



## Inductive and Unsupervised Representation Learning on Graph Structured Objects

Lichen Wang<sup>1</sup>, Bo Zong<sup>2</sup>, Qianqian Ma<sup>3</sup>, Wei Cheng<sup>2</sup>, Jingchao Ni<sup>2</sup>, Wenchao Yu<sup>2</sup>, Yanchi Liu<sup>2</sup>, Dongjin Song<sup>2</sup>, Haifeng Chen<sup>2</sup>, Yun Fu<sup>1</sup>

<sup>1</sup>Northeastern University <sup>2</sup>NEC Laboratories America <sup>3</sup>Boston University

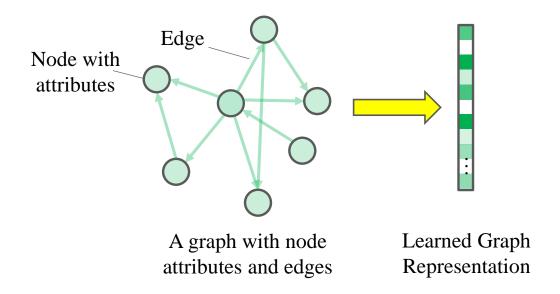
## Problem Setting

#### Input:

Graph with node attributes and edge attributes

Output:

Graph representation as a vector



Concept of Graph Representation Learning

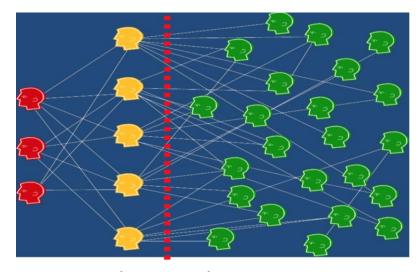
## Why Inductive and Unsupervised are Important?

Graph objects have a wide range of potential applications [1]:

- Social Network
  - Facebook, Twitter, WhatsApp
- Finance
  - Credit card fraud, Money laundry
- Logistics Industry:
  - eBay, Amazon, FedEx

#### **Problems:**

- Not enough labeled samples
- Learned model should be generalized to unseen data



Fake Social Account



**Credit Fraud** 

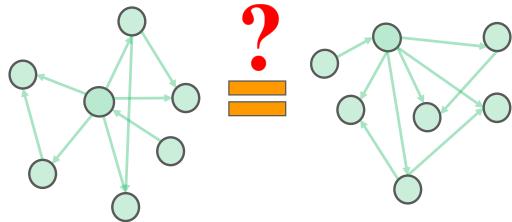


Computer Hack

## Challenges

- Existing approaches are in transductive setting
  - Difficult to handle unseen graphs
- Reconstruction-based approach
  - How similar of two graphs?
  - Graph Isomorphism is hard and rigid
  - Computational costly

We proposed a framework that addresses the practical need for graph representation learning in real-life applications

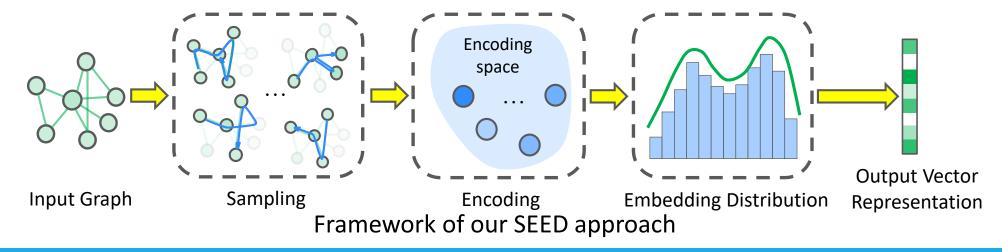


Isomorphism test is a necessary but hard and computational cost in graph representation learning

## The proposed Framework: SEED (1)

SEED: Sampling, Encoding, and Embedding Distributions

- Sampling: Random walk-based subgraph sampling from the input graph
  - Difficult to directly get whole graph representations
  - Could be easier to obtain representations for walks
- Encoding: Subgraph encoding via earliest visiting time
  - Make the process efficient and the representations effective



## The proposed Framework: SEED (2)

**SEED**: Sampling, Encoding, and Embedding Distributions

#### Embedding Distributions:

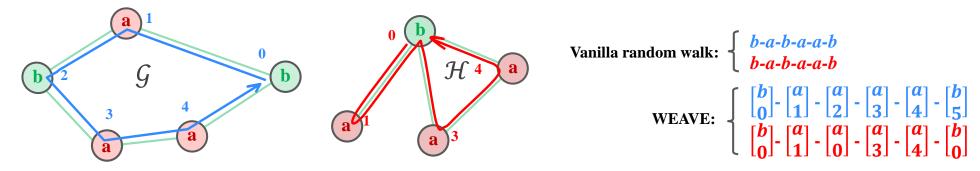
We encode a vector distribution into a single vector, which should preserve the similarity between vector distributions.

