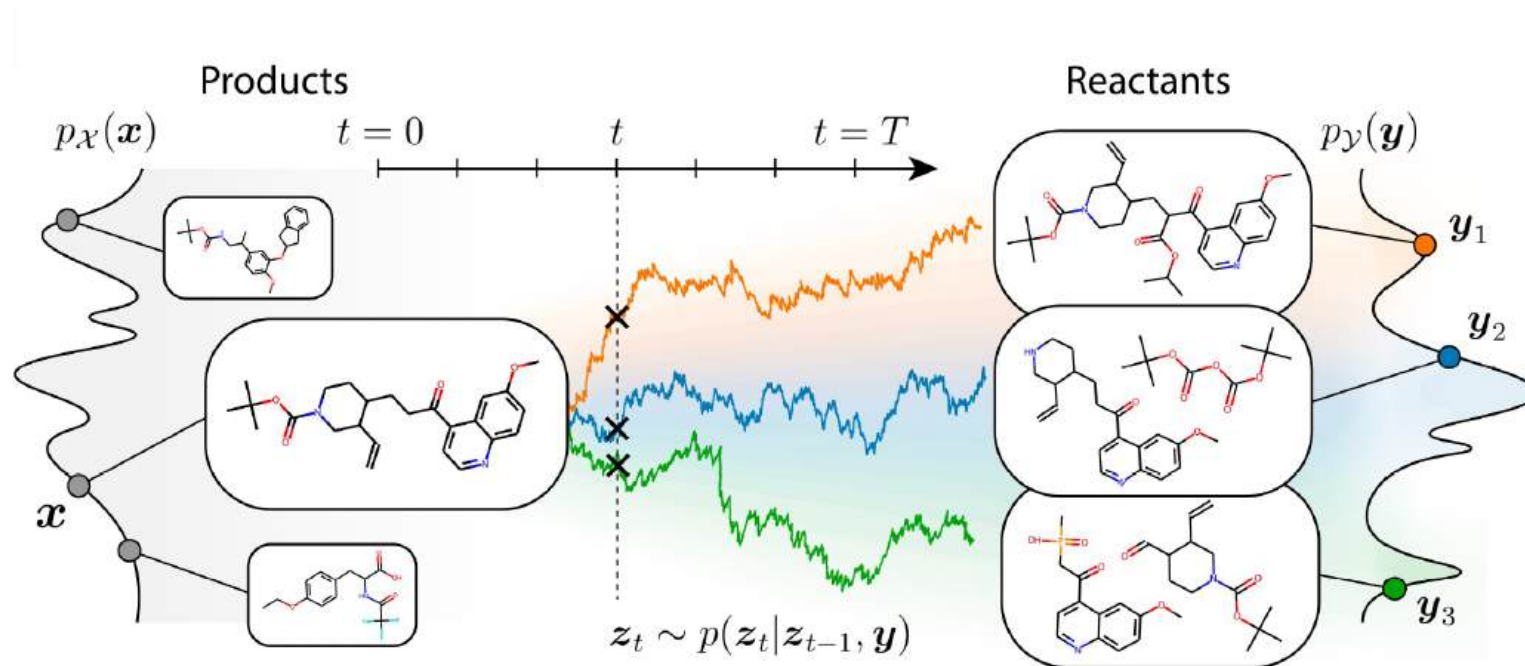


Generation of Metal-Organic Frameworks (MOF) for C capture



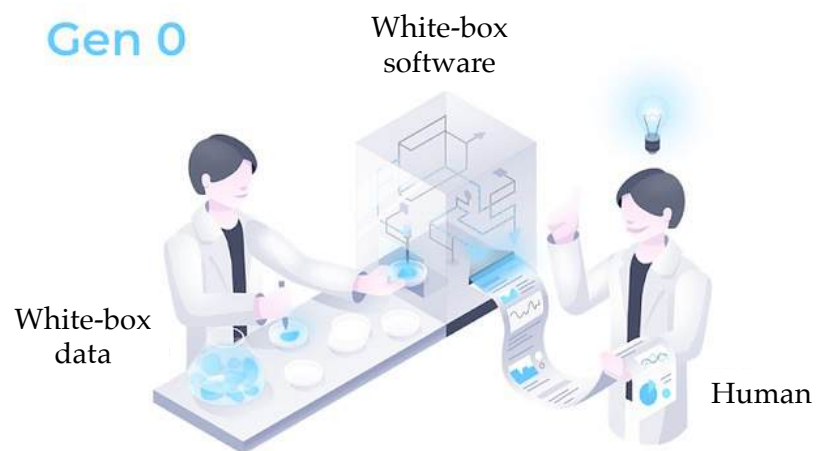
Example of generated MOF

## Future directions: Synthesis prediction



RetroBridge: generative model for retrosynthesis design

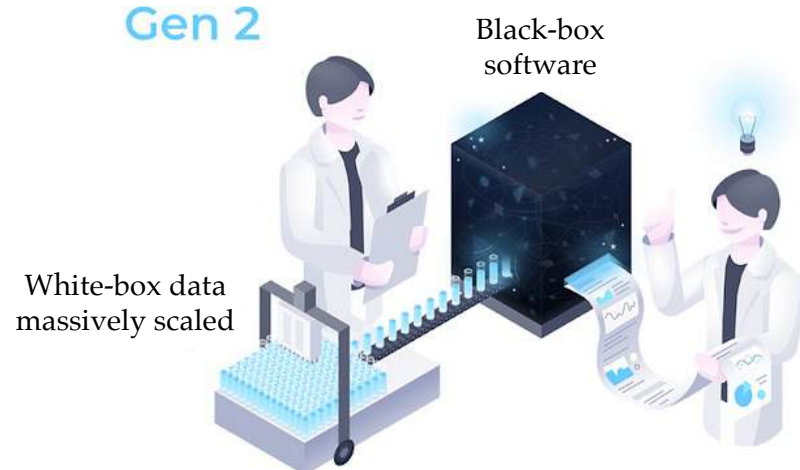
## Gen 0



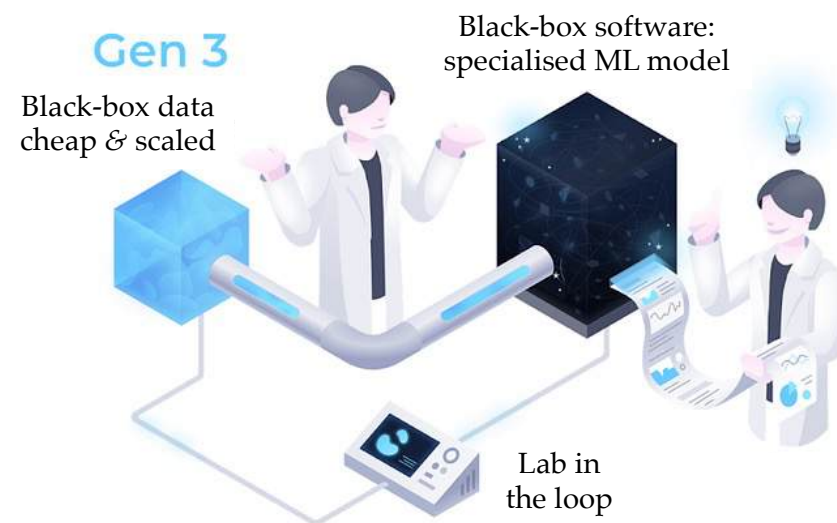
## Gen 1



## Gen 2



## Gen 3

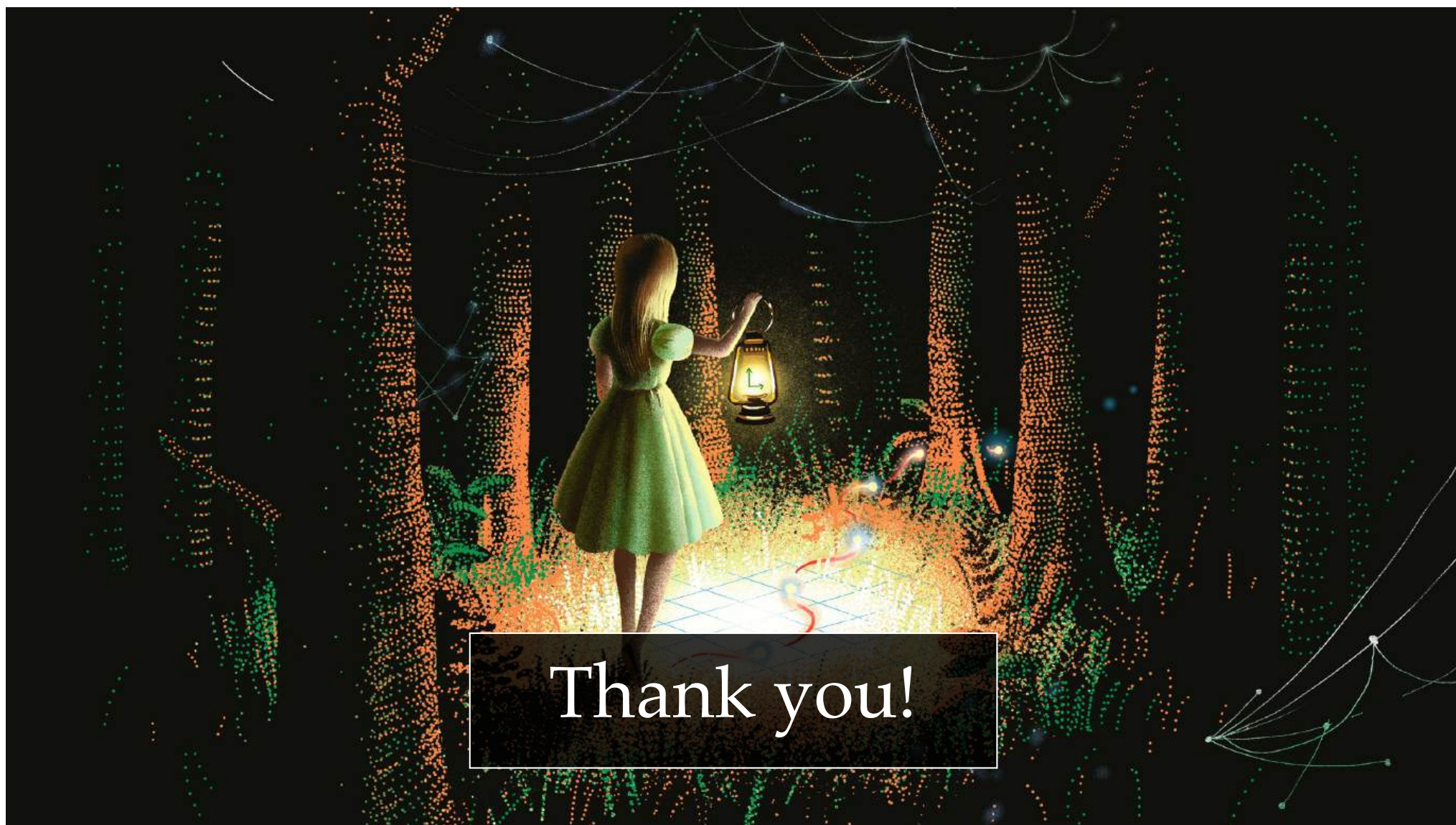


## *Conclusions*

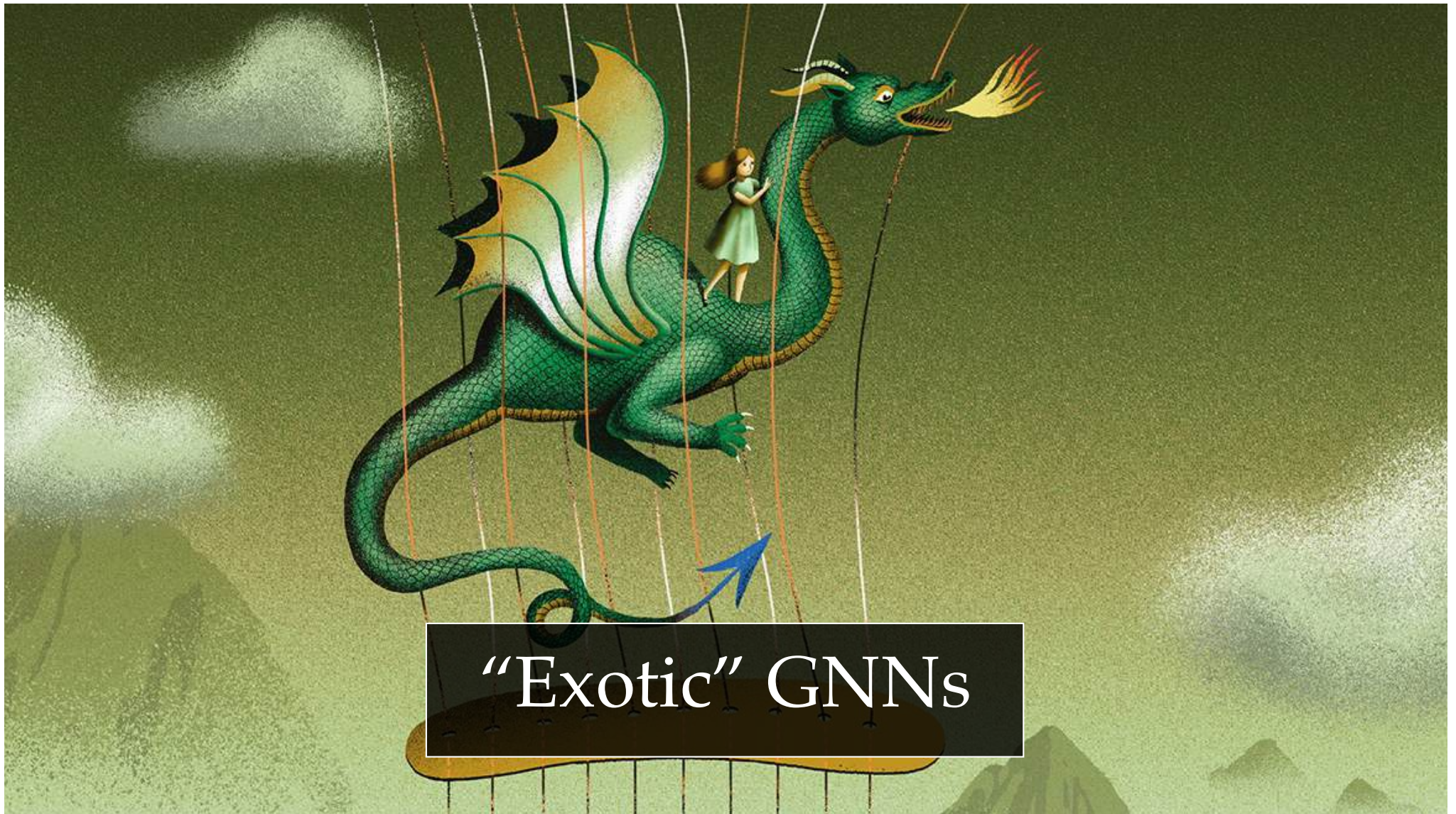
- Geometric deep learning is a powerful tool for molecular modelling
- Rootes in fundamental mathematical principles of invariance & symmetry
- Geometric generative models models
- Experimental validation!

“The knowledge of certain principles easily  
compensates the lack of knowledge of certain facts”

—Claude Adrien Helvétius

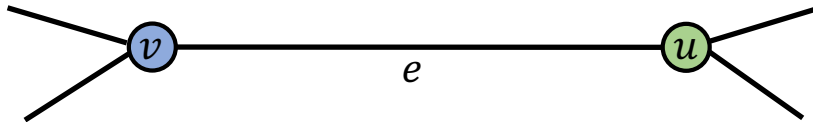


Thank you!

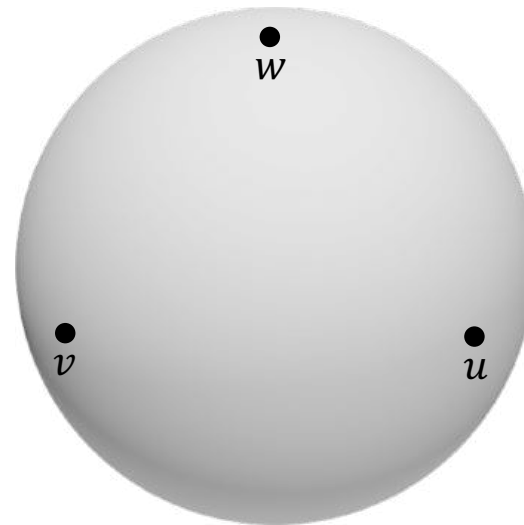


“Exotic” GNNs

# *Cellular Sheaves*

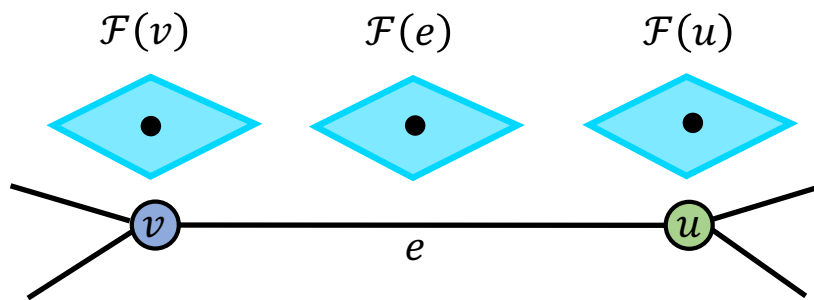


Graph

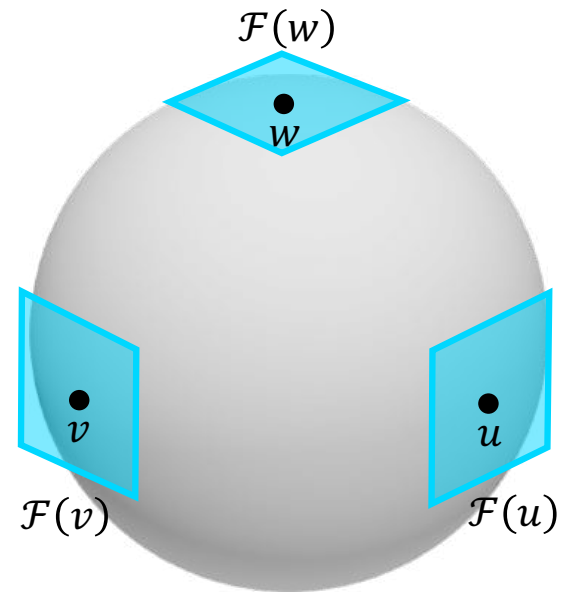


Manifold

# Cellular Sheaves

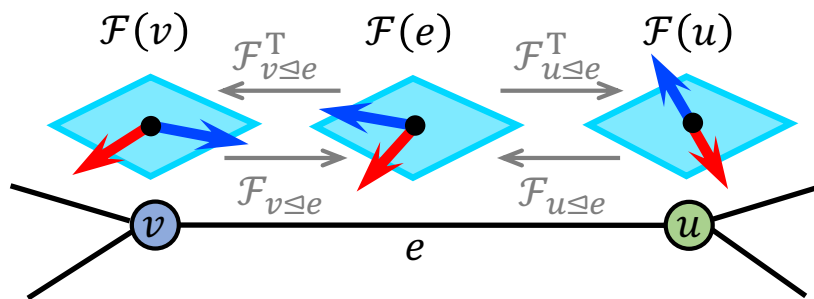


Cellular sheaf  $\mathcal{F}$

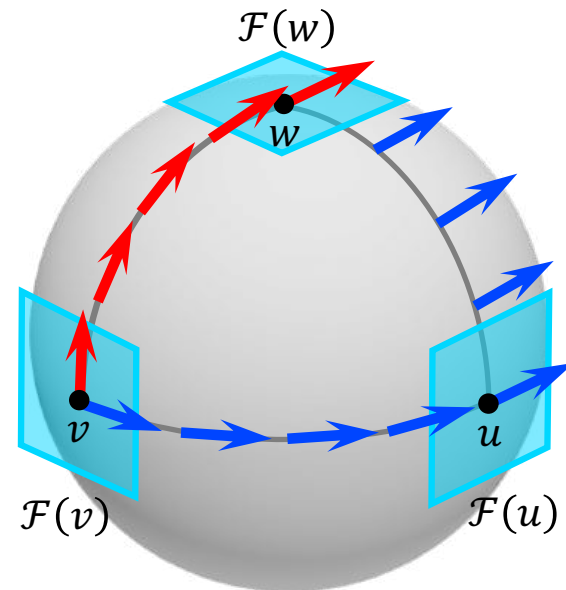


Manifold + Connection

# Cellular Sheaves

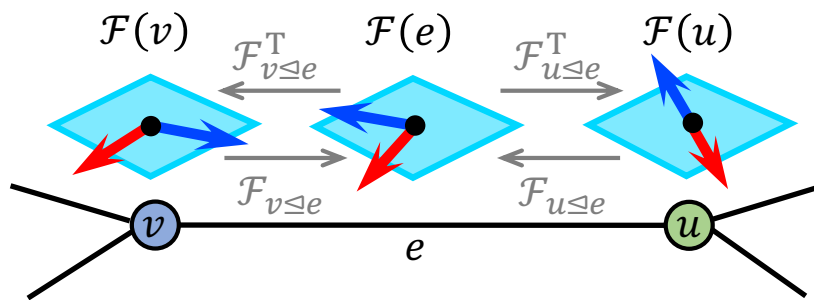


Cellular sheaf  $\mathcal{F}$

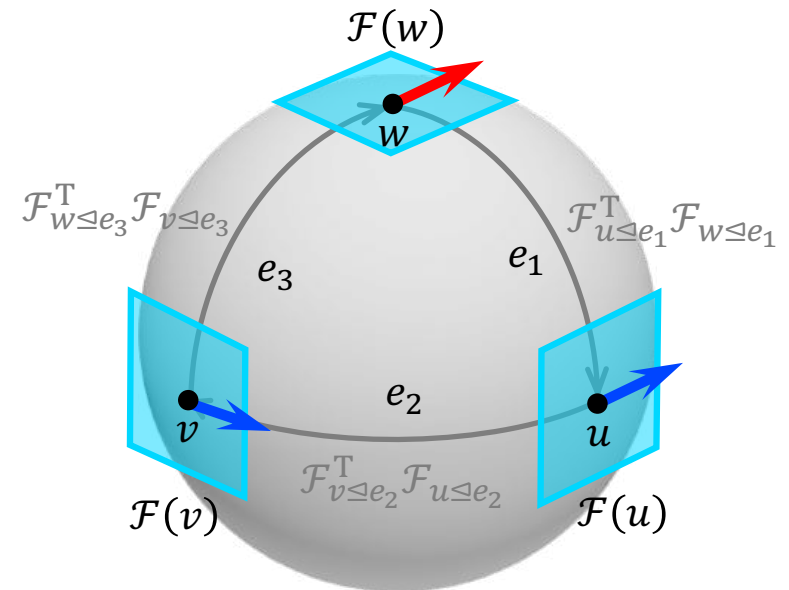


Manifold + Connection

# Cellular Sheaves

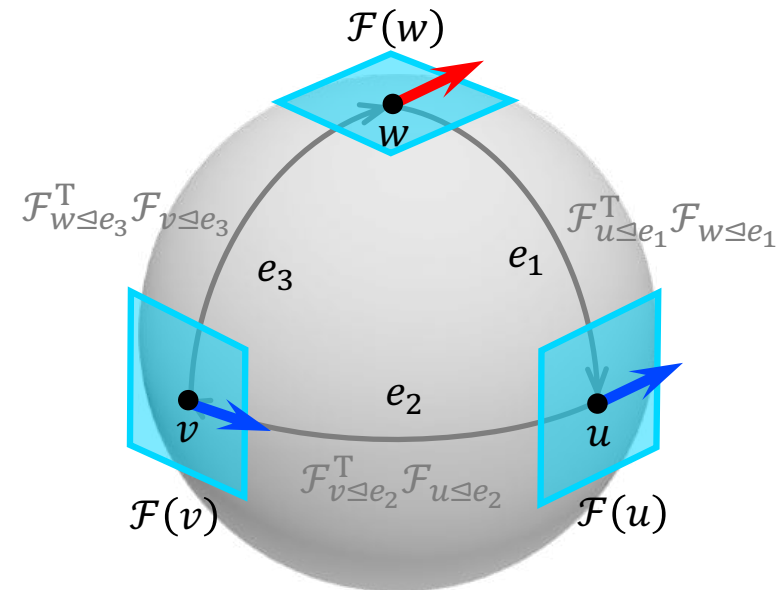
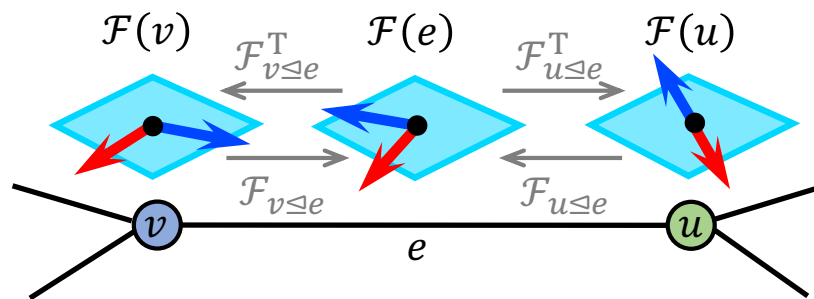


