Non-Homophilic Graph Pre-Training and Prompt Learning

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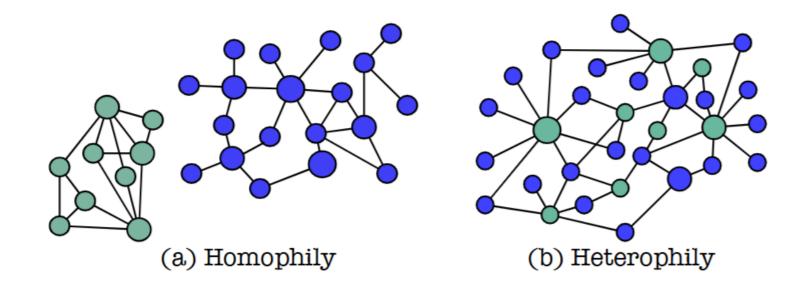
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- 1. Motivation & Challenges
- 2. Theoretical Insights
- 3. Proposed Model: ProNoG
- 4. Experiments
- 5. Conclusions

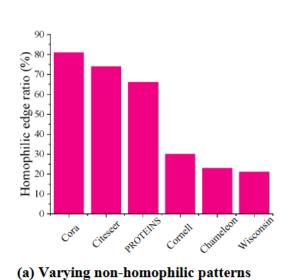
Motivation & Challenges



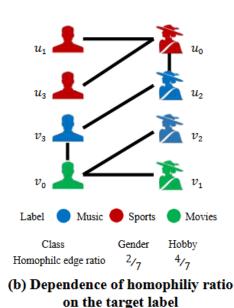
Real-world graphs are typically non-homophilic:

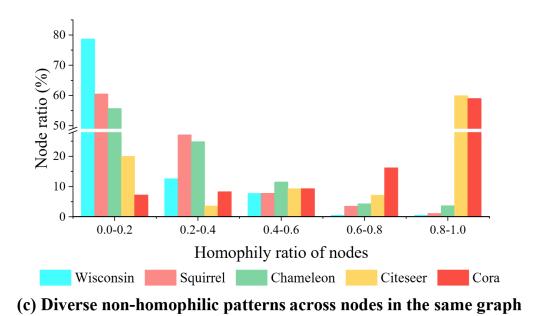
- They are neither strictly or uniformly homophilic;
- Mix both homophilic and heterophilic patterns.

Motivation & Challenges



across different graphs





- *C1:* How do we pre-train a graph model irrespective of the graph's homophily characteristics?
- C2: How do we capture the fine-grained, node-specific non-homophilic characteristics?

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Theoretical Insights

Contrastive pre-training method loss function

$$\mathcal{L}_T = -\sum_{u \in V} \ln P(u, \mathcal{A}_u, \mathcal{B}_u), \tag{4}$$

$$\sum_{u \in V} \operatorname{sim}(\mathbf{h}_u, \mathbf{h}_u)$$

$$P(u, \mathcal{A}_u, \mathcal{B}_u) \triangleq \frac{\sum_{a \in \mathcal{A}_u} \text{sim}(\mathbf{h}_u, \mathbf{h}_a)}{\sum_{a \in \mathcal{A}_u} \text{sim}(\mathbf{h}_u, \mathbf{h}_a) + \sum_{b \in \mathcal{B}_u} \text{sim}(\mathbf{h}_u, \mathbf{h}_b)}, \quad (5)$$

Definition of homophily task

Definition 1 (Homophily Task). On a graph G = (V, E), a pretraining task $T = (\{\mathcal{A}_u : u \in V\}, \{\mathcal{B}_u : u \in V\})$ is a homophily task if and only if, $\forall u \in V, \forall a \in \mathcal{A}_u, \forall b \in \mathcal{B}_u, (u, a) \in E \land (u, b) \notin E$. A task that is not a homophily task is called a non-homophily task. \square

Table 6: Positive and negative samples for homophily and non-homophily methods.

