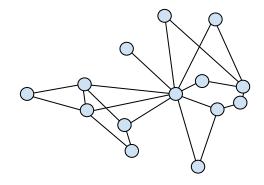




Graph Neural Networks Algorithmic Alignment & Necessity





Article

A Deep Learning Approach to Antibiotic Discovery

Cell

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About 9'650 results (0.36 seconds)

() The Guardian

Powerful antibiotic discovered using machine learni... first time

Tests on bacteria collected from patients showed that halicin killed Mycobacterium tuberculosis, the bug that causes TB, and strains of



Q

20 Feb 2020

Nature

Powerful antibiotics discovered using AI Proton block. Antibiotics work through a range of mechanisms, such as blocking the enzymes involved in cell-wall biosynthesis, DNA repair or ... 20 Feb 2020



MIT News

Artificial intelligence yields new antibiotic

Preliminary studies suggest that halicin kills bacteria by disrupting their ability to maintain an electrochemical gradient across their cell

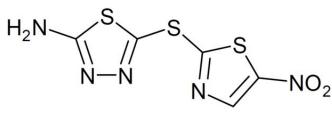
20 Feb 2020

Analytics Insight

Halicin: Enter Al Based Drugs To Fight Drug-Resistan..

This promising candidate is Halicin, a drug being explored for treating diabetes. Initially, it was identified as c-lun N-terminal kinase





Halicin

MLP is all you need?

Theorem 4.1.1 (universal approximation theorem):

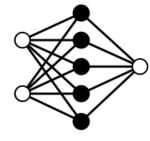
An arbitrary continuous function, defined on [0,1] can be arbitrary well uniformly approximated by a multilayer feed-forward neural network with one hidden layer (that contains only finite number of neurons) using neurons with arbitrary activation functions in the hidden layer and a linear neuron in the output layer. Formally:

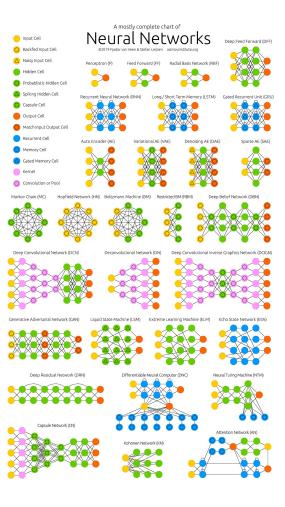
Let $\varphi(.)$ be the arbitrary activation⁵ function. Then $\forall f \in C([0,1]), \forall \varepsilon > 0: \exists n \in \mathbb{N}, w_i, a_i, b_i \in \mathbb{R}, i \in \{0...n\}$:

$$(A_n f)(x) = \sum_{i=1}^n w_i \varphi(a_i x + b_i)$$

as an approximation of the function f(.); that is

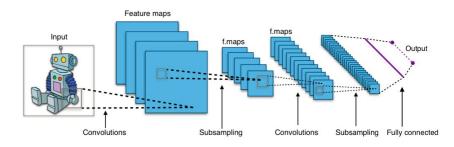
$$\sup_{x \in [0,1]} |(A_n f)(x) - f(x)| < \varepsilon$$

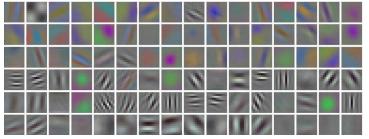




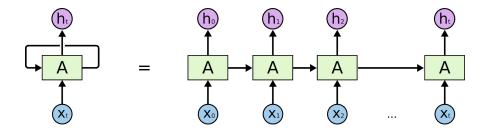
MLP is all you need? No!

• Inductive bias for Images: Convolutions





• Inductive bias for Time Series: Hidden states



MLP is all you need? No!

