Modeling Graph Structures: Graph Isomorphism and GNN

2022/09/23

Li Peng-Hsuan

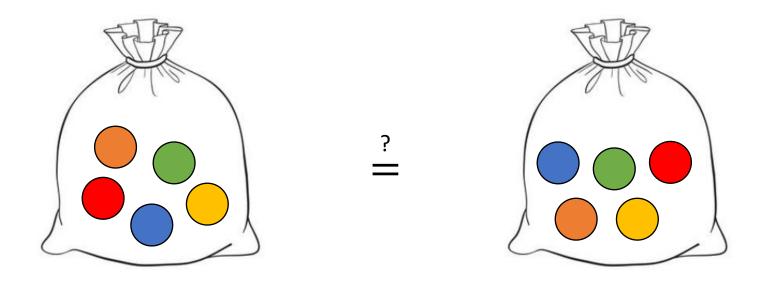
Items

- (-2019) Graph Isomorphism, Weisfeiler-Leman, and GNN
- (-2021) Beyond Weisfeiler-Leman: Heuristic and Theoretical Approaches
- (2022) A Sound Heuristic: Hierarchy of Local Isomorphism and GraphSNN

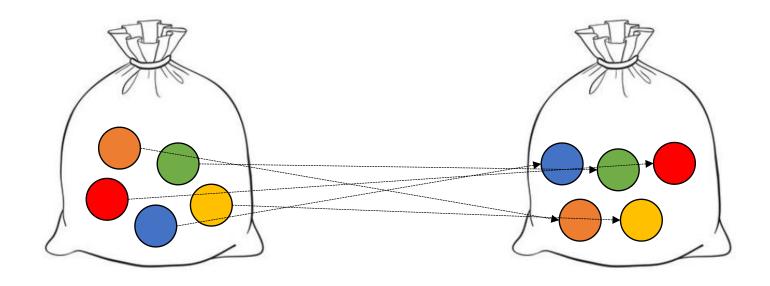
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Comparing Sets

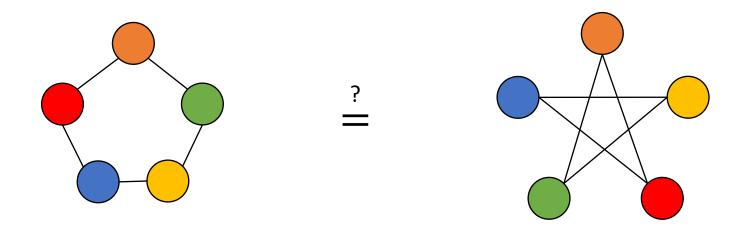


The Same Set



"=": a bijective mapping s.t. member labels are preserved

Comparing Graphs



Graph Isomorphism



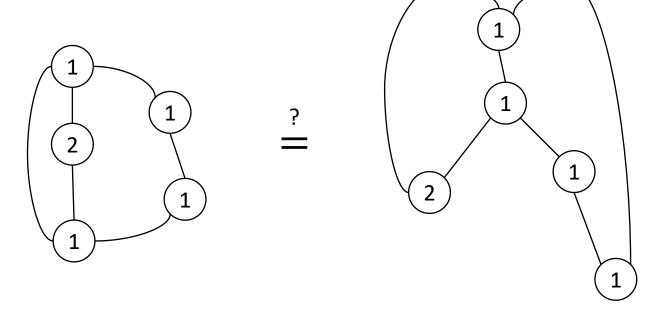
"=": a bijective mapping s.t. nodes (labels), edges (labels) are preserved

Graph Isomorphism Test

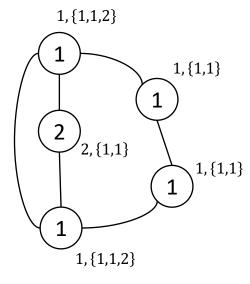
- Complexity
 - NP-completeness not known
 - The current algorithm with the best claim:

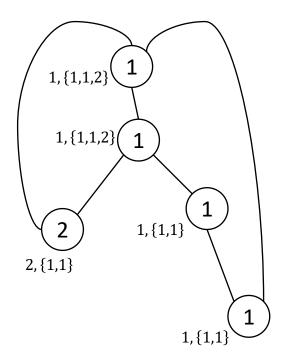
• Quasi-polynomial time $2^{O((\log n)^c)}$ with c=3