Pre-training task	Positive instances \mathcal{A}_u	Negative instances \mathcal{B}_u	Homophily task
Link prediction [26, 62, 64]	a node connected to node u	nodes disconnected to node u	Yes
DGI [48]	nodes in graph G	nodes in corrupted graph G'	No
GraphCL [60]	an augmented graph from graph G	augmented graphs from $G' \neq G$	No
GraphACL [55]	nodes with similar ego-subgraph to node u	nodes with dissimilar ego-subgraph to node u	No

Theoretical Insights

Theorems

THEOREM 1. For a homophily task T, adding a homophily sample always results in a smaller loss than adding a non-homophily sample.

Theorem 2. Consider a graph G = (V, E) with a label mapping function $V \to Y$, and let $y_v \in Y$ denote the label mapped to $v \in V$. Suppose the label mapping satisfies that

$$\forall u, a, b \in V, y_u = y_a \land y_u \neq y_b \Rightarrow sim(u, a) > sim(u, b).$$

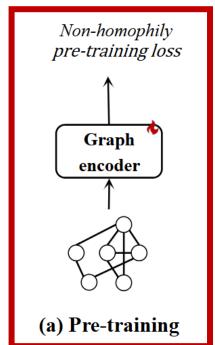
Let \mathbb{E}_T denote the expected number of homophily samples for a homophily task T on the graph G. Then, \mathbb{E}_T increases monotonically as the homophily ratio $\mathcal{H}(G)$ defined w.r.t. Y increases.

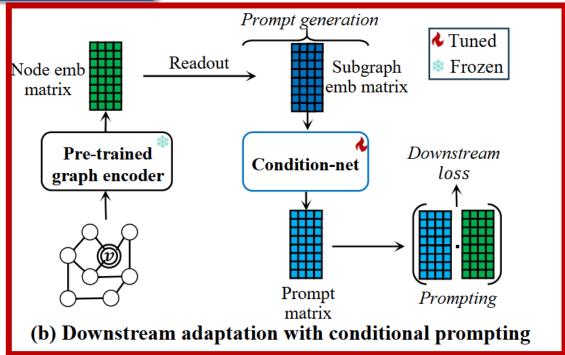
Insights

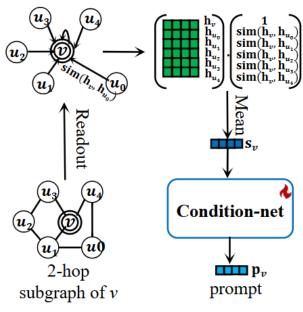
For non-homophilic graphs, especially those with low homophily ratio, non-homophily tasks are a better choice compared to homophily tasks when optimizing the training loss.

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Proposed Method: ProNoG







(c) Details of prompt generation

Figure 2: Overall framework of ProNoG.

Prompt generation

$$\mathbf{s}_v = \frac{1}{|S_v|} \sum_{u \in S_v} \mathbf{h}_u \cdot \operatorname{sim}(\mathbf{h}_u, \mathbf{h}_v),$$

$$\mathbf{p}_{t,v} = \mathsf{CondNet}(\mathbf{s}_v; \phi_t),$$

Prompt tuning

$$\tilde{\mathbf{h}}_{t,v} = \mathbf{p}_{t,v} \odot \mathbf{h}_v,$$

$$\mathcal{L}_{\text{down}}(\phi_t) = -\sum_{(x_i, y_i) \in \mathcal{D}_t} \ln \frac{\exp\left(\frac{1}{\tau} \text{sim}(\tilde{\mathbf{h}}_{t, x_i}, \bar{\mathbf{h}}_{t, y_i})\right)}{\sum_{c \in Y} \exp\left(\frac{1}{\tau} \text{sim}(\tilde{\mathbf{h}}_{t, x_i}, \bar{\mathbf{h}}_{t, c})\right)},$$

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Experiment

Table 2: Accuracy evaluation on few-shot node classification.

