

# Lossless Compression of Structured Convolutional Models (GNNs) via Lifting

**Gustav Sourek\*** & Filip Zelezny & Ondrej Kuzelka

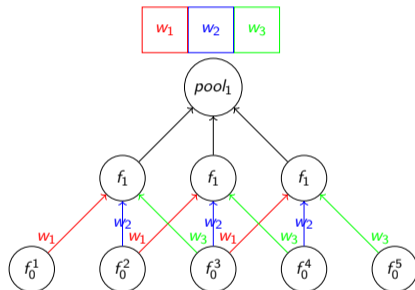
\* [souregus@fel.cvut.cz](mailto:souregus@fel.cvut.cz)

Czech Technical University in Prague

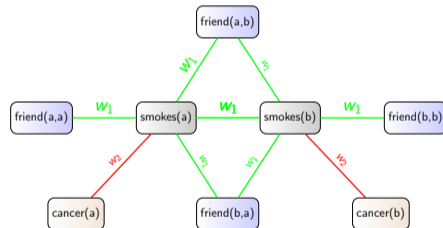
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# Lifted (Templated) Models

**Lifted** (templated) models exploit input sample **symmetries** using parameterized computation **templates**, while inducing **weight-sharing** in their respective computation graphs:



$w_1 : \forall X, Y : friends(X, Y) \implies (smokes(X) \iff smokes(Y))$   
 $w_2 : \forall X : smokes(X) \implies cancer(X)$



Templating in a CNN (left) and a lifted graphical model (MLN - right).

Templating improves **generalization** w.r.t. different sample transformations in pixel grids (CNNs), trees (RNNs), graphs (GNNs), and beyond (Lifted Relational Neural Networks).

## Lifted Inference

is a technique to exploit **computation graph symmetries** for **speedup**.

- known in *Statistical Relational Learning* and database query engines
- but so far *unexploited in deep learning!*

Q: *But do such computation graph symmetries occur in deep learning practice?*

- A: Yes, particularly in the recently explored **structured data** domains with **discrete-valued** elements such as social, biological, chemical graphs and networks.

## “Structured Convolutional Models?”

are simply the templated (convolutional) models applied to such structured data domains.

- e.g. the common **Graph Neural Networks** (GNNs)

To detect the symmetries in computation graphs, we partition its nodes into **equivalence classes**:

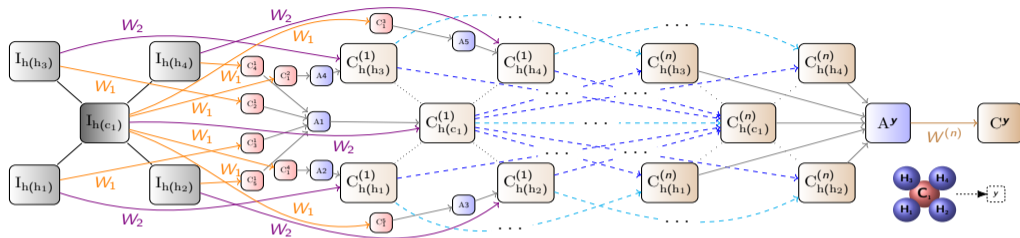
## Definition (functional equivalence)

We say that two nodes  $N_1, N_2 \in \mathcal{N}$  are **functionally equivalent** if, for any initialization of (shared) weights  $\mathcal{W}$ , it holds that  $value(N_1; \mathcal{W}) = value(N_2; \mathcal{W})$ .