Original

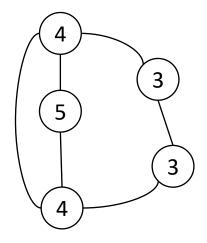


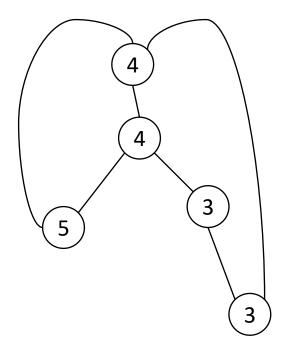
Collect neighbor



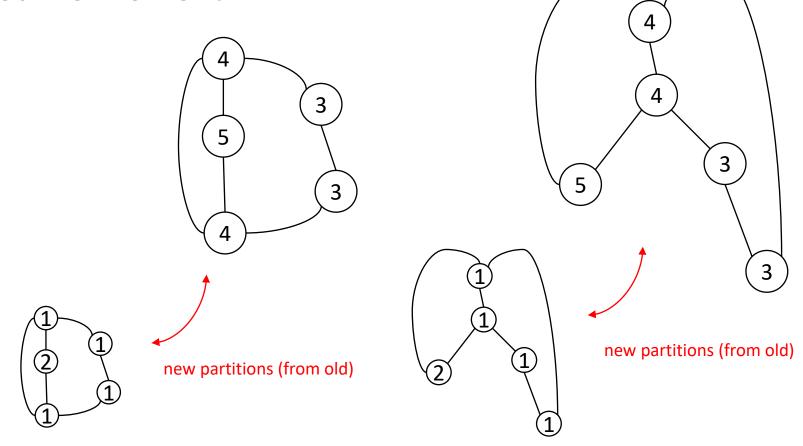


• Re-label

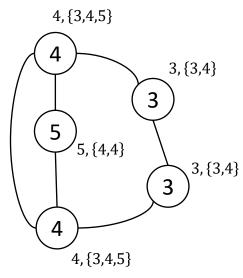


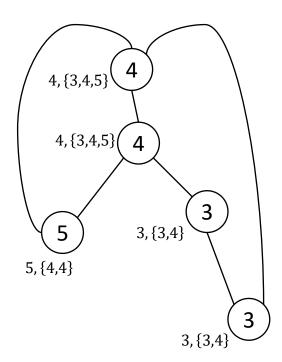


Check refinement

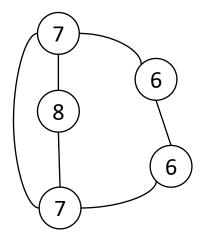


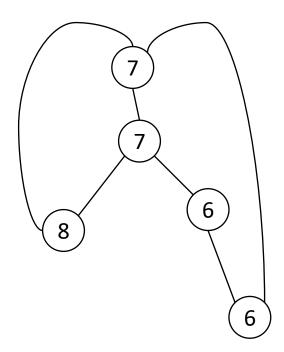
Collect neighbor



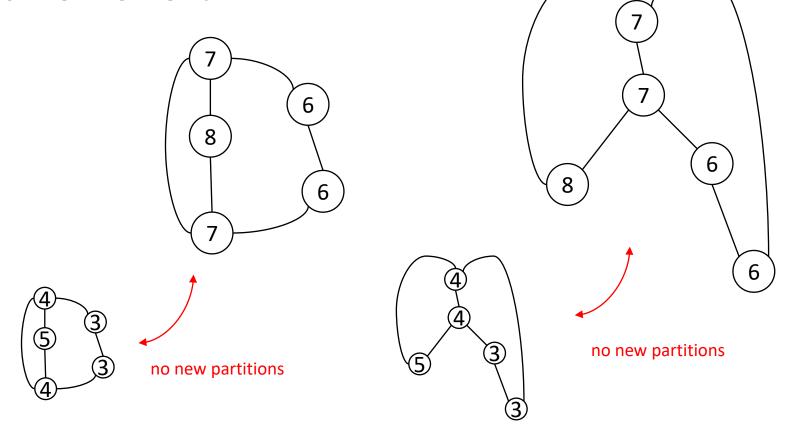


• Re-label

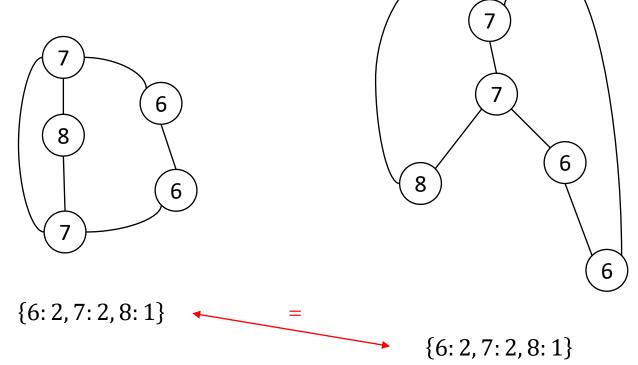




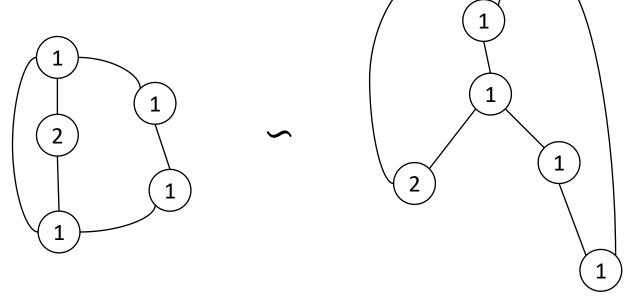
Check refinement



Count final labels



• Result: not discriminated



- Very fast
 - 0(n + e)
- Sound
 - Isomorphic graphs won't be discriminated
- Incomplete
 - Some non-isomorphic graphs are not discriminated

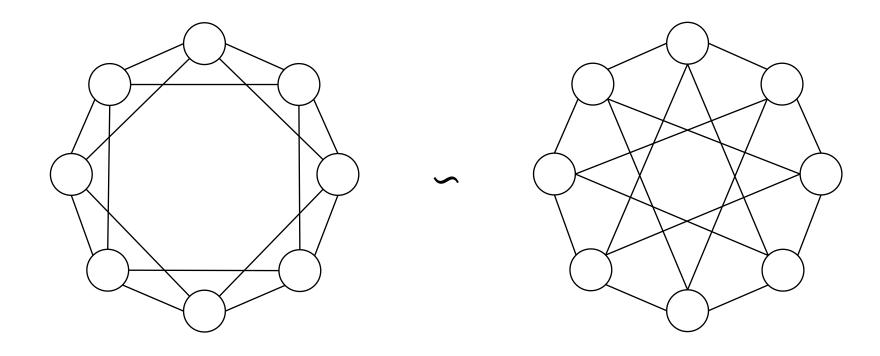
Weisfeiler-Leman: Limitations



Weisfeiler-Leman: Limitations



Weisfeiler-Leman: Limitations



GNN

- Graph Neural Networks (GNNs)
 - Each layer t maps each node and its neighbors from $R^{d_{t-1}}$ to R^{d_t}
 - (A message-passing framework)

