Knowledge Graph Embedding with PyKEEN in 2022

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C https://github.com/pykeen



\$ pip install pykeen



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Background







A *knowledge graph* is a set of entities, relations, and triples A **representation** is typically a vector representation for an entity or relation

Useful for *downstream tasks* like link prediction, clustering, entity alignment, question answering, dialogue

Where PyKEEN Started

Back in 2018, there was a huge variety of:

- Decoders/interaction functions (e.g., DistMult, TransE, ComplEx)
- Benchmarking datasets (e.g., FB15k-237, YAGO-310, etc.)
- Preprocessing workflows (e.g., adding inverse triples)
- Training procedures (e.g., OWA, sLCWA, LCWA, CWA)
- Evaluation procedures and metrics

What was missing:

- Ability to reproduce previous results
- Meaningful way to compare different formulations of KGE models
- A modular architecture
- Legible, reusable, extendable, sustainable code
- Documentation for newcomers
- A moment of introspection and philosophizing

PyKEEN has a modular architecture for KGEMs



7

PyKEEN is for Users

>>> from pykeen.pipeline import pipeline
>>> pipeline_result = pipeline(
... dataset='Nations',
... model='TransE',
...)
>>> pipeline_result.save_to_directory('nations_transe')

Train your first model

```
from pykeen.nn.modules import Interaction
```

class TransEInteraction(Interaction): def forward(self, h, r, t): return -(h + r - t).norm(p=2, dim=-1)

Implement your own model



Optimize your first model

>>> from pykeen.pipeline import pipeline
>>> # Run the pipeline
>>> pipeline_result = pipeline(dataset='Nations', model='RotatE')
>>> model = pipeline_result.model
>>> # Predict tails
>>> predicted_tails_df = model.get_tail_prediction_df('brazil', 'intergovorgs')

Predict new links

Interaction Functions (42)

- NodePiece
- InductiveNodePiece
- TuckER
- HolE
- QuatE
- FixedModel
- RotatE
- DistMultLiteral
- BoxE
- TransR
- ERMLP
- CrossE
- TransF

- ConvE
- NTN
- ComplExLiteral
- ERMLPE
- InductiveNodePieceGNN
- PairRE
- CompGCN
- CP
- KG2E
- UM
- TorusE
- ProjE
- TransE

- DistMult
- DistMA
- RESCAL
- SE
- ConvKB
- TransH
- MuRE
- AutoSF
- TransD
- DistMultLiteralGated
- SimplE
- RGCN
- ComplEx

Datasets (33)

- CSKG
- Countries
- ConceptNet
- Kinships
- OpenBioLinkLQ
- CoDExMedium
- Nations
- WK3l15k
- WD50KT
- CoDExSmall
- PharmKG
- Hetionet

- DB100K
- FB15k
- WN18RR
- OpenEA
- DBpedia50
- WK3I120k
- OGBBioKG
- PharmKG8k
- AristoV4
- CoDExLarge
- NationsLiteral
- YAGO310

- WN18
- UMLS
- BioKG
- OGBWikiKG2
- CKG
- Wikidata5M
- FB15k237
- DRKG
- CN3I
- OpenBioLink

PyKEEN Benchmark (2020)

Results

- SOTA can usually be achieved with arbitrary additional HPO
- RotatE was consistently the best performing model
- sLCWA + inverse relations is the best training paradigm
- CEL and MRL underperforming, NSSAL is usually the best
- Less complicated models can still perform
 well
- Old models can outcompete previous SOTA

New Questions

- When should we stop optimizing?
- Can we trust metrics?
- Are we really making fair evaluations?
- Are bigger, slower models really better?
- How much ablation is necessary given insight as to some obvious best pairs?

FB15k-237 Results



- New models proposed frequently, squeezing minimal gains on standard metrics
- New tools like batch normalization and improved optimizers lead to SOTA results.
- E.g., WN18-RR, TransE, 56.98% Hits@10

Bigger, more complex models aren't even necessarily better.

