Node Identifiers: Compact, Discrete Representations for Efficient Graph Learning

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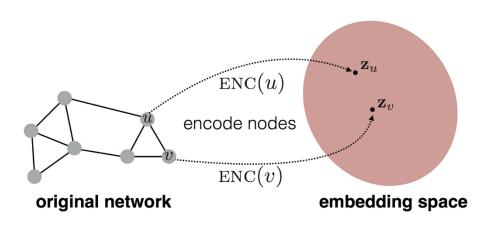
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Introduction: Challenges in GNNs

- ■Efficiency in Large-Scale Graphs
 - lacktriangle Message-passing requires full graph loading \rightarrow high inference compute costs (billions of edges).
 - ◆High-dimensional embeddings (128-256 dim) → storage and interpretability issues.

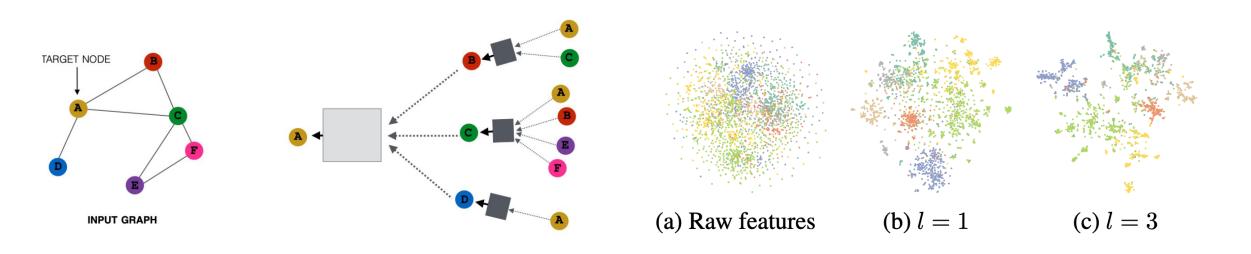




Message-passing Mechanism

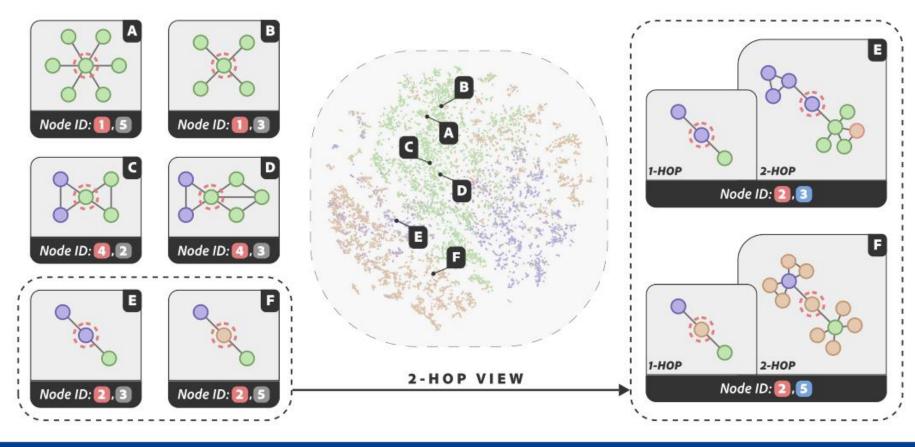
The message-passing mechanism creates new node representations, where each node gathers information from its neighbors and combines it to update its own embedding.

Due to the smoothing effect of message passing, the node representations generated by GNNs exhibit distinct clustering patterns.

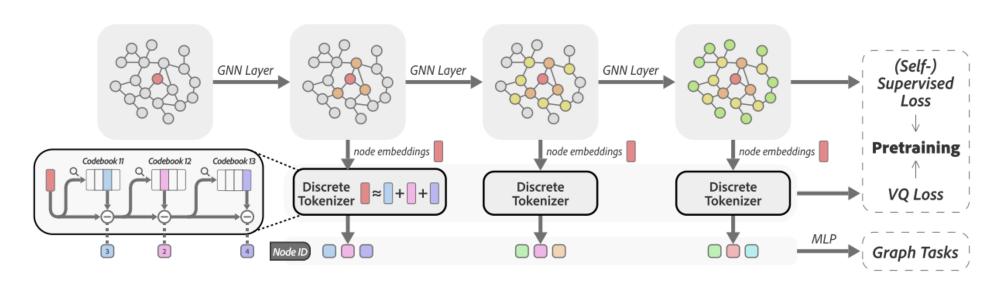


Our Solution: Node IDs

We present a novel end-to-end framework that generates highly compact (typically 6-15 dimensions), discrete (int4 type), and interpretable node representations—termed node identifiers (node IDs).