GNN

- The power of GNNs in modeling graph structures
 - GNNs are at most as powerful as Weisfeiler-Leman
 - GCN, GraphSAGE, GAT are less powerful than Weisfeiler-Leman
 - GIN meets the simple requirements to be as powerful as Weisfeiler-Leman

$$h_v^{(k)} = \text{MLP}^{(k)} \left(\left(1 + \epsilon^{(k)} \right) \cdot h_v^{(k-1)} + \sum_{u \in \mathcal{N}(v)} h_u^{(k-1)} \right)$$

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Beyond Weisfeiler-Leman: Heuristics

- Heuristic approaches
 - Add domain specific features
 - Add triangle, clique, cycle features
 - Add node identifiers
 - Arbitrary fixed id (for modeling one big graph)
 - Random id (for generalizability to unseen graphs)

Beyond Weisfeiler-Leman: Heuristics

- Heuristic approaches
 - ID-GNN
 - Fast
 - Add cycle count as node feature
 - Full
 - Individually expand a subgraph for each node
 - In each subgraph, distinguish the center node (and its duplicates) from other nodes

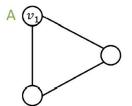
ID-GNN

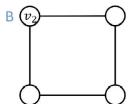
Node classification

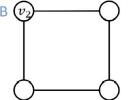
Example input graphs

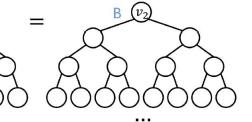
Existing GNNs' computational

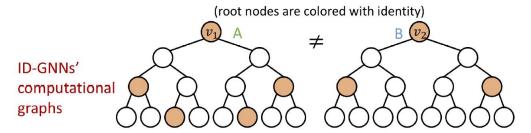
graphs



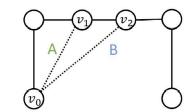


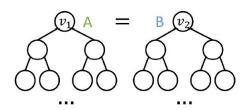




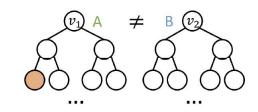


Link prediction

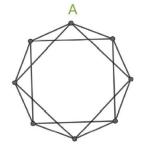


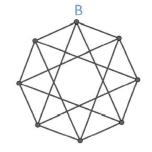


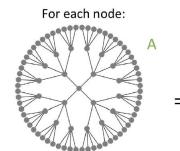
(v_0 is colored with identity)

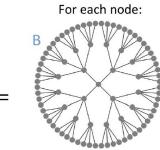


Graph classification

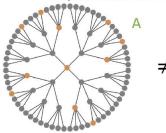


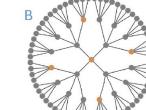






(root nodes are colored with identity)





A B Class labels



node with augmented identity

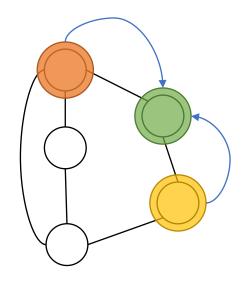


node without augmented identity

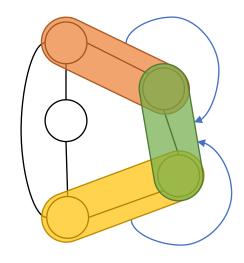
ID-GNN

		Node classification: real-world labels		Edge classification: link prediction				Graph classification: real-world labels			
		Cora	CiteSeer	ScaleFree	SmallWorld	ENZYMES	PROTEINS	ENZYMES	PROTEINS	BZR	ogbg-molhiv
GNNs	GCN SAGE GAT GIN	0.868±0.01 0.857±0.01	0.709 ± 0.01 0.726 ± 0.01 0.716 ± 0.01 0.719 ± 0.01	0.796 ± 0.01 0.541 ± 0.00 0.500 ± 0.00 0.802 ± 0.01	0.709 ± 0.00 0.512 ± 0.00 0.500 ± 0.00 0.722 ± 0.01	0.651 ± 0.01 0.546 ± 0.01 0.478 ± 0.01 0.654 ± 0.01	0.582 ± 0.01 0.491 ± 0.01	0.542 ± 0.01 0.555 ± 0.02	0.692 ± 0.01	0.852 ± 0.04 0.848 ± 0.03	0.747 ± 0.02 0.758 ± 0.01 0.742 ± 0.01 0.762 ± 0.03
ID-GNNs Fast	GCN SAGE GAT GIN	0.870 ± 0.02	0.742 ± 0.01	0.856 ± 0.03 0.898 ± 0.01 0.731 ± 0.02 0.837 ± 0.01	0.719 ± 0.00 0.743 ± 0.02 0.537 ± 0.00 0.759 ± 0.01	0.649 ± 0.01 0.671 ± 0.04 0.490 ± 0.01 0.718 ± 0.02				0.807±0.02 0.835±0.06 0.848±0.05 0.864 ± 0.03	0.772 ± 0.02 0.780 ± 0.01 0.740 ± 0.01 0.755 ± 0.02
ID-GNNs Full	GCN SAGE GAT GIN	0.875 ± 0.01		0.771 ± 0.04 0.741 ± 0.01 0.749 ± 0.01 0.815 ± 0.01	0.798±0.03 0.724±0.03 0.742±0.03 0.810 ± 0.03	0.838±0.01 0.819±0.01 0.824±0.01 0.846 ± 0.01	0.863 ± 0.01 0.859 ± 0.03		0.721 ± 0.01 0.738 ± 0.01	0.881±0.04 0.864±0.02 0.881±0.04 0.852±0.03	0.769±0.01 0.783 ± 0.02 0.739±0.01 0.756±0.00
Best ID-GNN over best GNN		1.0%	1.6%	9.6%	8.7%	19.2%	21.9%	8.3%	1.8%	2.5%	2.0%