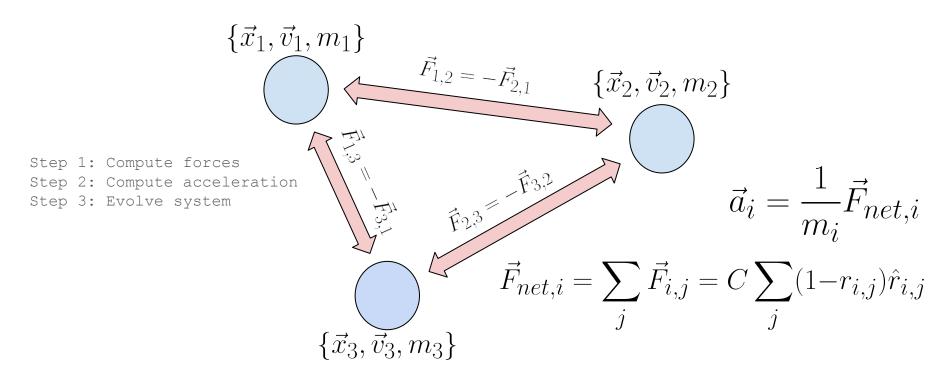
• Prior distribution

$$p(\theta|X) = \frac{p(X|\theta)p(\theta)}{p(X)}$$

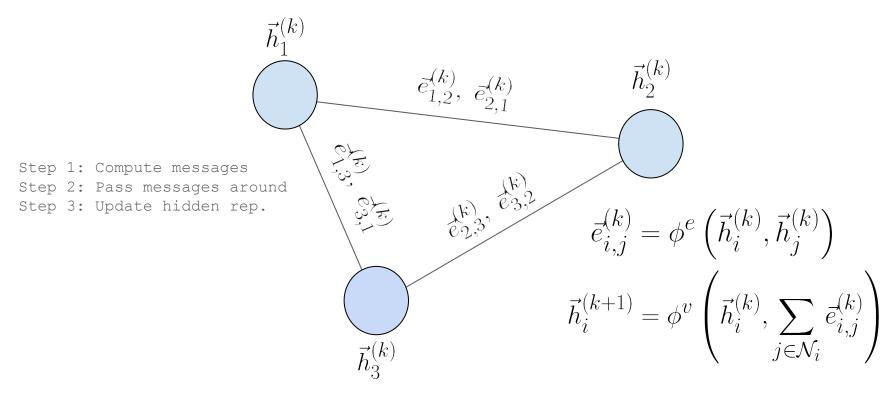
• Ridge / Lasso regularization

$$\mathcal{L} = \mathcal{L}\left(Y, f_{\theta}(X)\right) + \lambda \|\theta\|_{p}$$

Example: Particle Physics - Predict particle movement



Example: Particle Physics - Predict particle movement

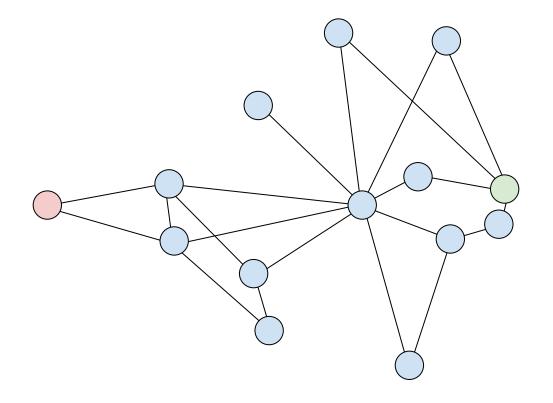


Example: Particle Physics - Predict particle movement

| Physics | GNNs |
|--|------------------------------------|
| Particle $\{ec{x_1},ec{v_1},m_1\}$ | Node $ec{h}_1^{(k)}$ |
| Force $ec{F_{i,j}}$ | Edge / message $ec{e}_{i,j}^{(k)}$ |
| Gravitation $(1\!-\!r_{i,j})\hat{r}_{i,j}$ | Edge model ϕ^e |
| Net force $\sum \bar{F}_{,j}$ | Aggregation $\sum f_{i,j}^{(k)}$ |
| Acceleration $\widetilde{a_i}$ | Node model ϕ^v |