Cellular sheaf  $\mathcal{F}$



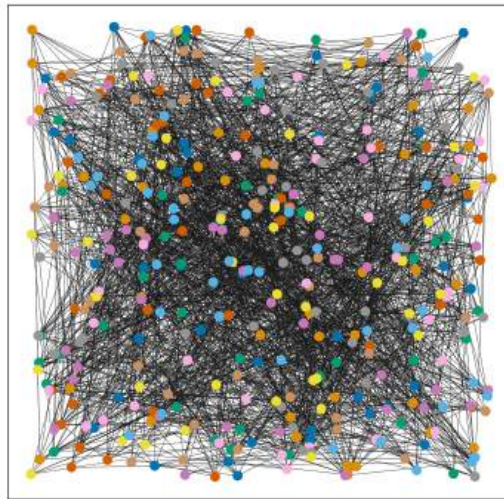
Analogy to parallel transport  
on manifolds

# Cellular Sheaves



Endow graph with "geometry" leading to richer diffusion  
with better separation, ability to cope with heterophily,  
and no oversmoothing

## *Diffusion on Cellular Sheaves*



$$\dot{\mathbf{X}}(t) = \Delta_{\mathcal{F}} \mathbf{X}(t) \quad \text{with i.c. } \mathbf{X}(0) = \mathbf{X}$$

Node classification = limit of sheaf diffusion equation  
with an appropriate sheaf

## *Alternative to Weisfeiler-Lehman for expressive power?*

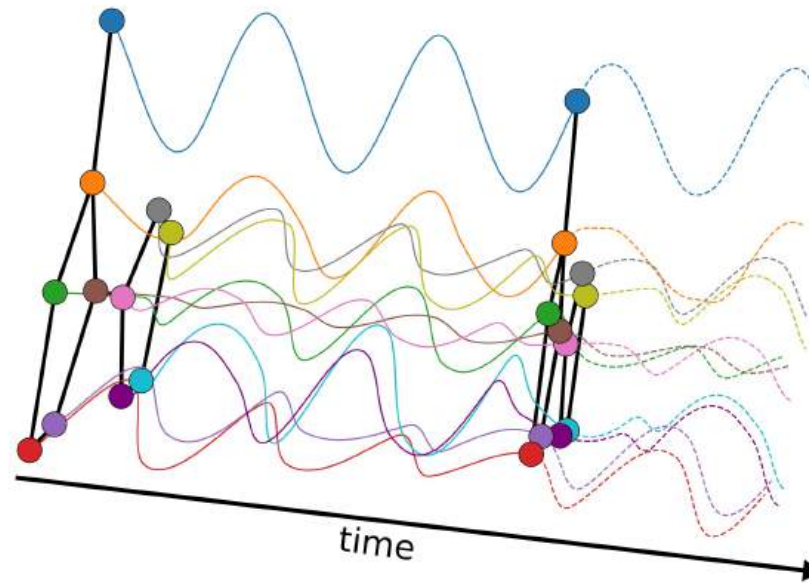
| Graph type   | # Node classes | Sheaf class $\mathcal{F}$ , $\dim=d$ |   |
|--------------|----------------|--------------------------------------|---|
| Homophilic   | 2              | Symmetric $d=1$                      | ✓ |
| Heterophilic | 2              | Symmetric $d=1$                      | ✗ |
|              | 2              | Non-symmetric $d=1$                  | ✓ |
|              | $\geq 3$       | Non-symmetric $d=1$                  | ✗ |
|              | $\leq 2d$      | Orthogonal, $d=\{2,4\}$              | ✓ |

The capability of sheaf diffusion to solve node classification problem in the limit

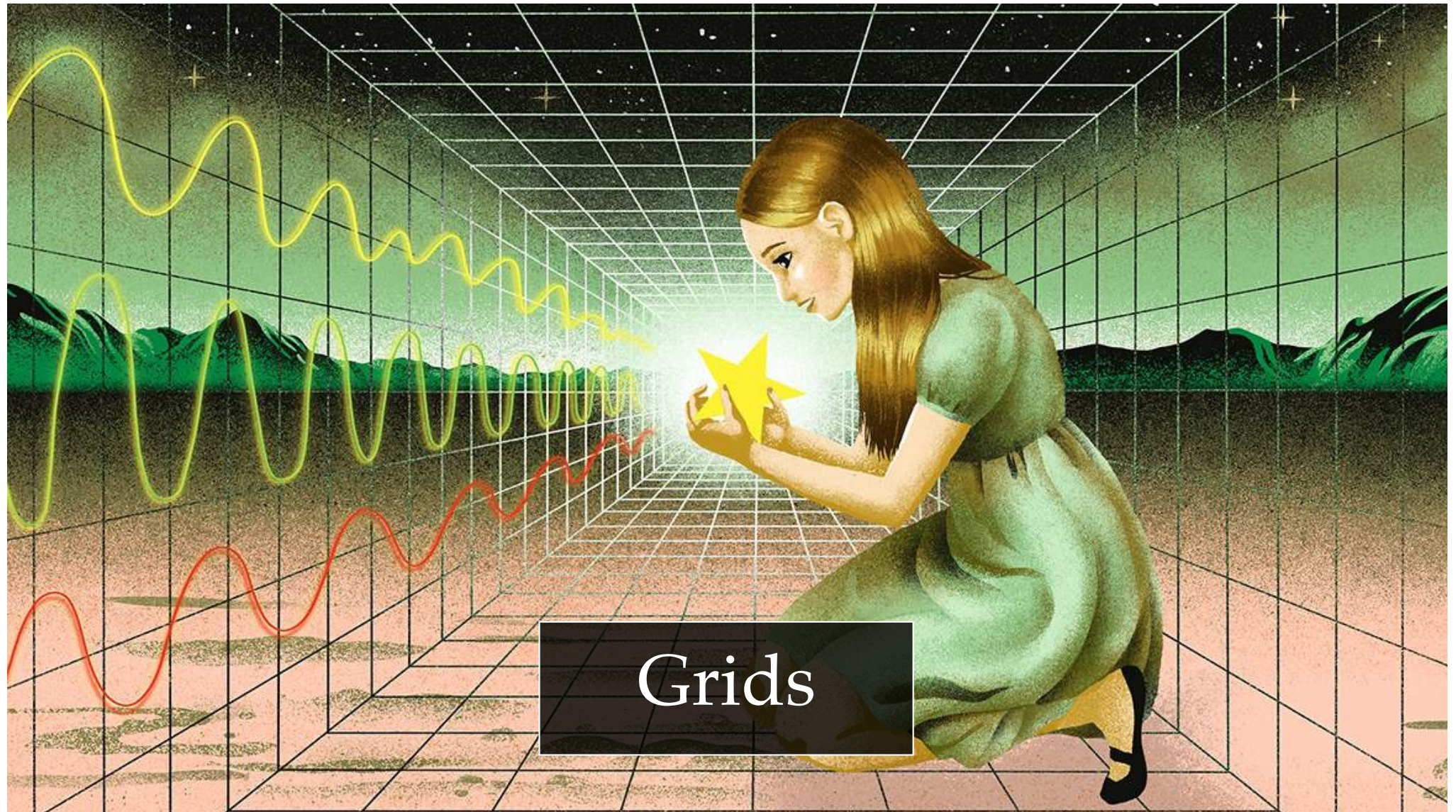
## *What do we gain from physics-inspired GNNs?*

- New perspectives on old problems (e.g. oversmoothing, bottlenecks, etc.)
- New architectures
  - Many GNNs can be formalised as a discretised Graph Diffusion equation
  - More efficient solvers (multistep, adaptive, implicit, multigrid, etc.)
  - Implicit schemes = multi-hop filters
- Principled architectural choices (residual connection, shared symmetric weights)
- Theoretical guarantees (e.g. stability, convergence, expressive power, etc.)
- Deep links to other fields less known in GNN literature (e.g. differential geometry and algebraic topology)
- Other physical models

# *Graph-Coupled Oscillators*

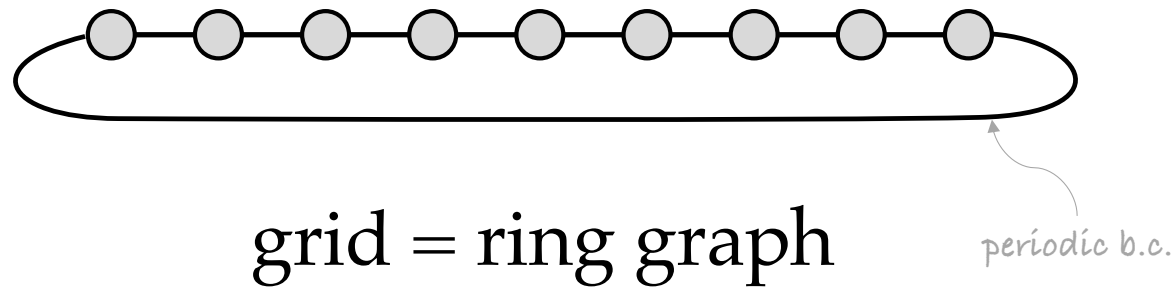


Dynamics of a system of coupled oscillators on a molecular graph



Grids

## *Grids vs Graphs*

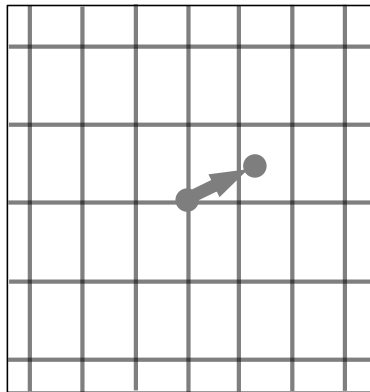
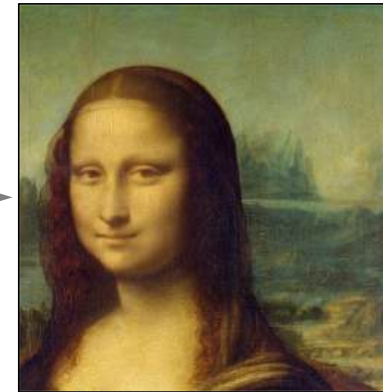


*“Lifting”*



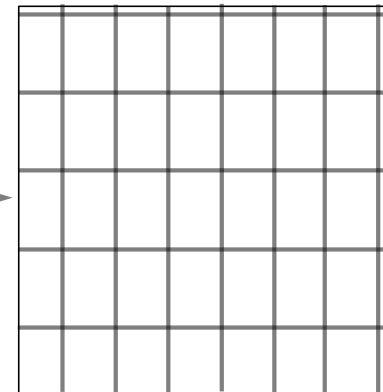
**Group representation**

$$- \rho(g): \mathcal{X}(\Omega) \rightarrow \mathcal{X}(\Omega) \longrightarrow$$

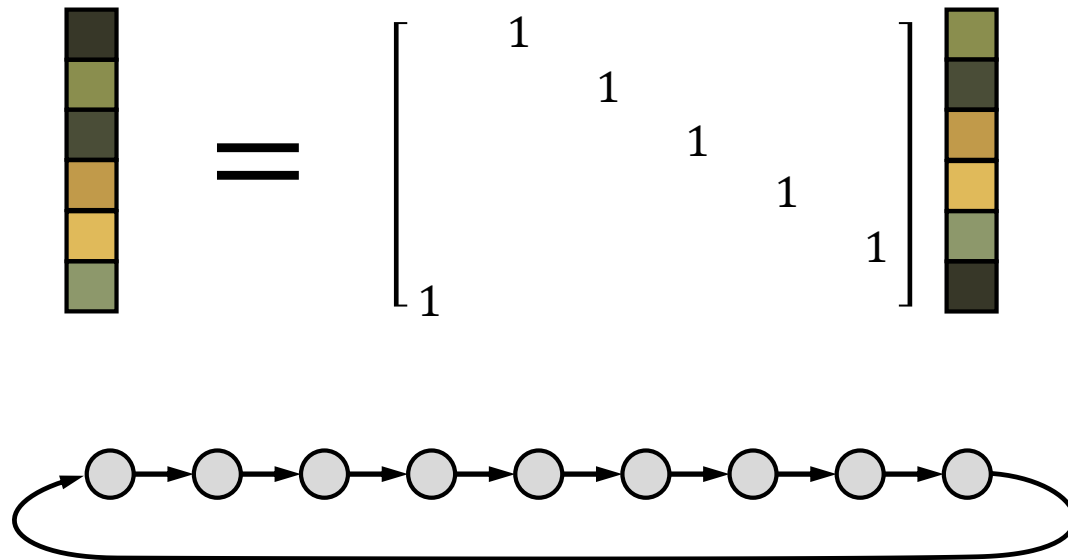


**group**

$$g: \Omega \rightarrow \Omega$$

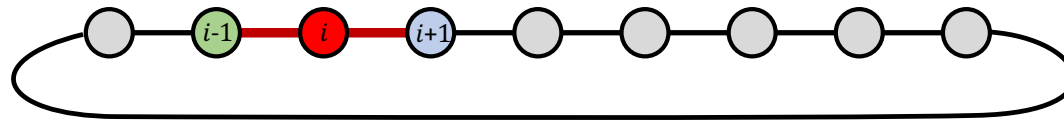


## *Shift operator*



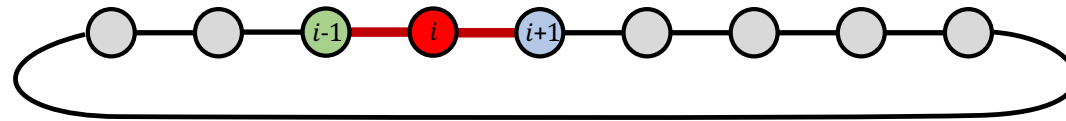
**Note:** Observe that the adjacency matrix of the directed ring graph is exactly the shift operator. We will use it when defining graph convolutions.

## *Grids vs Graphs*



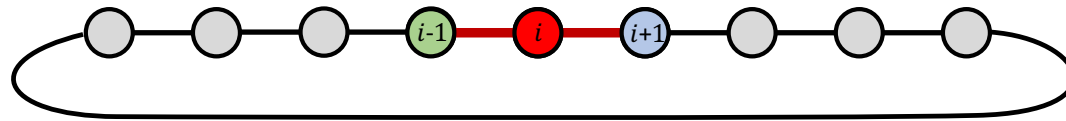
fixed neighbourhood structure

## *Grids vs Graphs*



fixed neighbourhood structure

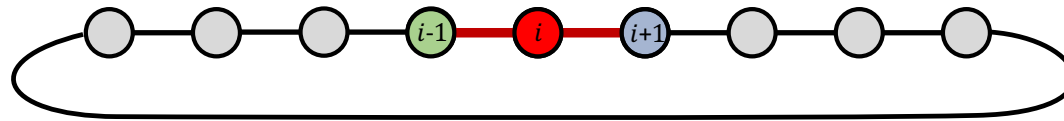
## *Grids vs Graphs*



local aggregation function

$$f(\mathbf{x}_i) = \phi(\mathbf{x}_i, \{\mathbf{x}_{i-1}, \mathbf{x}_{i+1}\})$$

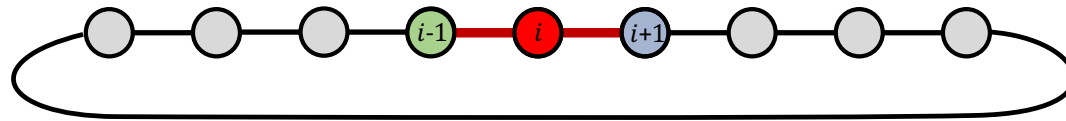
## *Grids vs Graphs*



local aggregation function

$$f(\mathbf{x}_i) = \phi(\mathbf{x}_{i-1}, \mathbf{x}_i, \mathbf{x}_{i+1})$$

## *Grids vs Graphs*



**linear** local aggregation function

$$f(\mathbf{x}_i) = a\mathbf{x}_{i-1} + b\mathbf{x}_i + c\mathbf{x}_{i+1}$$

## *Convolution*

$$f(\mathbf{X}) = \begin{bmatrix} \text{red } b & \text{blue } c & & & \text{green } a \\ \text{green } a & \text{red } b & \text{blue } c & & \\ & \text{green } a & \text{red } b & \text{blue } c & \\ \text{blue } c & & \text{green } a & \text{red } b & \\ & & & \text{green } a & \text{red } b \end{bmatrix} \begin{bmatrix} \text{gray } \mathbf{X} \end{bmatrix}$$

circulant matrix = convolution

# Convolution

vector of parameters  $\theta$

$$f(\mathbf{X}) = \begin{bmatrix} \textcolor{red}{b} & \textcolor{blue}{c} & & \textcolor{green}{a} \\ \textcolor{green}{a} & \textcolor{red}{b} & \textcolor{blue}{c} & \\ & & \textcolor{green}{a} & \textcolor{red}{b} & \textcolor{blue}{c} \\ \textcolor{blue}{c} & & \textcolor{green}{a} & \textcolor{red}{b} \end{bmatrix} \begin{bmatrix} \mathbf{X} \end{bmatrix}$$

circulant matrix  $\mathbf{C}(\theta)$

# Deriving Convolution from Symmetry

vector of parameters  $\theta$

$$f(\mathbf{X}) = \mathbf{C}(\theta) \mathbf{X}$$

circulant matrices commute  
circulant matrix  $\mathbf{C}(\theta)$

## *Deriving Convolution from Symmetry*

$$\begin{array}{c} \text{shift S} \\ \left[ \begin{array}{ccc} b & c & a \\ a & b & c \\ c & a & b \end{array} \right] \left[ \begin{array}{ccc} 1 & & \\ & 1 & \\ & & 1 \end{array} \right] \end{array} = \begin{array}{c} \text{shift S} \\ \left[ \begin{array}{ccc} 1 & & \\ & 1 & \\ & & 1 \end{array} \right] \left[ \begin{array}{ccc} b & c & a \\ a & b & c \\ c & a & b \end{array} \right] \end{array}$$

circulant matrix  $\Rightarrow$  commutes with shift

## *Deriving Convolution from Symmetry*

$$\begin{array}{c} \text{shift S} \\ \left[ \begin{array}{c} \begin{array}{c} \text{red } b \quad \text{blue } c \quad \text{green } a \\ \text{green } a \quad \text{red } b \quad \text{blue } c \\ \text{blue } c \quad \text{green } a \quad \text{red } b \end{array} \\ 1 \end{array} \right] \begin{array}{c} \text{shift S} \\ \left[ \begin{array}{c} 1 \\ 1 \\ 1 \end{array} \right] \end{array} = \begin{array}{c} \text{shift S} \\ \left[ \begin{array}{c} 1 \\ 1 \\ 1 \end{array} \right] \end{array} \left[ \begin{array}{c} \begin{array}{c} \text{red } b \quad \text{blue } c \quad \text{green } a \\ \text{green } a \quad \text{red } b \quad \text{blue } c \\ \text{blue } c \quad \text{green } a \quad \text{red } b \end{array} \\ 1 \end{array} \right]
 \end{array}$$

convolution  $\Rightarrow$  shift-equivariant

$$\mathbf{CS} = \mathbf{SC}$$

## *Deriving Convolution from Symmetry*

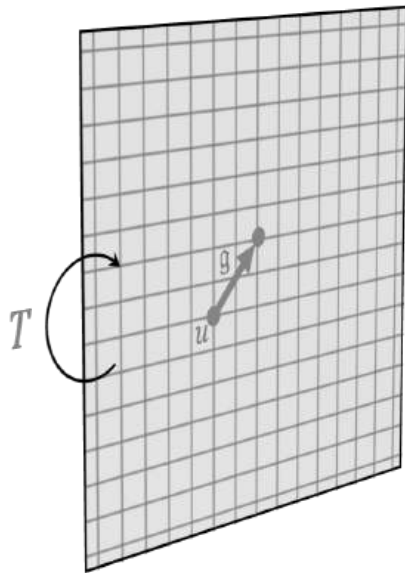
$$\begin{array}{c} \text{shift S} \\ \left[ \begin{array}{c} \begin{array}{c} \text{b} \text{ c} \text{ a} \\ \text{a} \text{ b} \text{ c} \\ \text{c} \text{ a} \text{ b} \end{array} \end{array} \right] \left[ \begin{array}{c} 1 \\ 1 \\ 1 \end{array} \right] = \left[ \begin{array}{c} \text{shift S} \\ \left[ \begin{array}{c} \begin{array}{c} \text{b} \text{ c} \text{ a} \\ \text{a} \text{ b} \text{ c} \\ \text{c} \text{ a} \text{ b} \end{array} \end{array} \right] \left[ \begin{array}{c} 1 \\ 1 \\ 1 \end{array} \right] \end{array} \right.$$

convolution  $\Leftrightarrow$  shift-equivariant

convolution **emerges** from translation symmetry

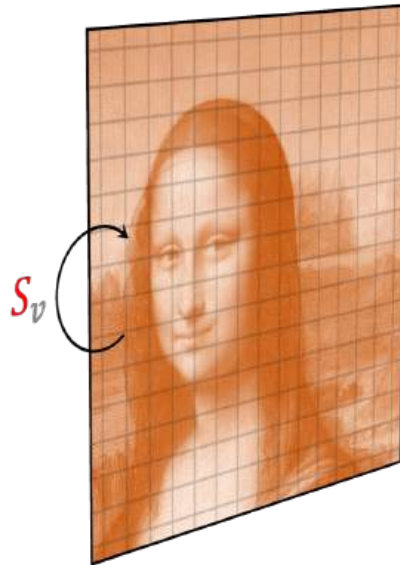
# *CNNs as an Instance of Geometric Deep Learning Blueprint*

Plane  $\mathbb{R}^2$



Translation group  $T(2)$

images  $\mathcal{X}(\mathbb{R}^2)$



Shift operator  $S$

$$S_v x(u) = x(u - v)$$

functions  $\mathcal{F}(\mathcal{X}(\Omega))$



Convolutional layer

$$(Sx \star y) = S(x \star y)$$

## Deriving Fourier Transform from Symmetry

same eigenbasis for all convolutions

different eigenvalues for each convolution

$$\begin{pmatrix} b & c & a \\ a & b & c \\ c & a & b \end{pmatrix} = \begin{pmatrix} | & & | \\ \mathbf{u}_1 & \dots & \mathbf{u}_n \\ | & & | \end{pmatrix} \begin{pmatrix} \lambda_1 & & \\ & \lambda_2 & \\ & & \lambda_n \end{pmatrix} \begin{pmatrix} \text{---} & \mathbf{u}_1^* & \text{---} \\ & \vdots & \\ \text{---} & \mathbf{u}_n^* & \text{---} \end{pmatrix}$$

commuting matrices are jointly  
diagonalisable

common eigenvectors of  $\mathbf{S}$

## Deriving Fourier Transform from Symmetry

Fourier basis

$$\mathbf{u}_k = \frac{1}{\sqrt{n}} \begin{bmatrix} 1 \\ e^{i\frac{2\pi}{n}k} \\ \vdots \\ e^{i\frac{2\pi}{n}(n-1)k} \end{bmatrix}$$

