

Bringing Your Own View: Graph Contrastive Learning without Prefabricated Data Augmentations

The 15th ACM International Conference on Web Search and Data Mining

Phoenix, Az, USA

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February 21–25, 2022

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> Motivations

- Unlike images, graph data are inherently heterogenous (e.g. pandemics, product co-purchase relation, molecules).
- The SOTA GraphCL [1] handles the heterogenousity with ad-hoc choices of augmentations (priors) for every datasets.
- * Rather than the **discrete** selection on prefabricated ones, can we directly learn and generate such priors, **continuously**?
- Question: What us the space, principle and framework for learnable GraphCL priors (GraphCL-LP)?

Method. Graph Generative Models as Learnable Priors

- ❖ We define the **space** of GraphCL priors as the set of stochastic mappings between graph manifolds $m: G \rightarrow G$.
- ❖ Naturally, we adopt the recent rising graph generative models (VGAE [2] here) for the prior space **parametrization**.
- Further, principled reward signals are introduced to convey messages from contrastive learning to generator training.
- ❖ Above components are assembled into the bi-level optimization **framework**.

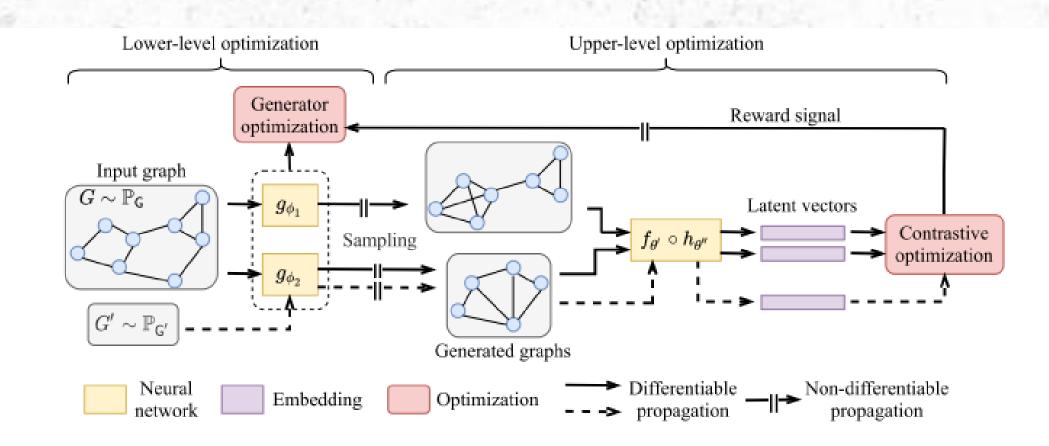


Figure 2: Pipeline of GraphCL with learned prior. Graph generative models g_{ϕ_1}, g_{ϕ_2} generate contrastive views for self-supervised contrasting, and then receive the reward for their parameter update.

> References

[1] Yuning You et al., "Graph Contrastive Learning with Augmentations", NeurIPS'20. [2] Thomas Kipf & Max Welling, "Variational Graph Auto-Encoders", NeurIPS'16 Workshop. [3] Chence Shi et al., "Graphaf: a flow-based autoregressive model for molecular graph generation ", ICLR'20.

> Method. Principles for Learning Priors to Contrast

- Information minimization (InfoMin). Encouraging contrastive views to share less mutual information.
- Information bottleneck (InfoBN). Diminishing the information overlap between each contrastive view and its latent representation.

> Experiments

We numerically show the competitive performance of GraphCL-LP versus SOTA methods.

