

GOOD-D: On Unsupervised Graph Out-Of-Distribution Detection

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https://github.com/yixinliu233/G-OOD-D.



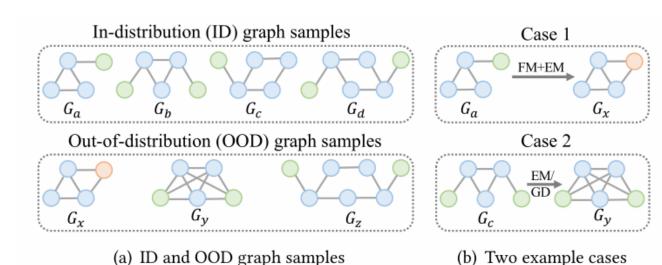
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Reported by Nengqiang Xiang



Introduction



data and its application for graph-structured data remains under-explored. Considering the fact that data labeling on graphs is commonly time-expensive and labor-intensive, the author studies the problem of unsupervised graph OOD detection,

Current endeavors mostly focus on grid-structured

Figure 1: Toy examples of (a) ID graphs $(G_a - G_d)$ and OOD graphs $(G_x - G_z)$; and (b) perturbation-based augmentations (e.g., feature modification (FM), edge modification (EM), and graph diffusion (GD)) introducing OOD samples.

To achieve this goal, the author develops a new graph contrastive learning framework GOOD-D for detecting OOD graphs without using any ground-truth labels.





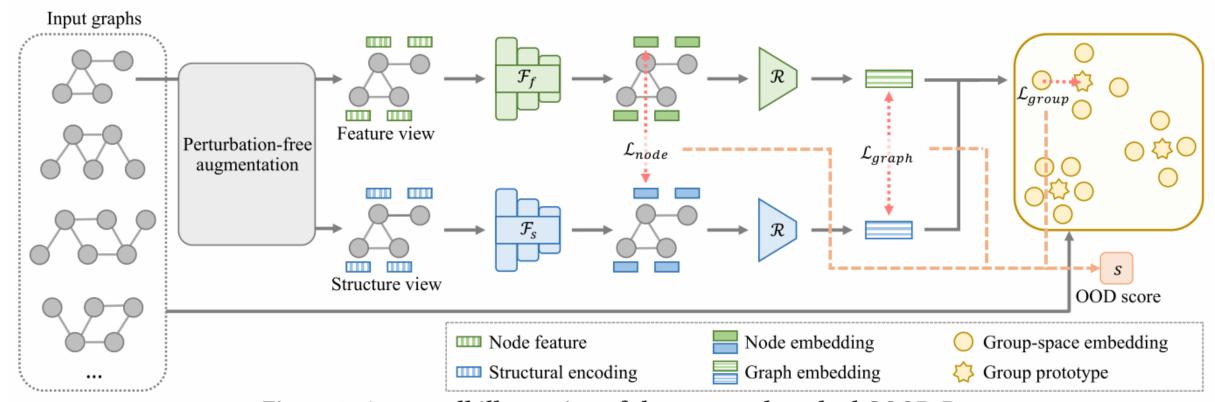
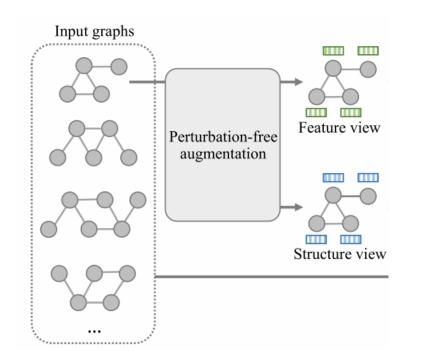


Figure 2: An overall illustration of the proposed method GOOD-D.



Method



PRELIMINARIES:

 $G = (\mathcal{V}, \mathcal{E}, \mathbf{X}) = (\mathbf{A}, \mathbf{X})$

ID dataset $\mathcal{D}^{in} = \{G_1^{in}, \cdots, G_{N_1}^{in}\} \in \mathbb{P}^{in}$

OOD dataset $\mathcal{D}^{out} = \{G_1^{out}, \cdots, G_{N_2}^{out}\} \in \mathbb{P}^{out}$ Train: ID dataset $\mathcal{D}_{train}^{in} \subset \mathcal{D}^{in}$