Methodology: NID Framework



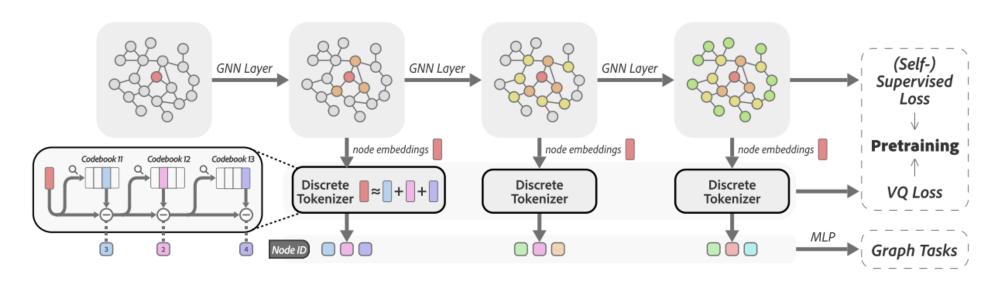
1. Node ID Generation:

 Residual VQ (RVQ) quantizes embeddings per layer into codewords (integer indices) tuples: (Each layer has M codebooks (RVQ))

Node_ID(
$$v$$
) = $(c_{\{11\}}, ..., c_{\{1M\}}, ..., c_{\{L1\}}, ..., c_{\{LM\}})$

2. Downstream Task Application.

Node ID Generation via RVQ



$$egin{aligned} \mathcal{L}_{ ext{NID}} &= \mathcal{L}_{\mathcal{G}} + \mathcal{L}_{ ext{VQ}}, \ \mathcal{L}_{ ext{VQ}} &= \sum_{l=1}^{L} \sum_{m=1}^{M} \| ext{sg}(oldsymbol{r}_{lm}) - oldsymbol{e}_{c_{lm}}^{lm} \| + eta \|oldsymbol{r}_{lm} - ext{sg}(oldsymbol{e}_{c_{lm}}^{lm}) \| \end{aligned}$$

No reconstruction loss \rightarrow guided by VQ loss.

Theoretical Analysis

Theorem 1. The optimizer C^* of VQ objective (7) satisfies that, for any x_u and x_v , $u, v \in V$ with different labels, Node_ $ID(u) \neq Node_{ID}(v)$. Then, as long as V_R uniformly include node IDs from all the classes, by training the linear head V with sufficient gradient descent steps, we can achieve that the classification error $\mathbb{1}[y_v \neq \arg\max_{i \in [P]} \hat{p}_{v,i}] = 0$ for any $v \in V$.

Theorem 1 illustrates that the optimized C* of VQ objective (7) ensures that the obtained IDs from different classes are distinct. Then, we demonstrate that with node IDs in the training set, a linear head can be learned to achieve a zero classification error.

Experiments: Key Results

Supervised Tasks (Node/Graph Classification, Link Prediction):

- Matches or outperforms SOTA GNNs.
- 10-1000x Faster Inference:

ogbn-products: $11.9s \rightarrow 0.7ms$ per inference.

Table 1: Node classification results in supervised representation learning over homophilic and heterophilic graphs (%). The baseline results are primarily taken from Polynormer (Deng et al., 2024).