Message passing framework: Algorithmic alignment with physical task

Example: Graph Algorithms





| for k = 1 ISI - 1: | |
|--|--|
| for u in S: | |
| d[k][u] = min _v d[k-1][v] + cost (v, u) | |

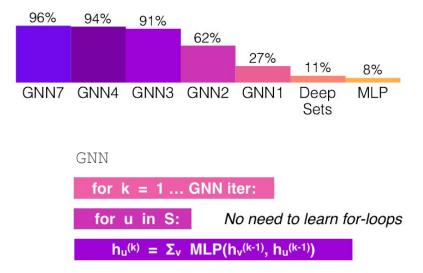
GNN



 $h_{u}^{(k)} = \Sigma_{v} MLP(h_{v}^{(k-1)}, h_{u}^{(k-1)})$

Example: Graph Algorithms





Can we mathematically define Algorithmic Alignment?

Definition 1.1 (PAC learning and sample complexity). Fix an error parameter $\epsilon > 0$ and failure probability $\delta \in (0,1)$ Suppose $\{x_i, y_i\}_{i=1}^{M}$ are i.i.d. samples from some distribution \mathcal{D} , and the data satisfies $y_i = g(x_i)$ for some underlying function g. Let $f = \mathcal{A}(\{x_i, y_i\}_{i=1}^{M})$ be the function generated by a learning algorithm \mathcal{A} . Then g is (M, ϵ, δ) -learnable with \mathcal{A} if

$$\mathbb{P}_{x \sim \mathcal{D}}\left[\|f(x) - g(x)\| \le \epsilon\right] \ge 1 - \delta.$$

The sample complexity $\mathcal{C}_{\mathcal{A}}(g,\epsilon,\delta)$ is the minimum M so that g is (M,ϵ,δ) -learnable with \mathcal{A} .

Can we mathematically define Algorithmic Alignment?

Definition 1.2 (Algorithmic alignment). Let g be a reasoning function and \mathcal{N} a neural network with n modules \mathcal{N}_i . The module functions $f_1, ..., f_n$ generate g for \mathcal{N} if, by replacing \mathcal{N}_i with f_i , the network \mathcal{N} simulates g. Suppose $\{x_i, y_i\}_{i=1}^M$ are i.i.d. samples from some distribution \mathcal{D} , and the data satisfies $y_i = g(x_i)$. Then \mathcal{N} (M, ϵ, δ) -algorithmically aligns with g if (1) $f_1, ..., f_n$ generate g and (2) there are learning algorithms \mathcal{A}_i for the \mathcal{N}_i 's such that

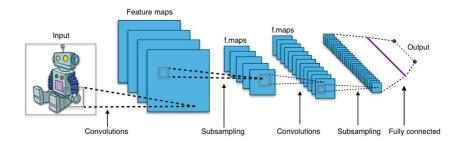
 $n \cdot \max_i C_{\mathcal{A}_i}(f_i, \epsilon, \delta) \leq M.$



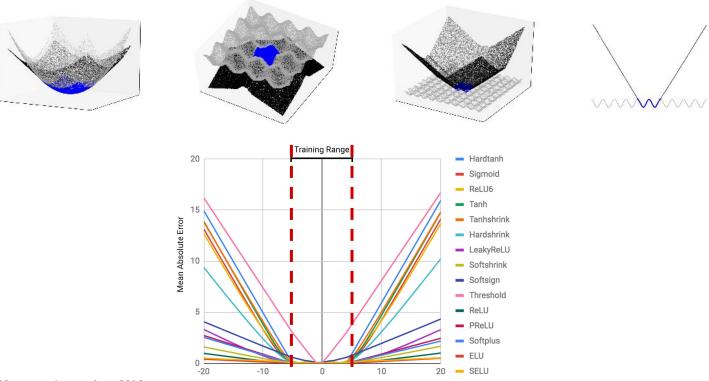
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$$n \cdot \max_i \mathcal{C}_{\mathcal{A}_i}(f_i, \epsilon, \delta) \le M.$$



When can GNNs extrapolate?