Fourier transform

$$\hat{\boldsymbol{\theta}} = \mathbf{U}^* \boldsymbol{\theta}$$

The diagram illustrates the Fourier transform of a vector  $\boldsymbol{\theta}$ . The vector  $\boldsymbol{\theta}$  is represented as a column of elements  $a, b, c$  with colored diagonal bands. This is equal to the product of a matrix  $\mathbf{U}$  (columns  $\mathbf{u}_1, \dots, \mathbf{u}_n$ ) and a diagonal matrix of eigenvalues  $\hat{\theta}_1, \hat{\theta}_2, \dots, \hat{\theta}_n$ . The matrix  $\mathbf{U}$  is formed by the Fourier basis vectors  $\mathbf{u}_k$ . The diagonal matrix has elements  $\hat{\theta}_1, \hat{\theta}_2, \dots, \hat{\theta}_n$ . The resulting vector  $\hat{\boldsymbol{\theta}}$  is shown as a row of elements  $u_1^*, \dots, u_n^*$ .

commuting matrices are jointly  
diagonalisable by Fourier Transform

*spatial domain*

Circulant matrix

$\mathbf{C}(\boldsymbol{\theta})$

$\mathbf{x}$

$\boldsymbol{\theta} \star \mathbf{x}$

$\mathbf{U}$



$\mathbf{U}^*$



DFT

IDFT



$\mathbf{U}^*$



$\hat{\mathbf{x}}$

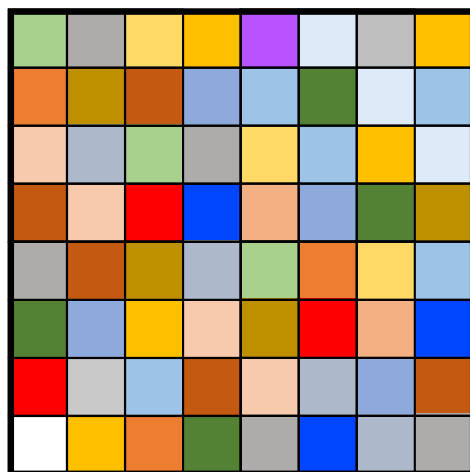
$\widehat{\boldsymbol{\theta} \star \mathbf{x}}$

$$\begin{bmatrix} \hat{\theta}_1 & & \\ & \ddots & \\ & & \hat{\theta}_n \end{bmatrix}$$

Element-wise product

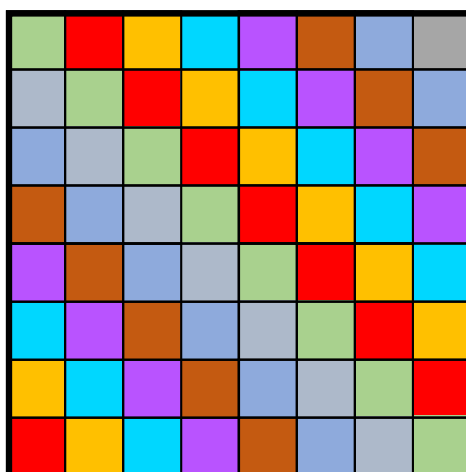
*frequency domain*

Fully connected



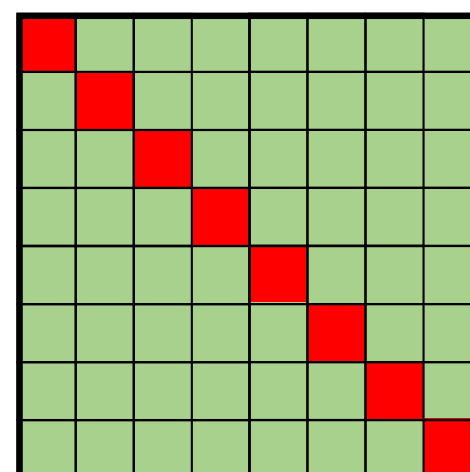
Trivial  $G = \{e\}$   
 $\mathcal{O}(n^2)$  DOF

Grids



Translation  
 $\mathcal{O}(n)$  DOF

Graphs / Sets

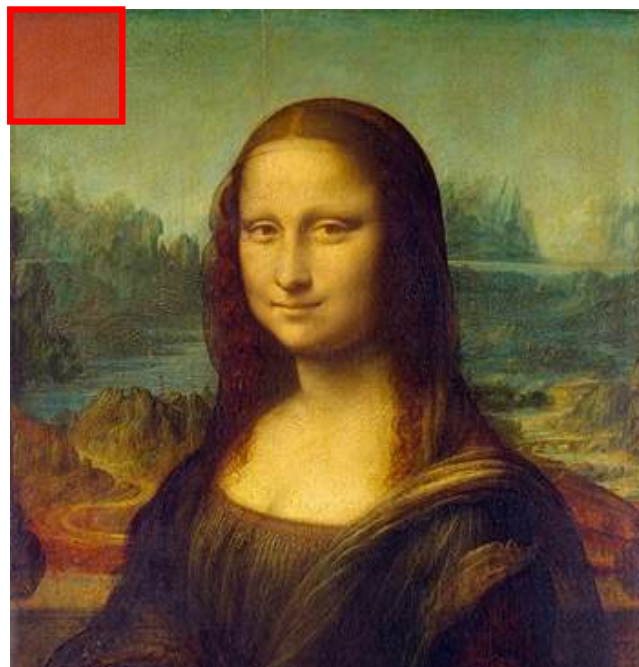


Permutation  
 $\mathcal{O}(1)$  DOF

An illustration depicting a group of people falling into a dark, swirling vortex. At the bottom of the vortex is a bright, circular opening showing a blue sky with white clouds. Five people are shown in various stages of falling: a woman in a green dress is in the foreground, upside down; a woman in a purple dress is falling towards the center; a woman in a blue dress is further in; a woman in a yellow dress is near the top; and a woman in an orange dress is at the very top. Red arrows indicate the direction of the fall. The background is dark with a faint, cracked texture.

# Groups

## *Convolution, revisited*



## *Convolution, revisited*

convolution = matching shifted filter

$$(\boldsymbol{x} \star \boldsymbol{\psi})(u) = \langle \boldsymbol{x}, S_u \boldsymbol{\psi} \rangle = \int_{-\infty}^{+\infty} \boldsymbol{x}(v) \boldsymbol{\psi}(u - v) dv$$

  
shift vector                      shift operator

**domain  $\Omega \cong$  symmetry group  $G$**   
i.e.,  $\star \psi: \mathcal{X}(\Omega) \rightarrow \mathcal{X}(\Omega)$

## Group Convolution

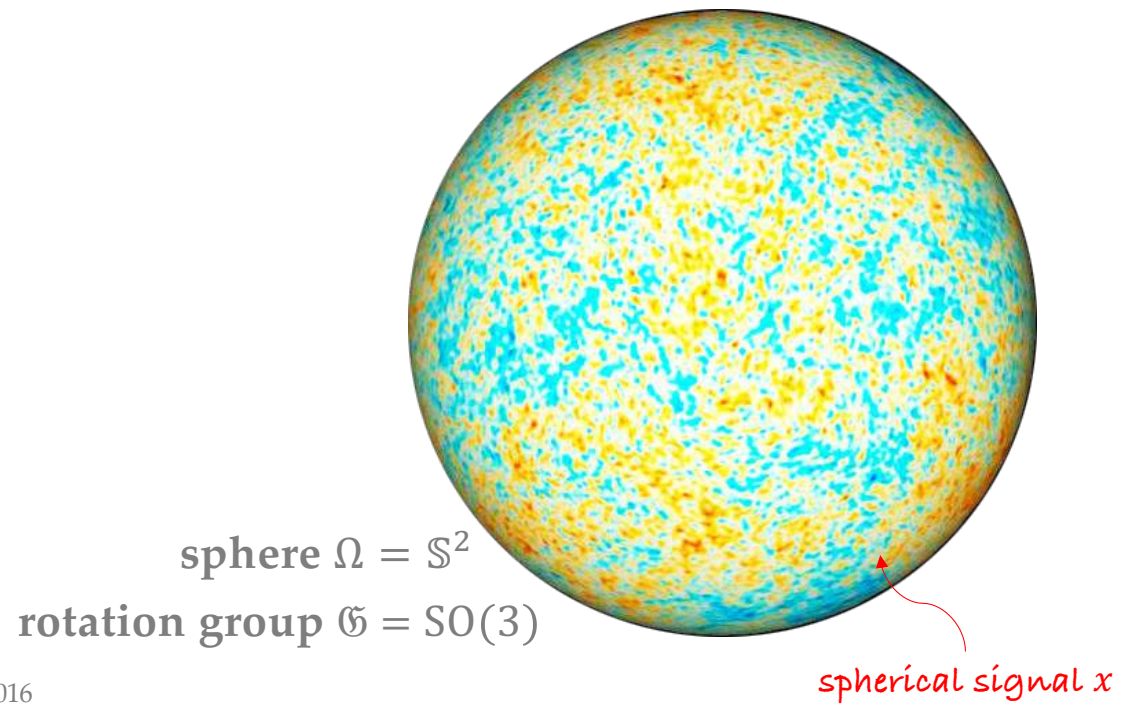
convolution = matching transformed filter

$$(\boldsymbol{x} \star \boldsymbol{\psi})(\boldsymbol{g}) = \langle \boldsymbol{x}, \boldsymbol{\rho}(\boldsymbol{g})\boldsymbol{\psi} \rangle = \int_{\Omega} \boldsymbol{x}(\boldsymbol{v})\boldsymbol{\psi}(\boldsymbol{g}^{-1}\boldsymbol{v})\mathrm{d}\boldsymbol{v}$$

  
group element                      group representation

**The convolution outputs a signal on the group  $G$**   
i.e.,  $\star \psi: \mathcal{X}(\Omega) \rightarrow \mathcal{X}(G)$

# *Convolution on the Sphere*

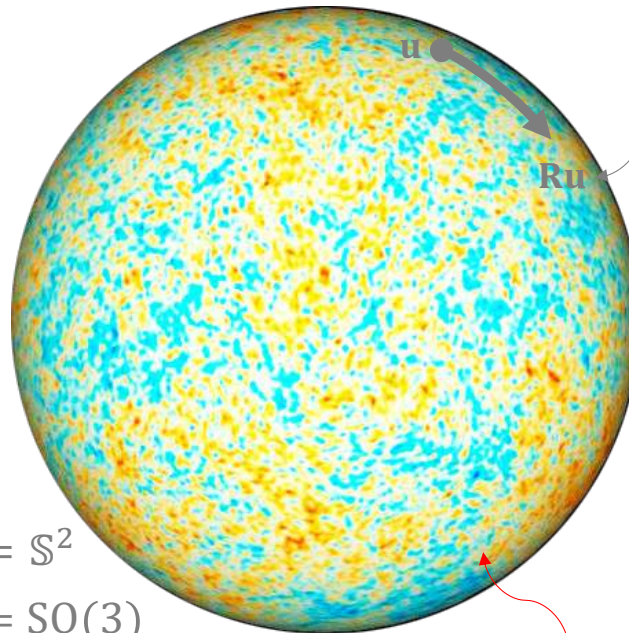


# Convolution on the Sphere

$$(x \star \psi)(\mathbf{R}) = \int_{\mathbb{S}^2} x(\mathbf{u}) \psi(\mathbf{R}^{-1} \mathbf{u}) d\mathbf{u}$$

signal on  $SO(3)$

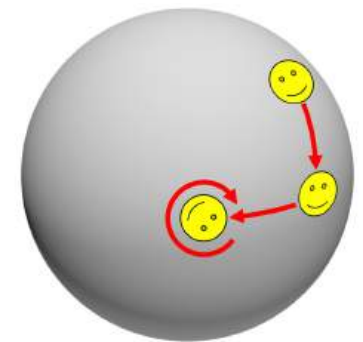
rotation transformation



sphere  $\Omega = \mathbb{S}^2$

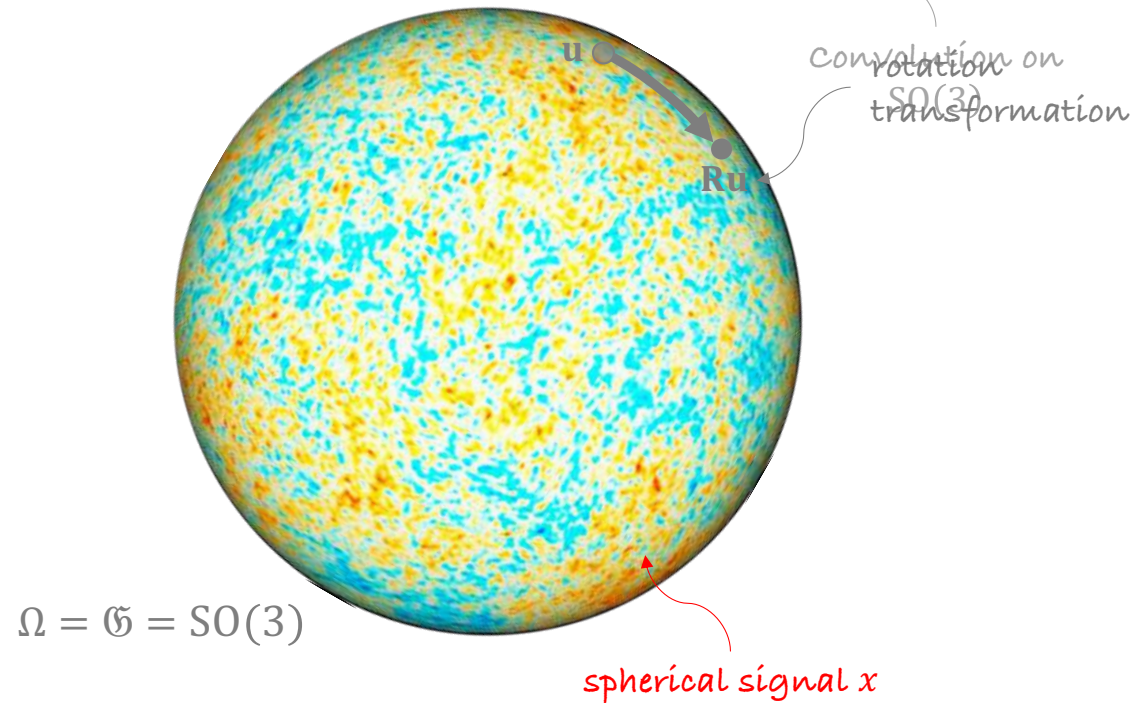
rotation group  $\mathfrak{G} = SO(3)$

spherical signal  $x$

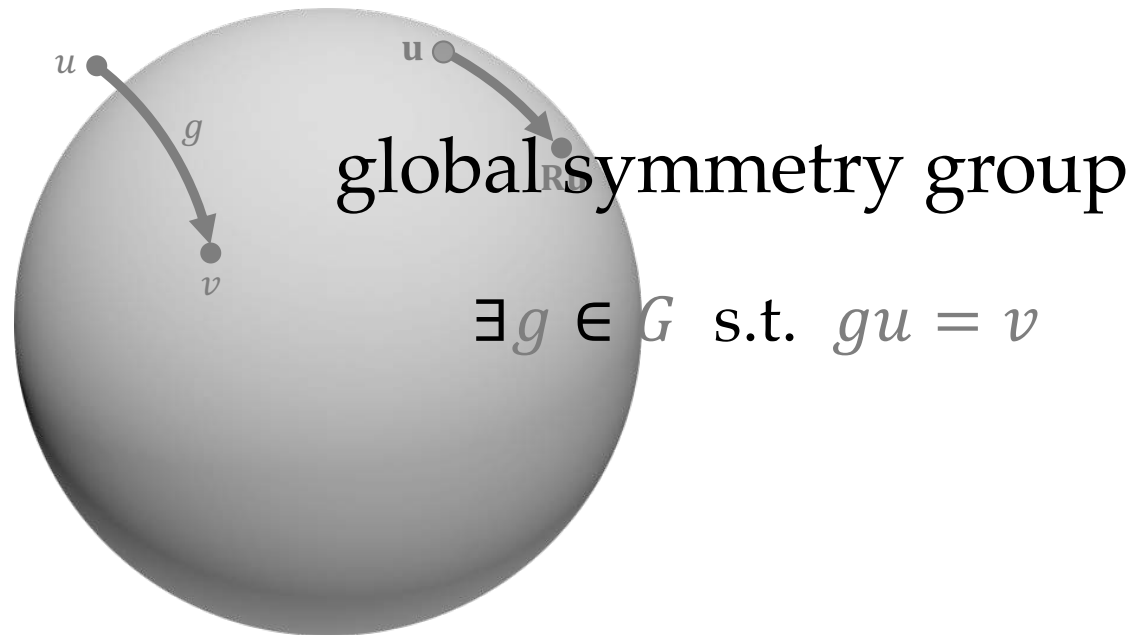


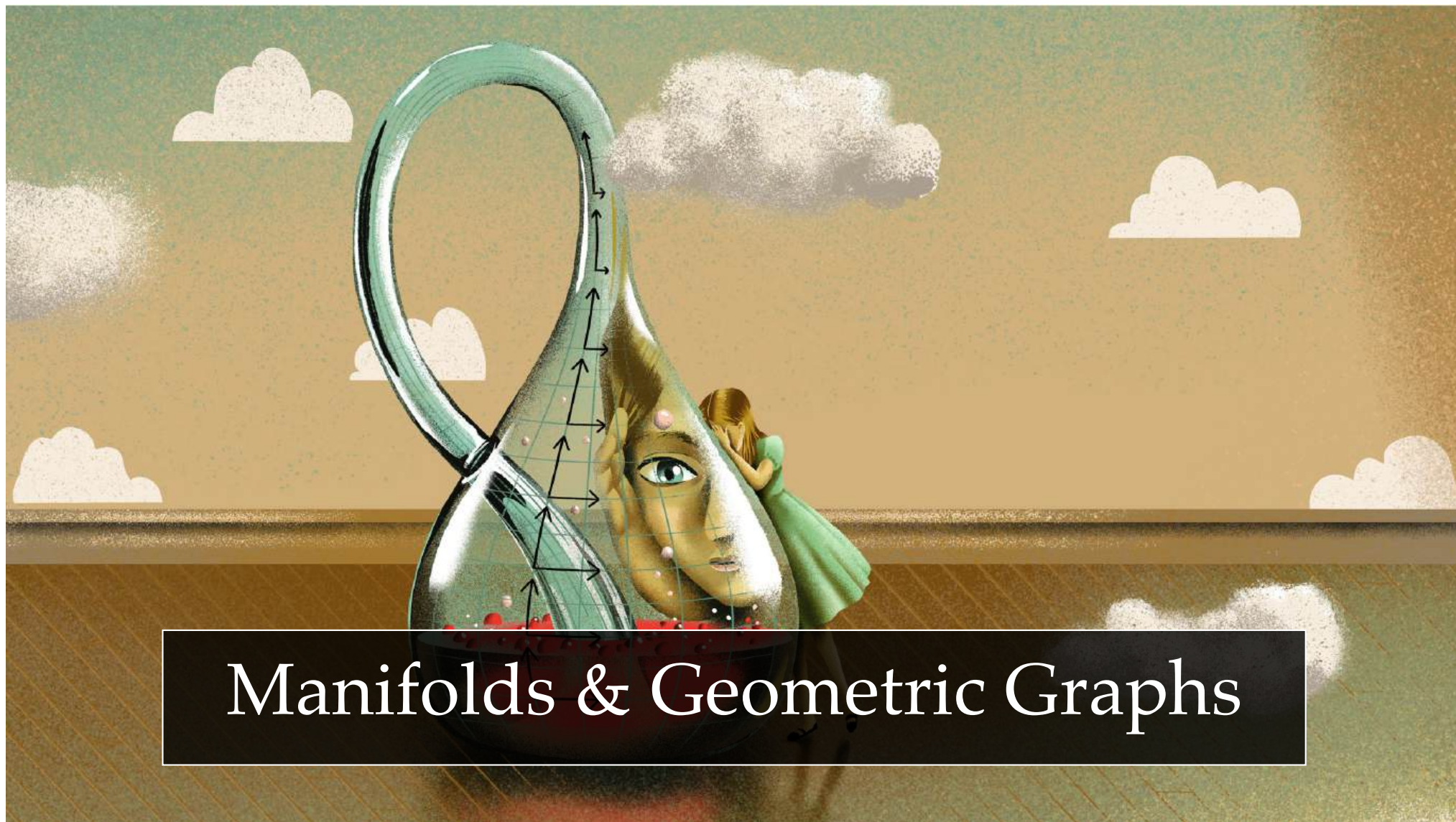
## Convolution on the Sphere

$$((x \star \psi) \star \phi)(\mathbf{R}) = \int_{\text{SO}(3)} (x \star \psi)(\mathbf{Q}) \phi(\mathbf{R}^{-1}\mathbf{Q}) d\mathbf{Q}$$



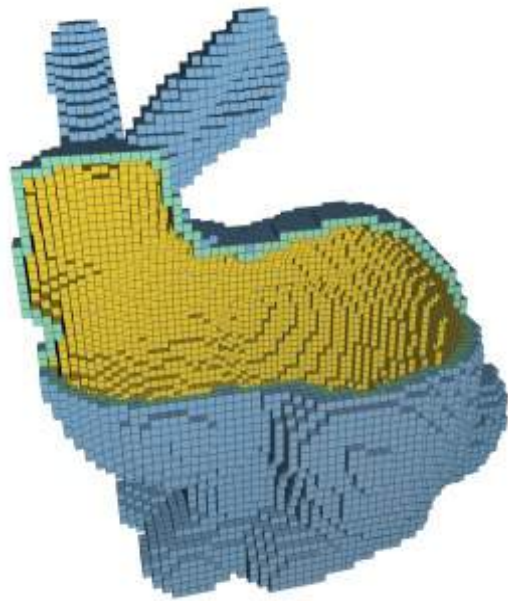
# *Homogeneous Spaces*



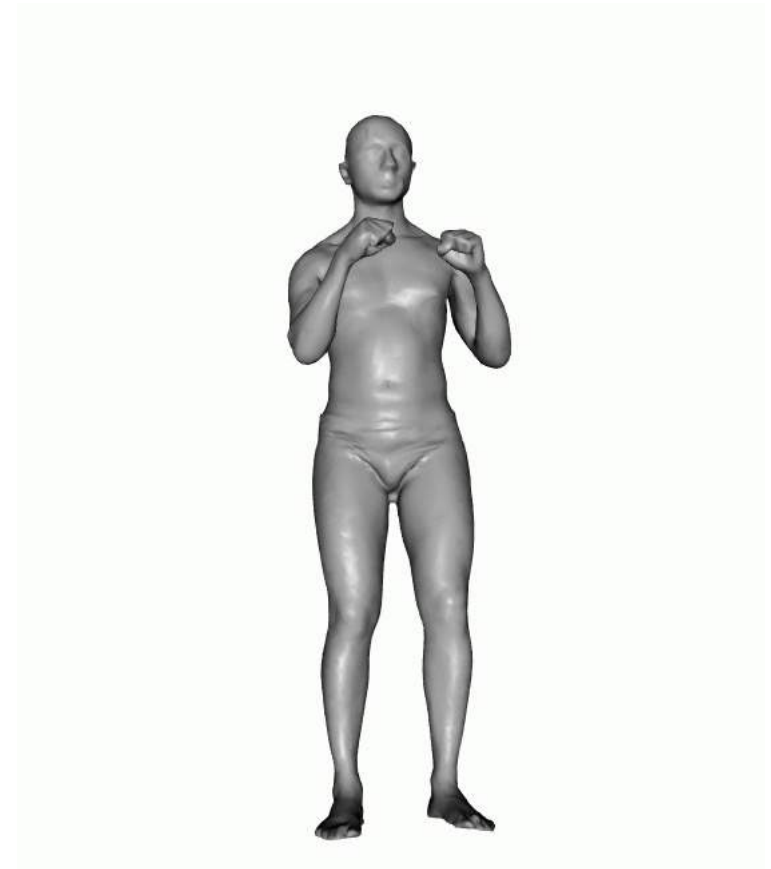
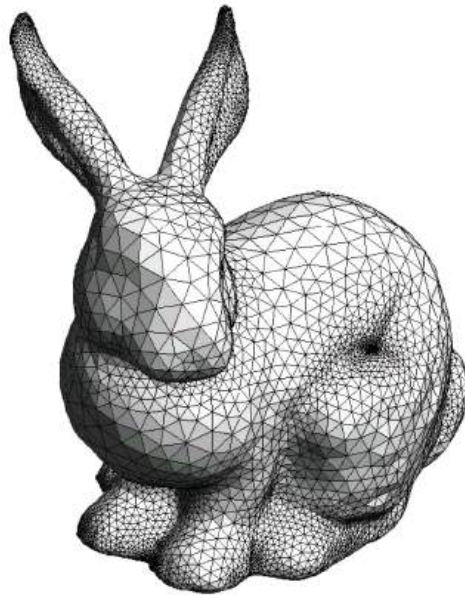