Transductive	Cora	CiteSeer	PubMed	Computer	Photo	CS	Physics	WikiCS	Squirrel	Chameleon	Ratings	Questions
# nodes # edges Metric	2,708 5,278 Accuracy†	3,327 4,732 Accuracy†	19,717 44,324 Accuracy↑	13,752 245,861 Accuracy†	7,650 119,081 Accuracy†	18,333 81,894 Accuracy†	34,493 247,962 Accuracy†	11,701 216,123 Accuracy†	2223 46,998 Accuracy†	890 8,854 Accuracy↑	24,492 32,927 Accuracy†	48,921 153,540 ROC-AUC↑
GPRGNN APPNP SGFormer Polynormer	87.87 ± 0.82 87.83 ± 0.92	$76.53 \pm 1.16 \\ 77.24 \pm 0.74$	88.43 ± 0.15 89.31 ± 0.54	90.18 ±0.17 92.42 ±0.66	94.32 ±0.14 95.58 ±0.36	94.49 ±0.07 95.71 ±0.24	96.54 ±0.07 96.75 ±0.26	78.87 ± 0.11 80.05 ± 0.46	36.88 ± 1.27 42.65 ± 2.41	39.93 ± 3.30 41.62 ± 3.13 45.21 ± 3.72 41.82 ± 3.45	54.14 ±0.62	55.48 ± 0.91 77.82 ± 1.31 73.81 ± 0.59 78.92 ± 0.89
Graph-MLP VQGraph							95.45 ±0.24 95.93 ±0.28		-	-	-	-
GCN NID _{GCN}										46.11 ± 3.16 46.29 ± 2.92		77.40 ± 1.07 96.85 ± 0.10
GAT NID _{GAT}	00122	77.08 ± 0.84 76.13 ± 1.35								43.44 ± 3.00 42.83 ± 3.42		78.35 ± 1.16 97.03 ± 0.02

Table 2: Node classification results in supervised representation Table 3: Graph-level performance in super-learning on large-scale graphs (%). vised representation learning from LRGB.

Transductive	ogbn-proteins	ogbn-arxiv	ogbn-products	pokec
# nodes	132,534	169,343	2,449,029	1,632,803
# edges	39,561,252	1,166,243	61,859,140	30,622,564
Metric	ROC-AUC↑	Accuracy↑	Accuracy↑	Accuracy↑
GPRGNN LINKX GraphGPS SGFormer Polynormer	$75.68 \pm 0.49 \\ 71.37 \pm 0.58 \\ 76.83 \pm 0.26 \\ 79.53 \pm 0.38 \\ 75.97 \pm 0.47$	71.10 ± 0.12 66.18 ± 0.33 70.97 ± 0.41 72.63 ± 0.13 71.82 ± 0.23	79.76 ± 0.59 71.59 ± 0.71 OOM 74.16 ± 0.31 82.97 ± 0.28	$78.83 \pm 0.05 \\ 82.04 \pm 0.07 \\ OOM \\ 73.76 \pm 0.24 \\ 85.95 \pm 0.07$
SAGE	79.43 ± 0.75	72.67 ± 0.31	83.27 ± 0.35	85.97 ± 0.21
Infer. Time	158.1ms	416.5ms	11.9s	129.6s
Storage Space	129.4MB	165.7MB	1.9GB	1.6GB
NID _{SAGE}	76.78 ± 0.59	70.52 ± 0.14	81.83 ± 0.26	85.63 ± 0.31
Infer. Time	0.4ms	0.3ms	0.7ms	27.1ms
Storage Space	0.4MB	1.2MB	17.5MB	16.4MB

•		
Inductive	Peptides-func	Peptides-struct
Avg. # nodes	150.9	150.9
Avg. # edges	307.3	307.3
Metric	AP↑	$MAE \downarrow$
GT	0.6326 ± 0.0126	0.2529 ± 0.0016
GraphGPS	0.6535 ± 0.0041	0.2500 ± 0.0012
GRIT	0.6988 ± 0.0082	0.2460 ± 0.0012
Exphormer	0.6527 ± 0.0043	0.2481 ± 0.0007
Graph ViT	0.6970 ± 0.0080	0.2449 ± 0.0016
GCN	0.6762 ± 0.0053	0.2512 ± 0.0007
Infer. Time	471.1ms	424.9ms
NID _{GCN}	0.6608 ± 0.0058	0.2589 ± 0.0014
Infer. Time	0.4ms	0.4ms

Node IDs, typically comprising 6 to 15 int4 integers, serve as effective node representations.

Experiments: Key Results

Unsupervised Tasks (Graph Clustering, Unsupervised Prediction):

- Matches or outperforms SOTA GNNs.
- Faster Clustering.

Table 5: Attributed graph clustering results; normalized mutual information, and F1-score (%).

