



Self-Supervised Graph Transformer on Large Molecular Data

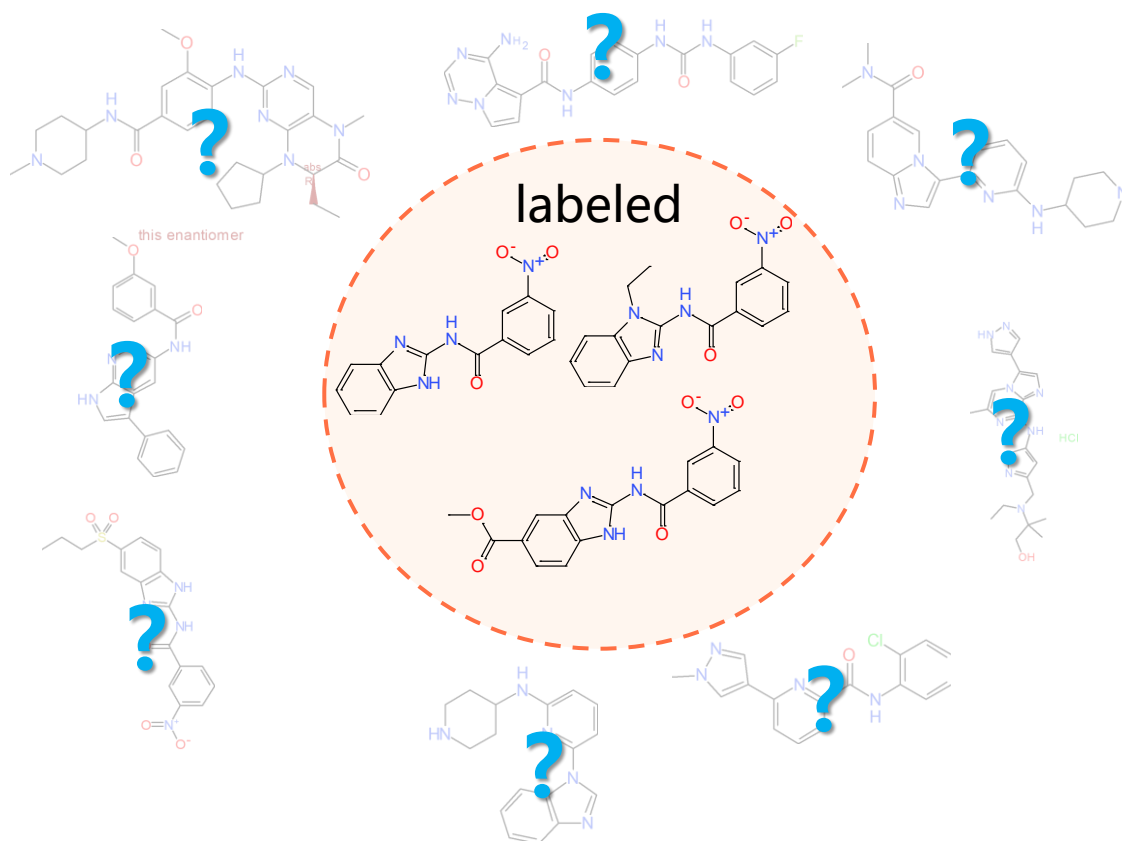
Yu Rong*, Yatao Bian*, Tingyang Xu, Weiyang Xie, Ying Wei, Wenbing Huang, Junzhou Huang