When can GNNs extrapolate?

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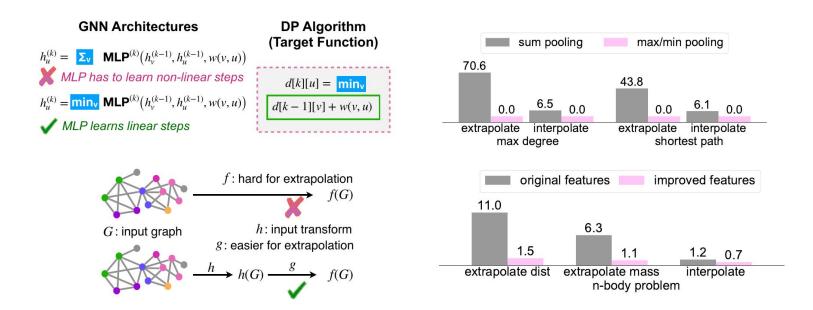
$$n \cdot \max_i \mathcal{C}_{\mathcal{A}_i}(f_i, \epsilon, \delta) \leq M.$$

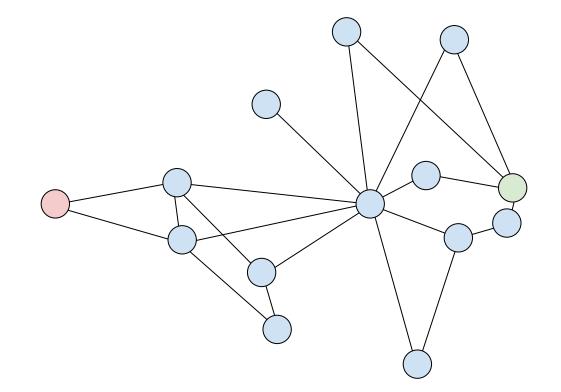
"easy to learn" = sample complexity grows **polynomial** = good **interpolation**

good **extrapolation** = algorithm steps can be represented by **linear** functions via MLP

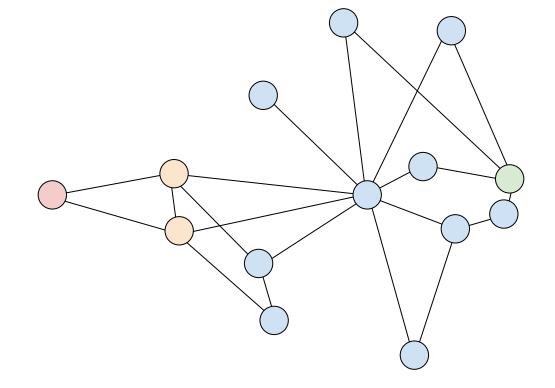
When can GNNs extrapolate?

good **extrapolation** = algorithm steps can be represented by **linear** functions via MLP