# Manifolds & Geometric Graphs

## *Why Manifolds?*



More efficient representation: no “waste”  
for internal structures



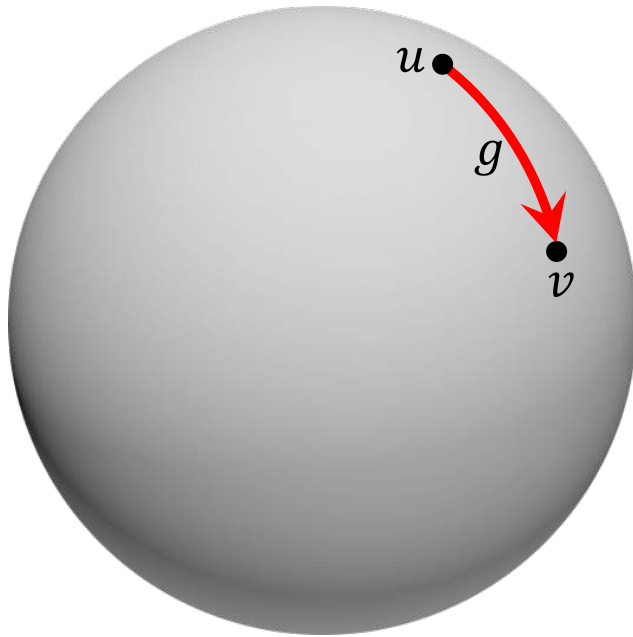
Natural model for  
deformable shapes

## *Why Manifolds?*

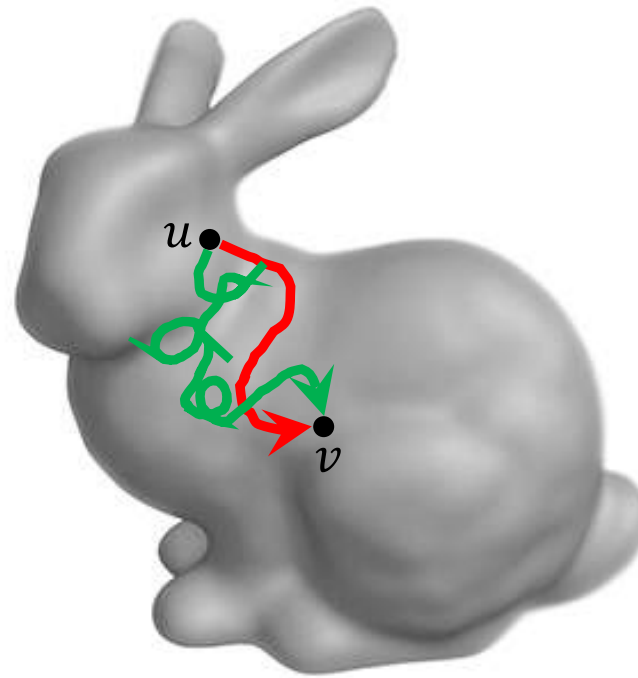
In protein modeling,  
abstract out internal  
structure that is irrelevant  
for interactions + allow  
some conformation  
changes



## *Homogeneous Spaces*

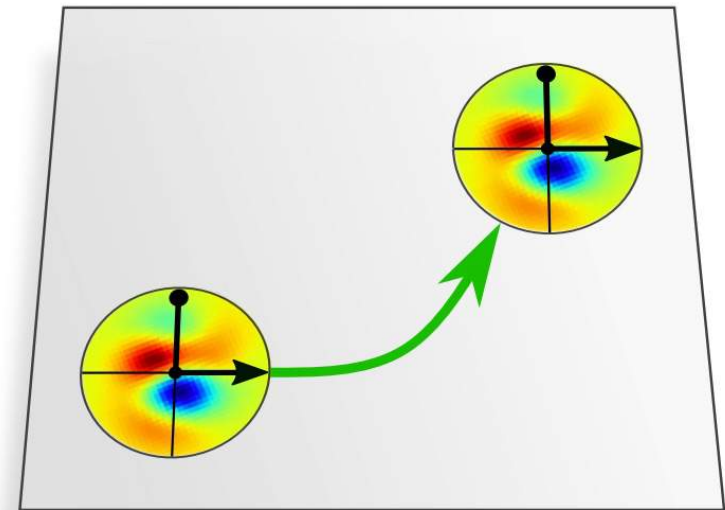
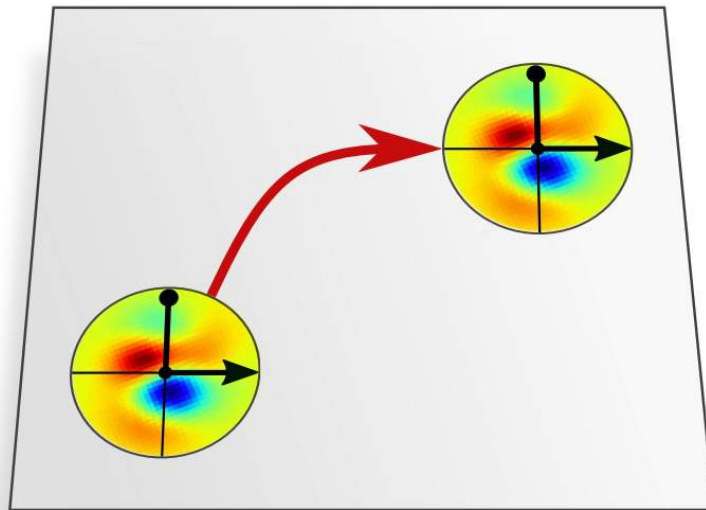


global symmetry group  
 $\exists g \in G$  s.t.  $gu = v$



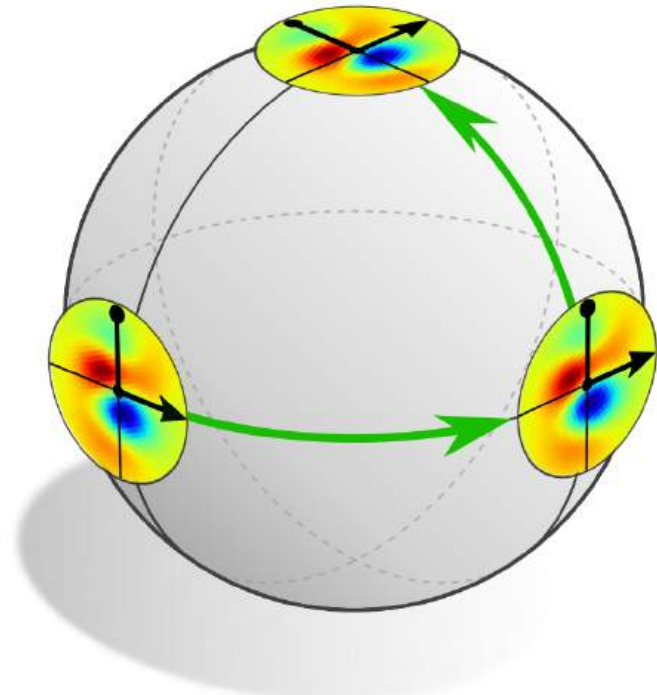
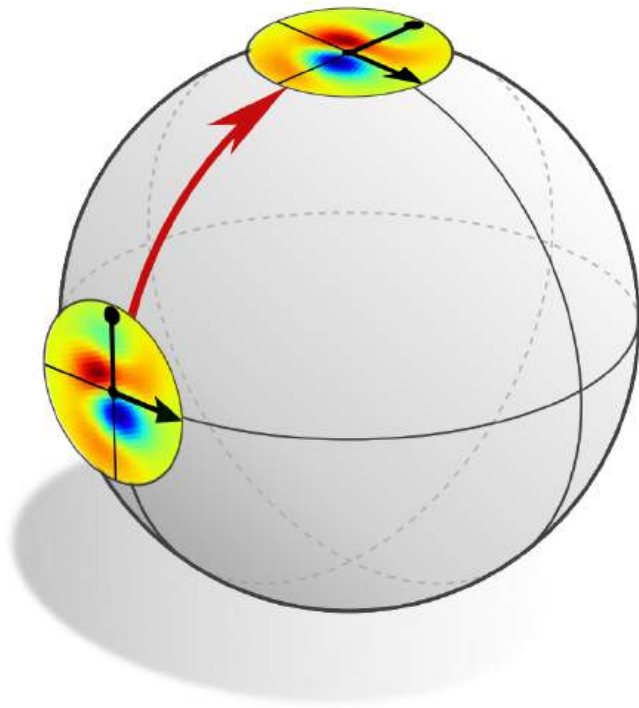
no global symmetry group

## *Euclidean Convolution*



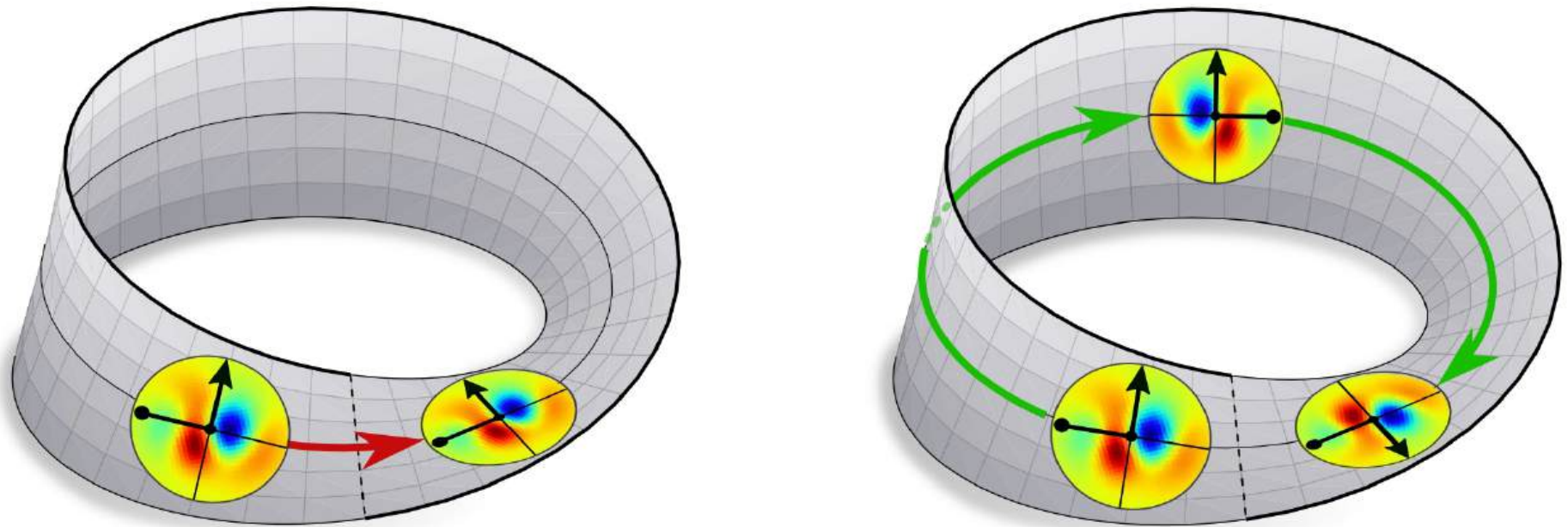
Euclidean space: Transport the filter around the domain

## Non-Euclidean Convolution



Manifold: Result of transport is *path dependent*

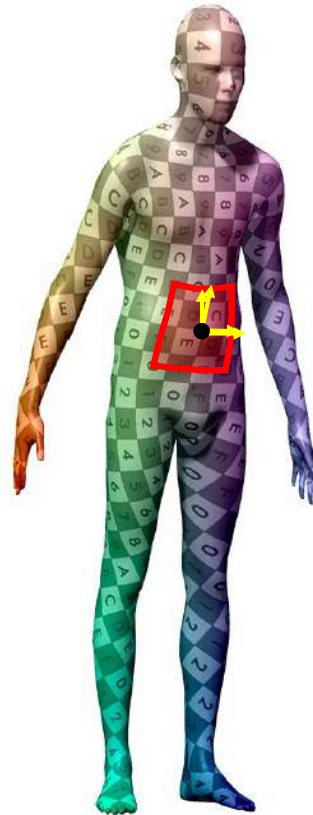
## Non-Euclidean Convolution



Manifold: Result of transport is *path dependent*

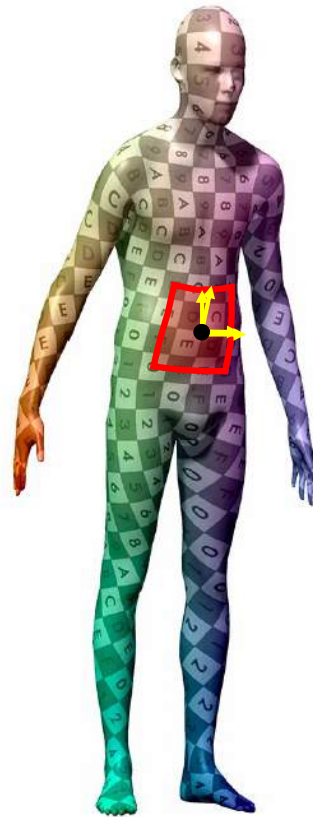
## *Two Types of Invariance*

**Local gauge  
transformation**



## *Two Types of Invariance*

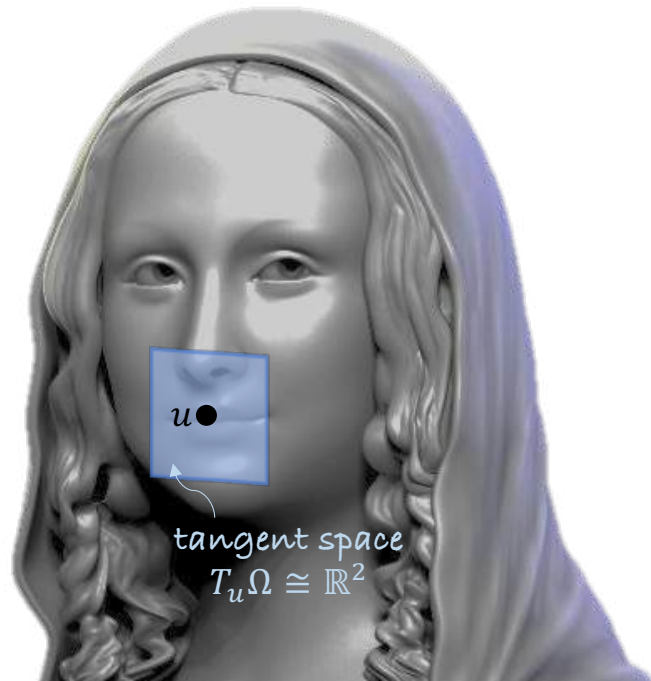
**Local gauge  
transformation**



**Global  
deformation**



# Manifolds



manifold  $\Omega$

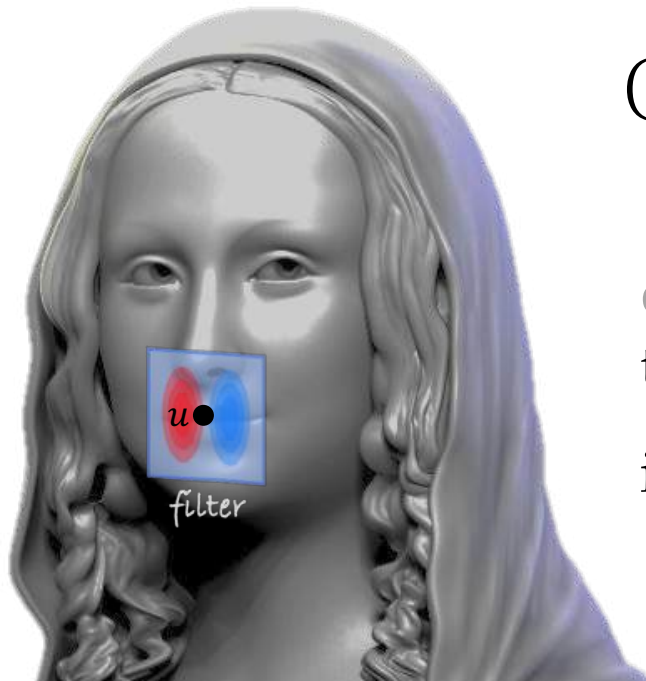
**manifold** = locally Euclidean space

**Riemannian metric** = local  
length / direction

**Intrinsic** quantity = expressed solely  
in terms of the Riemannian metric

**Isometry** = metric-preserving  
deformation

# Geodesic CNNs



manifold  $\Omega$

isometry group  $\text{Iso}(\Omega)$

Masci et B 2015; Boscaini et B 2016; Monti et B 2017

Exponential map  
 $\exp_u: T_u\Omega \rightarrow \Omega$

$$(\boldsymbol{x} \star \boldsymbol{\psi})(u) = \int_{T_u\Omega} \boldsymbol{\psi}(v) \boldsymbol{x}(\exp_u v) dv$$

$\exp_u$  is an intrinsic map allowing to express the signal  $\boldsymbol{x}$  locally in the tangent space  $T_u\Omega$

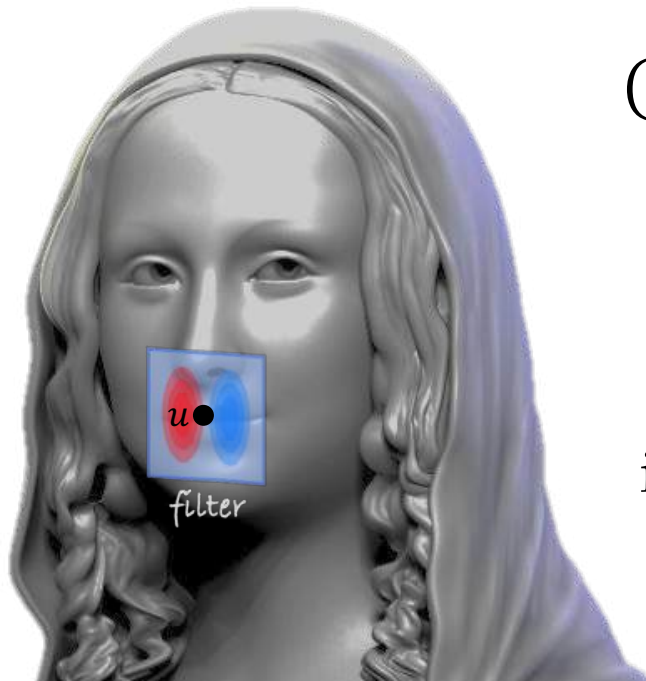
intrinsic filter = invariant to isometries

## *Geodesic CNNs*



Anisotropic intrinsic filters on a manifold

# Geodesic CNNs



manifold  $\Omega$

isometry group  $\text{Iso}(\Omega)$

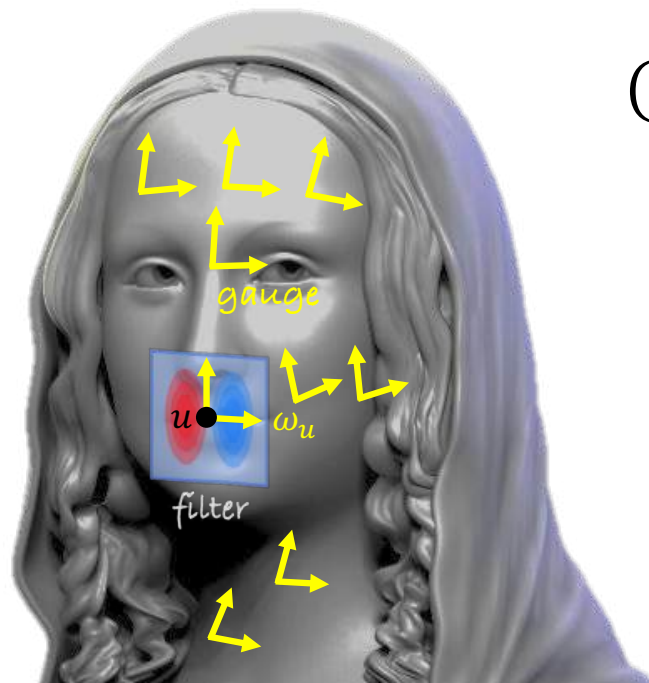
Masci et B 2015; Boscaini et B 2016; Monti et B 2017

$$(x \star \psi)(u) = \int_{T_u \Omega} \psi(v) x(\exp_u v) dv$$

Problem: these are abstract vectors!

intrinsic filter = invariant to isometries

# Geodesic CNNs

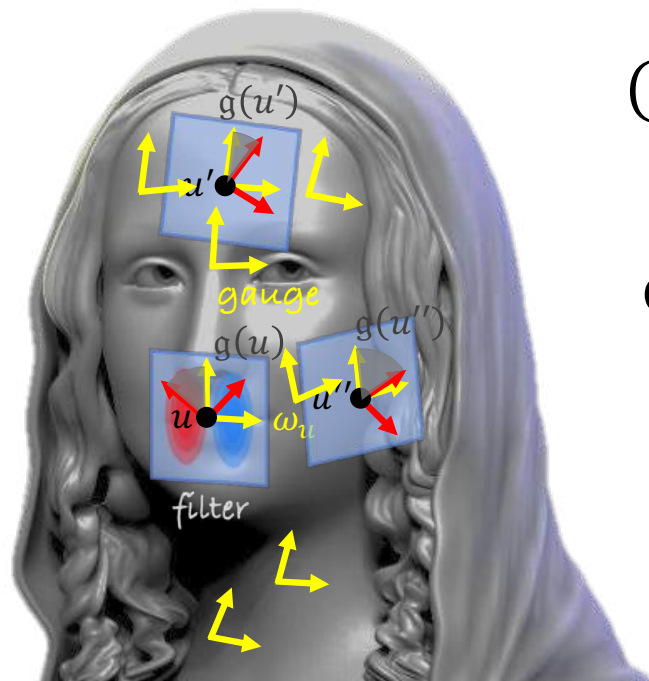


manifold  $\Omega$   
isometry group  $\text{Iso}(\Omega)$

local reference frame  
 $\omega_u: \mathbb{R}^2 \rightarrow T_u\Omega$

$$(x \star \psi)(u) = \int_{\mathbb{R}^2} \psi(\mathbf{v}) x(\exp_u \omega_u \mathbf{v}) d\mathbf{v}$$

# Gauge Transformations



manifold  $\Omega$   
structure group  $G$

Cohen et al. 2019; Weiler et al. 2021

$$(\boldsymbol{x} \star \boldsymbol{\psi})(u) = \int_{\mathbb{R}^2} \boldsymbol{\psi}(\mathbf{v}) \boldsymbol{x}(\exp_u \omega_u \mathbf{v}) d\mathbf{v}$$