Test: $\mathcal{D}_{test}^{in} \subset \mathcal{D}^{in} (\mathcal{D}_{test}^{in} \cap \mathcal{D}_{train}^{in} = \emptyset) \cup \mathcal{D}_{test}^{out} \subset \mathcal{D}^{out}$ Perturbation-free Graph Data Augmentation

$$G_{f} = (\mathbf{A}, \mathbf{X}) \quad G_{s} = (\mathbf{A}, \mathbf{S})$$

$$\mathbf{s}_{i}^{(rw)} = \begin{bmatrix} \mathbf{T}_{ii}, \mathbf{T}_{ii}^{2}, \cdots, \mathbf{T}_{ii}^{d_{s}^{(rw)}} \end{bmatrix} \in \mathbb{R}^{d_{s}^{(rw)}}, \quad (1)$$

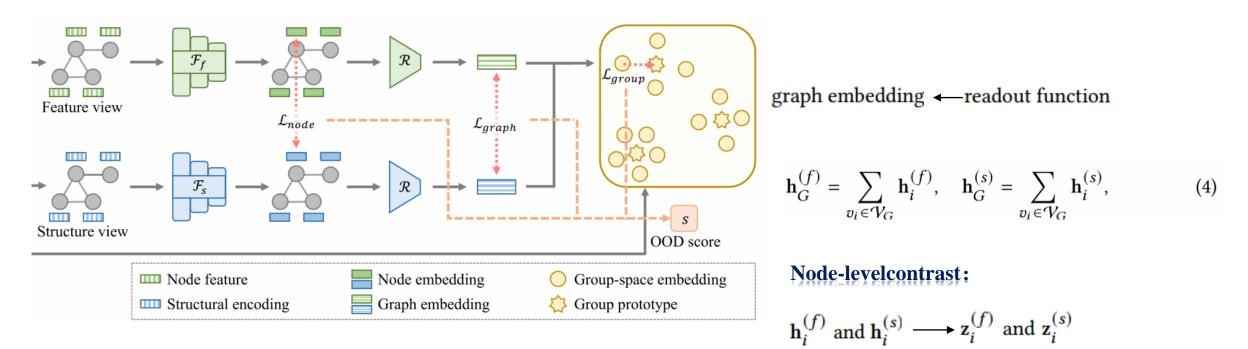
$$\mathbf{T} = \mathbf{A}\mathbf{D}^{-1} \quad \mathbf{D}_{ii} = \sum_{j} \mathbf{A}_{ij}$$

$$\mathbf{s}_{ik}^{(dg)} = \begin{cases} 1, k = \mathbf{D}_{ii} \text{ or } k = d_{s}^{(dg)} < \mathbf{D}_{ii} \\ 0, k \neq \mathbf{D}_{ii} \end{cases}, \quad (2)$$

$$\mathbf{s}_{i} = [\mathbf{s}_{i}^{(rw)} || \mathbf{s}_{i}^{(dg)}]$$



Method



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Hierarchical Graph Contrastive Learning

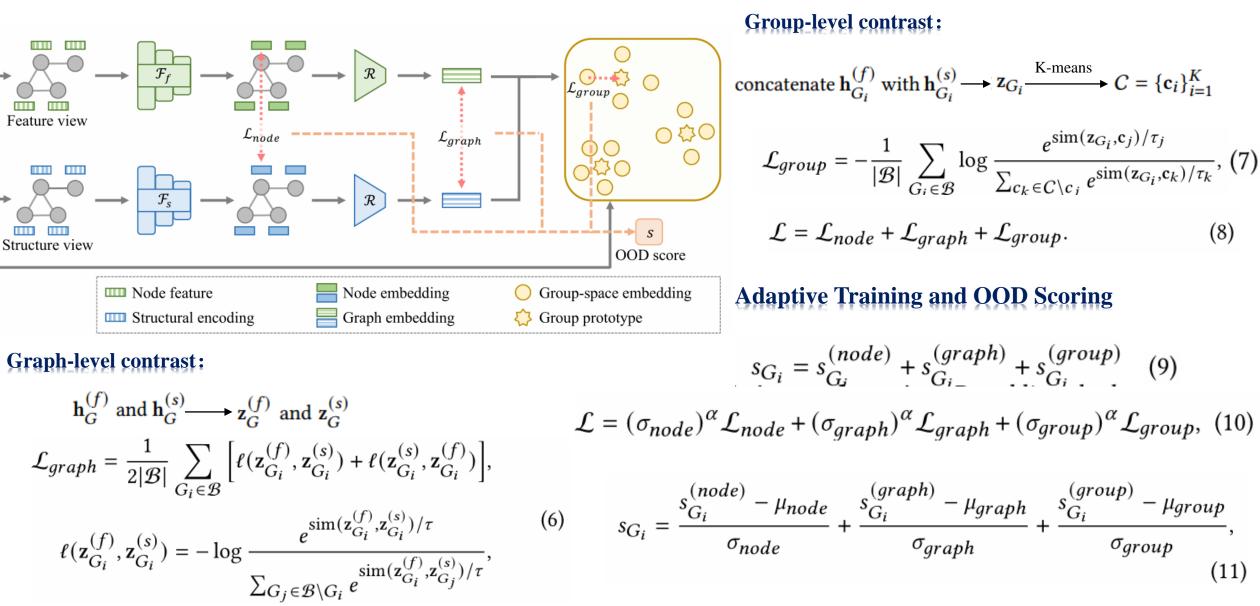
GNN encoders and readout function:

$$\mathbf{h}_{i}^{(f,l)} = \mathrm{MLP}^{(f,l)} \left(\mathbf{h}_{i}^{(f,l-1)} + \sum_{v_{j} \in \mathcal{N}(v_{i})} \mathbf{h}_{j}^{(f,l-1)} \right), \quad (3)$$
$$\mathbf{h}_{i}^{(f)} = [\mathbf{h}_{i}^{(f,1)} || \cdots || \mathbf{h}_{i}^{(f,L)}]$$

$$\mathcal{L}_{node} = \frac{1}{|\mathcal{B}|} \sum_{G_j \in \mathcal{B}} \frac{1}{2|\mathcal{V}_{G_j}|} \sum_{v_i \in \mathcal{V}_{G_j}} \left[\ell(\mathbf{z}_i^{(f)}, \mathbf{z}_i^{(s)}) + \ell(\mathbf{z}_i^{(s)}, \mathbf{z}_i^{(f)}) \right],$$
$$\ell(\mathbf{z}_i^{(f)}, \mathbf{z}_i^{(s)}) = -\log \frac{e^{\sin(\mathbf{z}_i^{(f)}, \mathbf{z}_i^{(s)})/\tau}}{\sum_{v_k \in \mathcal{V}_{G_j} \setminus v_i} e^{\sin(\mathbf{z}_i^{(f)}, \mathbf{z}_k^{(s)})/\tau}},$$
(5)



Method



(11)





Table 1: OOD detection results in terms of AUC (in percent, mean ± std). The best and runner-up results are highlighted with bold and <u>underline</u>, respectively.