Beyond Weisfeiler-Leman: Theoretical



Weisfeiler-Leman / GNN

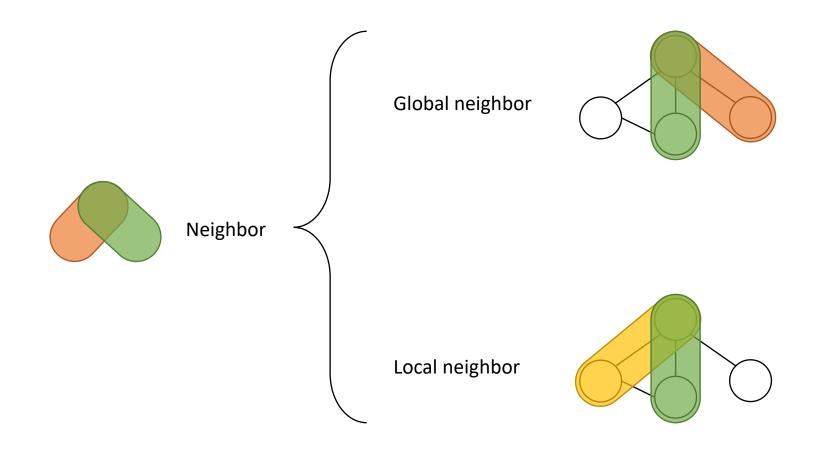


k-WL/k-GNN

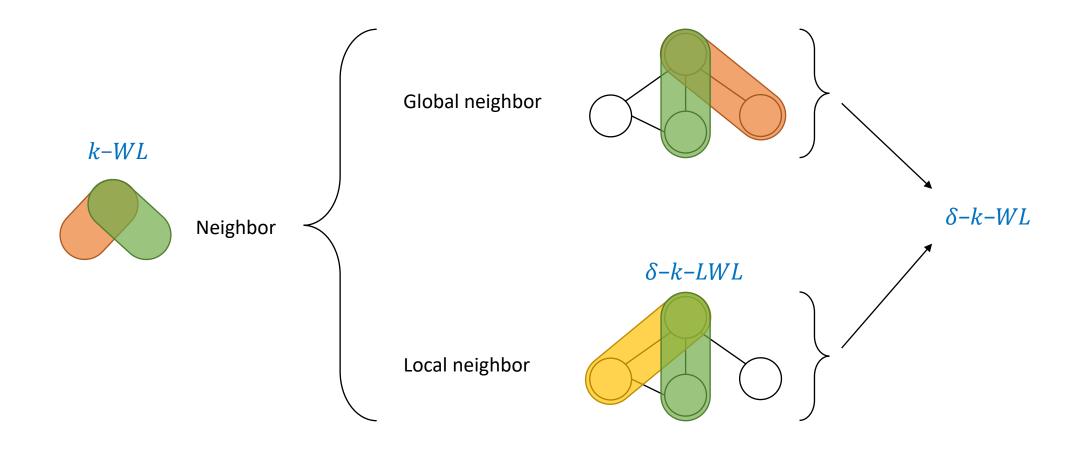
- Just like Weisfeiler-Leman / GNN, but
 - "Nodes" → k-node subgraphs
 - "Neighbors" → subgraphs with a (k-1)-node intersection

- Power in modeling graph structures
 - Weisfeiler-Leman $\equiv 2\text{-WL} \supset 3\text{-WL} \supset 4\text{-WL} \supset \cdots$
- Complexity
 - $O(n^k)$

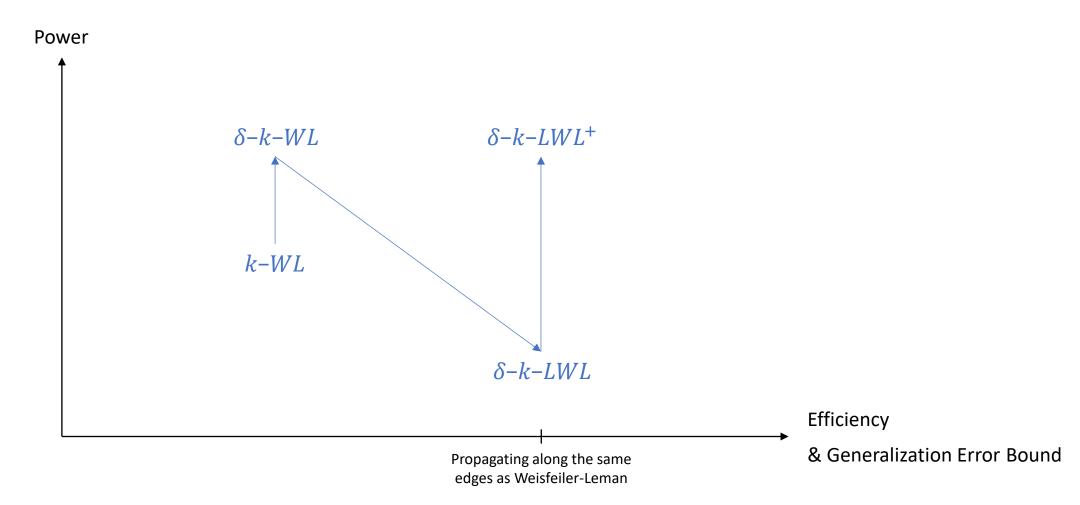
- 3-WL
 - Power in modeling graph structures
 - Weisfeiler-Leman $\equiv 2$ -WL $\supset 3$ -WL
 - Distinguishes all planar graphs
 - Complexity
 - $O(n^2)$