Gauge defined up to gauge transformation

$$g: \Omega \rightarrow G$$

## Structure Group

A gauge is defined up to a *gauge transformation*  $g: \Omega \rightarrow G$

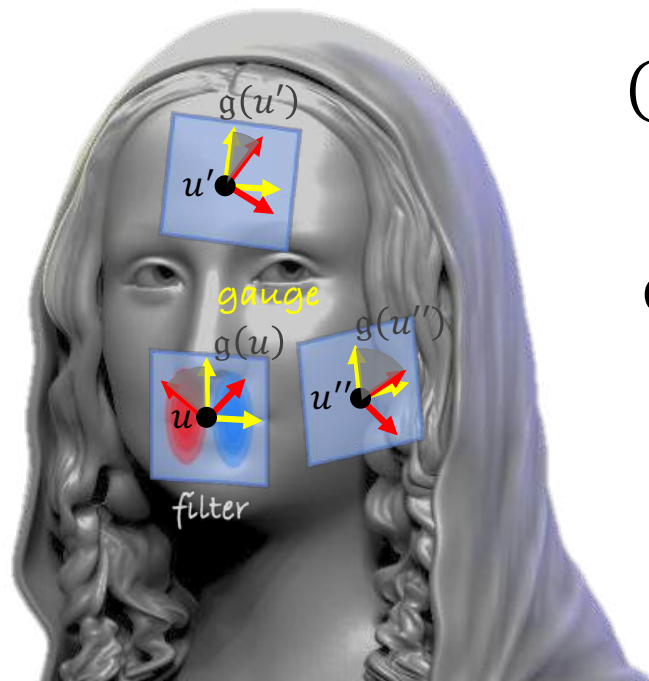
|                               |           |                                     |
|-------------------------------|-----------|-------------------------------------|
| • “Naked” manifold            | $GL(s)$   | invertible matrices                 |
| • Manifold+orientation        | $GL^+(s)$ | invertible matrices with $\det > 0$ |
| • Manifold+volume             | $SL(s)$   | matrices with $\det = 1$            |
| • Manifold+metric             | $O(s)$    | orthogonal matrices                 |
| • Manifold+metric+orientation | $SO(s)$   | orthogonal matrices with $\det = 1$ |
| • Manifold+frame field        | $\{id\}$  | identity (no ambiguity)             |

# Structure Group

**A gauge is defined up to a *gauge transformation*  $g: \Omega \rightarrow G$**

|                               |           |                                     |
|-------------------------------|-----------|-------------------------------------|
| • “Naked” manifold            | $GL(s)$   | invertible matrices                 |
| • Manifold+orientation        | $GL^+(s)$ | invertible matrices with $\det > 0$ |
| • Manifold+volume             | $SL(s)$   | matrices with $\det = 1$            |
| • Manifold+metric             | $O(s)$    | orthogonal matrices                 |
| • Manifold+metric+orientation | $SO(s)$   | orthogonal matrices with $\det = 1$ |
| • Manifold+frame field        | $\{id\}$  | identity (no ambiguity)             |

# Gauge-equivariant CNNs



manifold  $\Omega$   
 structure group  $G = \text{SO}(2)$

Cohen et al. 2019

$$(x \star \psi)(u) = \int_{\mathbb{R}^2} \psi(\mathbf{v}) \rho(\exp_u \omega_u \mathbf{v}) d\mathbf{v}$$

Gauge defined up to gauge transformation

$$g: \Omega \rightarrow \text{SO}(2)$$

gauge-equivariant filter

$$\psi(g^{-1}\mathbf{v}) = \rho(g^{-1})\psi(\mathbf{v})\rho(g)$$

# *“Hairy Ball” (a.k.a. Poincaré-Hopf) Theorem*

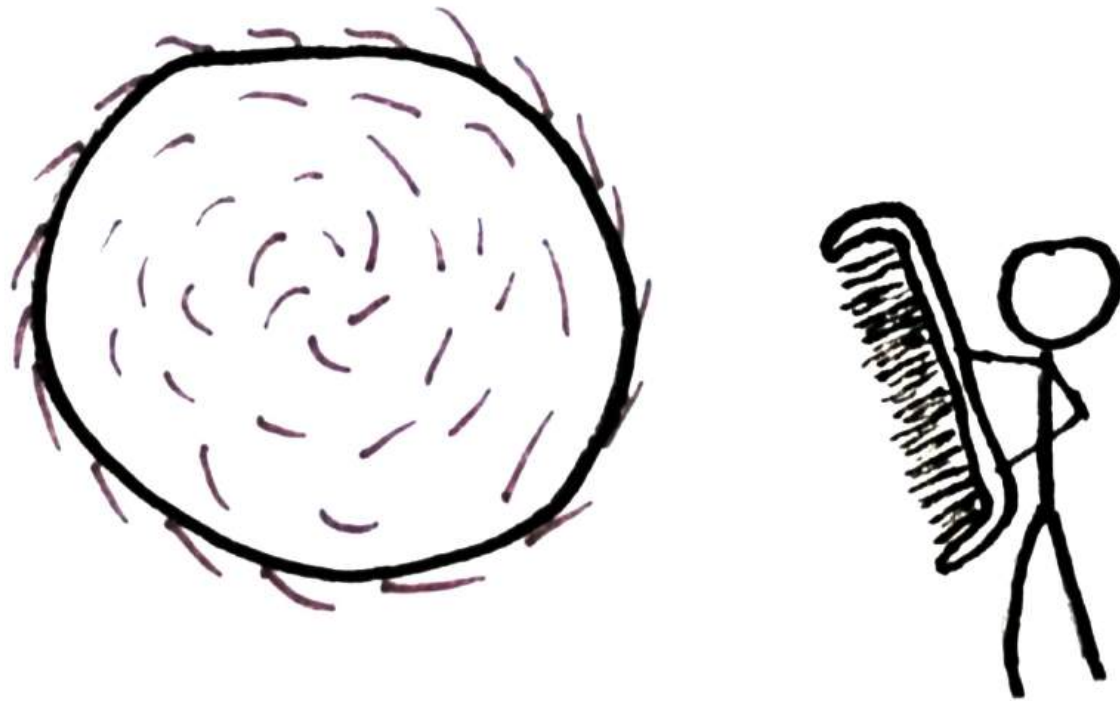
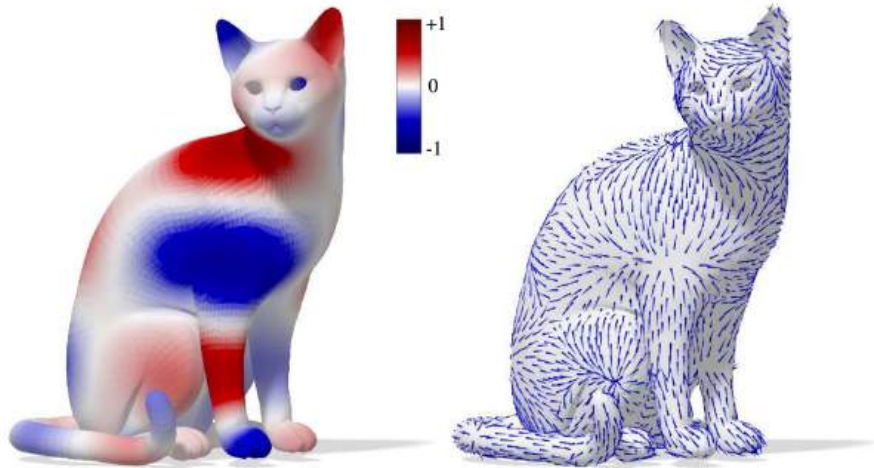
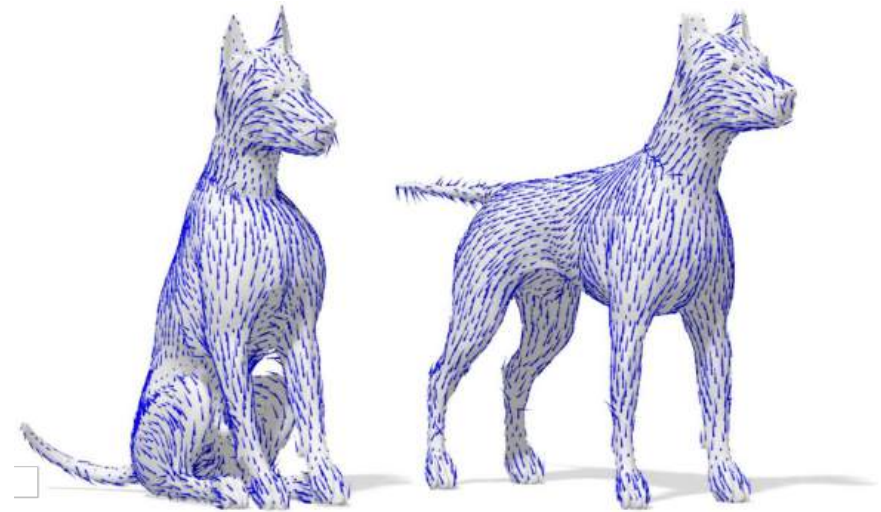


Image: Minutephysics

## *Theory vs Practice: Stable Gauges*



Gradient of intrinsic function

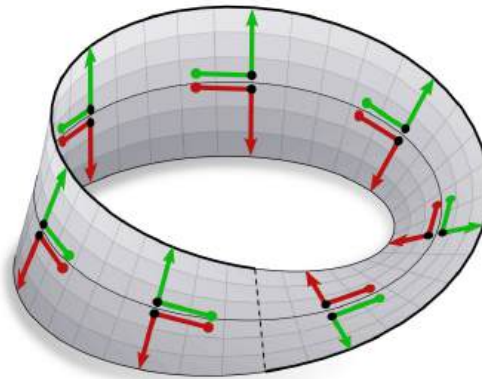


Deformation-invariant  
stable gauge

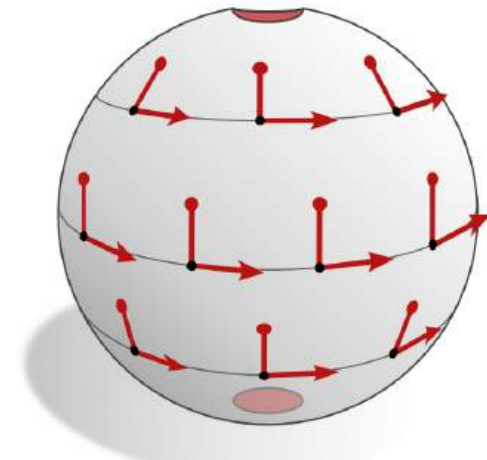
# Structure Group



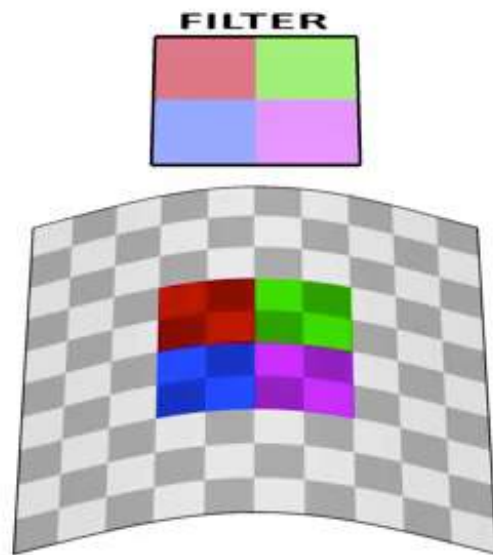
**rotation**  
 $SO(2)$



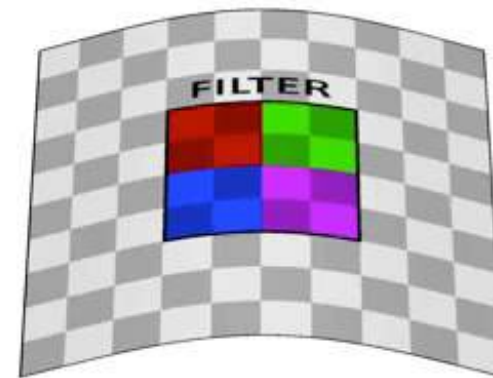
**reflection**  
 $R$



**fixed gauge**  
 $\{id\}$



**Euclidean (extrinsic)  
convolution**



**Geometric (intrinsic)  
convolution**

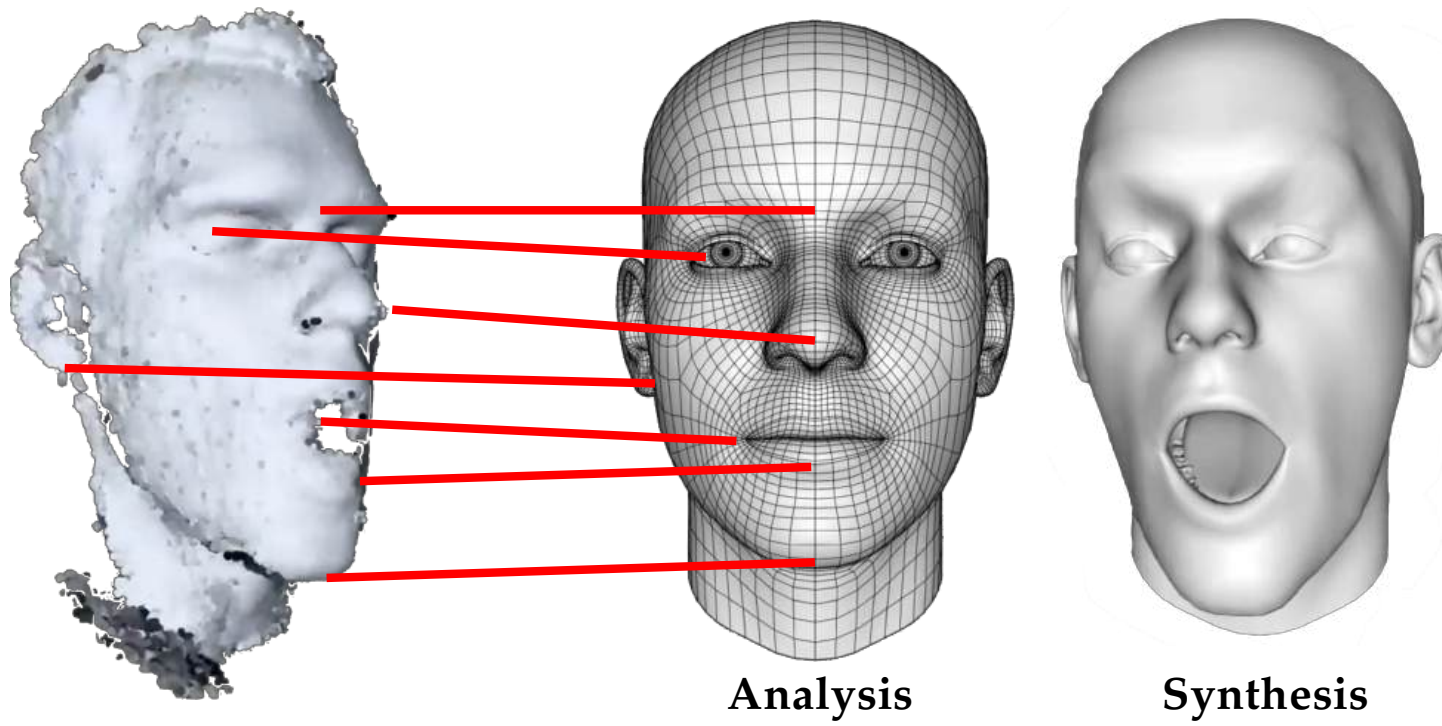
A whimsical illustration of a young girl with long blonde hair, seen from behind, wearing a bright green dress. She holds a glowing yellow lantern in her right hand, illuminating a path in a dark forest. The trees are tall and slender, their trunks and branches covered in a dense pattern of small, glowing orange and green dots. The ground is a mix of dark earth and patches of glowing orange and green. In the upper part of the image, there are faint, glowing lines and dots, resembling a constellation or a magical web. The overall atmosphere is magical and mysterious.

# Applications

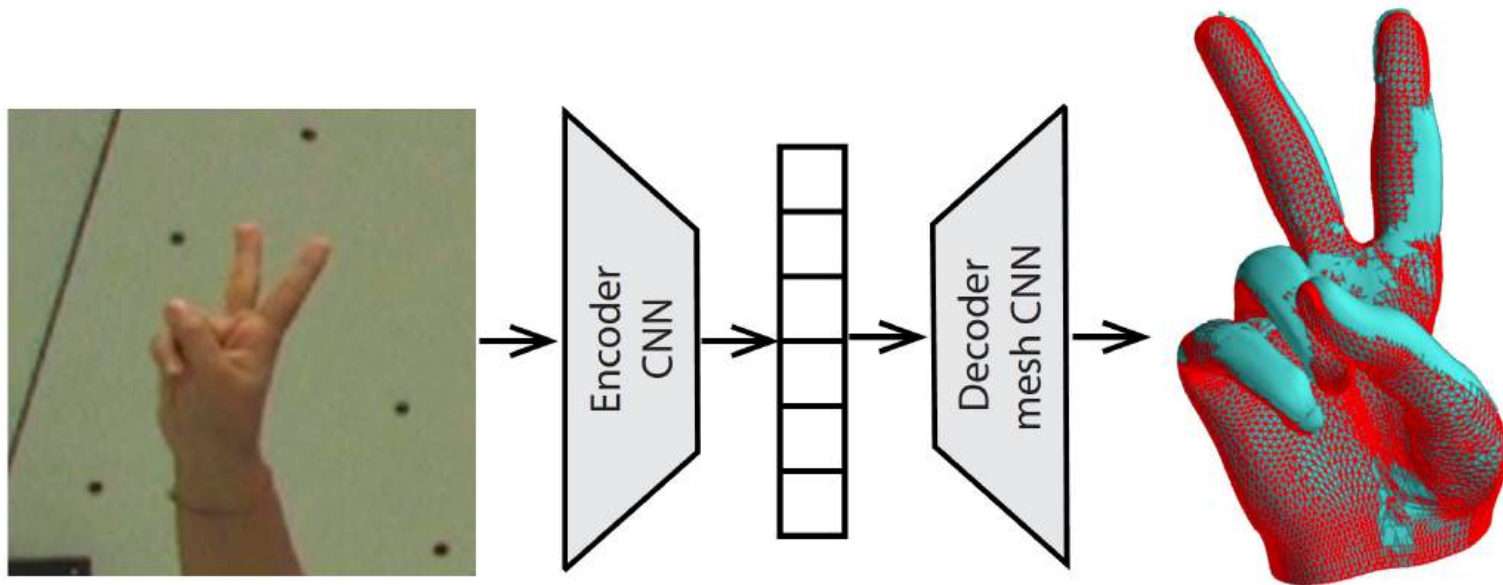
FaceShift 2015



## *Shape Analysis & Synthesis*



## *3D Hand Reconstruction*



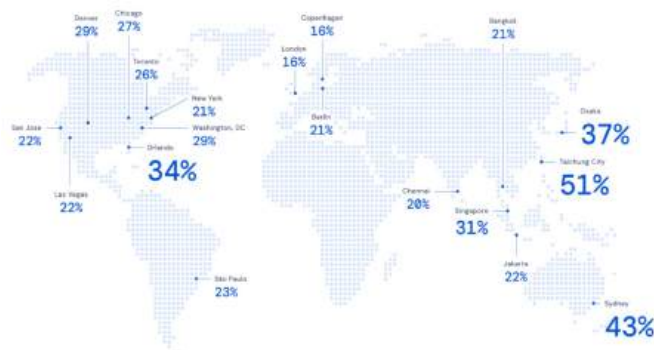


## Snap Acquires Ariel AI To Enhance AR Features

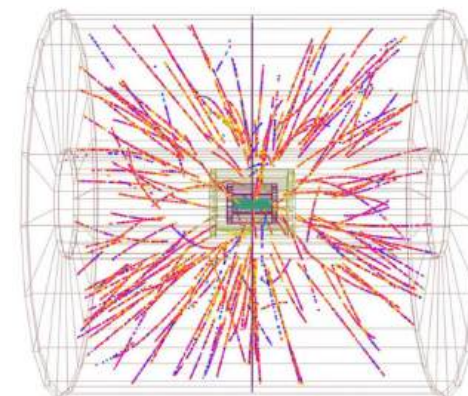




Fake news detection



Navigation



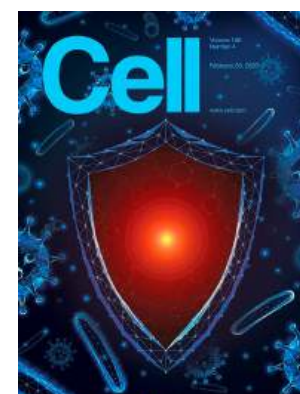
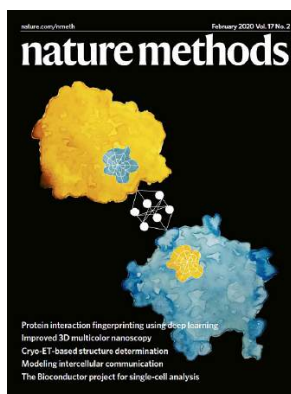
Particle physics