ID dataset	BZR	PTC-MR	AIDS	ENZYMES	IMDB-M	Tox21	FreeSolv	BBBP	ClinTox	Esol	Avg.
OOD dataset	COX2	MUTAG	DHFR	PROTEIN	IMDB-B	SIDER	ToxCast	BACE	LIPO	MUV	Rank
PK-LOF	42.22±8.39	51.04 ± 6.04	50.15±3.29	50.47 ± 2.87	48.03 ± 2.53	51.33 ± 1.81	49.16 ± 3.70	53.10 ± 2.07	50.00 ± 2.17	50.82±1.48	11.9
PK-OCSVM	42.55 ± 8.26	49.71 ± 6.58	50.17 ± 3.30	50.46 ± 2.78	48.07 ± 2.41	51.33 ± 1.81	48.82±3.29	53.05 ± 2.10	50.06 ± 2.19	51.00 ± 1.33	11.8
PK-iF	51.46 ± 1.62	54.29 ± 4.33	$51.10{\pm}1.43$	51.67 ± 2.69	50.67 ± 2.47	49.87 ± 0.82	52.28±1.87	51.47 ± 1.33	50.81 ± 1.10	50.85 ± 3.51	10.1
WL-LOF	48.99 ± 6.20	53.31 ± 8.98	50.77 ± 2.87	$52.66 {\pm} 2.47$	52.28 ± 4.50	51.92 ± 1.58	51.47 ± 4.23	$52.80{\pm}1.91$	51.29 ± 3.40	51.26 ± 1.31	9.3
WL-OCSVM	49.16 ± 4.51	53.31±7.57	50.98 ± 2.71	51.77 ± 2.21	51.38 ± 2.39	51.08 ± 1.46	50.38 ± 3.81	52.85 ± 2.00	50.77±3.69	50.97 ± 1.65	10.0
WL-iF	50.24±2.49	51.43 ± 2.02	50.10 ± 0.44	51.17 ± 2.01	51.07 ± 2.25	50.25 ± 0.96	52.60 ± 2.38	50.78 ± 0.75	50.41 ± 2.17	50.61±1.96	11.3
InfoGraph-iF	63.17±9.74	51.43±5.19	93.10±1.35	60.00 ± 1.83	58.73±1.96	56.28 ± 0.81	56.92±1.69	53.68 ± 2.90	48.51±1.87	54.16 ± 5.14	7.4
InfoGraph-MD	86.14±6.77	50.79 ± 8.49	69.02 ± 11.67	55.25 ± 3.51	$81.38{\scriptstyle\pm1.14}$	59.97 ± 2.06	58.05 ± 5.46	70.49 ± 4.63	48.12 ± 5.72	77.57 ± 1.69	6.5
GraphCL-iF	60.00±3.81	50.86 ± 4.30	92.90 ± 1.21	$61.33 {\pm} 2.27$	59.67 ± 1.65	56.81 ± 0.97	55.55 ± 2.71	59.41 ± 3.58	47.84 ± 0.92	62.12 ± 4.01	7.7
GraphCL-MD	83.64±6.00	73.03 ± 2.38	93.75 ± 2.13	52.87 ± 6.11	79.09 ± 2.73	$58.30{\pm}1.52$	60.31 ± 5.24	75.72 ± 1.54	51.58 ± 3.64	78.73 ± 1.40	4.3
OCGIN	76.66±4.17	80.38 ± 6.84	86.01±6.59	57.65±2.96	67.93±3.86	46.09±1.66	59.60 ± 4.78	61.21 ± 8.12	49.13 ± 4.13	54.04 ± 5.50	6.9
GLocalKD	75.75±5.99	70.63 ± 3.54	93.67 ± 1.24	57.18 ± 2.03	78.25 ± 4.35	66.28 ± 0.98	64.82 ± 3.31	73.15 ± 1.26	55.71 ± 3.81	86.83 ± 2.35	4.1
GOOD-D _{simp}	93.00±3.20	78.43 ± 2.67	98.91 ± 0.41	$61.89{\scriptstyle\pm2.51}$	79.71±1.19	$65.30{\pm}1.27$	70.48 ± 2.75	81.56 ± 1.97	66.13 ± 2.98	91.39 ± 0.46	2.2
GOOD-D	$94.99{\scriptstyle \pm 2.25}$	$81.21{\scriptstyle\pm2.65}$	$99.07{\scriptstyle\pm0.40}$	$\underline{61.84{\pm}1.94}$	79.94 ± 1.09	$66.50{\scriptstyle \pm 1.35}$	$80.13{\scriptstyle \pm 3.43}$	$82.91{\scriptstyle\pm2.58}$	$69.18{\scriptstyle \pm 3.61}$	$91.52{\scriptstyle \pm 0.70}$	1.2





Table 2: Anomaly detection results in terms of AUC (in percent, mean ± std). The best and runner-up results are highlighted with bold and <u>underline</u>, respectively.

