

How can we use random walks in deep learning on graphs?

Why do we care?

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Work done while at RWTH Aachen together with Jan Tönshoff, Hinrikus Wolf, and Martin Grohe

Introduction

Introduction: Graphs are Everywhere



Molecules



Social Networks

Introduction: Graphs are Everywhere



This talk focuses on Graph Classification

Graph Learning







• Process graphs of any size and structure



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- Process graphs of any size and structure
- Permutation Invariance



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Solution: Message Passing

Message Passing: Extensions

Equivalent to the 1-dimensional Weisfeiler-Leman algorithm.



Many extensions have been proposed:

• Random Node IDs [Abboud et al., 2020]



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- Add motif counts as features [Bouritsas et al., 2020]

	Motif	Description
3-node	4	2-star
	Δ	triangle
	\square	4-path
1 node	\sim	3-star
4-node		4-tailedtriangle
		4-cycle
	\square	4-chordalcycle
	\boxtimes	4-clique
5-node	Ø	5-clique

Message Passing: Extensions

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Are there alternatives?

Random Walks for Graph Learning

Random Walk Graph Kernel

- Compare graphs through common random walks
- based on the number of length $p \in [P]$ random walks

(0	1	0	1	0)	p
1	0	1	0	0	
0	1	0	1	1	
1	0	1	0	0	
0	0	1	0	0)	

Random Walk Graph Kernel

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- Various usecases:
 - Graph kernel, e.g. with SVM
 - Structural embedding, e.g. in Graph Transformers
 - As GNN, e.g. RWGNN [Nikolentzos and Vazirgiannis, 2020]

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Intuition based on random walks, deterministic computation

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Random Walk Based Node Embeddings

DeepWalk and Node2Vec

- 1. Sample random walks
- 2. Run Skip-Gram to get the embedding:
 - Positive: co-occuring nodes
 - Negative: other nodes
 - \implies Embedding is a random variable



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Node2Vec just encodes proximity, can we use more structure?

CRAWL

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- Construct a feature matrix for each walk
- Process features with 1D-CNNs
- Use result to update latent node embeddings

Input: Graph G = (V, E) with node and edge features h, g**Hyperparameters:** number m and length ℓ of walks, window size s of the CNN



Step 1: Sample m random walks of length ℓ
































Step 2: Compute feature matrix for each walk with window size s





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	(1)	101 1	
(h(1))	00000	0000	000
h(2)	g(1,2)	0000	000
h(4)	g(2,4)	0000	100
h(3)	g(4,3)	0000	110
h(6)	g(3,6)	0000	000
h(8)	g(6,8)	0000	000
h(7)	g(8,7)	0000	100
h(6)	g(7,6)	0010	100
h(5)	g(6,5)	0000	000
h(2)	g(5,2)	0000	000 /

 $X(w_1, h, q, 4)$

Column 1: Node features



(h(1))		000
h(2)		000
h(4)		
h(3)		
h(6)		
h(8)		
h(7)		
h(6)		
h(5)		
h(2)		000/

 h_w

Column 2: Edge features



g_w		
00000		000
g(1,2)		
g(2,4)		
g(4,3)		
g(3,6)		
g(6,8)		
g(8,7)		
g(7,6)		
g(6,5)		
g(5,2)		000,
	g_w 00000 g(1,2) g(2,4) g(3,6) g(6,8) g(7,6) g(6,5) g(5,2)	$\begin{array}{cccc} g_w \\ 00000 & 0000 \\ g(1,2) & 0000 \\ g(2,4) & 0000 \\ g(4,3) & 0000 \\ g(3,6) & 0000 \\ g(6,8) & 0000 \\ g(6,8) & 0000 \\ g(7,6) & 0010 \\ g(6,5) & 0000 \\ g(5,2) & 0000 \end{array}$

CRAWL Layer



CRAWL Layer

Column 4: Binary edge features (1 of current node and (*j*+1)-th predecessor are connected)

 A^s_w



000		(h(1))
000		h(2)
100		h(4)
110		h(3)
000		h(6)
000		h(8)
100		h(7)
100		h(6)
000		h(5)
000 ,		h(2)

Again within the window We skip the first node (always 1) Step 2: The feature matrix fully describes induced subgraphs of size s



	(
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h(5)	g(6,5)	0000	000
$\setminus h(2)$	g(5,2)	0000	000,

 $X(w_1 \ h \ a \ 4)$

Step 2: The feature matrix fully describes induced subgraphs of size s

$$w_1 = (1, 2, 4, 3, 6, 8, 7, 6, 5, 2)$$



(h(1))	00000	0000	000 \
h(2)	g(1,2)	0000	000
h(4)	g(2,4)	0000	100
h(3)	g(4,3)	0000	110
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h(8)	g(6,8)	0000	000
h(2)			000,
	$egin{array}{c} h(1) \\ h(2) \\ h(2) \\ h(3) \\ h(3) \\ h(6) \\ h(6) \\ h(6) \\ h(6) \\ h(5) \\ h(2) \end{array}$	$egin{array}{cccc} h(1) & 00000 \ h(2) & g(1,2) \ h(4) & g(2,4) \ h(3) & g(4,3) \ h(6) & g(3,6) \ h(8) & g(6,8) \ h(7) & g(8,7) \ h(6) & g(7,6) \ h(5) & g(6,5) \ h(2) & g(5,2) \ \end{array}$	