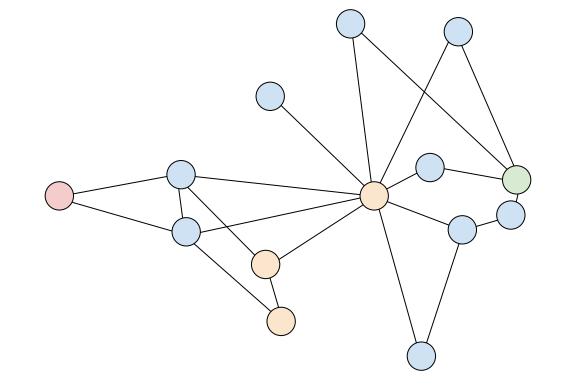




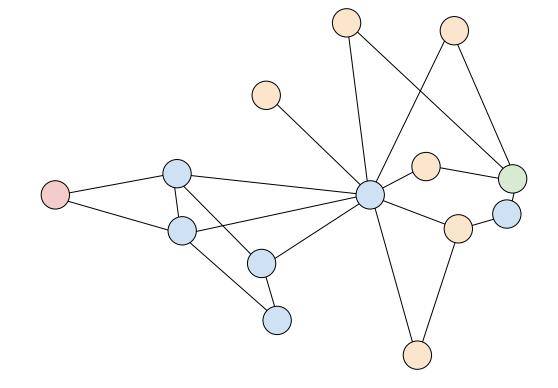
1 hop



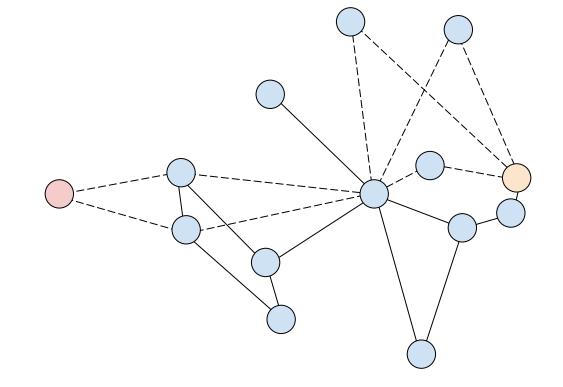
2 hops



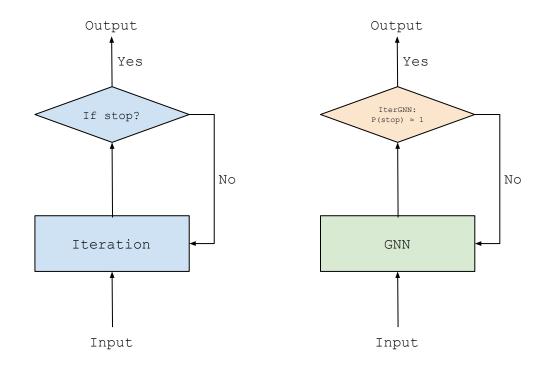
3 hops



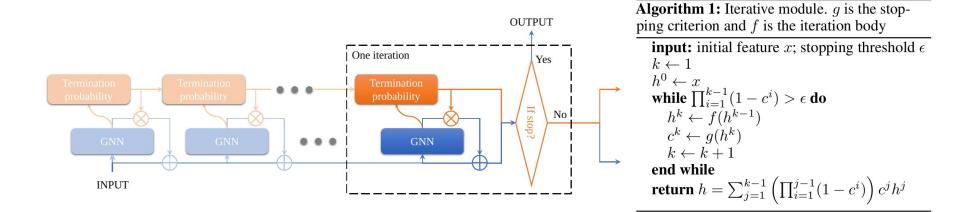
4 hops



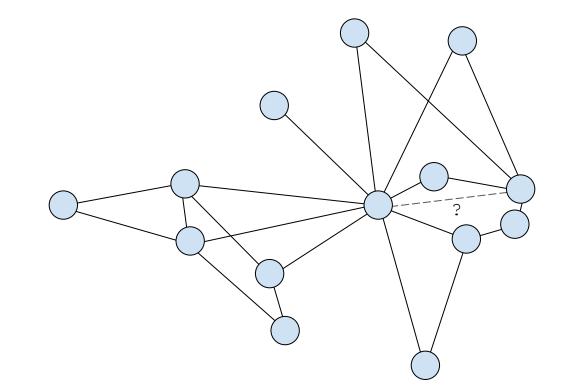
Idea: Learn termination with IterGNN



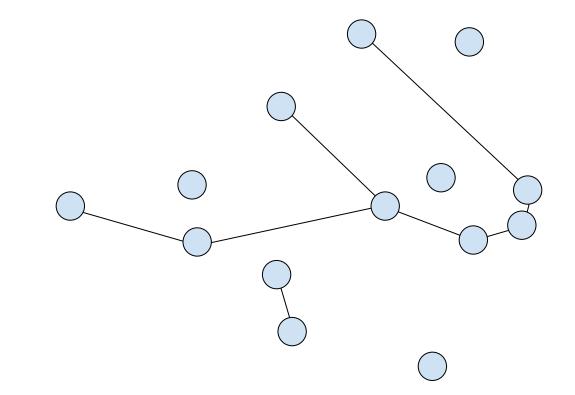
Idea: Learn termination with IterGNN



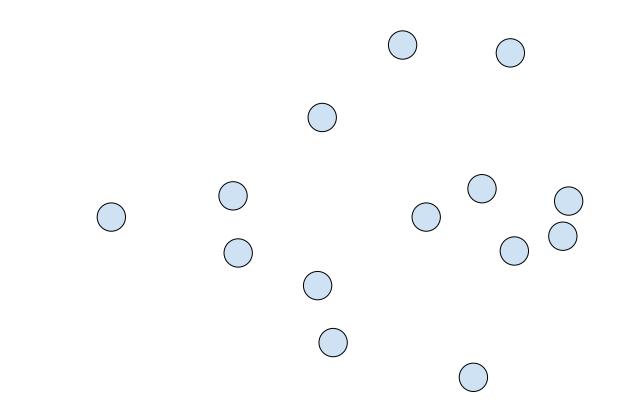
Static graph structure



Static graph structure



Static graph structure