Pure math



Structural biology



Drug discovery

Safe spaces for South  
Asia's vultures p. 1086

Synthetic Notch receptors  
enhance T cell therapies p. 1112

Dietary fiber fights  
diabetes p. 1151

# Science

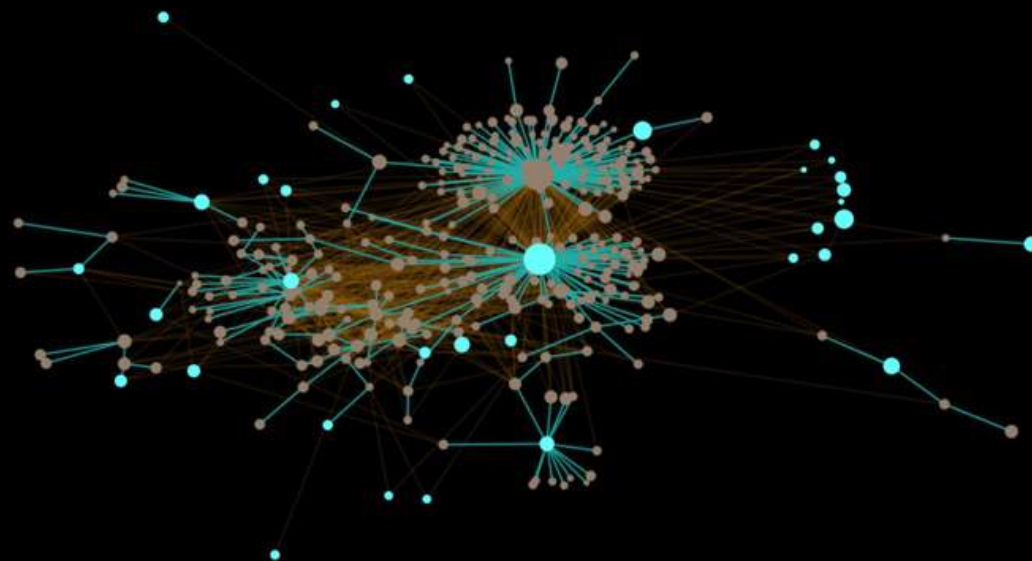
\$15  
9 MARCH 2018  
sciencemag.org

AAAS

## HOW LIES SPREAD

On social media,  
false news beats the truth  
pp. 1094 & 1146

Vosoghi et al. 2018



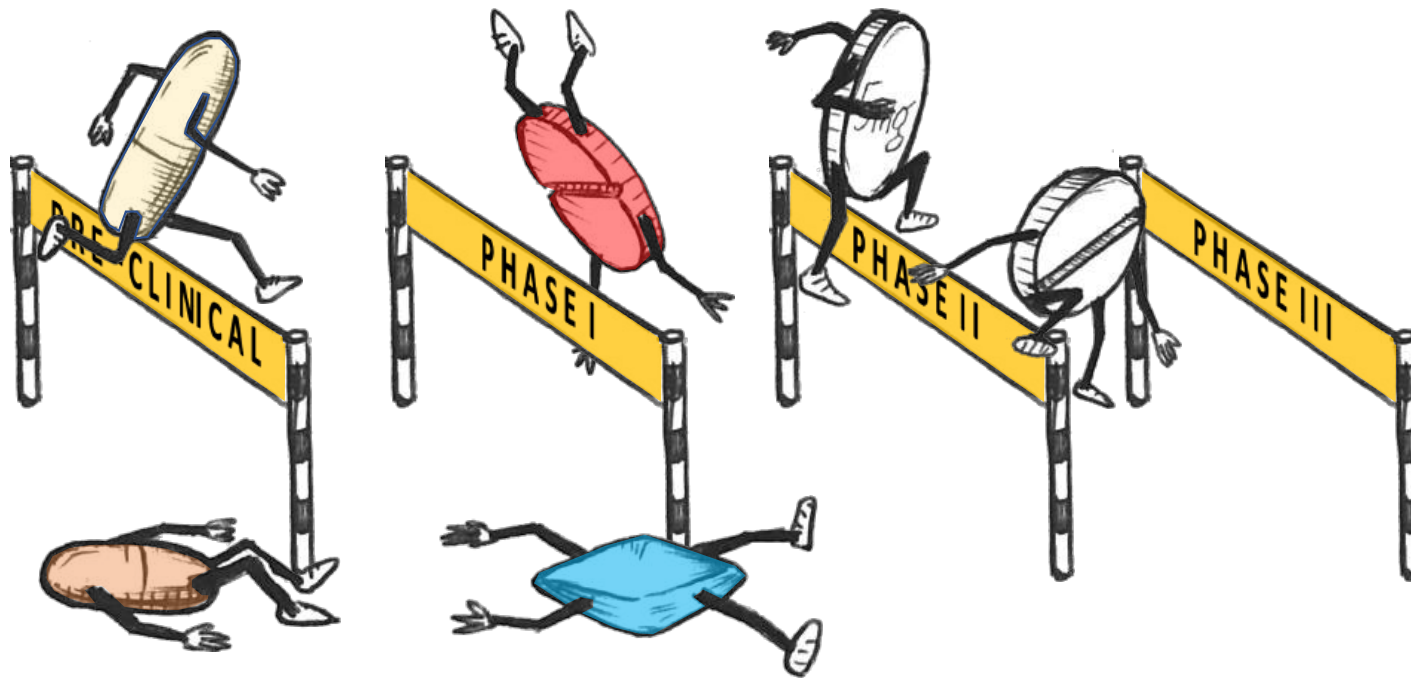
FABULA

Monti et B 2019

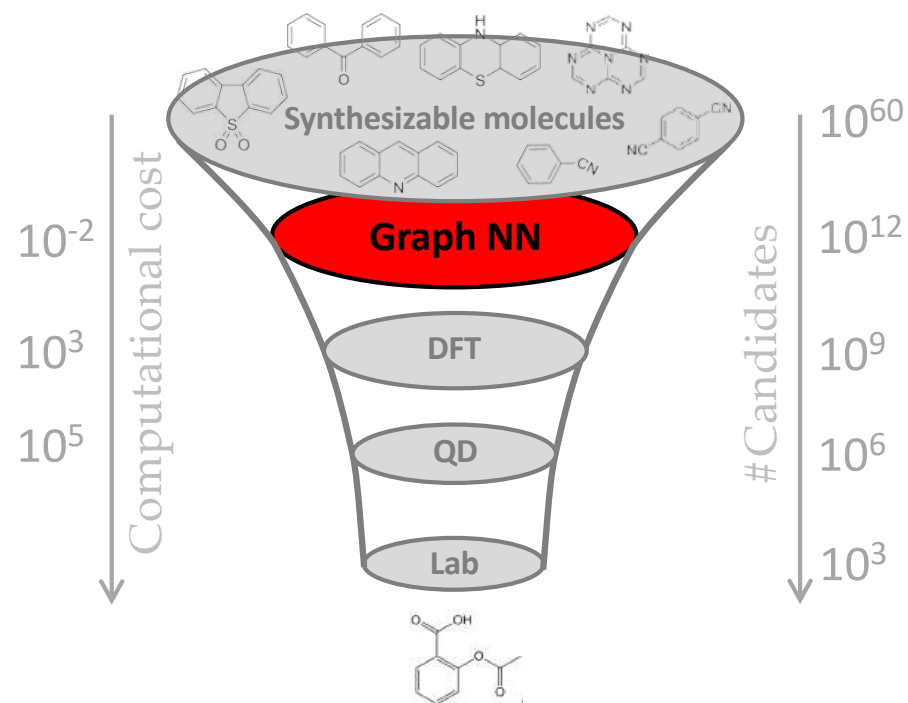
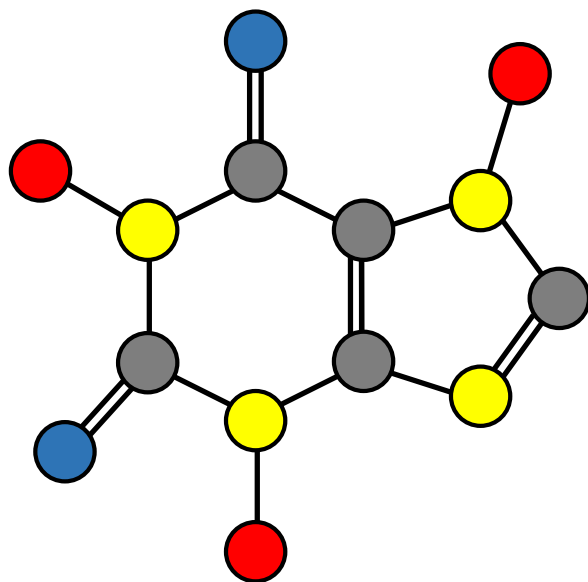


Acquired by Twitter in 2019

## *Drug Discovery & Design*

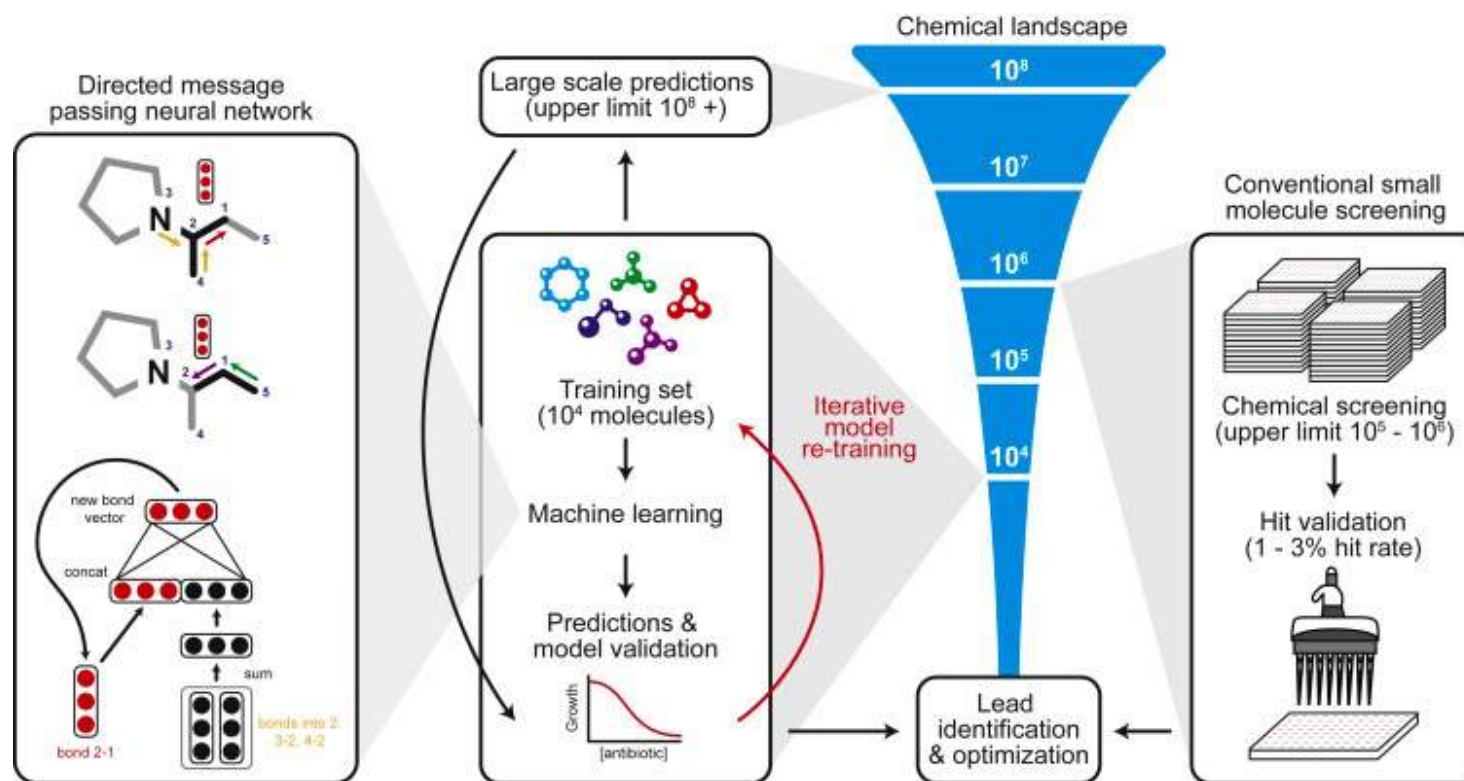


# Virtual Drug Screening

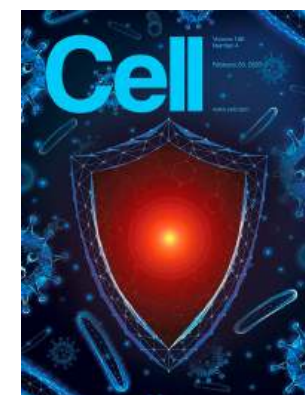


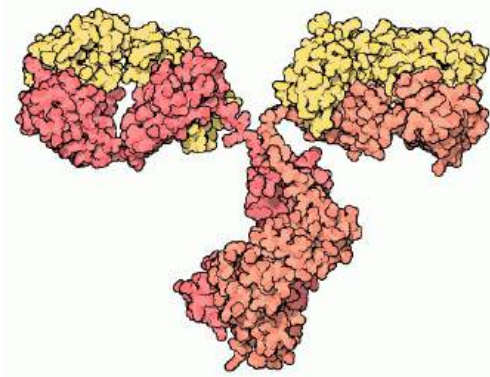
"Computational funnel"

# New Antibiotic Discovery

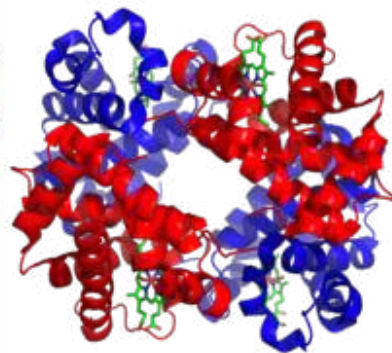


Stokes et al. 2020

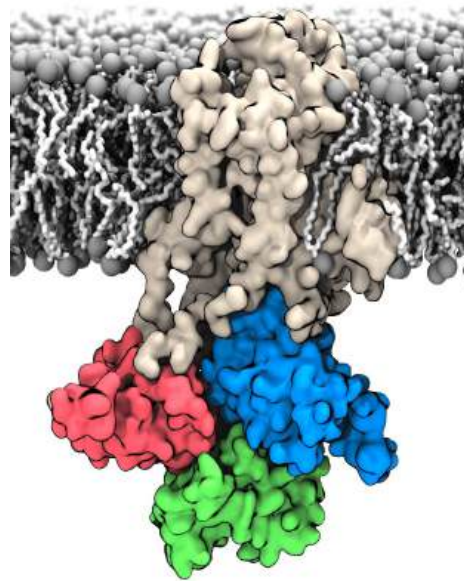




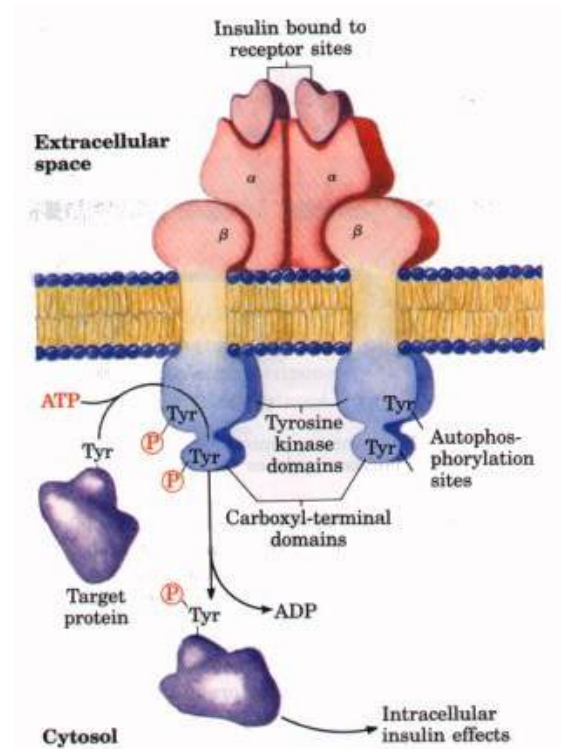
Defense (antibody)



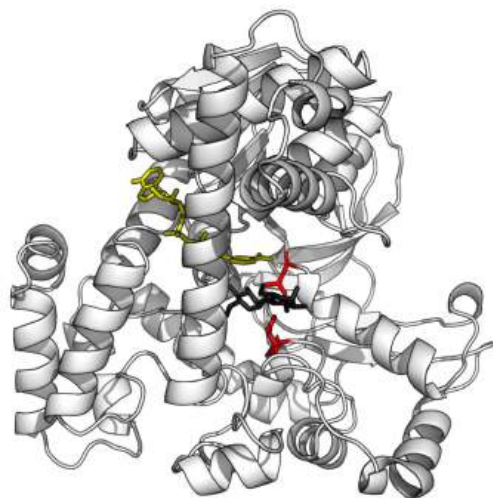
Storage (haemoglobin)



Transport (calcium pump)

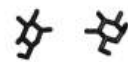


Communication (insulin)



Catalysis (enzyme)

Maltose substrate



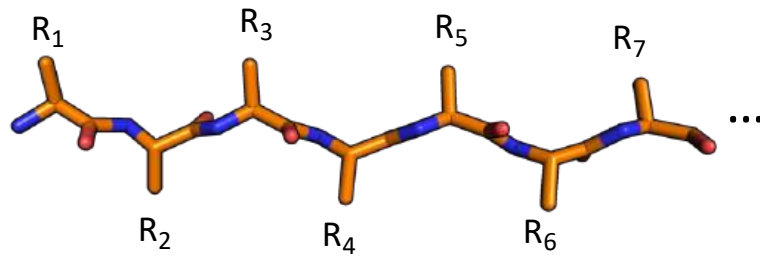
Glucose products



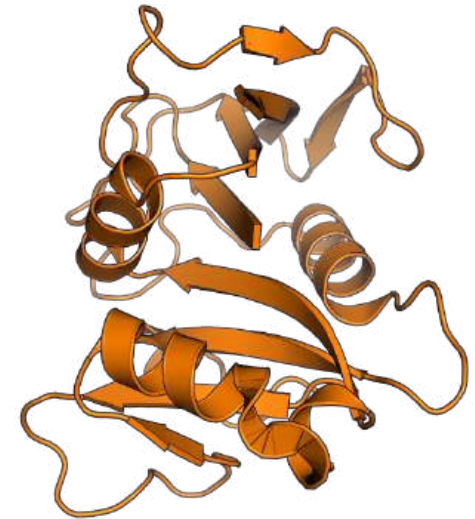
Structure (collagen)

# *Protein Folding*

Protein folding



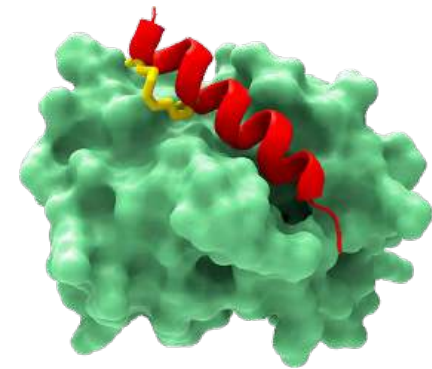
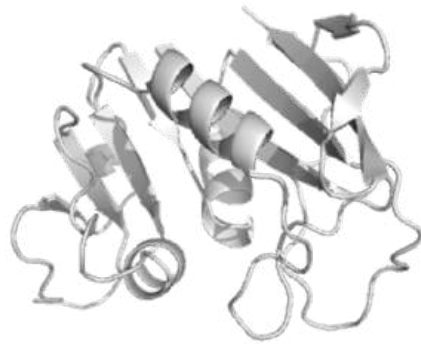
Primary protein  
structure



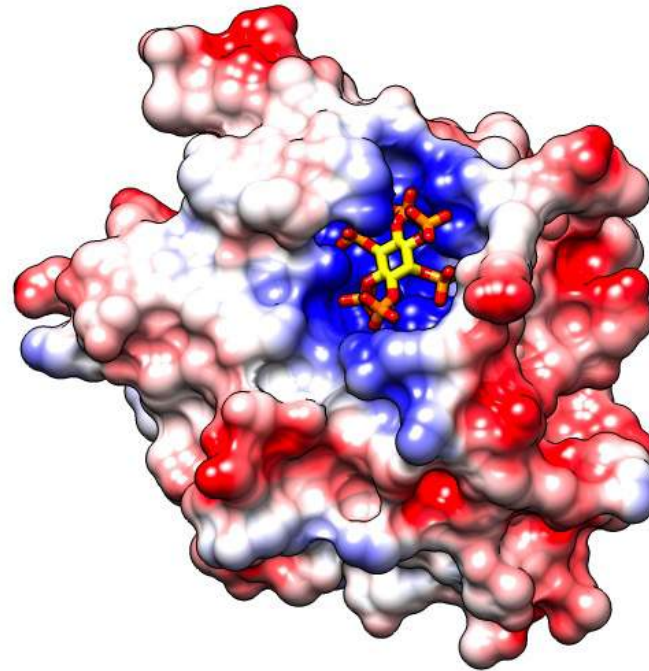
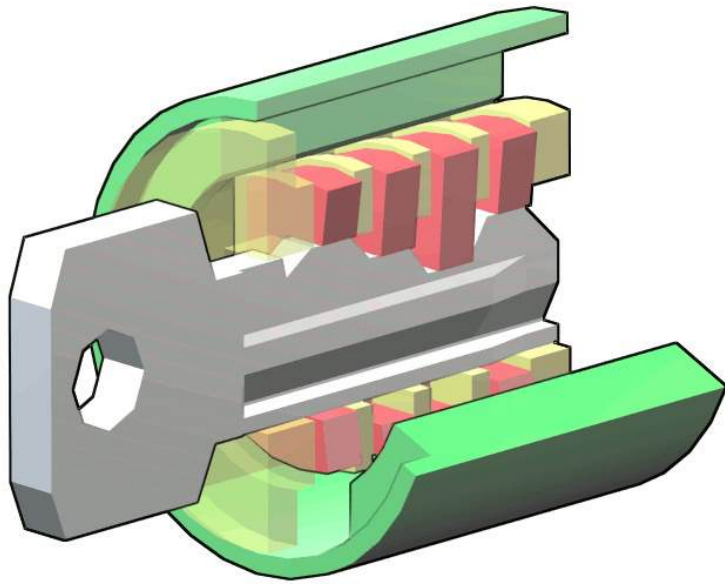
Tertiary protein  
structure

Sequence → Structure → Function

L G C V L A W N T N S K

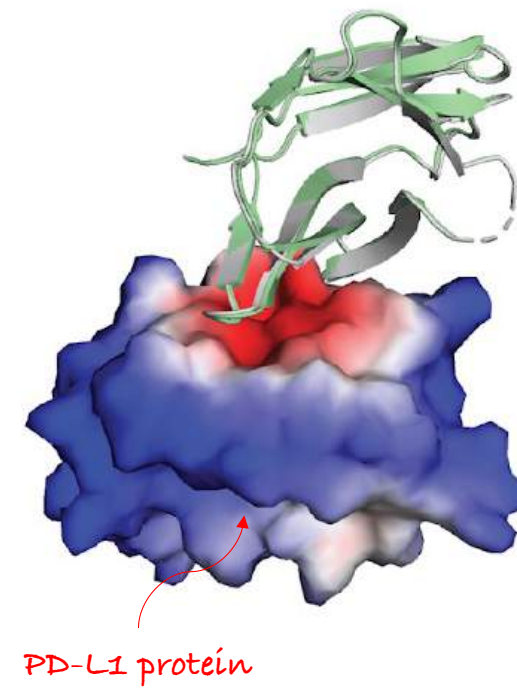
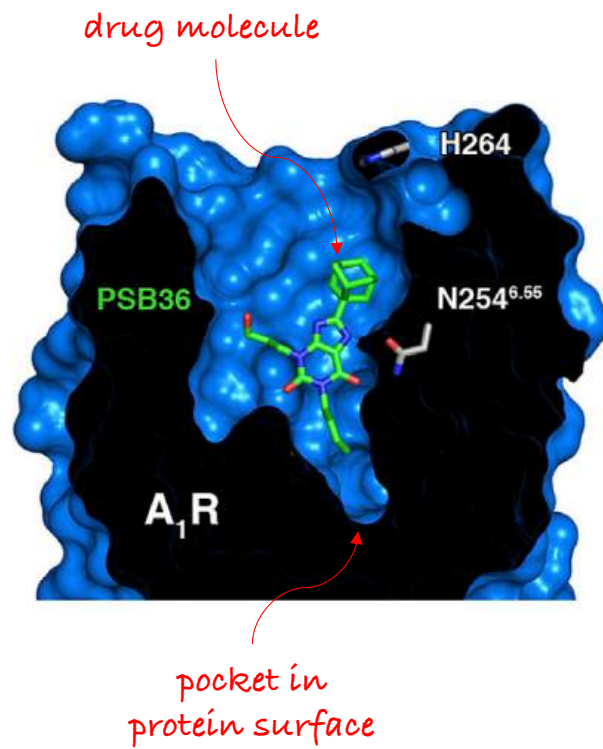