	Co:	ra F1↑	CiteS NMI↑	Seer F1↑	PubN NMI↑	Med F1↑	Comp NMI↑	outer F1↑	Pho NMI↑	oto F1↑	Phys	sics F1↑	ogbn-a NMI↑	arxiv F1↑
SBM	36.2	30.2	15.3	19.1	16.4	16.7	48.4	34.6	59.3	47.4	45.4	30.4	31.9	28.3
AGC	34.1	28.9	25.5	27.5	18.2	18.4	51.3	35.3	59.0	44.2	-	-	-	-
SDCN	27.9	29.9	31.4	41.9	19.5	29.9	24.9	45.2	41.7	45.1	50.4	39.9	15.3	28.8
DAEGC	8.3	13.6	4.3	18.0	4.4	11.6	42.5	37.3	47.6	45.0	-	_	-	-
NOCD	46.3	36.7	20.0	24.1	25.5	20.8	44.8	37.8	62.3	60.2	51.9	28.7	20.7	38.2
DiffPool	32.9	34.4	20.0	23.5	20.2	26.3	22.1	38.3	35.9	41.8 -	-	_	-	
MinCut	35.8	25.0	25.9	20.1	25.4	15.8	-	_	-	-	48.3	24.9	36.0	27.1
Ortho	38.4	26.6	26.1	20.5	20.3	13.9	_	-	-	-	44.7	23.7	35.6	26.7
DMoN	48.8	48.8	33.7	43.2	29.8	33.9	49.3	45.4	63.3	61.0	56.7	42.4	37.6	45.7
DGCluster	62.1	54.5	41.0	32.2	32.6	34.6	60.4	52.2	77.3	75.9	65.7	49.2	31.2	32.4
Clustering Time	93.6	ms	119.6	óms	405.5	5ms	286.1	lms	204.	6ms	547.4	4ms	2.7	s
NID _{DGCluster}	70.5	73.9	54.1	63.3	40.6	50.9	62.1	58.2	75.6	75.4	69.8	65.4	32.4	35.6
Clustering Time	78.3	ms	77.2	ms	292.5	5ms	223.6	óms	140.	6ms	442.0	Oms	1.8	s

pervised representation learning (%).

Metric	Cora Accuracy↑	CiteSeer Accuracy↑	PubMed Accuracy↑	dim
GAE	71.5 ± 0.4	65.8 ± 0.4	72.1 ±0.5	16
DGI	82.3 ± 0.6	71.8 ± 0.7	76.8 ± 0.6	512
MVGRL	83.5 ± 0.4	73.3 ± 0.5	80.1 ± 0.7	512
InfoGCL	83.5 ± 0.3	73.5 ± 0.4	79.1 ± 0.2	512
CCA-SSG	84.0 ± 0.4	73.1 ± 0.3	81.0 ± 0.4	512
MLP	57.8 ± 0.5	54.7 ± 0.4	73.3 ± 0.6	500
GraphMAE	84.2 ± 0.4	73.4 ± 0.4	81.1 ± 0.4	512
NID _{MAE}	80.8 ± 0.7	74.2 ± 0.6	76.4 ± 0.8	6

Table 6: Node classification results in unsu- Table 7: Graph classification results in unsupervised representation learning on TUDataset; Accuracy (%).

# graphs	NCI1 4.110	PROTEINS 1,113	DD 1,178	MUTAG 188	COLLAB 5.000	RDT-B 2,000	RDT-M5K 4,999	IMDB-B 1.000
Avg. # nodes	.,	39.1	284.3	17.9	74.5	429.7	508.5	19.8
InfoGraph	76.2 ± 1.0	74.4 ± 0.3	72.8 ± 1.7	89.0 ± 1.1	70.6 ± 1.1	82.5 ± 1.4	53.4 ± 1.0	73.0 ± 0.8
MVGRL	-	-	-	89.7 ± 1.1	-	84.5 ± 0.6	-	74.2 ± 0.7
JOAO	78.3 ± 0.5	74.0 ± 1.1	77.4 ± 1.1	87.6 ± 0.7	69.3 ± 0.3	86.4 ± 1.4	56.0 ± 0.2	70.8 ± 0.2
GraphMAE	80.4 ± 0.3	75.3 ± 0.4	-	88.1 ± 1.3	80.3 ± 0.5	88.0 ± 0.2	-	75.5 ± 0.6
AD-GCL	69.6 ± 0.5	73.5 ± 0.6	74.4 ± 0.5	-	73.3 ± 0.6	85.5 ± 0.7	53.0 ± 0.8	71.5 ± 1.0
GraphCL	77.8 ± 0.4	74.3 ± 0.4	78.6 ± 0.4	86.8 ± 1.3	71.3 ± 1.1	89.5 ± 0.8	55.9 ± 0.2	71.1 ±0.4
NID _{CL}	75.9 ± 0.6	75.1 ± 0.5	77.8 ± 1.1	88.6 ± 1.7	76.9 ± 0.3	90.7 ± 0.9	55.0 ± 0.5	72.3 ± 1.2
AutoGCL	82.0 ± 0.2	75.8 ±0.3	77.5 ± 0.6	0010 - 110	70.1 ± 0.6	88.5 ± 1.4	56.7 ± 0.1	73.3 ±0.4
NID _{AutoGCL}	78.2 ± 1.5	75.9 ± 0.6	77.2 ± 0.9	90.4 ± 0.8	74.5 ± 1.1	89.8 ± 0.7	54.2 ± 0.6	72.4 ± 0.8