Method	PK-OCSVM	PK-iF	WL-OCSVM	WL-iF	InfoGraph-iF	GraphCL-iF	OCGIN	GLocalKD	GOOD-D _{simp}	GOOD-D
PROTEINS-full	50.49 ± 4.92	60.70 ± 2.55	51.35 ± 4.35	$61.36{\pm}2.54$	57.47±3.03	60.18 ± 2.53	70.89 ± 2.44	$77.30{\scriptstyle \pm 5.15}$	74.74±2.28	71.97±3.86
ENZYMES	53.67 ± 2.66	$51.30{\scriptstyle \pm 2.01}$	55.24 ± 2.66	51.60 ± 3.81	53.80 ± 4.50	$53.60{\pm}4.88$	58.75 ± 5.98	$\underline{61.39{\scriptstyle\pm8.81}}$	61.23 ± 4.58	$63.90{\scriptstyle\pm3.69}$
AIDS	50.79 ± 4.30	51.84 ± 2.87	50.12 ± 3.43	61.13 ± 0.71	70.19 ± 5.03	79.72 ± 3.98	78.16 ± 3.05	93.27 ± 4.19	94.09 ± 1.75	$97.28{\scriptstyle\pm0.69}$
DHFR	47.91±3.76	52.11 ± 3.96	50.24 ± 3.13	50.29 ± 2.77	52.68±3.21	51.10 ± 2.35	49.23 ± 3.05	56.71±3.57	62.71±3.38	62.67 ± 3.11
BZR	46.85 ± 5.31	55.32 ± 6.18	50.56 ± 5.87	52.46 ± 3.30	63.31 ± 8.52	60.24 ± 5.37	65.91±1.47	69.42 ± 7.78	74.48 ± 4.91	$75.16{\scriptstyle \pm 5.15}$
COX2	50.27 ± 7.91	50.05 ± 2.06	49.86 ± 7.43	50.27 ± 0.34	53.36 ± 8.86	52.01 ± 3.17	53.58 ± 5.05	59.37 ± 12.67	60.46 ± 12.34	$62.65{\scriptstyle\pm8.14}$
DD	48.30 ± 3.98	71.32 ± 2.41	47.99 ± 4.09	70.31 ± 1.09	55.80±1.77	59.32 ± 3.92	72.27 ± 1.83	$80.12{\scriptstyle \pm 5.24}$	72.24 ± 1.82	73.25 ± 3.19
NCI1	49.90 ± 1.18	50.58 ± 1.38	50.63 ± 1.22	50.74 ± 1.70	50.10 ± 0.87	$49.88 {\pm} 0.53$	71.98 ± 1.21	68.48 ± 2.39	59.56±1.62	61.12 ± 2.21
IMDB-B	50.75 ± 3.10	50.80 ± 3.17	54.08 ± 5.19	$50.20{\scriptstyle \pm 0.40}$	56.50 ± 3.58	$56.50 {\pm} 4.90$	60.19 ± 8.90	52.09 ± 3.41	65.49 ± 1.06	$65.88{\scriptstyle \pm 0.75}$
REDDIT-B	45.68 ± 2.24	46.72 ± 3.42	49.31 ± 2.33	48.26 ± 0.32	68.50 ± 5.56	$71.80{\pm}4.38$	75.93 ± 8.65	77.85 ± 2.62	87.87 ± 1.38	$88.67{\scriptstyle\pm1.24}$
COLLAB	49.59 ± 2.24	50.49 ± 1.72	52.60 ± 2.56	$50.69{\scriptstyle \pm 0.32}$	46.27 ± 0.73	47.61 ± 1.29	60.70 ± 2.97	52.94 ± 0.85	62.10 ± 0.63	$72.08{\scriptstyle\pm0.90}$
HSE	57.02 ± 8.42	56.87 ± 10.51	62.72 ± 10.13	53.02 ± 5.12	53.56±3.98	51.18 ± 2.71	64.84 ± 4.70	59.48 ± 1.44	69.18 ± 1.89	$69.65{\scriptstyle\pm2.14}$
MMP	46.65 ± 6.31	50.06 ± 3.73	55.24 ± 3.26	52.68 ± 3.34	54.59 ± 2.01	$54.54{\pm}1.86$	$71.23{\scriptstyle \pm 0.16}$	67.84 ± 0.59	70.18 ± 1.14	70.51 ± 1.56
p53	46.74 ± 4.88	50.69 ± 2.02	54.59 ± 4.46	50.85 ± 2.16	52.66 ± 1.95	53.29 ± 2.32	58.50 ± 0.37	$\underline{64.20{\scriptstyle\pm0.81}}$	$66.48{\scriptstyle \pm 0.56}$	62.99 ± 1.55
PPAR-gamma	53.94 ± 6.94	45.51 ± 2.58	57.91 ± 6.13	$49.60{\scriptstyle \pm 0.22}$	51.40 ± 2.53	50.30 ± 1.56	$71.19{\scriptstyle \pm 4.28}$	64.59 ± 0.67	66.85±2.19	$\underline{67.34{\pm}1.71}$
Avg. Rank	8.7	7.7	6.9	7.5	6.5	6.9	3.5	3.1	2.3	1.7





Table 3: Ablation study results of GOOD- D_{simp} and its variants in terms of AUC (in percent, mean \pm std).