## *Lock-Key Metaphor*

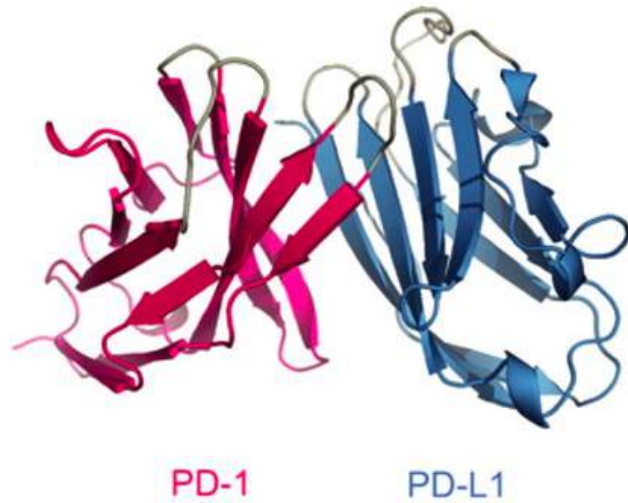


Emil Fischer "Schlüssel-Schloss-Prinzip" 1894

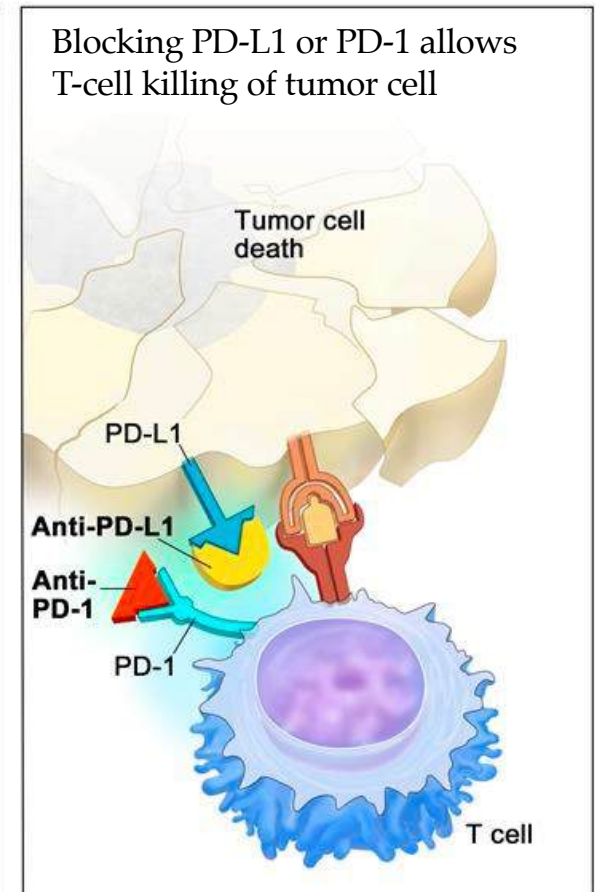
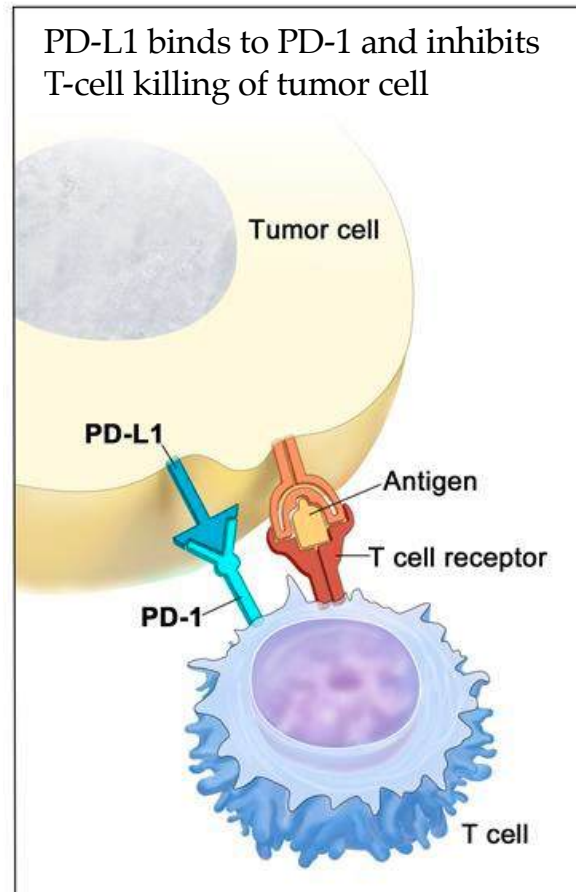
# Biologic Drug Design



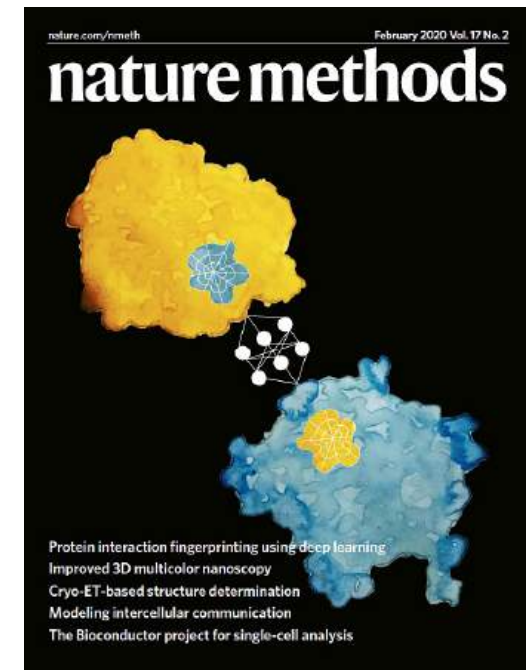
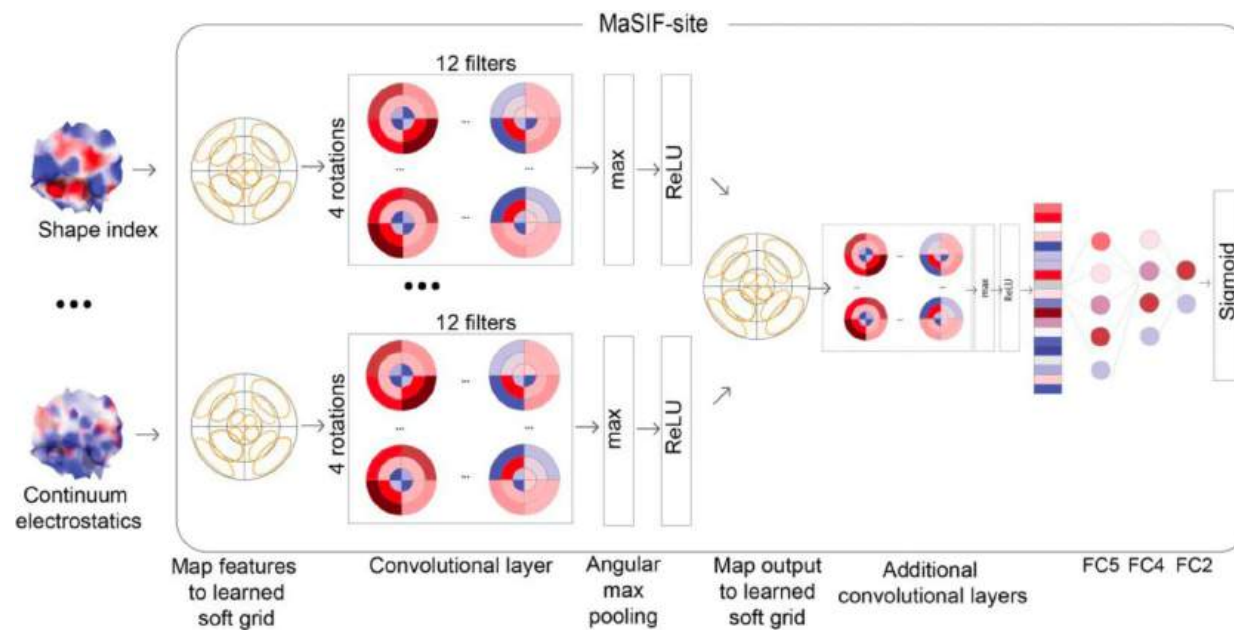
# Immunotherapy



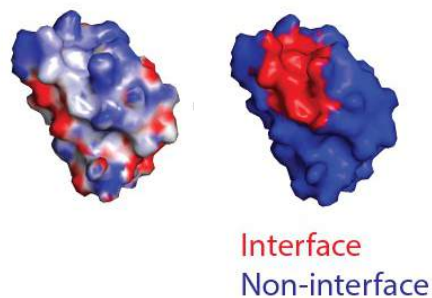
2018 Nobel Prize  
PD-proteins role in  
immunotherapy



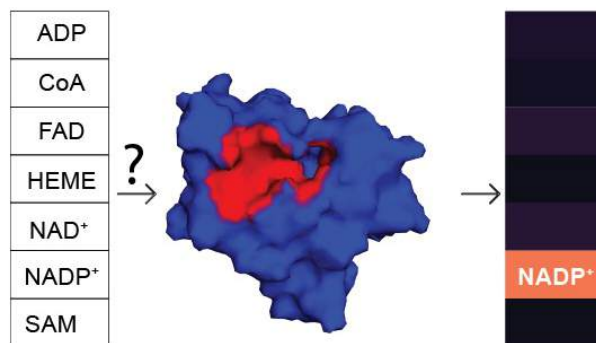
# *MaSIF: Geometric ML for Protein Function Prediction*



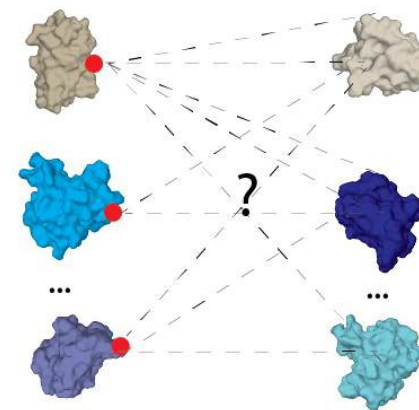
# *MaSIF Applications*



Interface site prediction  
**MaSIF-site**



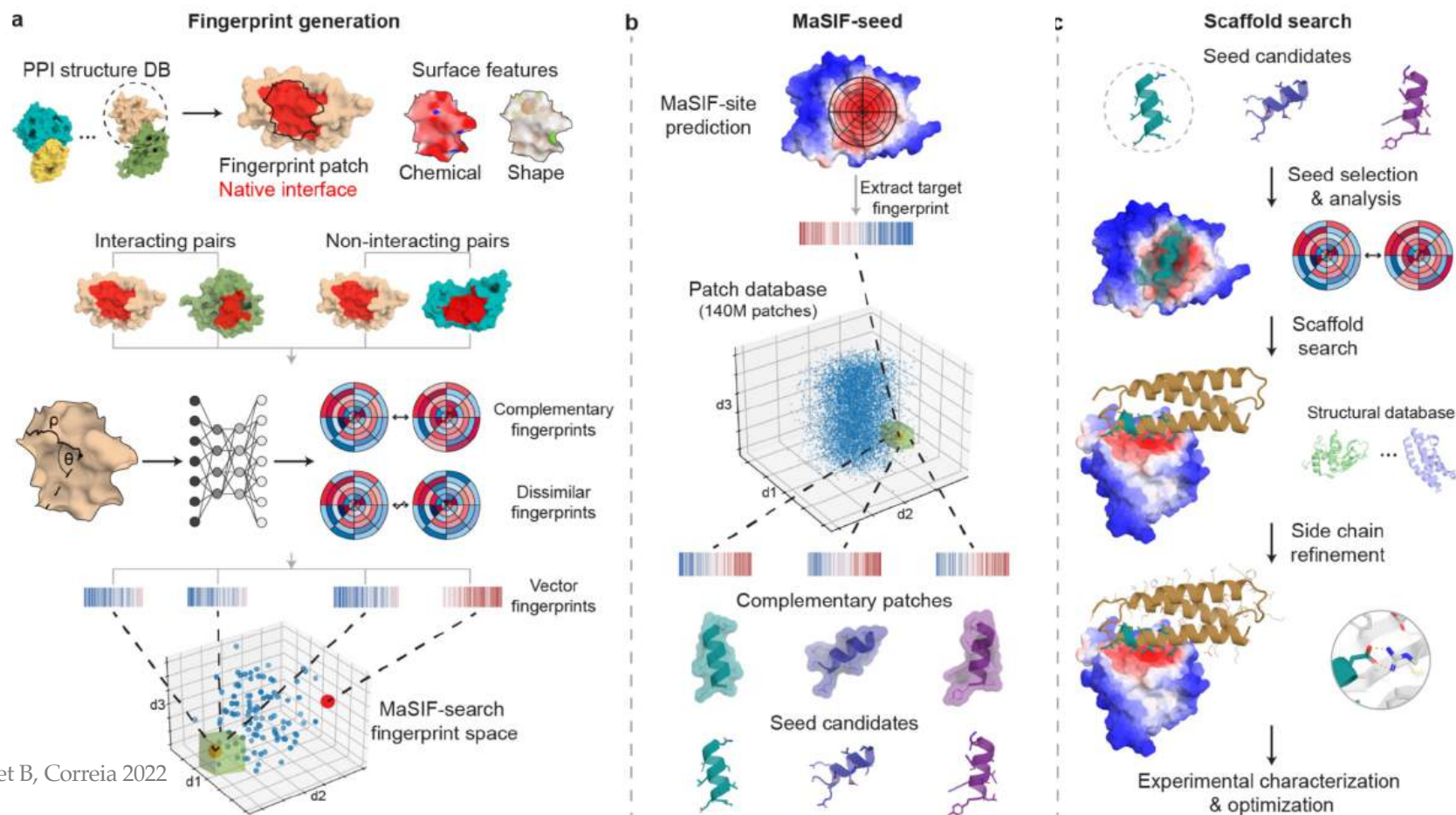
Pocket classification  
**MaSIF-ligand**



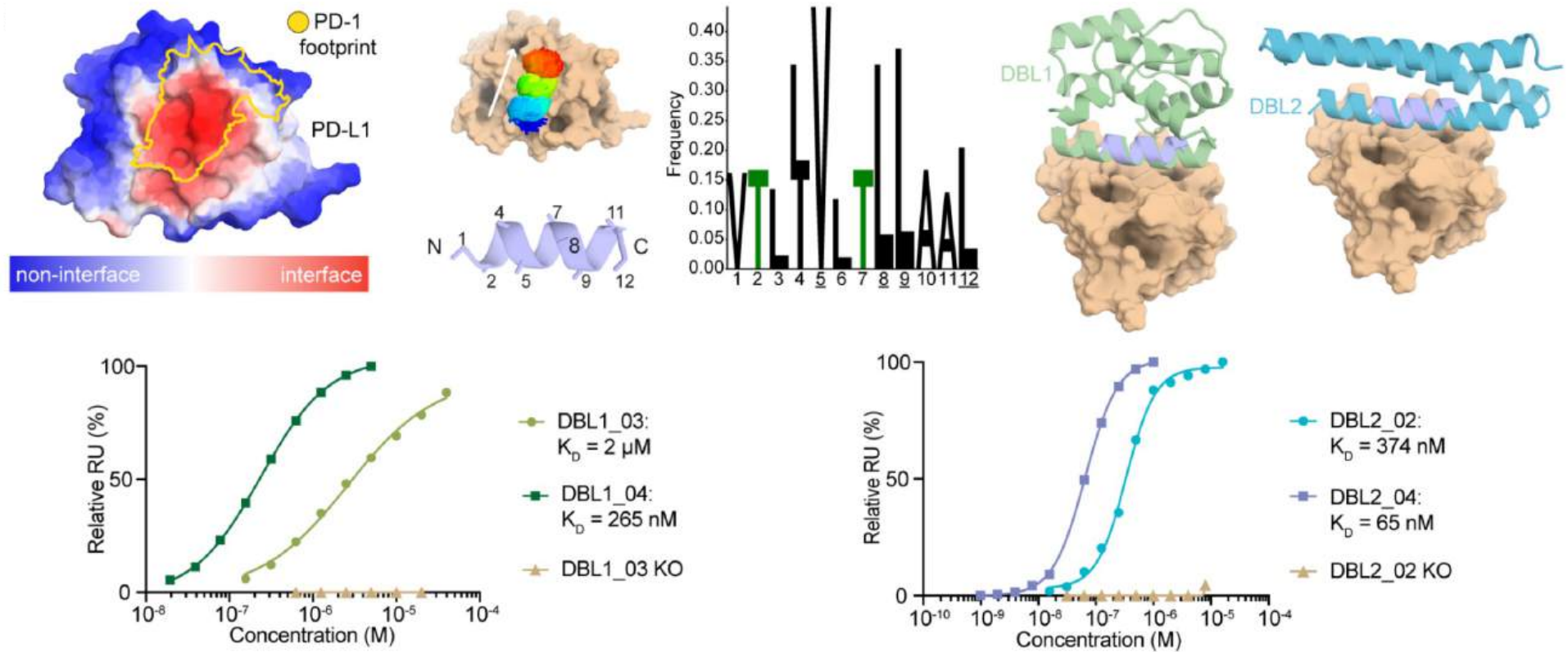
Fast PPI search  
**MaSIF-search**



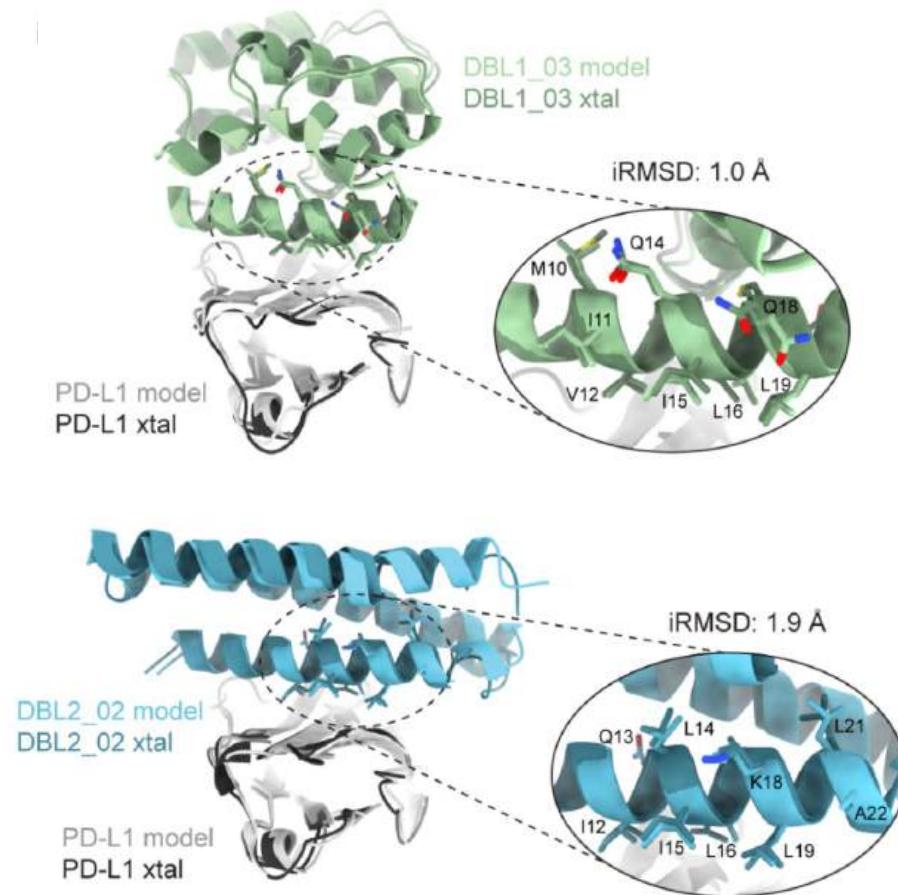
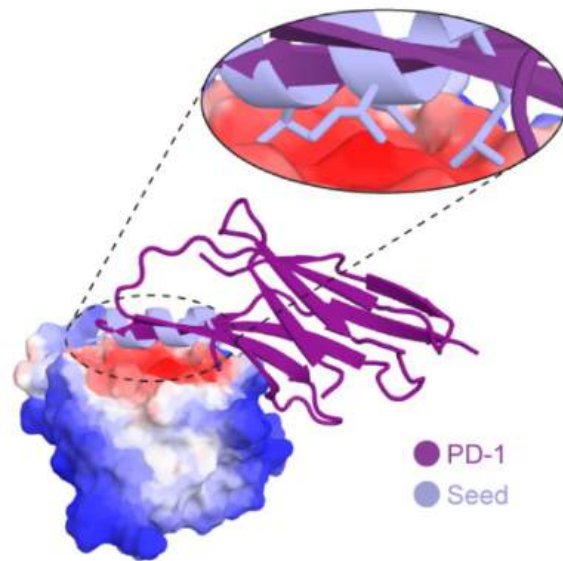
# *De novo protein design with MaSIF*



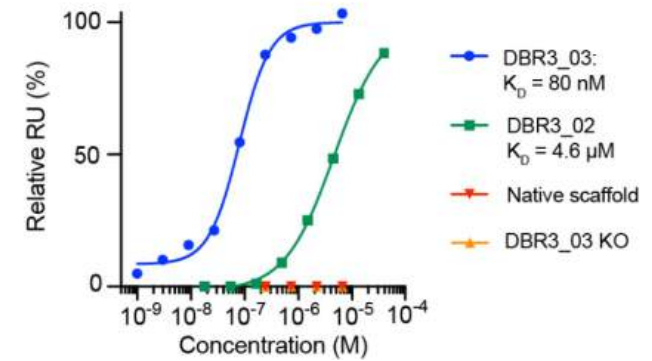
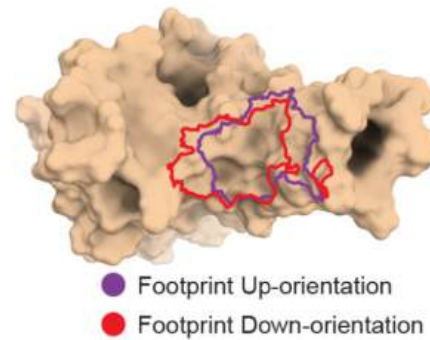
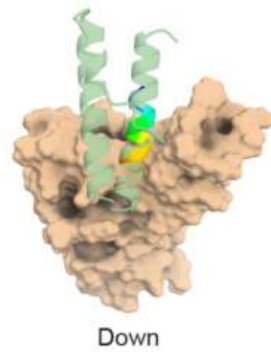
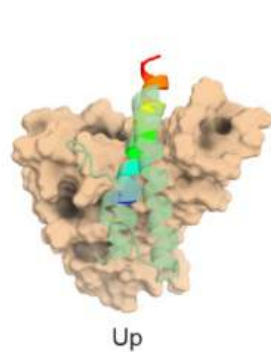
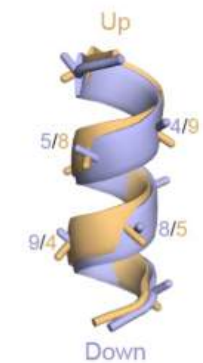
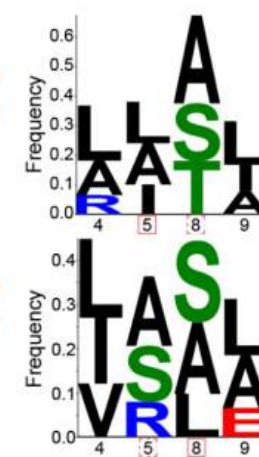
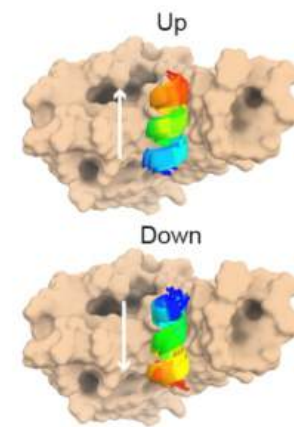
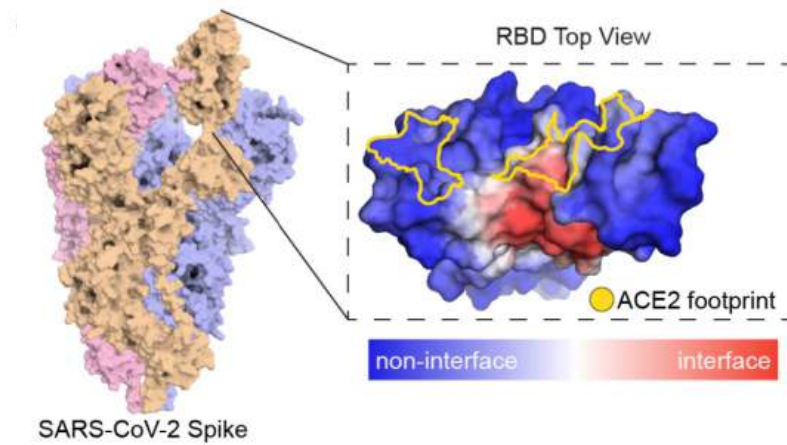
# PD-L1 binder design