Tencent AI Lab

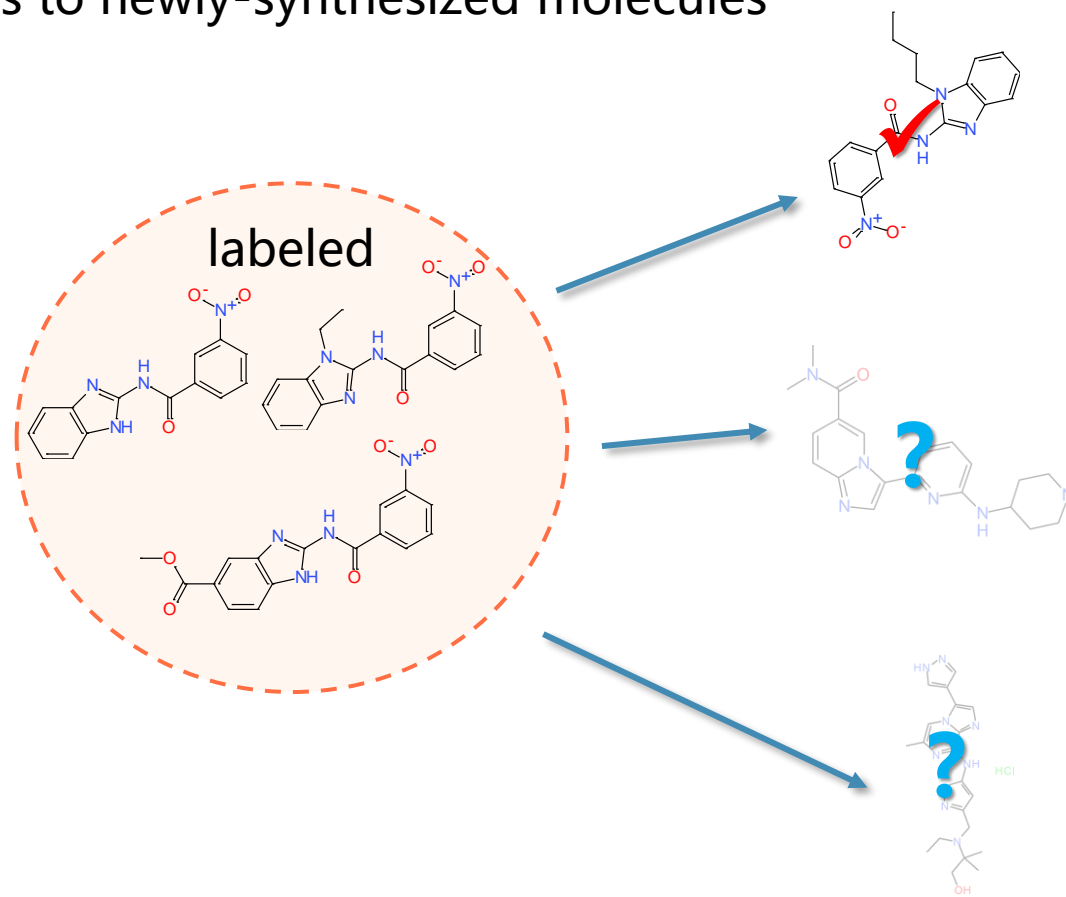
Tsinghua University

2020-10-21

- GNNs are widely adopted for molecular tasks.
- Challenges
 - Insufficient labeled molecules for supervised training
 - Poor generalization capabilities to newly-synthesized molecules



- GNNs are widely adopted for molecular tasks.
- Challenges
 - Insufficient labeled molecules for supervised training
 - Poor generalization capabilities to newly-synthesized molecules



- **GROVER**: **G**raph **R**epresentation fr**O**m self-super**V**ised m**E**ssage passing t**R**ansformer
- Overview of this molecular representation learning framework



GROVER

Integrating message passing networks with the Transformer-style architecture

delivers

More expressive encoders of molecules

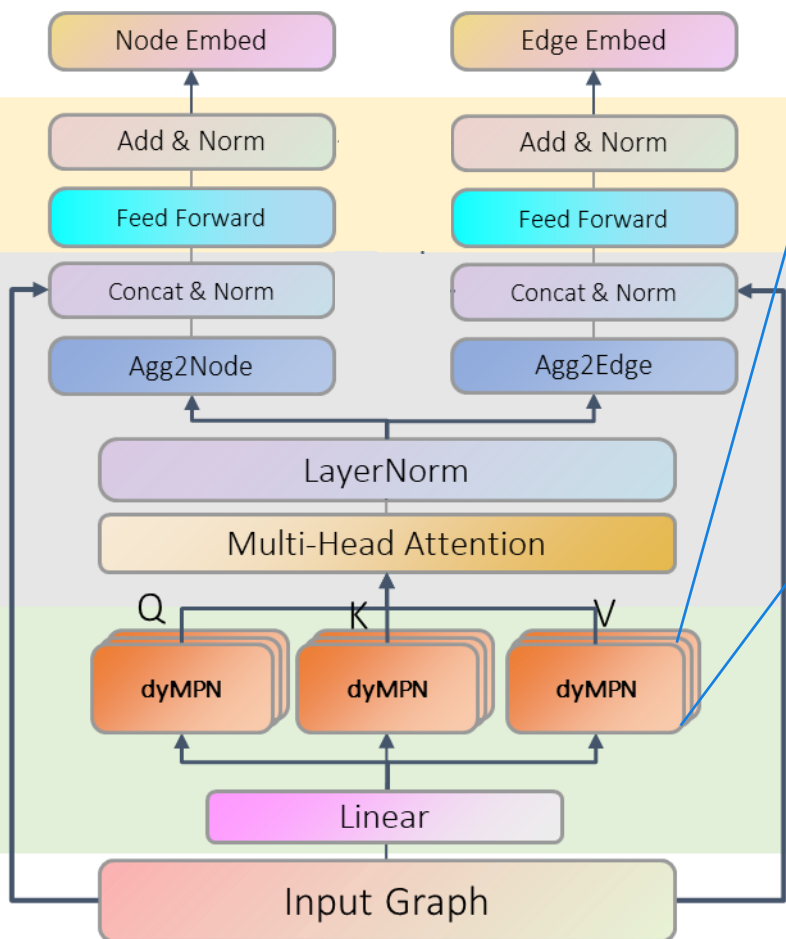
Carefully designed self-supervised tasks in node, edge & graph levels