How to overcome static graph structure?

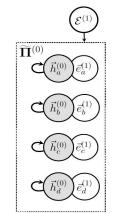
Idea: Augment the graph with dynamic edges

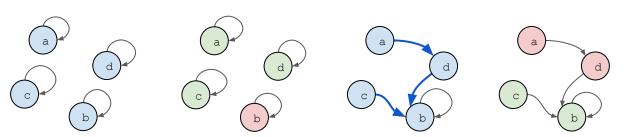
(1) encode entity representations

(2) compute new hidden representations(3) decode answer

(4) calc pointer mask

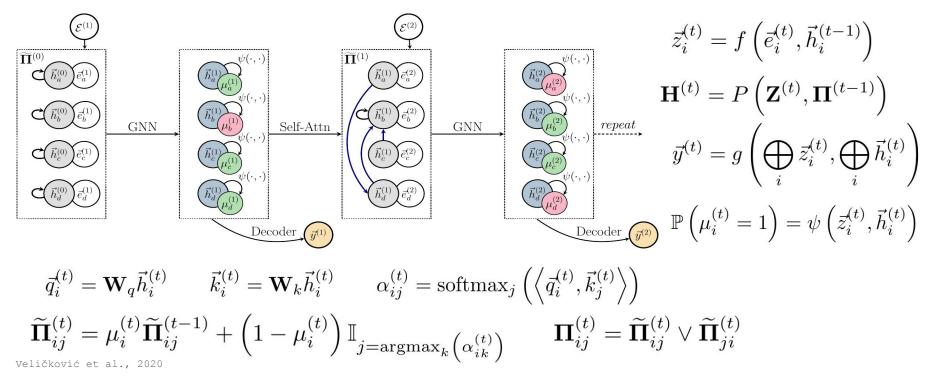
(5) re-estimate pointer via self-attention





How to overcome static graph structure?

Idea: Augment the graph with inferred edges



When not to use GNNs?



When *should* we use GNNs?

