TorchDrug: A Powerful and Flexible Machine Learning Platform for Drug Discovery

Zhaocheng Zhu\textsuperscript{1,2}
Chence Shi\textsuperscript{1,2}
Zuobai Zhang\textsuperscript{1,2}
Shengchao Liu\textsuperscript{1,2}
Minghao Xu\textsuperscript{1,2}
Xinyu Yuan\textsuperscript{3}
Yangtian Zhang\textsuperscript{4}
Junkun Chen\textsuperscript{5}
Huiyu Cai\textsuperscript{1,2}
Jiarui Lu\textsuperscript{1,2}
Chang Ma\textsuperscript{3}
Runcheng Liu\textsuperscript{5}
Louis-Pascal Xhonneux\textsuperscript{1,2}
Meng Qu\textsuperscript{1,2}
Jian Tang\textsuperscript{1,6,7}
\textsuperscript{1}Mila - Quebec AI Institute
\textsuperscript{2}University of Montreal
\textsuperscript{3}Peking University
\textsuperscript{4}Shanghai Jiao Tong University
\textsuperscript{5}Tsinghua University
\textsuperscript{6}HEC Montreal
\textsuperscript{7}CIFAR AI Research Chair

Abstract

Machine learning has huge potential to revolutionize the field of drug discovery and is attracting increasing attention in recent years. However, lacking domain knowledge (e.g., which tasks to work on), standard benchmarks and data preprocessing pipelines are the main obstacles for machine learning researchers to work in this domain. To facilitate the progress of machine learning for drug discovery, we develop TorchDrug, a powerful and flexible machine learning platform for drug discovery built on top of PyTorch. TorchDrug benchmarks a variety of important tasks in drug discovery, including molecular property prediction, pretrained molecular representations, de novo molecular design and optimization, retrosynthesis prediction, and biomedical knowledge graph reasoning. State-of-the-art techniques based on geometric deep learning (or graph machine learning), deep generative models, reinforcement learning and knowledge graph reasoning are implemented for these tasks. TorchDrug features a hierarchical interface that facilitates customization from both novices and experts in this domain. Tutorials, benchmark results and documentation are available at https://torchdrug.ai Code is released under Apache License 2.0.

Keywords: AI for drug discovery, geometric deep learning, graph machine learning, deep generative models, knowledge graphs

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1. Introduction

Drug discovery is a long and costly process, taking on average 10 years and costing 2.5 billion US dollars to develop a new drug (DiMasi et al., 2016). Machine learning has huge potential to accelerate the process of drug discovery by extracting evidence through mining and analyzing data in the biomedical domain (e.g., scientific literature, bioassays, and clinical trials). Recently, machine learning methods have made significant progress in many drug discovery tasks, such as protein structure prediction (Baek et al., 2021; Jumper et al., 2021), molecular property prediction (Duvenaud et al., 2015; Hu et al., 2019), de novo molecular design and optimization (You et al., 2018; Shi et al., 2020b), reaction prediction (Jin et al., 2017; Bradshaw et al., 2018), retrosynthesis prediction (Dai et al., 2019; Shi et al., 2020a), and drug repurposing (Wang et al., 2020; Zhao et al., 2020). However, it remains a challenge for machine learning researchers to work in this domain for a few reasons: (1) lacking domain knowledge of what are important tasks in the domain; (2) no standard benchmarks of different methods due to their completely different implementations; (3) the large cost of implementing complicated data preprocessing pipelines for each task.

To accelerate the process of drug discovery through machine learning, we see a critical need to develop an open-source machine learning platform for drug discovery. Here we present such a platform, called TORCHDRUG. TORCHDRUG provides a hierarchical interface to accommodate different demands in the development of drug discovery. At the low level, TORCHDRUG encapsulates graphs and molecules as basic data structures, and provides GPU-accelerated graph operations, along with standard datasets in a PyTorch-style interface. At the mid-level, TORCHDRUG supplies popular building blocks of graph representation learning models (e.g., MPNN (Gilmer et al., 2017)), which can be used to quickly construct models for drug discovery. The high level contains reusable routines for a variety of important tasks in drug discovery, ranging from molecular property prediction, pretrained molecular representations, de novo molecule design and optimization, retrosynthesis prediction to biomedical knowledge graph reasoning (e.g., for drug repurposing). Figure 1 presents an overview of the TORCHDRUG library. TORCHDRUG has received more than 5,000 downloads on PyPI and Anaconda since its first release in August 2021.
2. Existing Systems and Implementations

**Graph Machine Learning Systems.** The most prominent packages are PyTorch-Geometric (PyG) (Fey and Lenssen, 2019) and Deep Graph Library (DGL) (Wang et al., 2019), which are targeted at building graph neural networks (GNNs) in PyTorch (Paszke et al., 2019). DGL additionally supports MXNet (Chen et al., 2015) backend. Other similar packages include GraphNets (Battaglia et al., 2018), StellarGraph (Data61, 2018), Spektral (Grattarola and Alippi, 2020), tf_geometric (Hu et al., 2021) for Tensorflow (Abadi et al., 2016), CogDL (Cen et al., 2021) for PyTorch, and Jraph (Godwin* et al., 2020) for JAX (Bradbury et al., 2018). All these libraries cover the low-level graph operations (e.g., batch of graphs) and mid-level models (e.g., GIN (Xu et al., 2018)) for GNN architectures. By contrast, DIG (Liu et al., 2021) focuses on high-level tasks on graphs, such as graph generation and self-supervised learning. To our best knowledge, there is no general graph machine learning system targeting at the research and development need of drug discovery tasks.

