### SAME: Uncovering GNN Black Box with Structureaware Shapley-based Multipiece Explanation







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# A brief intro: XAI in graph



- Deep graph models becoming more widespread
- Black-box graph models are the mainstream
  - Graph Convolutional Network (GCN)
  - Graph Attention Network (GAT)
  - Graph Isomorphism Network (GIN)

▶ ...

- Various concerns about model transparency
- Analyzing the influence of a single node or edge is not enough.

### Motivation



Brain Networks Associated with Specific Cognitive Task



Functional Groups Associated with Molecular Property



Social Groups Associated with Single Person

- The characteristics and properties within a graph or node tend to be jointly influenced by more than one high-order connected community of the graph.
- > To design an explanation method: Retain important nodes while avoiding irrelevant nodes.

## Methodology



- (a) Important substructure initialization phase
- Search the single connected important substructure.
- (b) Explanation exploration phase
- Provide a candidate set of explanations
- Optimize the combination of different important substructures.



Expansion-based Monte Carlo Tree Search (MCTS)

Root Node: Empty graph



- Root Node: Empty graph
- Expand within 1-hop neighbors of the associate substructure
- Choose the best children according to the Shapley value



- Root Node: Empty graph
- Expand within 1-hop neighbors of the associate substructure
- Leaf Node: The substructure reaches the maximum size predefined
- > Backpropagation to update the previous nodes



- Root Node: Empty graph
- Expand within 1-hop neighbors of the associate substructure
- Leaf Node: The substructure reaches the predefined maximum size
- Backpropagation to update the previous nodes
- Important substructure set: All the substructures in the MCTS



Important Substructure Set



#### **Expansion-based Monte Carlo Tree Search (MCTS)**

Root Node: Empty graph



- Root Node: Empty graph
- Expand an important substructure
- Leaf Node: The size reaches the threshold



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- Root Node: Empty graph
- Expand an important substructure
- Leaf Node: The size reaches the threshold
- Backpropagation to update the previous nodes
- > Explanation Candidate Set: All the leaf nodes

Explanation Candidate Set



### Experiments

Table 2: Comparison of our SAME and other baseline using fidelity.

Dataset	Graph classification					Node classif.
	Molecular graph		Semantic graph		Synthetic graph	
Methods	BBBP	MUTAG	Graph-SST2	Graph-SST5	<b>BA-2Motifs</b>	BA-Shapes
Grad-CAM [22]	$0.226 \pm 0.036$	$0.261 {\pm} 0.018$	$0.257 \pm 0.056$	$0.229 \pm 0.042$	$0.472 {\pm} 0.010$	-
GNNExplainer [35]	$0.148 \pm 0.041$	$0.188 {\pm} 0.031$	$0.143 {\pm} 0.041$	$0.170 \pm 0.046$	$0.442 {\pm} 0.026$	$0.154 {\pm} 0.000$
PGExplainer [19]	$0.197 \pm 0.043$	$0.156 {\pm} 0.004$	$0.219 {\pm} 0.040$	$0.207 {\pm} 0.036$	$0.431 \pm 0.011$	$0.135 {\pm} 0.020$
GNN-LRP [25]	$0.111 \pm 0.040$	$0.253 {\pm} 0.030$	$0.103 \pm 0.042$	$0.131 \pm 0.057$	$0.146 \pm 0.010$	$0.155 {\pm} 0.000$
SubgraphX [38]	$0.433 \pm 0.073$	$0.379 {\pm} 0.030$	$0.262 {\pm} 0.027$	$0.283 \pm 0.042$	$0.493 \pm 0.003$	$0.181 {\pm} 0.005$
GStarX [40]	$0.117 \pm 0.043$	$\underline{0.656{\pm}0.096}$	$\overline{0.183 \pm 0.050}$	$0.186 \pm 0.050$	$\overline{0.476 \pm 0.014}$	-
SAME Relative Improve	0.489±0.034   12.9%↑	0.702±0.125 7.01%↑	0.373±0.042 42.3%↑	0.393±0.022 38.9%↑	0.549±0.004 11.3%↑	0.214±0.000 18.2%↑

Note: The fidelity results are averaged across different sparsity from 0.5 to 0.8. The quantitative results are presented in the form of mean  $\pm$  std. The previous SOTA results on different datasets are marked with an underline. *Relative Improve* denotes the relative improvement of our SAME method over the SOTA methods.

Table 3: Comparison of inference time (in seconds) on different datasets.

Dataset	BBBP	MUTAG	Graph-SST2	Graph-SST5	BA-2Motifs	BA-Shapes
Grad-CAM [22]	0.16	0.23	0.39	0.44	0.14	-
GNNExplainer [35]	7.56	1.96	7.64	19.39	1.89	2.72
PGExplainer [19]	0.15	0.21	0.35	0.43	0.12	0.13
GNN-LRP [25]	2.37	1.97	5.84	5.47	3.30	51.77
SubgraphX [38]	26.72	151.75	36.48	71.32	85.50	162.80
GStarX 40	84.54	25.24	30.64	54.49	77.99	-
SAME	7.86	5.67	6.06	8.83	8.19	14.08

Note: The PGExplainer needs training before inferring the explanation.

#### **Fidelity**

- A higher fidelity demonstrates a better explainability.
- SAME outperforms the SOTA baselines among different tasks and datasets.

#### **Inference Time**

SAME consistently achieves much lower computational cost compared to GStarX and SubgraphX, reflecting its efficiency and robustness.



### **MUTAG** dataset

SAME achieves to provide the explanations the same as the ground truth (-NO<sub>2</sub>) which are labeled by human experts.

### **BA-2Motifs dataset**

SAME exactly finds the groundtruth explanation (a 5-node-housestructure motif) compared to other baselines.

### Experiments

Grad-	CAM GNN	Explainer	PGExplainer	
of scr	eam a of s	cream a	of scream	a
cons. str	uct. carefully cons.	struct. – carefully c	ons. struct. care	efully
that tort	ured is that to	ortured is t	hat tortured	is
and un	set. – – and –	unset a	and unset.	
but al	ve unques. but	alive unques.	but alive und	ques.
GNN-LRP	SubgraphX	GStarX	S	SAME(ours)
of scream a	of scream a	of scream	a of	scream a
cons. struct. carefully	cons. struct. carefull	y cons. struct.	carefully cons.	struct. carefully
that tortured is	that tortured is	that tortured	is that	tortured is
and unset	and unset	and unset.	and	unset. – ––

Sentence: "a carefully structured scream of consciousness that is tortured and unsettling -- but unquestionably alive."

#### Graph-SST2 dataset

SAME can well capture the adjectives-or-adverbs-like graph structures than other baselines.

# Thanks for your attention!