Node IDs, typically comprising 6 to 15 int4 integers, serve as effective node representations.

usage rates (%).

Usage rate↑	Cora	CiteSeer	PubMed
VQGraph	1.3	0.8	18.1
NID_{GCN}	84.7	97.9	79.1
$NID_{GCN(M=1)}$	83.3	81.3	78.1

Table 8: Comparison of codebook Table 9: Average GEDs of 1-hop Table 10: Accuracy vs Inference Time. subgraphs among nodes.

GEDs↓	Cora	CiteSeer	PubMed
Random VQGraph	7.21 6.85	4.83 4.73	9.61 9.03
NID _{GCN}	6.15	3.89	6.22

	Cor	nputer	ogbn-products		
Metric	Acc↑	Time↓	Acc↑	Time↓	
GCN	93.78	119.6ms	82.33	12.8s	
SAGE	93.59	95.7ms	83.27	11.9s	
VQGraph	90.28	1.4ms	79.17	1.6ms	
NID _{SAGE}	93.32	0.5ms	81.83	0.7ms	

Avoiding Codebook Collapse:

It was observed that VQGraph suffers from severe codebook collapse. In contrast, NID achieves high codebook utilization, effectively avoiding codebook collapse.

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Subgraph Retrieval:

Using the Graph Edit Distance (GED) of Node IDs for subgraph matching yields superior results compared to the existing VQGraph tokenizer.

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NID _{SAGE}	93.32	0.5ms	81.83	0.7ms

Inference Acceleration:

On the ogbn-products dataset (with millions of nodes), NID reduces inference time from 11.9 seconds to 0.7 milliseconds.

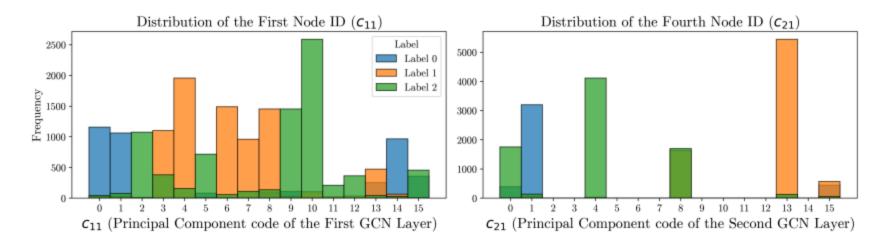


Figure 5: Codeword distributions of c_{11} and c_{21} in PubMed colored by the ground-truth labels.

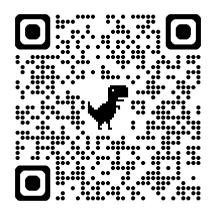
Interpretability:

By analyzing the distribution of Node IDs' codeword indices, it was found that they can effectively distinguish between nodes of different categories, demonstrating strong interpretability.

Conclusions

Node IDs without reconstruction task:

- No performance drop \rightarrow seamless integration with existing GNNs
- Compact (6-15 dim int4) \rightarrow ideal for large-scale
- ullet Interpretable ullet meaningful and human-understandable node features



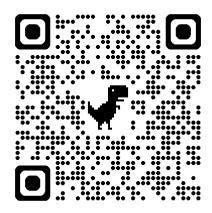
https://github.com/LUOyk1999/NodeID

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- Interpretable \rightarrow meaningful and human-understandable node features

Thanks for listening!



https://github.com/LUOyk1999/NodeID