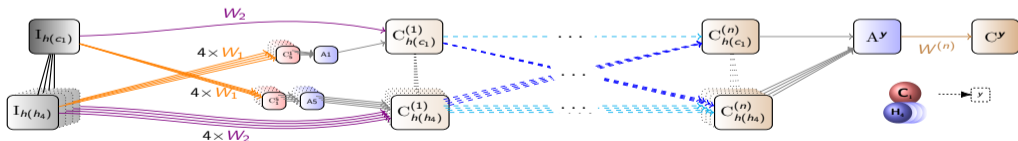
The compression algorithm then works very simply in 2 steps

- 1 precalculate the equivalence classes of neurons
- 2 iterate the computation graph and replace all nodes with a single equivalent

# GNN compression example



is compressed into **equivalent** GNN computation graph:



## Models:

- classic GCNs, graph-SAGE, GIN, and some extensions (graphlet networks)
- also GNNs modified into knowledge-base embedding (KBE) mode

## Learning tasks:

- *Molecule classification*
  - various (large) molecular datasets
- *Knowledge base completion (KBC)*
  - various mid-sized KBs such as Kinships, Nations, and UMLS

# Lossless Compression Results

The models were implemented within the framework of *Lifted Relational Neural Networks*<sup>1</sup> (LRNNs), but we also compared with specialized GNN frameworks of PyG<sup>2</sup> and DGL<sup>3</sup>:

Model	Lifting (s)	LRNNs (s)	PyG (s)	DGL (s)
GCN	<b>0.25 ± 0.01</b>	0.75 ± 0.01	3.24 ± 0.02	23.25 ± 1.94
g-SAGE	<b>0.34 ± 0.01</b>	0.89 ± 0.01	3.83 ± 0.04	24.23 ± 3.80
GIN	<b>1.41 ± 0.10</b>	2.84 ± 0.09	11.19 ± 0.06	52.04 ± 0.41

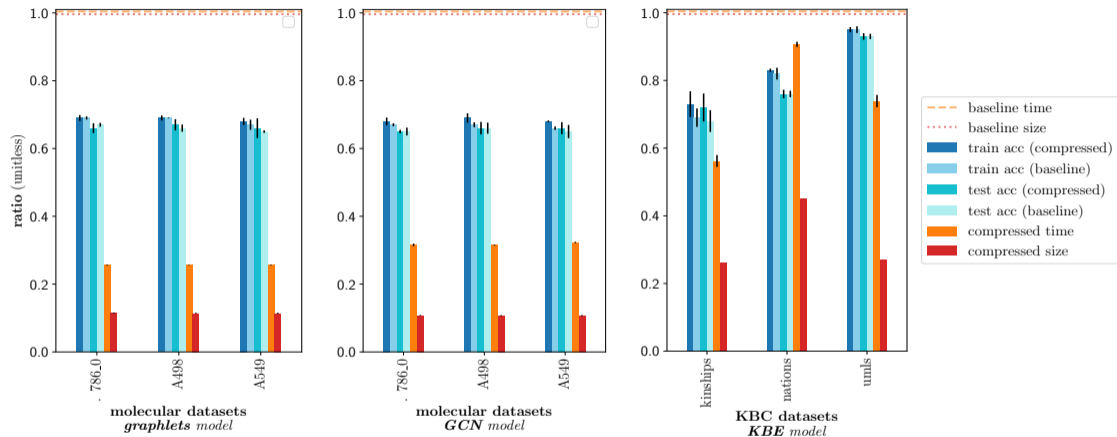
Training times *per epoch* across different models and frameworks over 3000 molecules.

<sup>1</sup><https://github.com/GustikS/NeuraLogic>

<sup>2</sup>[https://github.com/rusty1s/pytorch\\_geometric](https://github.com/rusty1s/pytorch_geometric)

<sup>3</sup><https://www.dgl.ai/>

# Lossless Compression Results



Comparison of 3 different baseline models of graphlets (left), GCNs (middle), and KBEs (right) with their compressed versions over molecule classification (left, middle) and knowledge-base completion (right).



- The **symmetries are indeed common** in structured (discrete) data domains
  - especially in the molecular graphs, but also elsewhere
- The resulting compression rates and speedups are **quite significant**
  - easily 2-5x improvement in classic GNN classification settings
- The technique is **very simple** and can be adopted by any templated model
  - and can be easily extended into a lossy compression setting for further speedup
- The experiments and the LRNN framework itself are available at Github
  - Experiments: <https://github.com/GustikS/NeuraLifting>
  - LRNN: <https://github.com/GustikS/NeuraLogic>
  - email: [souregus@fel.cvut.cz](mailto:souregus@fel.cvut.cz)