$\delta - k - LWL / \delta - k - LGNN$



$\delta - k - LWL^+ / \delta - k - LGNN^+$



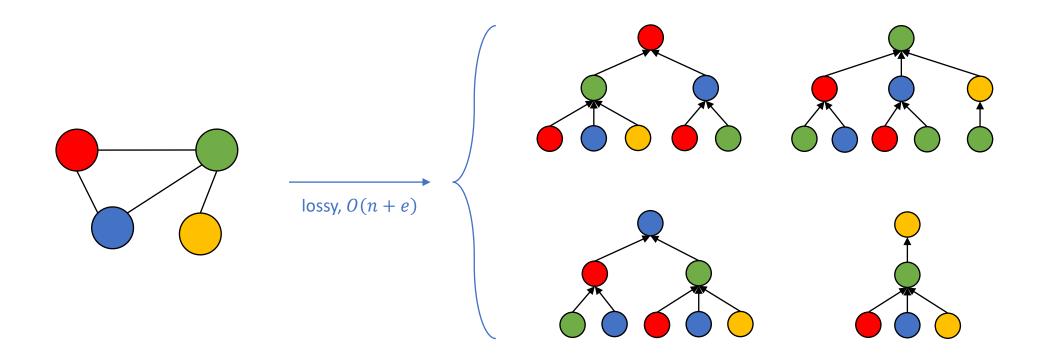
$\delta - k - LWL^+ / \delta - k - LGNN^+$

M d 1	Dataset										
Method	ENZYMES	IMDB-BINARY	IMDB-MULTI	NCI1	NCI109	PTC_FM	PROTEINS	REDDIT-BINARY			
GR SP 1-WL WLOA	29.7 ± 0.6 40.7 ± 0.9 50.7 ± 1.2 56.8 ± 1.6	58.9 ± 1.0 58.5 ± 0.4 72.5 ± 0.5 72.7 ± 0.9	39.0 ± 0.8 39.4 ± 0.3 50.0 ± 0.5 50.1 ± 0.7	$66.1 \pm 0.4 74.0 \pm 0.3 84.2 \pm 0.3 84.9 \pm 0.3$	66.3 ± 0.2 73.0 ± 0.4 84.3 ± 0.3 85.2 ± 0.3	61.3 ± 1.1 61.3 ± 1.3 62.6 ± 2.0 61.8 ± 1.5	71.2 ± 0.6 75.6 ± 0.5 72.6 ± 1.2 73.2 ± 0.6	60.0 ± 0.2 84.6 ± 0.3 72.8 ± 0.5 88.1 ± 0.4			
Gin-0 Gin-ε	38.8 ±1.7 39.4 ±1.7	72.7 ± 0.9 72.7 ± 0.9 72.9 ± 0.6	49.9 ±0.8 49.6 ±0.9	78.5 ± 0.5 78.6 ± 0.3	76.7 ± 0.8 77.0 ± 0.5	58.2 ±3.3 57.7 ±2.0	71.3 ±0.9 71.1 ±0.8	89.8 ±0.6 90.3 ±0.3			
2-WL	36.7 ± 1.7 42.3 ± 1.1	68.2 ± 1.1 67.8 ± 0.8	48.1 ± 0.5 47.0 ± 0.7	67.1 ±0.3 Oot	$67.5_{\pm 0.2}$	$62.3 \pm 1.6 \\ 61.5 \pm 1.7$	$75.0 \pm 0.8 \\ Oom$	Оом Оом			
$\overline{\mathcal{S}} = \frac{\overline{\delta}}{\delta - 2 - WL}$ $\delta - 3 - WL$	$37.5 \pm 1.2 \\ 43.0 \pm 1.4$	68.1 ± 1.1 67.5 ± 1.0	47.9 ± 0.7 $47.3 \pm 0/9$	$\begin{array}{c} 67.0 \pm 0.5 \\ Oot \end{array}$	$\begin{array}{c} 67.2 \pm 0.4 \\ OOT \end{array}$	$61.9 \pm 0.9 \\ 61.2 \pm 2.0$	$75.0 \pm 0.4 \\ Oom$	OOM Oom			
$\begin{array}{c} \overline{\delta\text{-2-LWL}} \\ \overline{\delta} \\ \delta\text{-2-LWL}^+ \\ \delta\text{-3-LWL}^+ \\ \delta\text{-3-LWL}^+ \end{array}$	56.6 ± 1.2 52.9 ± 1.4 57.6 ± 1.2 56.8 ± 1.2	73.3 ± 0.5 75.7 ± 0.7 72.8 ± 1.2 76.2 ± 0.8	50.2 ± 0.6 62.5 ± 1.0 49.3 ± 1.0 64.2 ± 0.9	84.7 ± 0.3 91.4 ± 0.2 83.4 ± 0.2 82.7 ± 0.5	84.2 ± 0.4 89.3 ± 0.2 82.4 ± 0.4 81.9 ± 0.4	60.3 ± 3.2 62.6 ± 1.6 61.3 ± 1.6 61.3 ± 2.0	75.1 ±0.3 79.3 ±1.1 OOM OOM	89.7 ±0.4 91.1 ±0.5 Oom Oom			