enables

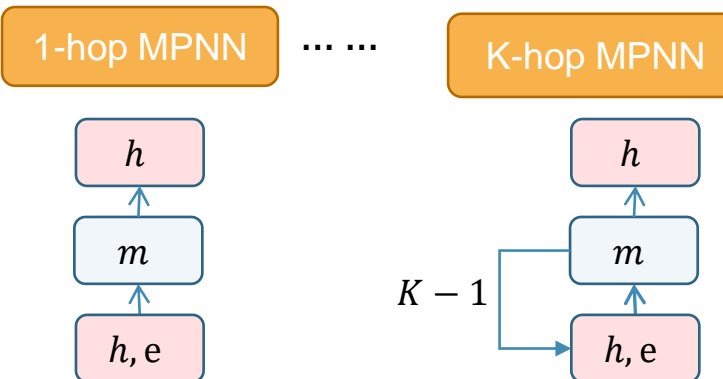
Rich structural and semantic information of molecules from enormous unlabeled data

GTransformer Architecture

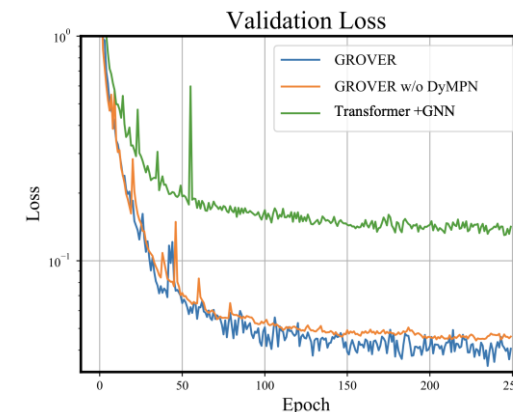
- Output for both node embedding and edge embeddings.
- **Multi-Head Attention:** model global interaction between nodes/edges.
- **Long-range Residual Connection:** alleviating the vanishing gradient and over-smoothing.
- **MPNN:** Extract local structural information of graphs.
- **dyMPN:** Randomize the message passing hops for the dynamic receptive field modeling.