Methods	Wisconsin	Squirrel	Chameleon	Cornell	PROTEINS	ENZYMES	Citeseer	Cora
GCN	21.39 ± 6.56	20.00 ± 0.29	25.11 ± 4.19	21.81 ± 4.71	43.32 ± 9.35	48.08 ± 4.71	31.27 ± 4.53	28.57 ± 5.07
GAT	28.01 ± 5.40	21.55 ± 2.30	24.82 ± 4.35	23.03 ± 13.19	31.79 ± 20.11	35.32 ± 18.72	30.76 ± 5.40	28.40 ± 6.25
H2GCN	23.60 ± 4.64	21.90 ± 2.15	25.89 ± 4.96	32.77 ± 14.88	29.60 ± 6.99	37.27 ± 8.73	26.98 ± 6.25	34.58 ± 9.43
FAGCN	35.03 ± 17.92	20.91 ± 1.79	22.71 ± 3.74	28.67 ± 17.64	32.63 ± 9.94	35.87 ± 13.47	26.46 ± 6.34	28.28 ± 9.57
DGI	28.04 ± 6.47	20.00 ± 1.86	19.33 ± 4.57	32.54 ± 15.66	45.22 ± 11.09	48.05 ± 14.83	45.00 ± 9.19	54.11 ± 9.60
GraphCL	29.85 ± 8.46	21.42 ± 2.22	27.16 ± 4.31	24.69 ± 14.06	46.15 ± 10.94	48.88 ± 15.98	43.12 ± 9.61	51.96 ± 9.43
DSSL	28.46 ± 10.31	20.94 ± 1.88	27.92 ± 3.93	20.36 ± 5.38	40.42 ± 10.08	66.59 ± 19.28	39.86 ± 8.60	40.79 ± 7.31
GraphACL	34.57 ± 10.46	24.44 ± 3.94	26.72 ± 4.67	33.17 ± 16.06	42.16 ± 13.50	47.57 ± 14.36	35.91 ± 7.87	46.65 ± 9.54
GPPT	27.39 ± 6.67	20.09 ± 0.91	24.53 ± 2.55	25.09 ± 2.92	35.15 ± 11.40	35.37 ± 9.37	21.45 ± 3.45	15.37 ± 4.51
GraphPrompt	31.48 ± 5.18	21.22 ± 1.80	25.36 ± 3.99	31.00 ± 13.88	47.22 ± 11.05	53.54 ± 15.46	45.34 ± 10.53	54.25 ± 9.38
GraphPrompt+	31.54 ± 4.54	21.24 ± 1.82	25.73 ± 4.50	31.65 ± 14.48	46.08 ± 9.96	57.68 ± 13.12	45.23 ± 10.01	$\overline{52.51} \pm 9.73$
ProNoG	44.72 ± 11.93	24.59 ± 3.41	30.67 ± 3.73	37.90 ± 9.31	48.95 ± 10.85	72.94 ± 20.23	49.02 ± 10.66	57.92 ± 11.50

Results are reported in percent. The best method is bolded and the runner-up is underlined.

Experiment

Table 3: Accuracy evaluation on few-shot graph classification.