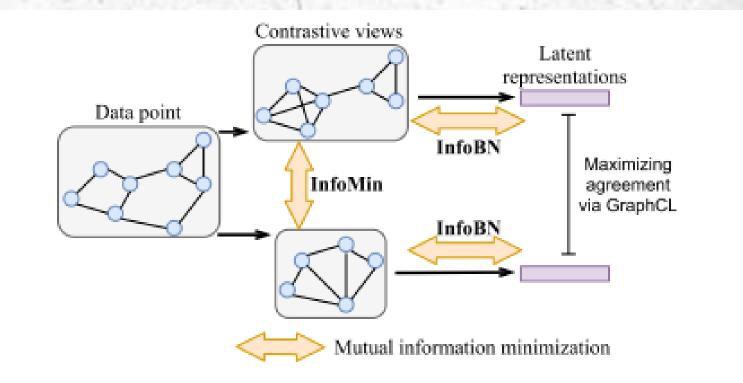


Figure 3: Schematic diagram of the InfoMin and InfoBN principles to guide the prior learning in GraphCL.

Table 2: Semi-supervised learning on small-scale benchmarks from TUDataset (the first four) and large-scale ones from OGB (the last two). Shown in red are the best three accuracies (%) for TUDataset and the best for ogbg-ppa and F1-score (%) for ogbg-code. The SOTA results compared here are as published under the same experimental setting (- indicates that results were not available in corresponding publications).

Methods	COLLAB	RDT-B	RDT-M5K	GITHUB	ogbg-ppa	ogbg-code
No pre-train	73.71±0.27	86.63±0.27	51.33±0.44	60.87±0.17	56.01±1.05	17.85±0.60
Augmentations	74.19 ± 0.13	87.74±0.39	52.01 ± 0.20	60.91 ± 0.32	-	_
GAE	75.09±0.19	87.69±0.40	53.58 ± 0.13	63.89±0.52	-	-
Infomax	73.76 ± 0.29	88.66±0.95	53.61±0.31	65.21±0.88	-	-
ContextPred	73.69 ± 0.37	84.76 ± 0.52	51.23 ± 0.84	62.35±0.73	-	-
GraphCL	74.23 ± 0.21	89.11 ±0.19	52.55 ± 0.45	65.81±0.79	57.77±1.25	22.45 ± 0.17
LP-InfoMin	74.66±0.14	88.03±0.46	53.00±0.26	62.71±0.54	59.10 ±0.88	23.50±0.22
LP-InfoBN	74.61 ± 0.28	87.64±0.33	53.05 ± 0.14	62.64±0.37	55.48 ± 0.97	23.31 ± 0.22
LP-Info(Min&BN)	74.84 ± 0.31	87.81 ± 0.45	53.32 ± 0.23	63.11±0.33	57.31±0.99	23.61±0.27

Further analysis show: graph generation quality usually aligns with downstream performance; and also molecule-specific generator (GraphAF here) alone does not significantly benefit molecular datasets.

Table 5: Link prediction performance (AUROC and AUPRC, %) of VGAE generators on eight pre-training datasets. Better link prediction results are marked in red if accompanied with better downstream performances, as shown in Table 2, 3 and 4.

	Principles	COLLAB	RDT-B	RDT-M5K	GITHUB	ogbg-ppa	ogbg-code	Trans-Mol	Trans-PPI
AIDOC (%)	InfoMin	71.28	97.32	99.08	78.68	96.53	92.39	64.54	71.20
AUROC (%)	InfoBN	69.44	97.29	99.31	81.20	95.24	94.06	83.55	71.32
AUPRC (%)	InfoMin	80.84	96.62	98.67	78.49	95.94	90.08	64.14	69.34
AUFRC (%)	InfoBN	79.13	96.59	98.97	80.47	95.30	91.66	82.51	70.65

Table 6: Learned prior performance with different generators under the guidance of InfoMin, in the transfer learning setting on molecular datasets. Red numbers indicate the best performances (AUROC, %).

Methods	BBBP	Tox21	ToxCast	SIDER	ClinTox	MUV	HIV	BACE
VGAE	71.47±0.66	74.60 ± 0.70	63.13±0.30	60.52±0.75	72.39 ± 1.50	70.51±2.25	76.43 ± 0.85	78.86±1.66
GraphAF	70.55±0.63	73.51 ± 0.43	62.03±0.33	61.32 ± 1.32	77.47±1.91	72.25 ± 1.18	76.30±1.34	78.43±2.36

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