- Each input graph is reduced into a set of vectors, each of which is the representation for a sampled subgraph.
- Given that we have sampled a sufficient number of subgraphs, if two input graphs are similar, their vector distributions should be similar

### Sampling & Encoding

WEAVE: Random Walk with EArliest Visit timE).

- Random walk (RW) in graphs
- Revisit information: earliest visiting time
- Advantages:
  - RW: easy to reconstruct, but no loop info preserved
  - RW + revisit: easy to reconstruct with loop info
  - RW with revisit contains more structural info



Encoding results of Vanilla random walk and WEAVE. WEAVE could distinguish the difference of the two graphs.

### **Embedding Distribution**

- Insight: Walk distribution representation similarity ⇒ graph similarity
- Theoretical: as proved, distribution  $R_{\mathcal{G}} = R_{\mathcal{H}}$  if graph  $\mathcal{G}$  and  $\mathcal{H}$  are isomorphic
- Option 1: Identity kernel
  - We assume  $r_{\mathcal{A}} \sim N(\mu_1, I)$  and  $r_{\mathcal{H}} \sim N(\mu_2, I)$ , it is simple but surprisingly effective.

$$\hat{\mu}_{\mathcal{G}} = \frac{1}{s} \sum_{i=1}^{s} \mathbf{z}_{i} \qquad \qquad \hat{\mu}_{\mathcal{H}} = \frac{1}{s} \sum_{i=1}^{s} \mathbf{h}_{i}$$

Option 2: Commonly adopted kernels

$$\hat{\mu}_{\mathcal{G}}' = \frac{1}{s} \sum_{i=1}^{s} \hat{\phi}(\mathbf{z}_i; \theta_m) \quad \hat{\mu}_{\mathcal{H}}' = \frac{1}{s} \sum_{i=1}^{s} \hat{\phi}(\mathbf{h}_i; \theta_m) \quad D(P_{\mathcal{G}}, P_{\mathcal{H}}) = \|\hat{\mu}_{\mathcal{G}}' - \hat{\mu}_{\mathcal{H}}'\|_2^2$$

#### Theoretical Insights

Theorem: Given graphs g and  $\mathcal{H}$ , distribution  $R_g = R_{\mathcal{H}}$  if graph g and  $\mathcal{H}$  are isomorphic The theorem holds for the situations:

- Graphs without any attributes
- Graphs with node attributes
- Graphs with node and edge attributes

### Experiments (1)

- Seven graph datasets
- Two down-stream tasks:
  - Clustering
  - Classification
- Our approach obtains the highest performance.
  - Up to 10% improvements