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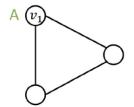
Weisfeiler-Leman / GNN

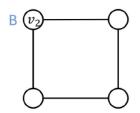


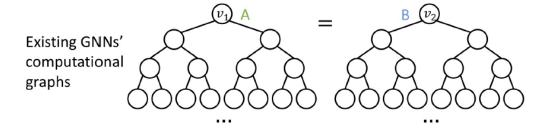
Weisfeiler-Leman / GNN

Node classification

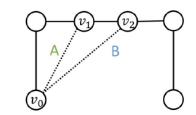
Example input graphs

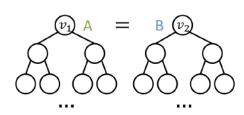




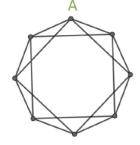


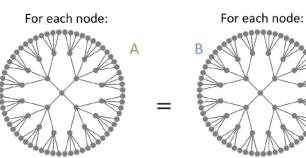
Link prediction

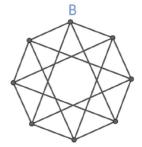




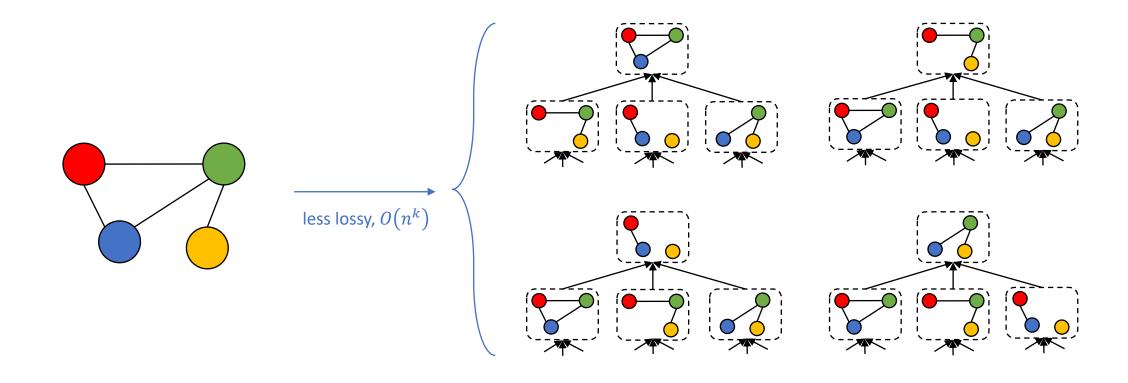
Graph classification



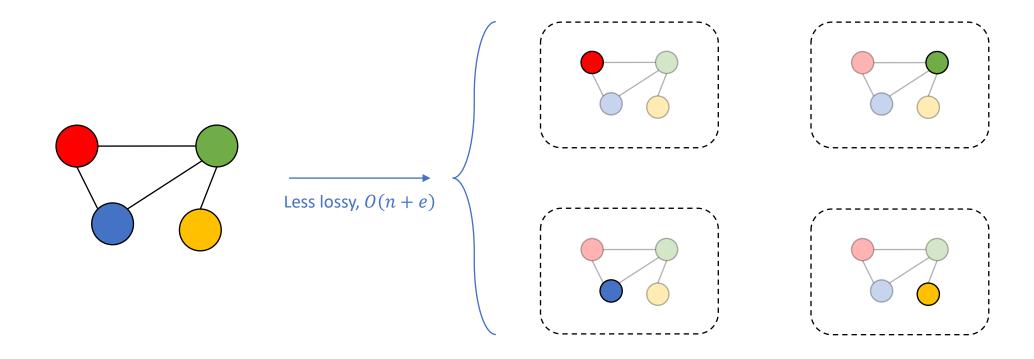




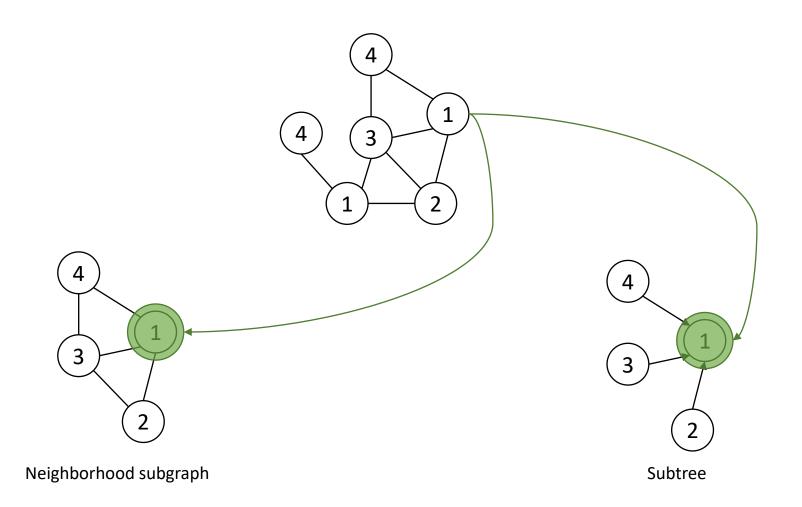
k-WL/k-GNN



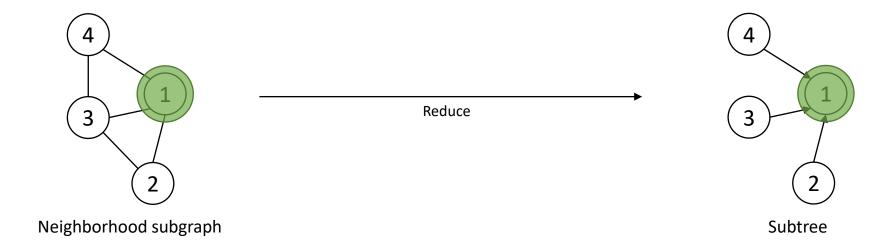
Modeling Local Structures



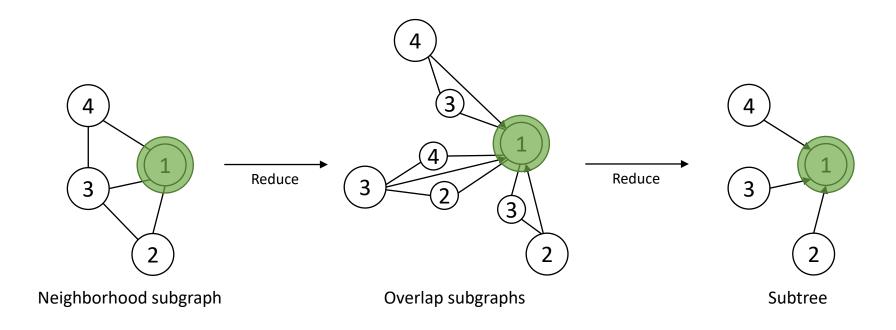
Modeling Local Structures



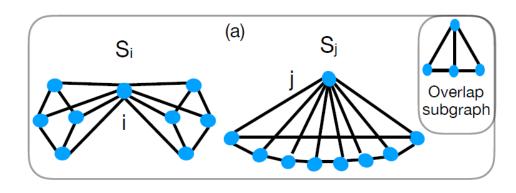
Modeling Local Structures



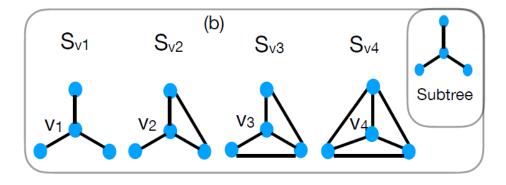
Hierarchy of Local Isomorphism



Hierarchy of Local Isomorphism

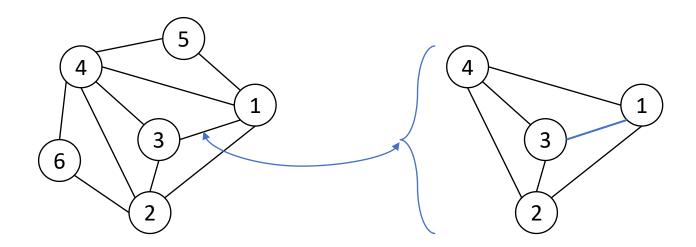


Overlap-isomorphic



Subtree-isomorphic

Edge ↔ Overlap Subgraph



- For each edge
 - Let S be its overlap subgraph with n nodes, e edges
 - Compute the overlap subgraph feature $\omega(S) \equiv \frac{e}{(n-1)n} n^{\lambda}$
