

Supplementary Material: Faithful Explanations for Graph Classification using Logic

Alessio Ragno¹, Marc Plantevit², and Céline Robardet¹

¹ INSA Lyon, CNRS, LIRIS UMR 5205, F-69621 Villeurbanne, France
`{alessio.ragno,celine.robardet}@insa-lyon.fr`

² EPITA Research Laboratory (LRE), FR-94276, Le Kremlin-Bicêtre, France
`marc.plantevit@epita.fr`

1 Models hyperparameters and accuracy

Dataset	Accuracy	Batch size	Dropout	Epochs	Hid. Dim	L2	LR
Ba2Motifs	100.00 \pm 0.00	128	0	3000	16	1e-4	0.001
MUTAG	84.74 \pm 8.02	128	0.5	3000	32	1e-4	0.001
Mutagenicity	82.21 \pm 1.87	32	0.5	3000	32	1e-4	0.001
NCI1	81.87 \pm 1.39	128	0	3000	32	1e-4	0.001
BBBP	87.95 \pm 2.07	32	0.5	3000	16	1e-4	0.001
PROTEINS	72.59 \pm 3.04	32	0	3000	32	1e-4	0.001

Table 1: Performance and hyperparameters for selected datasets

2 Explanation Performances

Table 2: Fidelity Scores when using the top 1, top 3 and top 5 nodes as hard mask. Values are reported as $\mu \pm \sigma$ over 5 seeds. The highest result is highlighted in bold, while values within one σ of the best result are underlined.

BA2Motifs				MUTAG		
Top Nodes	1	3	5	1	3	5
GNNEexpl.	5.0 ± 3.0	13.2 ± 5.5	21.0 ± 5.8	18.9 ± 10.8	42.1 ± 9.4	57.9 ± 13.3
PGExpl.	24.8 ± 3.3	24.6 ± 3.8	24.0 ± 5.5	23.2 ± 15.8	34.7 ± 17.5	40.0 ± 19.6
IG	16.4 ± 13.2	17.2 ± 15.4	21.0 ± 13.8	17.9 ± 20.1	27.4 ± 12.2	37.9 ± 13.1
SubGraphX	47.6 ± 30.0	48.4 ± 13.5	48.0 ± 12.8	27.4 ± 11.7	48.4 ± 6.1	58.9 ± 10.7
GStarX	14.2 ± 7.2	46.8 ± 2.9	50.0 ± 1.3	25.3 ± 11.7	49.5 ± 16.5	62.1 ± 15.8
TELL (ours)	57.4 ± 21.4	64.0 ± 20.3	58.0 ± 21.2	42.1 ± 11.0	66.3 ± 14.0	65.3 ± 12.3
Mutagenicity				NCI1		
Top Nodes	1	3	5	1	3	5
GNNEexpl.	7.6 ± 1.9	16.0 ± 3.4	21.9 ± 3.6	9.0 ± 1.3	19.3 ± 1.6	26.7 ± 2.5
PGExpl.	12.6 ± 1.8	22.0 ± 2.6	26.5 ± 2.0	14.5 ± 1.7	20.0 ± 2.8	26.3 ± 2.1
IG	6.9 ± 2.4	14.3 ± 5.1	17.7 ± 7.3	10.3 ± 2.7	16.5 ± 3.2	21.6 ± 2.8
SubGraphX	12.4 ± 3.8	21.9 ± 4.3	28.2 ± 3.0	14.7 ± 1.9	23.6 ± 2.4	29.6 ± 3.2
GStarX	17.6 ± 1.2	36.5 ± 4.1	49.4 ± 5.7	12.9 ± 2.6	23.3 ± 4.4	29.2 ± 5.5
TELL (ours)	20.0 ± 5.8	34.0 ± 6.9	40.8 ± 6.0	24.4 ± 6.5	33.1 ± 8.4	36.6 ± 10.9
BBBP				PROTEINS		
Top Nodes	1	3	5	1	3	5
GNNEexpl.	5.0 ± 1.6	9.3 ± 2.0	12.8 ± 2.1	12.7 ± 4.3	21.7 ± 3.7	28.8 ± 5.4
PGExpl.	5.1 ± 1.5	10.3 ± 0.6	13.3 ± 1.0	12.9 ± 3.4	20.4 ± 3.6	26.4 ± 5.4
IG	3.9 ± 1.6	8.1 ± 2.7	12.8 ± 4.9	8.7 ± 3.5	20.8 ± 3.9	28.3 ± 3.6
SubGraphX	5.8 ± 1.3	10.7 ± 3.3	14.6 ± 3.6	12.2 ± 2.8	24.9 ± 4.8	32.0 ± 3.2
GStarX	8.0 ± 1.6	15.5 ± 3.9	20.7 ± 6.3	16.2 ± 6.1	27.7 ± 4.9	41.5 ± 5.5
TELL (ours)	15.5 ± 13.8	25.1 ± 15.9	29.8 ± 18.3	12.5 ± 4.0	33.7 ± 3.6	41.6 ± 2.8