Sample a random-hop MPNN at each iteration



Better generalization



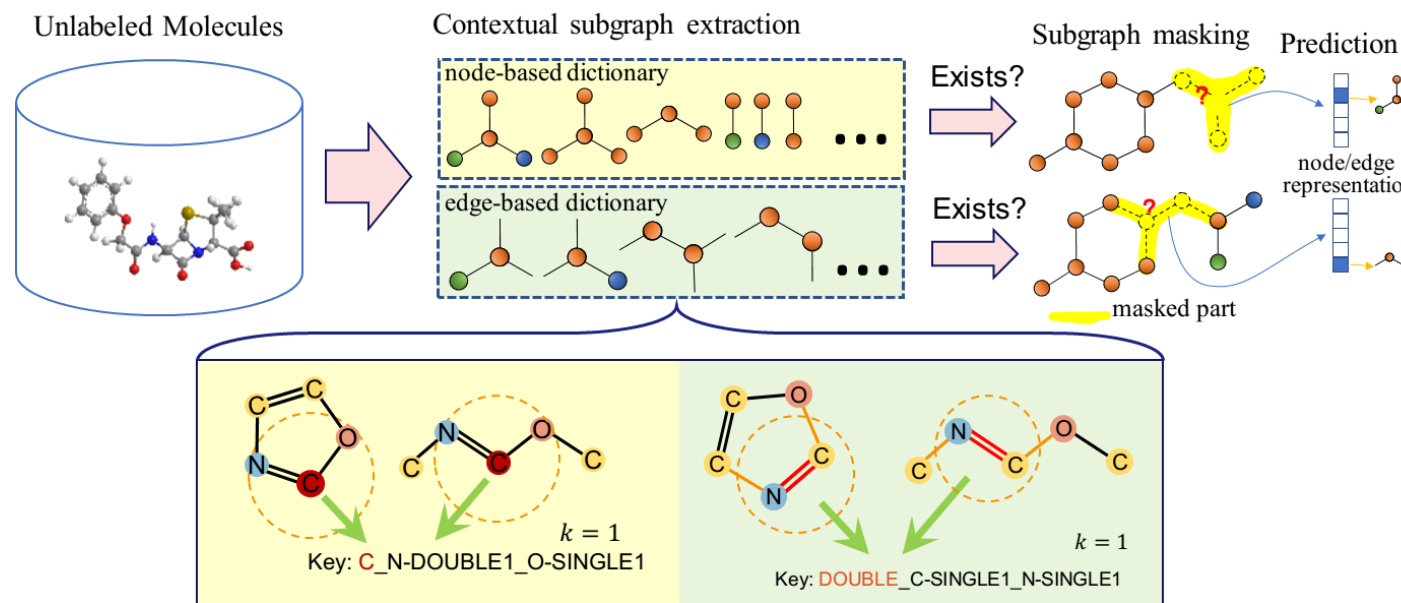
Self-supervised Tasks Construction

Good self-supervision task shall have *reliable* and *cheap* prediction target

Node/edge level task:
contextual property
prediction

target reflects contextual property:
recurrent statistical properties of
local subgraph

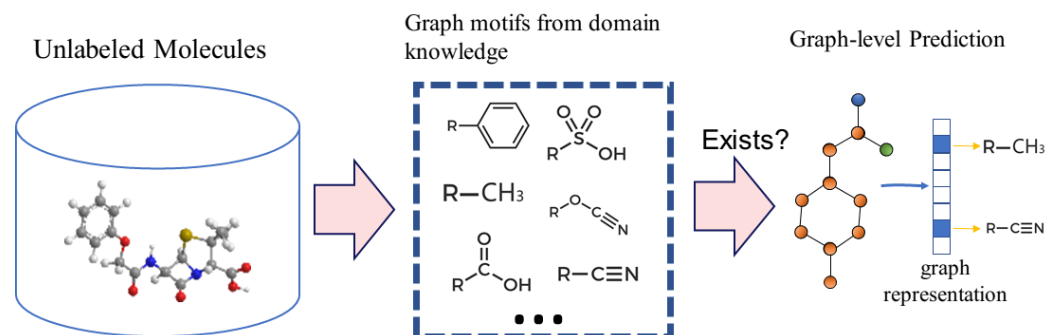
A multi-class classification problem



Graph level task:
motif prediction

Motifs: recurrent sub-graphs, such
as functional groups.

A multi-label classification problem



Experimental Results

Pre-training GROVER with 100M params on 10M unlabelled molecules

Verifying on downstream tasks with fine-tuning

Significant improvement (more than 6% on average) over SOTA models on 11 challenging benchmarks

Dataset # Molecules	Classification (Higher is better)					
	BBBP 2039	SIDER 1427	ClinTox 1478	BACE 1513	Tox21 7831	ToxCast 8575
TF_Robust [40]	0.860 _(0.087)	0.607 _(0.033)	0.765 _(0.085)	0.824 _(0.022)	0.698 _(0.012)	0.585 _(0.031)
GraphConv [24]	0.877 _(0.036)	0.593 _(0.035)	0.845 _(0.051)	0.854 _(0.011)	0.772 _(0.041)	0.650 _(0.025)
Weave [23]	0.837 _(0.065)	0.543 _(0.034)	0.823 _(0.023)	0.791 _(0.008)	0.741 _(0.044)	0.678 _(0.024)
SchNet [45]	0.847 _(0.024)	0.545 _(0.038)	0.717 _(0.042)	0.750 _(0.033)	0.767 _(0.025)	0.679 _(0.021)
MPNN [13]	0.913 _(0.041)	0.595 _(0.030)	0.879 _(0.054)	0.815 _(0.044)	0.808 _(0.024)	0.691 _(0.013)
DMPNN [63]	0.919 _(0.030)	0.632 _(0.023)	0.897 _(0.040)	0.852 _(0.053)	0.826 _(0.023)	0.718 _(0.011)
MGCN [30]	0.850 _(0.064)	0.552 _(0.018)	0.634 _(0.042)	0.734 _(0.030)	0.707 _(0.016)	0.663 _(0.009)
AttentiveFP [61]	0.908 _(0.050)	0.605 _(0.060)	0.933 _(0.020)	0.863 _(0.015)	0.807 _(0.020)	0.579 _(0.001)
N-GRAM [29]	0.912 _(0.013)	0.632 _(0.005)	0.855 _(0.037)	0.876 _(0.035)	0.769 _(0.027)	- ⁴
HU. et.al[18]	0.915 _(0.040)	0.614 _(0.006)	0.762 _(0.058)	0.851 _(0.027)	0.811 _(0.015)	0.714 _(0.019)
GROVER _{base}	0.936 _(0.008)	0.656 _(0.006)	0.925 _(0.013)	0.878 _(0.016)	0.819 _(0.020)	0.723 _(0.010)
GROVER _{large}	0.940 _(0.019)	0.658 _(0.023)	0.944 _(0.021)	0.894 _(0.028)	0.831 _(0.025)	0.737 _(0.010)

★ Code and models will be released soon.