ſ.	ſ.	ſ	BZR	PTC-MR	AIDS	ENZYMES	IMDB-M	Tox21	FreeSolv	BBBP	ClinTox	Esol
\mathcal{L}_{node}	\mathcal{L}_{graph}	Lgroup	COX2	MUTAG	DHFR	PROTEIN	IMDB-B	SIDER	ToxCast	BACE	LIPO	MUV
\checkmark	-	-	83.51 ± 4.14	72.48 ± 3.77	96.84 ± 0.58	60.85 ± 2.95	$79.34{\pm}1.81$	62.58 ± 0.67	59.48 ± 2.20	69.53 ± 2.29	53.29 ± 4.32	86.49 ± 1.20
-	\checkmark	-	87.44 ± 4.66	77.84 ± 3.71	97.60 ± 1.05	56.74±1.96	75.22 ± 1.91	65.07 ± 1.32	$78.40{\scriptstyle\pm6.44}$	77.66 ± 2.29	70.11 ± 2.44	89.57 ± 2.80
-	-	\checkmark	79.21 ± 5.60	74.83 ± 8.54	89.47 ± 1.85	50.43 ± 7.41	72.91 ± 2.75	54.84 ± 2.56	58.16 ± 6.23	58.09 ± 5.43	58.46 ± 5.35	83.35 ± 2.71
\checkmark	\checkmark	-	93.14 ± 3.63	77.53 ± 4.02	98.90 ± 0.42	61.48 ± 3.46	79.55 ± 1.35	65.44 ± 1.13	71.45 ± 4.23	80.43 ± 2.57	65.89 ± 4.57	90.94 ± 1.16
\checkmark	-	\checkmark	85.01 ± 3.05	76.10 ± 3.01	96.87 ± 0.52	59.69 ± 1.89	79.69 ± 1.67	63.01 ± 0.97	56.30 ± 5.33	69.66 ± 2.45	54.14 ± 4.01	86.31±1.99
-	\checkmark	\checkmark	86.59 ± 5.24	77.97 ± 4.00	97.22 ± 1.35	55.51 ± 4.39	76.17 ± 1.65	$65.48{\scriptstyle\pm0.78}$	77.38 ± 5.19	79.77 ± 4.39	$70.20{\scriptstyle \pm 1.01}$	88.33 ± 1.35
\checkmark	\checkmark	\checkmark	93.00 ± 3.20	$78.43{\scriptstyle \pm 2.67}$	$98.91{\scriptstyle\pm0.41}$	$61.89{\scriptstyle\pm2.51}$	$79.71{\scriptstyle\pm1.19}$	$65.30{\pm}1.27$	70.48 ± 2.75	$81.56{\scriptstyle \pm 1.97}$	66.13 ± 2.98	$91.39{\scriptstyle \pm 0.46}$

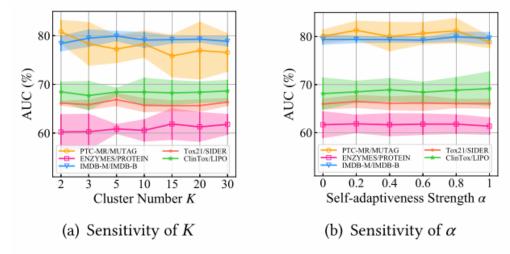


Figure 3: Parameter sensitivity of *K* and α .



Experiments

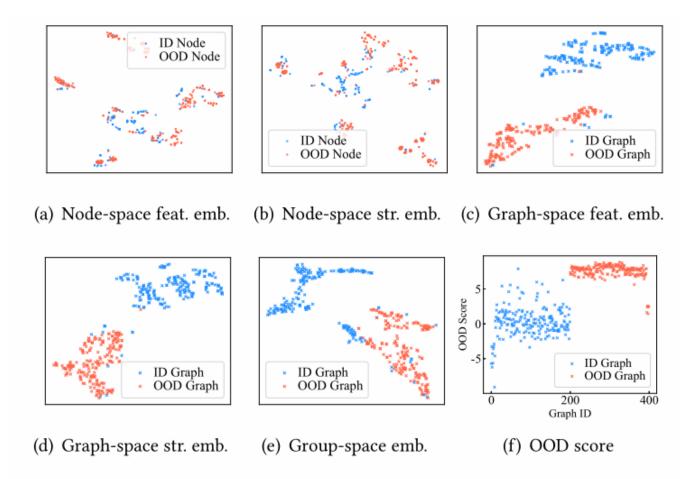


Figure 4: Visualization on AIDS/DHFR dataset pair. (a)-(e): t-SNE visualization of testing sample embeddings (emb.) of feature (feat.) or structure (str.) view at different embedding spaces. (f): OOD scores of GOOD-D on testing samples.