Motivation

- Different local context of each node
  - Biology: \(v_1\)
  - Bioinformatics: \(v_2\)
  - Computer science: \(v_3\)

**Q:** Can we allow each node to be parameterized by its own weight matrix?

Localization: Localize the global GNN model for each node

The proposed model: LGNN

Conclusions

- LGNN consistently achieves significant performance boosts
- GAT-based models generally attain better performance than GCN- and GIN-based models
- Increasing the number of parameters alone cannot achieve the effect of localization
- Utilizing only one module consistently outperforms the global model
- The node-level localization tends to perform better than edge-level localization.
- Modeling both jointly results in the best performance

Experiments

- Evaluation
  - Accuracy, Micro-F
- Baselines
  - Embedding models: DeepWalk [1], Planetoid [2]
  - GNN models: GCN [3], GAT [4], GIN [5]
  - GNN-FiLM [6]: GCN-FiLM, GAT-FiLM, GIN-FiLM

Node classification

<table>
<thead>
<tr>
<th>Method</th>
<th>#Params (G)</th>
<th>#Params (Loc)</th>
<th>#Classes</th>
<th>#Features</th>
<th>DeepWalk</th>
<th>Planetoid</th>
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<td>105.00k</td>
<td>80.16k</td>
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<td>77.51k</td>
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<td>93.88k</td>
<td>91.21k</td>
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Ablation study

- Utilizing only one module consistently outperforms the global model
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Reference