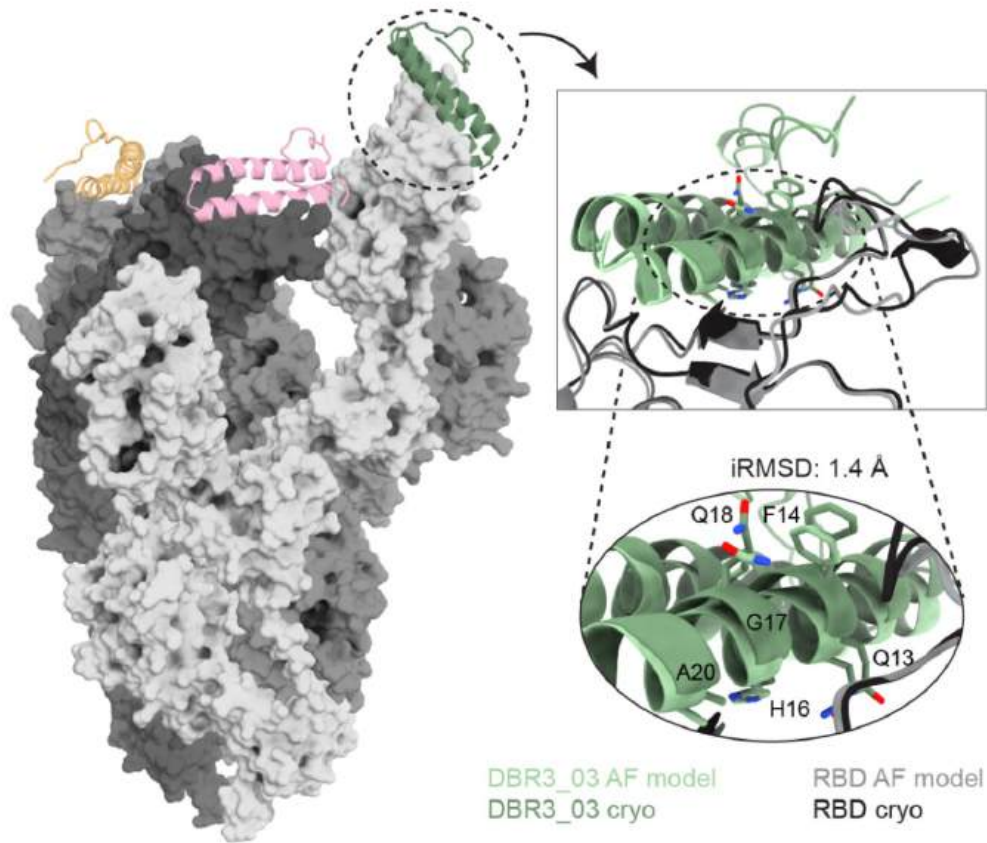
## *PD-L1 binder structure*



# *SARS-CoV-2 spike binder design*



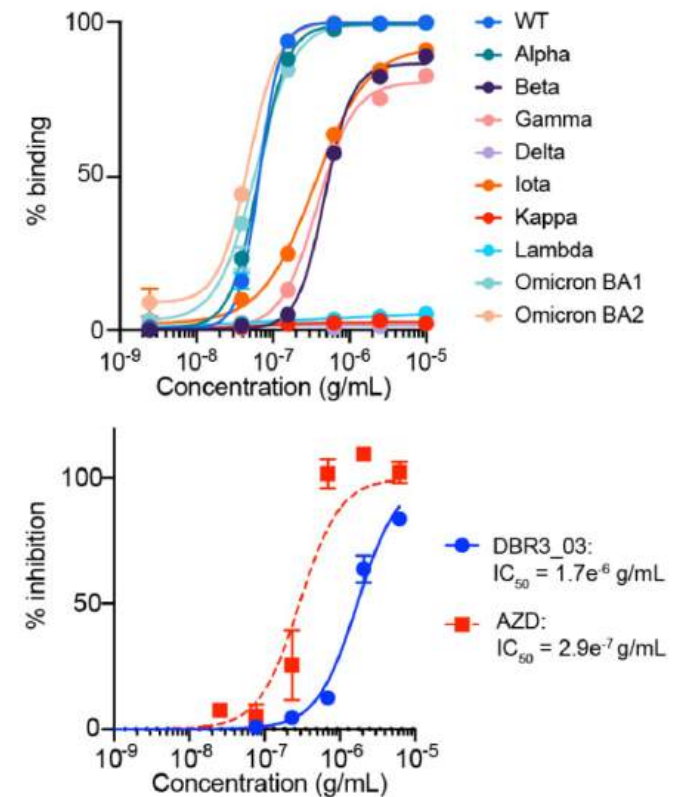
# *SARS-CoV-2 spike binder function*



Gainza et B, Correia 2022

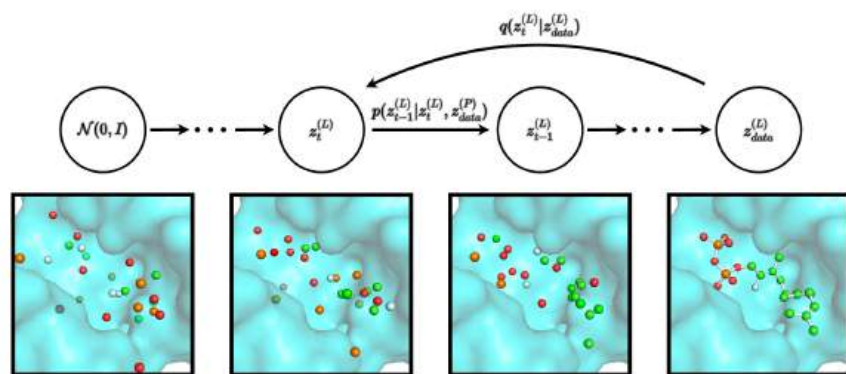
Structure

## Binding spike protein in multiple virus variants



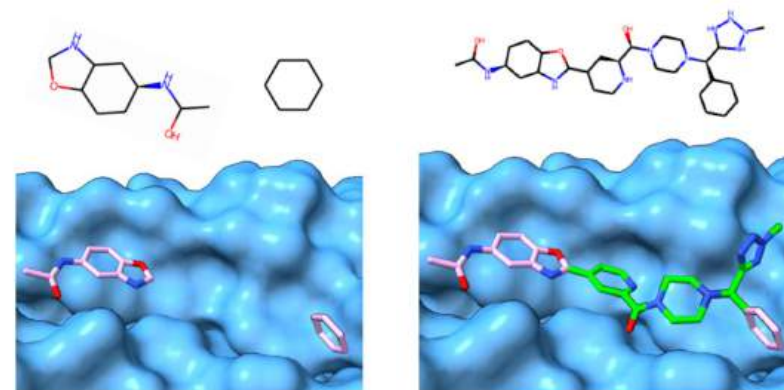
Pseudovirus neutralisation

# Structure-Based Drug Design



Equivariant diffusion model conditioned on target pocket 3D structure

Schneuing et B, Welling, Correia 2022



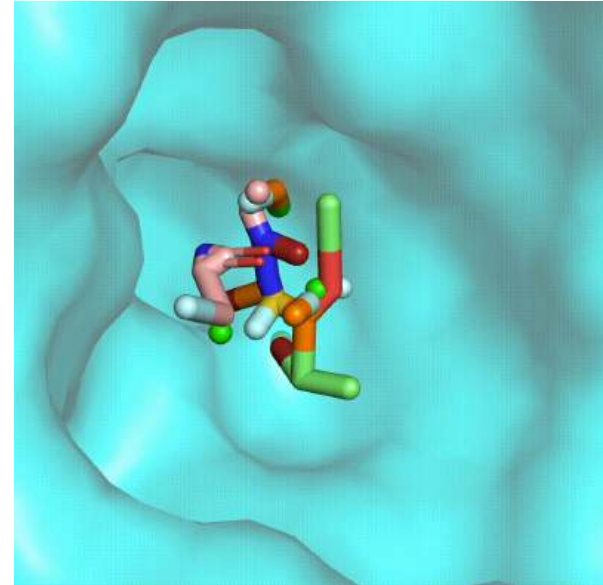
DiffLinker: Impainting of molecular fragments conditioned on target pocket

Igashov et B, Welling, Correia 2022



“Painting of an astronaut riding a dog on the Moon”

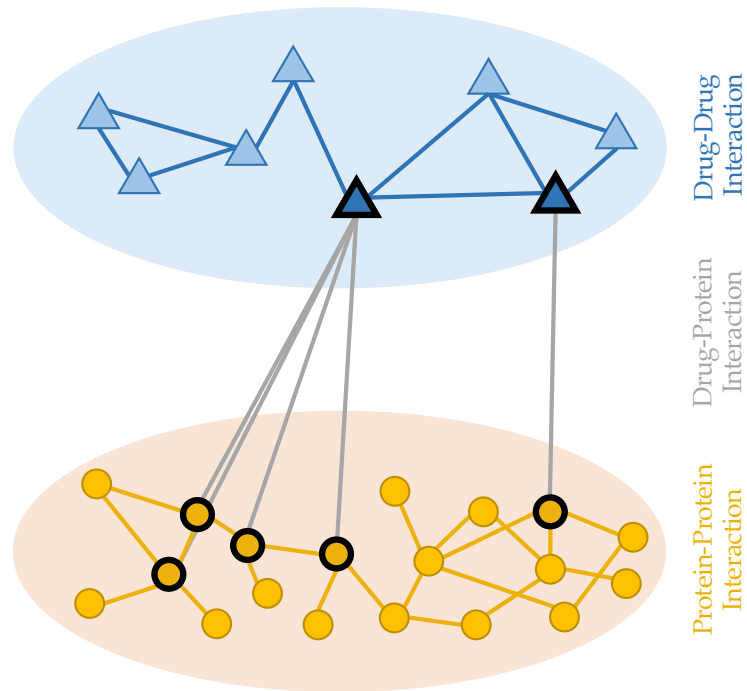
DALL-E 2023 (prompt by B)



“Drug-like molecule binding a protein pocket”

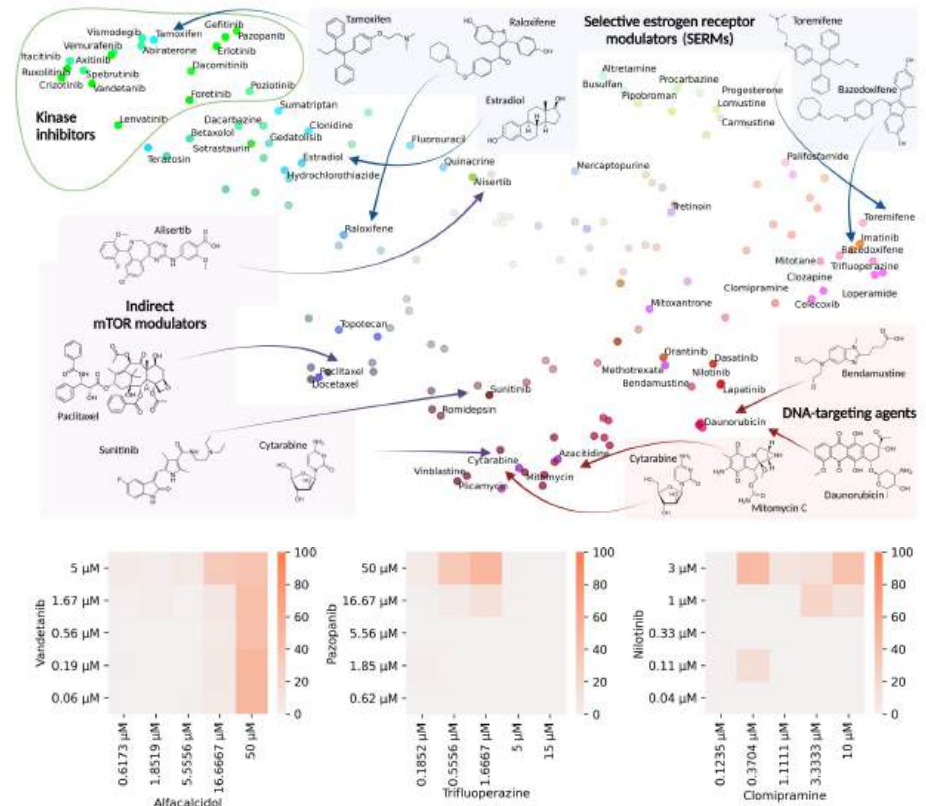
Schneuing et Welling, B, Correia 2022

# Drug Repositioning



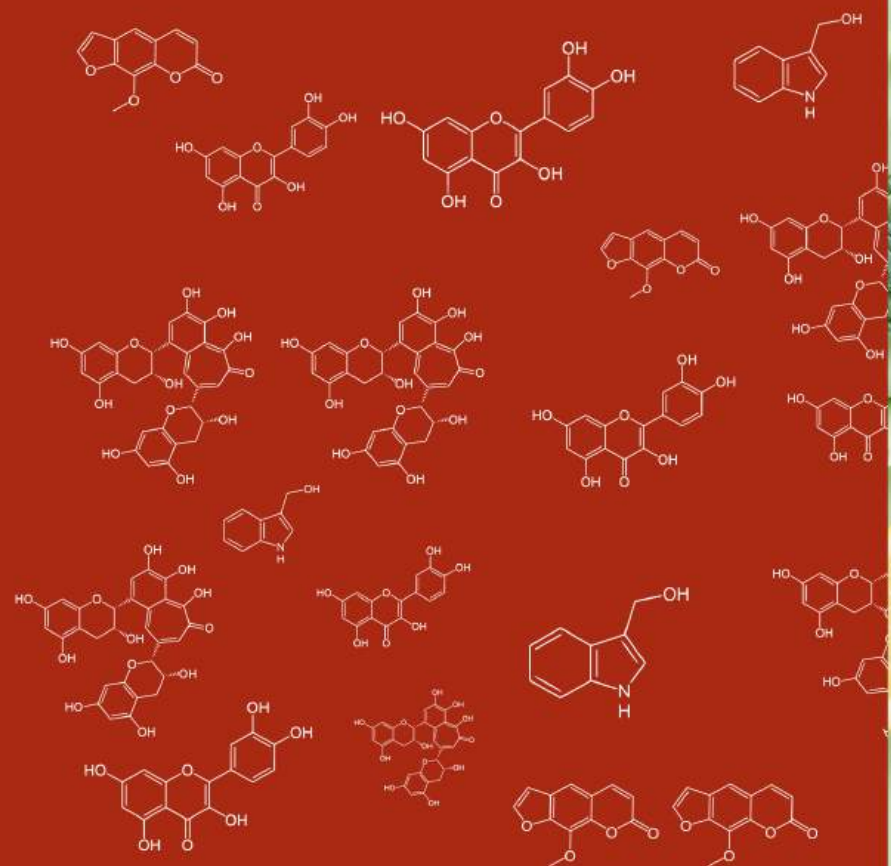
Drug side effect prediction

Zitnik et al. 2018



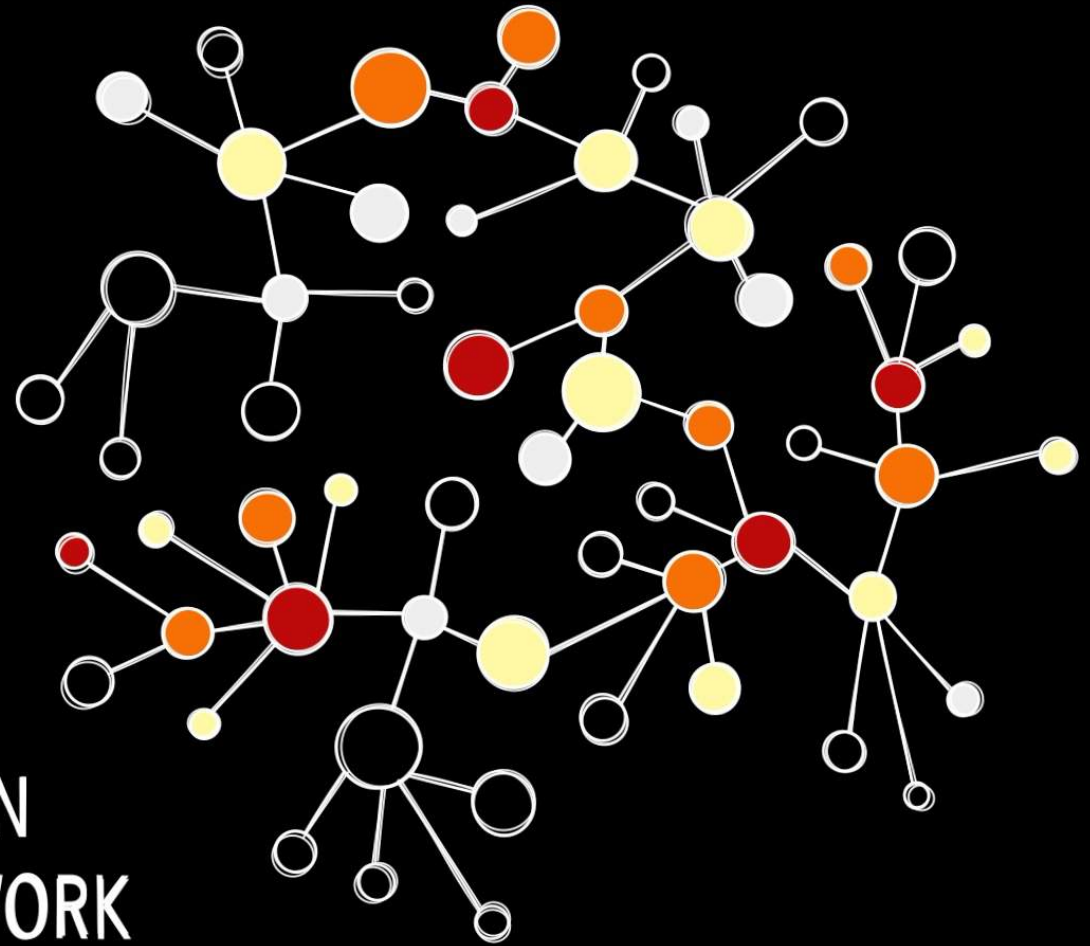
Drug synergy prediction

Bertin et B, Bengio 2021 (RECOVER & Gates Foundation)



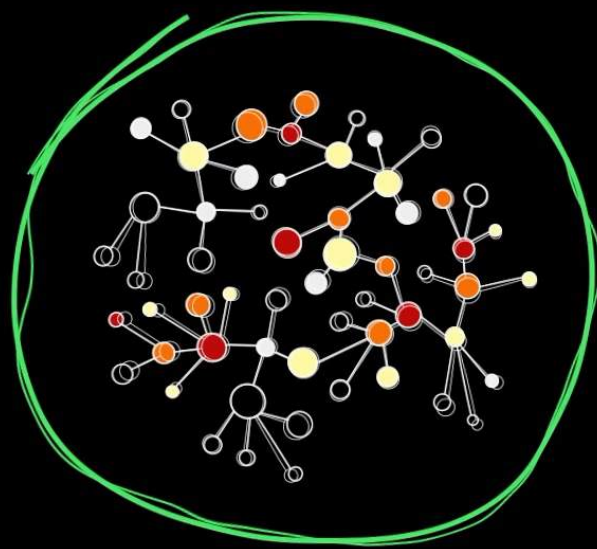
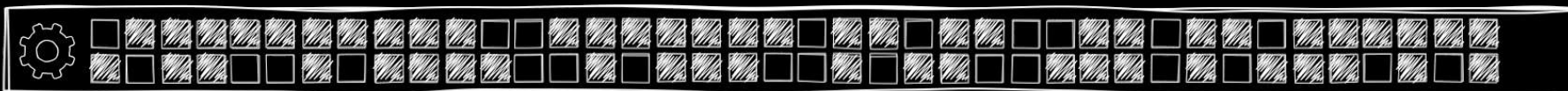


*Hyperfoods*

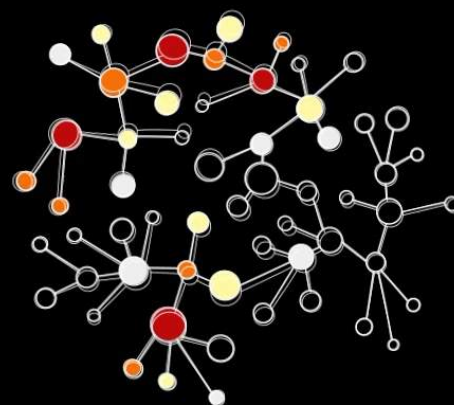


# PROTEIN-PROTEIN INTERACTION NETWORK

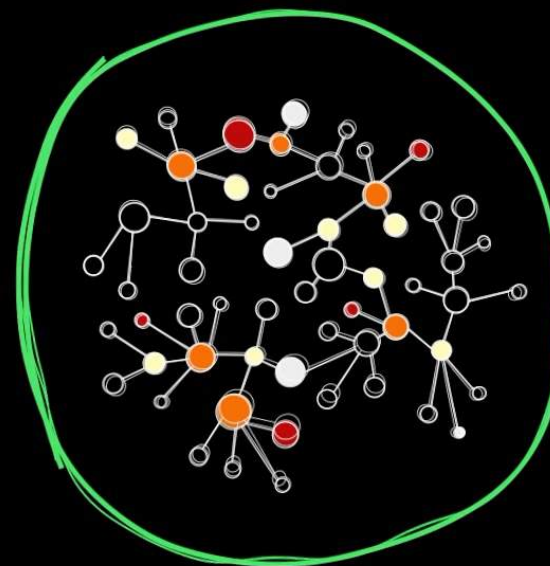
Veselkov et B 2019



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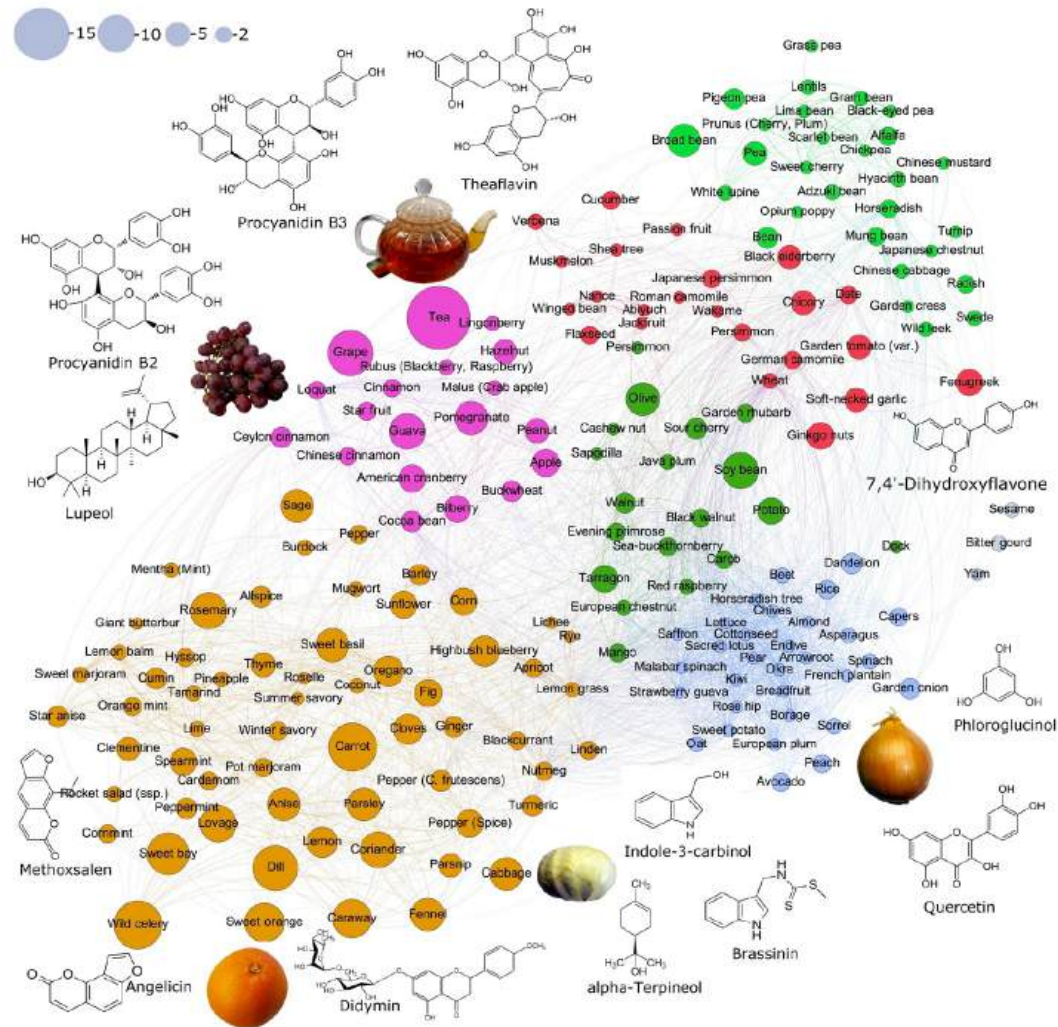


non ANTICANCER



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# Hyperfoods



Video: Vodafone Foundation / Recipes: Bruno Barbieri  
Based on Laponogov et B 2020

“The knowledge of certain principles easily  
compensates the lack of knowledge of certain facts”

—Claude Adrien Helvétius



Thank you!