Methods	Wisconsin	Squirrel	Chameleon	Cornell	PROTEINS	ENZYMES	BZR	COX2
GCN	21.39 ± 6.56	11.77 ± 3.10	17.21 ± 4.80	26.36 ± 4.35	51.66 ± 10.87	19.30 ± 6.36	45.06 ± 16.30	43.84 ± 13.94
GAT	24.93 ± 7.59	20.70 ± 1.51	25.71 ± 3.32	22.66 ± 12.46	51.33 ± 11.02	20.24 ± 6.39	46.28 ± 15.26	51.72 ± 13.70
H2GCN	22.23 ± 6.38	20.69 ± 1.42	26.76 ± 3.98	23.11 ± 11.78	53.81 ± 8.85	19.40 ± 5.57	50.28 ± 12.13	53.70 ± 11.73
FAGCN	23.81 ± 9.50	20.83 ± 1.43	25.93 ± 4.03	25.71 ± 13.12	55.45 ± 11.57	19.95 ± 5.94	50.93 ± 12.41	50.22 ± 11.50
DGI	29.77 ± 6.22	20.50 ± 1.52	24.29 ± 4.33	18.60 ± 12.79	50.32 ± 13.47	21.57 ± 5.37	49.97 ± 12.63	54.84 ± 14.76
GraphCL	27.93 ± 5.27	<u>21.01</u> ± 1.86	26.45 ± 4.30	20.03 ± 10.05	54.81 ± 11.44	19.93 ± 5.65	50.50 ± 18.62	47.64 ± 22.42
DSSL	22.05 ± 3.90	20.74 ± 1.61	26.19 ± 3.72	18.38 ± 10.63	52.73 ± 10.98	23.14 ± 6.71	49.04 ± 8.75	54.23 ± 14.17
GraphACL	22.98 ± 5.89	20.80 ± 1.28	26.28 ± 3.93	26.50 ± 17.18	56.11 ± 13.95	20.28 ± 5.60	49.24 ± 17.87	49.59 ± 23.93
	28.34 ± 3.89	21.22 ± 1.80	26.51 ± 4.67	24.06 ± 13.71	53.61 ± 8.90	21.85 ± 6.17	50.46 ± 11.46	55.01 ± 15.23
GraphPrompt+	26.95 ± 7.42	20.80 ± 1.45	26.03 ± 4.17	25.31 ± 7.65	54.55 ± 12.61	21.85 ± 5.15	53.26 ± 14.99	$\overline{54.73} \pm 14.58$
ProNoG	31.54 ± 5.30	20.92 ± 1.37	28.50 ± 5.30	27.17 ± 9.58	<u>56.11</u> ± 10.19	22.55 ± 6.70	51.62 ± 14.27	56.46 ± 14.57

Experiment 50 Accuracy (%) Accuracy 52 0.4-0.6 0.6-0.8 0.8-1.0 0.4-0.6 0.6-0.8 0.0 - 0.20.2 - 0.40.2 - 0.4Homophily ratio of nodes Homophily ratio of nodes Wisconsin Cornell 70 60 Accuracy (%) Accuracy 0.0-0.2 0.2-0.4 0.4-0.6 0.6-0.8 0.8-1.0 0.0-0.2 0.2-0.4 0.4-0.6 0.6-0.8 0.8-1.0 Homophily ratio of nodes Homophily ratio of nodes Cora Citeseer

Figure 4: Results on different node patterns.

ProNoG

GraphPrompt

GraphACL

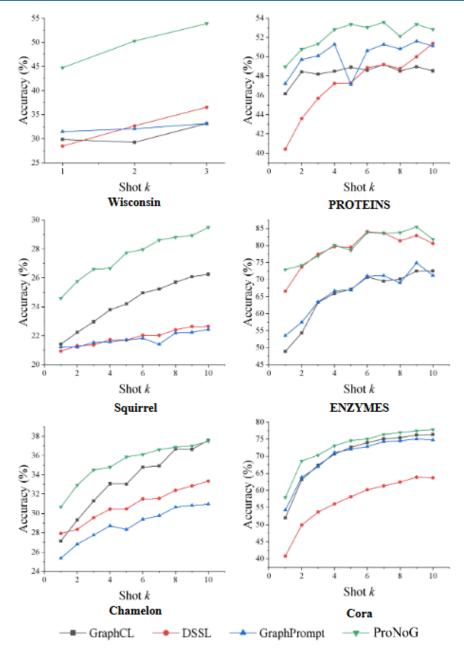


Figure 3: Impacts of different shots on node classification.

Conclusions

- We explored pre-training and prompt learning on non-homophilic graphs.
- We revisited graph pre-training on non-homophilic graphs, providing theoretical insights into the choice of pre-training tasks.
- For downstream adaptation, we proposed a condition-net to generate a series of prompts conditioned on node-specific non-homophilic patterns.
- We conducted extensive experiments showing that ProNoG significantly outperforms diverse state-of-the-art baselines.

Experiment

Thank you! Questions?

• ProNoG paper & github repo:

GCoT: Chain-of-Thought Prompt Learning for Graphs

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