 - $\rightarrow \omega \propto \text{density} \cdot \text{order}$
 - $\rightarrow \lambda$: the weight of order vs. density

- For each edge
 - Let S be its overlap subgraph with n nodes, e edges
 - Compute the overlap subgraph feature $\omega(S) \equiv \frac{e}{(n-1)n} n^{\lambda}$
 - $\rightarrow \omega \propto \text{density} \cdot \text{order}$
 - $\rightarrow \lambda$: the weight of order vs. density
- Incorporate (pre-computed) ω into GNN propagation

- The power of GraphSNN in modeling graph structures
 - Strictly more powerful than Weisfeiler-Leman / GNN
 - While having the same complexity

Method	Cora	Citeseer	Pubmed	NELL	ogbn-arxiv
GCN	81.5 ± 0.4	70.3 ± 0.5	79.0 ± 0.5	66.0 ± 1.7	71.74 ± 0.29
$GraphSNN_{GCN}$	$\textbf{83.1} \pm \textbf{1.8}$	72.3 ± 1.5	$\textbf{79.8} \pm \textbf{1.2}$	68.3 ± 1.6	72.20 ± 0.90
GAT	83.0 ± 0.6	72.6 ± 0.6	78.5 ± 0.3	-	-
$GraphSNN_{GAT}$	$\textbf{83.8} \pm \textbf{1.2}$	73.5 ± 1.6	79.6 ± 1.4	-	-
GIN	77.6 ± 1.1	66.1 ± 1.5	77.0 ± 1.2	61.5 ± 2.3	-
$GraphSNN_{GIN}$	$\textbf{79.2} \pm \textbf{1.7}$	68.3 ± 1.5	$\textbf{78.8} \pm \textbf{1.3}$	63.8 ± 2.7	-
GraphSAGE	79.2 ± 3.7	71.6 ± 1.9	77.4 ± 2.2	63.7 ± 5.2	71.49 ± 0.27
$GraphSNN_{GraphSAGE}$	$\textbf{80.5} \pm \textbf{2.5}$	$\textbf{72.7} \pm \textbf{3.2}$	79.0 ± 3.5	66.3 ± 5.6	71.80 ± 0.70