| G         |                | <b>D</b>    | Methods | SAGE                  | GIN    | GMN    | SEED                         | SAGE   | GIN    | GMN    | SEED   |
|-----------|----------------|-------------|---------|-----------------------|--------|--------|------------------------------|--------|--------|--------|--------|
| Setting   |                | Datasets    | Metric  | Node Feature Excluded |        |        | Node Feature <b>Included</b> |        |        |        |        |
|           |                | Dezzer      | ACC     | 0.3853                | 0.4913 | 0.4924 | 0.4927                       | 0.3840 | 0.4930 | 0.4808 | 0.4810 |
|           |                |             | NMI     | 0.0079                | 0.0958 | 0.0726 | 0.1277                       | 0.0003 | 0.0893 | 0.0651 | 0.0566 |
|           |                | MUTAG       | ACC     | 0.6649                | 0.4997 | 0.4990 | 0.8014                       | 0.6649 | 0.4963 | 0.4910 | 0.7260 |
|           | Clustering     |             | NMI     | 0.0150                | 0.0946 | 0.0825 | 0.3214                       | 0.0070 | 0.0933 | 0.0917 | 0.1567 |
|           |                | NCI1        | ACC     | 0.5098                | 0.5221 | 0.5022 | 0.5510                       | 0.5070 | 0.5204 | 0.5005 | 0.5441 |
|           |                |             | NMI     | 0.0003                | 0.0015 | 0.0034 | 0.0073                       | 0.0002 | 0.0013 | 0.0042 | 0.0089 |
| Cluste    |                | PROTEINS    | ACC     | 0.5657                | 0.5957 | 0.5966 | 0.5957                       | 0.5657 | 0.5957 | 0.5957 | 0.5957 |
| Clusic    |                |             | NMI     | 0.0013                | 0.0038 | 0.0117 | 0.0518                       | 0.0004 | 0.0034 | 0.0067 | 0.0689 |
|           |                | COLLAB      | ACC     | 0.5208                | 0.5458 | 0.5173 | 0.5973                       | -      | -      | -      | -      |
|           |                |             | NMI     | 0.0025                | 0.0729 | 0.0193 | 0.2108                       | -      | -      | -      | -      |
|           |                | IMDB-BINARY | ACC     | 0.5069                | 0.6202 | 0.5010 | 0.5776                       | -      | -      | -      | -      |
|           |                |             | NMI     | 0.0002                | 0.0459 | 0.0093 | 0.0241                       | -      | -      | -      | -      |
|           |                | IMDB-MULTI  | ACC     | 0.3550                | 3607   | 0.3348 | 0.3816                       | -      | -      | -      | -      |
| 5         |                |             | NMI     | 0.0019                | 0.0185 | 0.0112 | 0.0214                       | -      | -      | -      | -      |
|           | Classification | Dezzer      | ACC     | 0.3775                | 0.5094 | 0.5427 | 0.6327                       | 0.3754 | 0.5270 | 0.5627 | 0.7451 |
|           |                | MUTAG       | ACC     | 0.6778                | 0.6778 | 0.6889 | 0.8112                       | 0.6889 | 0.6778 | 0.6889 | 0.8222 |
|           |                | NCI1        | ACC     | 0.5410                | 0.5571 | 0.5123 | 0.6105                       | 0.5328 | 0.5231 | 0.5133 | 0.6151 |
| Classific |                | PROTEINS    | ACC     | 0.6846                | 0.7387 | 0.6216 | 0.7207                       | 0.7027 | 0.7207 | 0.6357 | 0.7462 |
|           |                | COLLAB      | ACC     | 0.5650                | 0.6170 | 0.5460 | 0.6720                       | -      | -      | -      | -      |
|           |                | IMDB-BINARY | ACC     | 0.5400                | 0.7310 | 0.5140 | 0.7660                       | -      | -      | -      | -      |
|           |                | IMDB-MULTI  | ACC     | 0.3866                | 0.3843 | 0.3478 | 0.4466                       | -      | -      | -      | -      |

**Clustering & Classification Performance** 

### Experiments (2)

How parameters impact the output quality?

- Subgraph extraction with different sampling number and walk length.
  - Quantitative performance
  - t-SNE[1] visualization

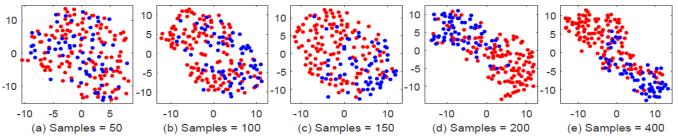
#### Summary

 More sampling number and walk length could improve the learned representation quality

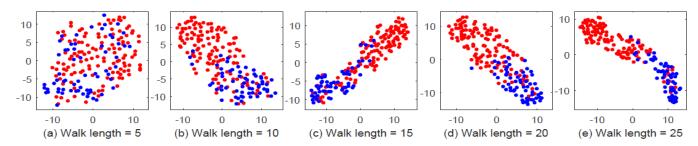
| Sampling | Classification | Clustering |        |  |
|----------|----------------|------------|--------|--|
| Number   | Accuracy       | ACC        | NMI    |  |
| 25       | 0.6832         | 0.6649     | 0.0031 |  |
| 50       | 0.6778         | 0.6649     | 0.0005 |  |
| 100      | 0.7778         | 0.6649     | 0.0537 |  |
| 150      | 0.7889         | 0.6968     | 0.1081 |  |
| 200      | 0.7778         | 0.7633     | 0.2100 |  |
| 300      | 0.7833         | 0.7502     | 0.1995 |  |
| 400      | 0.8389         | 0.7628     | 0.1928 |  |
| 800      | 0.8111         | 0.7660     | 0.1940 |  |

|   | Walk   | Classification | Clustering |        |  |  |
|---|--------|----------------|------------|--------|--|--|
| _ | Length | Accuracy       | ACC        | NMI    |  |  |
|   | 5      | 0.7278         | 0.6649     | 0.0534 |  |  |
|   | 10     | 0.7778         | 0.7633     | 0.2100 |  |  |
|   | 15     | 0.8167         | 0.7723     | 0.2495 |  |  |
|   | 20     | 0.8778         | 0.8245     | 0.3351 |  |  |
|   | 25     | 0.8722         | 0.8218     | 0.3380 |  |  |
| _ | 30     | 0.8743         | 0.8285     | 0.3321 |  |  |

#### Classification & clustering performance



t-SNE visualization with different sampling numbers



t-SNE visualization with different work length









# Thank you!

Welcome to contact: wanglichenxj@gmail.com for questions