 $X(w_1, h, g, 4)$





$$\begin{array}{c} 000 & 000 \\ 000 & 000 \\ 000 & 100 \\ 000 & 110 \\ 000 & 000 \\ 000 & 000 \\ 000 & 000 \\ 000 & 100 \\ 010 & 100 \\ 000 & 000 \\$$

C















Step 4: Pool the output (Every node averages all *c_i* where it was the center of the walk)



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CRAWL Network



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Every layer updates a node embedding

\implies Fully compatible with message passing and graph transformer layers

Experiments & Expressiveness

Method	ZINC	MOLPCBA	CSL
	Test MAE \downarrow	Test AP ↑	Test Acc \uparrow (%)
GIN [Xu et al., 2019]	0.526 ± 0.051	0.2703 ± 0.0023	$10.0\pm~0.0$
GCN [Kipf and Welling, 2017]	0.367 ± 0.011	0.2483 ± 0.0037	$10.0~\pm~0.0$
3WLGNN [Maron et al., 2019]	0.303 ± 0.068	-	95.7 ± 14.9
PNA [Corso et al., 2020]	0.142 ± 0.010	0.2838 ± 0.0035	$10.0~\pm~0.0$
PHC-GNN [Le et al., 2021]	0.164 ± 0.003	$\textbf{0.2947} \pm \textbf{0.0026}$	-
GSN [Bouritsas et al., 2020]	0.108 ± 0.018	-	-
GINE+ [Brossard et al., 2020]	-	$\textbf{0.2979} \pm \textbf{0.0030}$	-
GPS [Rampášek et al., 2022]	$\textbf{0.070} \pm \textbf{0.004}$	0.2907 ± 0.0028	-
CRAWL	0.085 ± 0.004	$\textbf{0.2986} \pm \textbf{0.0025}$	$100.0~\pm~0.0$

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- Output of CRAWL is a random variable.
- CRAWL is permutation invariant. (Because random walks are, too.)
- CRAWL can (theoretically) detect any substructure with up to s nodes.
 - \cdot Caveat: The feature matrix is not permutation invariant \implies the CNN has to cope
- Substructures need to be traversed to be detected.

MPGNNs cannot distinguish the following graphs:



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Distinguished by CRAWL with s = 3 and non-backtracking walks.

Theorem (informal)

CRAWL sees things that even higher-order MPGNNs cannot.

Theorem (formal)

For every $k \ge 1$ there are graphs of maximum degree 3 that are distinguishable by CRaWl with window size and walk length $O(k^2)$, but not by k-WL (and hence not by k-dimensional GNNs).

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Those graphs are standard CFI graphs.

CRAWL vs MPGNNs

For the other direction:



CRAWL vs MPGNNs

For the other direction:



Indistinguishable to CRAWL with s = o(n).

CRAWL vs MPGNNs

For the other direction:



Indistinguishable to CRAWL with s = o(n).

Distinguishable with 1-WL in $\mathcal{O}(n)$ steps.

(Small) Conclusion

Conclusion

CRAWL:

• Distinguishes local structures (it can detect triangles!)

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Future Work:

• Node- & edge-level tasks

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- Random walk strategies

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Future Work:

- Node- & edge-level tasks
- Random walk strategies
- $\cdot\,$ Use transformers for processing the feature matrix

Excursion: Baseline Training

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On the LRGB Dataset

Long-Range Graph Benchmark







Peptides-Func Peptides-Struct

Superpixel Pascal and COCO

PCQM-Contact (link prediction)

Long-Range Graph Benchmark







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- Focus on long-range interaction
- Young dataset (from summer 2022), rapidly adopted

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Baseline Tuning



16/19

Feature Normalization

- Input features may have very different ranges
- Not all GNNs use internal normalization
- \Rightarrow Feature normalization

reported +normalization 0.4 +tuning 0.3 Test F1 0.2 0.1 0.0 GCN GINE GatedGCN GPS CRaWI

PascalVOC-SP

Link Prediction Metric: Filtering False Negatives



- a) Implementation erroneously uses "raw MRR"
- b) After hyperparameter tuning
- c) Switching to "filtered MRR"
- d) Filtering self-loops
 - Can never be true edges
 - Emphasized by dot-product

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We argue that d) is the best metric for this task

Second Conclusion

CRaWl

- There are alternatives to standard MPGNNs (and Graph Transformers)
- Random walks are good at capturing local structure
 - $\cdot\,$ And long-range interactions for extended window sizes (\rightarrow LRGB)
- CRaWl layers are fully compatible with other layers (MPGNN, GT)

Second Conclusion

CRaWl

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- CRaWl layers are fully compatible with other layers (MPGNN, GT)

LRGB

- Baseline tuning is vitally important (always!)
- \cdot Message passing is much better than reported
 - What does that tell us about long-range interactions or the LRGB datasets?
- \cdot Currently, the link prediction metric is broken

References

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How many walks? Which length?

- Default: m = |V|. Start one walk at each vertex.
- Training: $\ell = 50$, Testing: $\ell = 100$

Walk Strategies:

- uniform
- non-backtracking
- Many more: pq-Walks,...

Which window size s?

• Default: s = 8