Method	MUTAG	PTC-MR	PROTEINS	D&D	BZR	COX2	IMDB-B	RDT-M5K
WL	90.4 ± 5.7	59.9 ± 4.3	75.0 ± 3.1	79.4 ± 0.3	78.5 ± 0.6	81.7 ± 0.7	73.8 ± 3.9	52.5 ± 2.1
RetGK	90.3 ± 1.1	62.5 ± 1.6	75.8 ± 0.6	81.6 ± 0.3	-	-	71.9 ± 1.0	-
GNTK	90.0 ± 8.5	67.9 ± 6.9	75.6 ± 4.2	75.6 ± 3.9	83.6 ± 2.9	-	76.9 ± 3.6	-
P-WL	90.5 ± 1.3	64.0 ± 0.8	75.2 ± 0.3	78.6 ± 0.3	-	-	-	-
WL-PM	87.7 ± 0.8	61.4 ± 0.8	-	78.6 ± 0.2	-	-	-	-
WWL	87.2 ± 1.5	66.3 ± 1.2	74.2 ± 0.5	79.6 ± 0.5	84.4 ± 2.0	78.2 ± 0.4	74.3 ± 0.8	-
FGW	88.4 ± 5.6	65.3 ± 7.9	74.5 ± 2.7	-	85.1 ± 4.1	77.2 ± 4.8	63.8 ± 3.4	-
DGCNN	85.8 ± 1.7	58.6 ± 2.5	75.5 ± 0.9	79.3 ± 0.9	-	-	70.0 ± 0.9	48.7 ± 4.5
CapsGNN	86.6 ± 6.8	66.0 ± 1.8	76.2 ± 3.6	75.4 ± 4.1	-	-	73.1 ± 4.8	52.9 ± 1.5
[†] GraphSAGE	85.1 ± 7.6	63.9 ± 7.7	75.9 ± 3.2	72.9 ± 2.0	-	-	72.3 ± 5.3	50.0 ± 1.3
†GIN	89.4 ± 5.6	64.6 ± 7.0	75.9 ± 2.8	-	-	-	75.1 ± 5.1	57.5 ± 1.5
†GraphSNN (S)	91.57 ± 2.8	66.70 ± 3.7	76.83 ± 2.5	81.97 ± 2.6	88.69 ± 3.2	82.86 ± 3.1	77.86 ± 3.6	58.43 ± 2.3
†GraphSNN (R)	91.24 ± 2.5	66.96 ± 3.5	76.51 ± 2.5	82.46 ± 2.7	88.97 ± 2.9	83.13 ± 3.5	76.93 ± 3.3	58.51 ± 2.7
GraphSNN (S)	94.70 ± 1.9	70.58 ± 3.1	78.42 ± 2.7	83.92 ± 2.3	91.12 ± 3.0	86.28 ± 3.3	$\textbf{78.51} \pm \textbf{2.8}$	59.86 ± 2.6
GraphSNN (R)	94.14 ± 1.2	71.01 ± 3.6	$\textbf{78.21} \pm \textbf{2.9}$	$\textbf{84.61} \pm \textbf{1.5}$	$\textbf{91.88} \pm \textbf{3.2}$	86.72 ± 2.9	77.87 ± 3.1	60.23 ± 2.2

Method	ogbg-molhiv	ogbg-moltox21	ogbg-moltoxcast	ogbg-ppa	ogbg-molpcba
GIN	75.58 ± 1.40	74.91 ± 0.51	63.41 ± 0.74	68.92 ± 1.00	22.66 ± 0.28
GIN+VN	75.20 ± 1.30	76.21 ± 0.82	66.18 ± 0.68	70.37 ± 1.07	27.03 ± 0.23
GSN	77.99 ± 1.00	-	-	-	-
PNA	79.05 ± 1.30	-	-	-	28.38 ± 0.35
ID-GNN	78.30 ± 2.00	-	-	-	-
Deep LRP	77.19 ± 1.40	-	-	-	-
GraphSNN	78.51 ± 1.70	75.45 ± 1.10	65.40 ± 0.71	70.66 ± 1.65	24.96 ± 1.50
GraphSNN+VN	79.72 ± 1.83	76.78 ± 1.27	67.68 ± 0.92	72.02 ± 1.48	28.50 ± 1.68

	Method	MUTAG	PTC-MR	PROTEINS	BZR	IMDB-B
GSN	GSN-e	90.6 ± 7.5	68.2 ± 7.2	76.6 ± 5.0	-	77.8 ± 3.3
	GSN-v	92.2 ± 7.5	67.4 ± 5.7	74.5 ± 5.0	-	76.8 ± 2.0
ID-GNNs	ID-GNN Fast	96.5 ± 3.2	61.9 ± 5.4	78.0 ± 3.5	86.4 ± 3.0	-
	ID-GNN Full	93.0 ± 5.6	62.5 ± 5.3	77.9 ± 2.4	88.1 ± 4.0	-
Ours	GraphSNN	91.57 ± 2.8	66.70 ± 3.7	76.83 ± 2.5	88.69 ± 3.2	77.86 ± 3.6
	1 -GNN $_{NT}$	82.7 ± 0.0	51.2 ± 0.0	-	-	69.4 ± 0.0
k-WL	1-GNN	82.2 ± 0.0	59.0 ± 0.0	-	-	71.2 ± 0.0
GNNs	1-2-3-GNN $_{NT}$	84.4 ± 0.0	59.3 ± 0.0	-	-	70.3 ± 0.0
	1-2-3-GNN	86.1 ± 0.0	60.9 ± 0.0	-	-	74.2 ± 0.0
Ours	GraphSNN	87.30 ± 3.1	61.63 ± 2.8	74.01 ± 3.2	82.72 ± 3.9	74.81 ± 3.5