Table 3: InvFidelity Scores when using the top $N - 1$, top $N - 3$ and $N - 5$ nodes as hard mask. Values are reported as $\mu \pm \sigma$ over 5 seeds. The highest result is highlighted in bold, while values within one σ of the best result are underlined.

BA2Motifs				MUTAG		
Top Nodes	$N - 1$	$N - 3$	$N - 5$	$N - 1$	$N - 3$	$N - 5$
GNNExpl.	3.6 ± 2.1	16.4 ± 6.7	24.0 ± 6.8	16.8 ± 12.2	40.0 ± 20.7	56.8 ± 14.7
PGExpl.	24.6 ± 5.0	25.0 ± 3.8	24.4 ± 2.2	26.3 ± 8.8	49.5 ± 7.9	52.6 ± 11.0
IG	35.0 ± 22.4	40.6 ± 24.2	38.4 ± 18.8	37.9 ± 16.1	55.8 ± 19.6	61.1 ± 16.8
SubGraphX	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	30.5 ± 3.9	56.8 ± 14.3	61.1 ± 12.7
GStarX	0.2 ± 0.4	0.2 ± 0.4	0.0 ± 0.0	16.8 ± 8.4	45.3 ± 13.6	57.9 ± 11.0
TELL (ours)	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	12.6 ± 10.8	22.1 ± 13.1	28.4 ± 14.4
Mutagenicity				NCI1		
Top Nodes	$N - 1$	$N - 3$	$N - 5$	$N - 1$	$N - 3$	$N - 5$
GNNExpl.	7.5 ± 0.7	14.7 ± 1.3	18.7 ± 2.1	10.5 ± 2.0	20.6 ± 0.1	27.3 ± 2.1
PGExpl.	11.4 ± 1.3	21.8 ± 1.3	27.3 ± 1.9	13.4 ± 1.5	23.4 ± 2.9	27.9 ± 2.9
IG	23.6 ± 4.6	37.6 ± 6.9	44.5 ± 9.2	23.4 ± 2.3	34.2 ± 4.1	39.3 ± 3.5
SubGraphX	8.5 ± 2.9	13.8 ± 3.2	19.6 ± 5.0	11.1 ± 0.9	23.4 ± 2.1	28.6 ± 3.0
GStarX	6.5 ± 2.1	8.8 ± 3.2	9.3 ± 3.1	16.1 ± 1.3	31.3 ± 5.1	37.5 ± 6.1
TELL (ours)	4.5 ± 2.2	7.6 ± 2.8	10.9 ± 3.3	5.2 ± 2.0	11.4 ± 3.3	17.3 ± 4.5
BBBP				PROTEINS		
Top Nodes	$N - 1$	$N - 3$	$N - 5$	$N - 1$	$N - 3$	$N - 5$
GNNExpl.	4.4 ± 1.8	9.0 ± 2.4	12.2 ± 2.5	9.5 ± 2.7	20.6 ± 6.9	29.0 ± 5.0
PGExpl.	6.3 ± 1.5	11.7 ± 2.0	13.6 ± 2.3	11.3 ± 4.3	23.9 ± 4.1	26.6 ± 4.0
IG	10.5 ± 2.4	19.0 ± 3.3	23.7 ± 1.9	19.7 ± 5.8	30.4 ± 6.4	39.0 ± 6.5
SubGraphX	4.1 ± 1.9	8.2 ± 2.2	11.4 ± 2.6	10.5 ± 4.9	22.0 ± 5.5	28.8 ± 5.7
GStarX	5.8 ± 3.1	12.2 ± 9.0	18.2 ± 15.9	10.0 ± 4.3	15.3 ± 2.5	23.1 ± 6.3
TELL (ours)	3.4 ± 2.7	8.8 ± 8.2	12.4 ± 11.7	7.9 ± 3.3	19.1 ± 4.1	28.9 ± 6.4

Table 4: Stability Scores when using the top $N - 1$, top $N - 3$ and $N - 5$ nodes as hard mask. Values are reported as $\mu \pm \sigma$ over 5 seeds. The highest result is highlighted in bold, while values within one σ of the best result are underlined.