**Drug Discovery Implementations.** Another stream of software is dedicated to the implementation of drug discovery tasks. For example, DeepChem (Ramsundar et al., 2019) provides standard datasets and models for molecule property prediction. You et al. (2018) implements a codebase for conducting research on de novo molecular design. Dai et al. (2019); Shi et al. (2021) develop two delicate packages for retrosynthesis prediction and 3D molecular conformation prediction, respectively. However, these efforts are mostly targeted on a specific task with a limited range of models, which restricts the development and benchmarking of new fundamental models. Other implementations like Therapeutics Data Commons (TDC) (Huang et al., 2021) and ATOM3D (Townshend et al., 2020) focus on datasets and evaluation toolkits for drug discovery tasks, but lack implementation of models.

By comparison, **TorchDrug** is a graph machine learning system for drug discovery, with flexible interface for low-level operations, mid-level models and high-level tasks.

3. Key Features

**TorchDrug** offers two key features: 1) low-level data structures and graph operations that can be manipulated with minimal domain knowledge and GPU acceleration. 2) mid-level datasets, layers, models and high-level tasks that support rapid prototyping of ideas.

3.1 Data Structures and Graph Operations

The core data structures of **TorchDrug** are homogeneous graphs, knowledge graphs (together in `data.Graph`), and molecules (`data.Molecule`). Like tensors in PyTorch, these data structures are designed to be the first-class citizen in **TorchDrug**, and serve as input and output of many functions. Our data structures support a lot of graph operations, such as node masking (`data.Graph.node_mask`), extracting connected components (`data.Graph.connected_components`) and converting ions to molecules (`data.Molecule.ion_to_molecule`), as well as their batched variants. All the graph operations are implemented based on standard PyTorch operations, which support auto differentiation and can be seamlessly switched between CPUs and GPUs. For example, the following code snippet creates a batch of 4 molecules, sends it to a GPU, repeats the batch and visualizes the results.
from torchdrug import data
smiles_list = ['CCSCCSP(=S)(OC)OC', 'CCOC(=O)N', 'N(Nc1ccccc1)c2ccccc2', 'NC(=O)c1cccnc1']
mols = data.PackedMolecule.from_smiles(smiles_list)
mols = mols.cuda()
mols = mols.repeat(2)
mols.visualize(num_row=1)

The data structures also contain several predefined node-level, edge-level and graph-level attributes that are useful for building machine learning models. For example, the type of atoms in a molecule may be used as an input feature to some property prediction model. Users may also register arbitrary attributes depending on their tasks. All the attributes are automatically maintained in all of our graph operations.

3.2 Datasets, Layers, Models and Tasks

Datasets. The datasets module provides 30 common datasets for 5 drug discovery tasks. These datasets inherit the Dataset class from PyTorch and further provide data loading and _getitem_ functions, which facilitates the interaction with dataloaders in PyTorch.

Layers and Models. The layers and models modules implement layers and models for representation learning respectively. This lets users switch between standard models or custom models from standard layers. Our interface follows the convention in PyTorch, which minimizes the cognitive load of users. Classes in layers (e.g., GCNConv) are similar to the layers in torch.nn, while classes in models (e.g., GCN) are similar to torchvision.models.

Tasks. The tasks module contains high-level routines of machine learning tasks in drug discovery. Typically, these include dataset preprocessing, prediction, training and evaluation. Each task is abstracted as a model-agnostic class in tasks, which can be used with any basic representation learning models (e.g., GIN (Xu et al., 2018)). Currently, TorchDrug supports 5 tasks: property prediction, pretrained molecular representations, de novo molecule design, retrosynthesis and biomedical knowledge graph reasoning. A full list of tasks and models supported by TorchDrug are showed in Table 1.

| Task | Model |
|------|-------|
| Property Prediction | Neural Fingerprint [Duvenaud et al., 2015], ChebyNet [Defferrard et al., 2016], GCN [Kipf and Welling, 2016], GIN [Xu et al., 2018], GAT [Velić et al., 2018] |
| Pretrained Molecular Representation | InfoGraph [Sun et al., 2019a], Edge Prediction [Hamilton et al., 2017], Attribute Masking [Hu et al., 2019] |
| De Novo Molecule Design and Optimization | GCPN [You et al., 2018], GraphAF [Shi et al., 2020] |
| Retrosynthesis Prediction | G2Gs [Shi et al., 2020a], TransE [Bordes et al., 2013], DistMult [Yang et al., 2014], ComplEx [Trouillon et al., 2016], SimplE [Kazemi and Poole, 2018], RotatE [Sun et al., 2019b], KBGAT [Nathani et al., 2019] |
| Biomedical Knowledge Graph Reasoning | NeuralLP [Yang et al., 2017], KIBGAT [Xiaowei et al., 2019], TransE [Bordes et al., 2013], SimplE [Kazemi and Poole, 2018], RotatE [Sun et al., 2019b], KBGAT [Nathani et al., 2019] |

4. Conclusion

We present TorchDrug, a powerful and flexible machine learning platform for drug discovery. It has the potential to accelerate the research and development of drug discovery. In the future, we plan to further add tasks and models for protein representation learning.
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