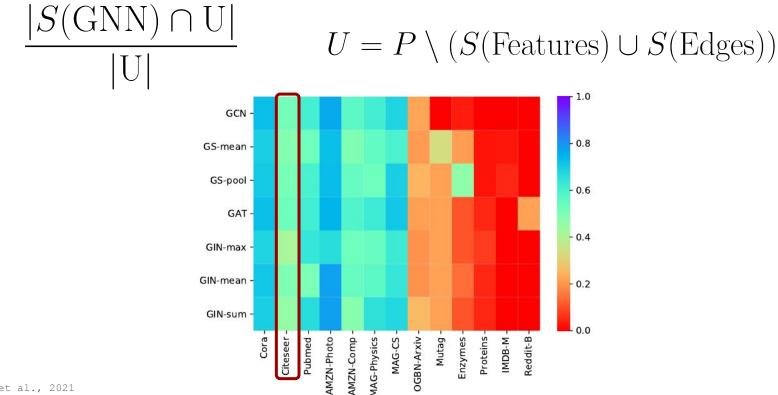
 $S = \{ p \in P | M \text{ solves } p \}$

"better than random guessing"

$$\text{ForE} = \frac{|S(\text{Edges}) \cup S(\text{Features})|}{|P|}$$

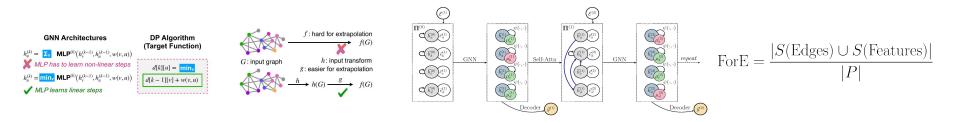
| Dataset | Features | Edges | $\mathbb{E}(FandE)$ | FandE | ForE | GNN |
|-------------|----------|-------|---------------------|-------|-------|-------|
| Cora | 0.586 | 0.346 | 0.203 | 0.192 | 0.74 | 0.828 |
| Citeseer | 0.544 | 0.412 | 0.224 | 0.235 | 0.721 | 0.699 |
| Pubmed | 0.693 | 0.407 | 0.282 | 0.246 | 0.854 | 0.779 |
| AMZN-Photo | 0.777 | 0.286 | 0.222 | 0.172 | 0.891 | 0.909 |
| AMZN-Comp | 0.652 | 0.391 | 0.255 | 0.235 | 0.808 | 0.809 |
| MAG-Physics | 0.915 | 0.507 | 0.464 | 0.475 | 0.947 | 0.949 |
| MAG-CS | 0.924 | 0.136 | 0.126 | 0.129 | 0.932 | 0.933 |
| OGBN-Arxiv | 0.658 | 0.411 | 0.271 | 0.281 | 0.788 | 0.726 |
| Mutag | 0.45 | 0.55 | 0.248 | 0.45 | 0.55 | 0.55 |
| Enzymes | 0.4 | 0.333 | 0.133 | 0.2 | 0.533 | 0.65 |
| Proteins | 0.607 | 0.643 | 0.39 | 0.607 | 0.643 | 0.616 |
| IMDB-M | 0.26 | 0.293 | 0.076 | 0.24 | 0.313 | 0.287 |
| Reddit-B | 0.76 | 0.775 | 0.589 | 0.76 | 0.775 | 0.77 |

When *should* we use GNNs?



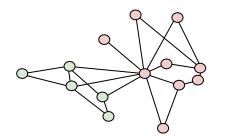
Faber et al., 2021

Famous last words

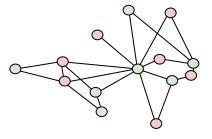


architectural overfitting to characteristics of evaluation data

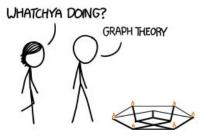
graph homophily

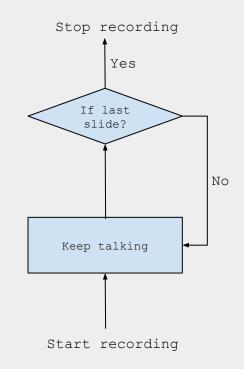


graph heterophily



Thank you for your attention! Looking forward to the discussion!





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