BA2Motifs				MUTAG		
Top Nodes	$N - 1$	$N - 3$	$N - 5$	$N - 1$	$N - 3$	$N - 5$
GNNEexpl.	62.0 ± 0.8	64.2 ± 1.1	67.6 ± 1.0	75.8 ± 2.2	77.5 ± 2.2	81.5 ± 1.4
PGExpl.	98.5 ± 0.5	97.8 ± 0.6	97.6 ± 0.4	99.4 ± 0.3	99.2 ± 0.5	99.0 ± 0.2
IG	30.9 ± 24.7	28.7 ± 25.8	37.2 ± 37.9	58.7 ± 9.4	34.9 ± 20.1	14.2 ± 34.2
SubGraphX	76.1 ± 8.4	11.2 ± 6.3	8.6 ± 4.8	42.4 ± 6.4	31.1 ± 9.0	35.5 ± 7.0
GStarX	96.1 ± 3.0	94.1 ± 3.1	93.9 ± 4.1	55.9 ± 12.8	8.2 ± 24.4	-6.1 ± 20.7
TELL (ours)	99.5 ± 0.7	92.4 ± 6.6	92.2 ± 6.4	97.3 ± 1.7	94.4 ± 3.2	93.3 ± 1.7
Mutagenicity				NCI1		
Top Nodes	$N - 1$	$N - 3$	$N - 5$	$N - 1$	$N - 3$	$N - 5$
GNNEexpl.	70.5 ± 0.8	72.5 ± 0.5	72.5 ± 1.0	74.0 ± 0.8	74.9 ± 0.6	75.6 ± 0.6
PGExpl.	99.2 ± 0.1	98.0 ± 0.2	96.5 ± 0.2	99.7 ± 0.1	99.4 ± 0.1	98.9 ± 0.2
IG	53.5 ± 10.8	31.1 ± 11.8	21.6 ± 11.2	49.7 ± 10.6	30.0 ± 10.4	20.6 ± 8.8
SubGraphX	63.8 ± 6.1	59.7 ± 7.5	57.5 ± 7.4	40.3 ± 7.7	36.7 ± 7.4	37.5 ± 6.0
GStarX	82.4 ± 5.4	73.0 ± 10.1	67.7 ± 12.3	64.2 ± 2.7	34.1 ± 9.1	23.5 ± 10.8
TELL (ours)	94.5 ± 2.4	89.5 ± 5.3	85.7 ± 6.2	93.8 ± 1.6	88.7 ± 3.6	85.3 ± 3.9
BBBP				PROTEINS		
Top Nodes	$N - 1$	$N - 3$	$N - 5$	$N - 1$	$N - 3$	$N - 5$
GNNEexpl.	72.1 ± 0.2	74.0 ± 0.4	74.4 ± 0.7	90.4 ± 0.5	91.0 ± 0.9	88.5 ± 1.3
PGExpl.	99.6 ± 0.1	99.0 ± 0.4	98.1 ± 0.3	99.8 ± 0.1	99.5 ± 0.2	97.3 ± 0.7
IG	53.8 ± 5.9	28.1 ± 4.3	19.4 ± 3.3	49.7 ± 17.2	28.9 ± 19.4	21.0 ± 16.5
SubGraphX	60.0 ± 1.7	48.9 ± 8.7	47.8 ± 7.8	52.5 ± 10.0	46.5 ± 9.9	45.2 ± 9.6
GStarX	81.9 ± 5.7	66.0 ± 15.0	53.2 ± 27.8	75.7 ± 8.3	63.3 ± 4.8	49.5 ± 10.0
TELL (ours)	95.3 ± 6.6	90.8 ± 10.8	88.9 ± 10.8	99.0 ± 1.0	97.7 ± 2.3	<u>96.7 ± 3.6</u>