Reported in: Ali, M., et al. (2020). Bringing Light Into the Dark: A Large-scale Evaluation of Knowledge Graph Embedding Models Under a Unified Framework. http://arxiv.org/abs/2006.13365



Adoption

Pharmaceutical Industry - AstraZeneca

- Core business of pharmaceutical is to identify safe, active modulators of disease
- Bonner *et al.* applied link prediction to biomedical knowledge graphs
 - Chemogenomics between chemical and protein
 - Target identification between protein and disease
 - Drug repositioning between chemical and disease
- Reference: <u>http://arxiv.org/abs/2112.06567</u>



Academia (Highlights)

- Ontologies
 - <u>https://repository.kaust.edu.sa/handle/10754/6634</u> <u>30</u>
- Biomedicine
 - <u>https://doi.org/10.1093/bioinformatics/btaa274</u>
 - <u>https://openreview.net/forum?id=qI-IS8DPq_N</u>
- Precision and Personalized Medicine
 - https://doi.org/10.1093/bioinformatics/btab340
- Bibliometrics and Meta-research
 - https://arxiv.org/abs/1904.12211
 - <u>https://recnlp2019.github.io/papers/RecNLP2019</u>
 <u>paper_20.pdf</u>

- Bias Detection
 - o <u>https://arxiv.org/abs/2109.10697</u>
- Entity Typing
 - <u>https://dl.acm.org/doi/abs/10.1145/346021</u>
 <u>0.3493563</u>
- Industry 4.0
 - <u>https://link.springer.com/chapter/10.1007/9</u> 78-3-030-59051-2_12

Current and Future Directions

Graph Neural Networks

- PyKEEN implements two GNN-based KGE models: R-GCN and CompGCN
- Goal: more easily integrate components like RGCNConv in PyKEEN models
- **Goal:** better promote reusability of PyKEEN components

602	+ class PygRGCNLayer(Layer):
603	+ """An alternate implementation of the R-GCN layer using PyG."""
604	+
605	+ definit(
606	+ self,
607	+ input_dim: int,
608	+ num_relations: int,
609	+ output_dim: Optional[int] = None,
610	+ use_bias: bool = True,
611	+):
612	+ """Initialize the PyG convolution."""
613	+ from torch_geometric.nn import RGCNConv
614	+
615	+ super()init()
616	+ self.conv = RGCNConv(
617	+ in_channels=input_dim,
618	+ out_channels=output_dim,
619	+ num_relations=num_relations,
620	+ bias=use_bias,
621	+)
622	+
623	+ def reset_parameters(self): # noqa: D102
624	+ self.conv.reset_parameters()
625	+
626	+ def forward(
627	+ self,
628	+ x: torch.FloatTensor,
629	<pre>+ edge_index: Tuple[torch.LongTensor, torch.LongTensor],</pre>
630	+ edge_type: torch.LongTensor,
631	+): # noqa: D102
632	+ return self.conv(x, edge_index, edge_type)
633	+
634	+

Better Evaluation Metrics

Problem: Ranked-based metrics for link prediction on knowledge graphs are dataset-dependent



Solution: introduce additional affine statistical adjustments (like Bonferroni in statistics) inspired by Berrendorf, *et al.* (2020)

Adjustment by expectation and optimum

$$M^*(r_1,...,r_n) = \frac{M(r_1,...,r_n) - E[M]}{\max(M) - E[M]}$$

- adjusted mean rank index (AMRI)
- adjusted mean reciprocal rank index (AMRRI)
- adjusted geometric mean rank index (AGMRI)
- adjusted hits @ k index (AH@K)

Adjust by expectation and variance (z-score)

$$M^*(r_1,\ldots,r_n) = \frac{M(r_1,\ldots,r_n) - E[M]}{\sqrt{\operatorname{Var}[M]}}$$

- z-mean rank (zMR)
- z-mean reciprocal rank (zMRR)
- *z*-geometric mean rank (zGMR)
- z-hits @ k (zH@K)

Entity Alignment with KGE Models

Problem: we often need to integrate different KGs but not all entities have mappings

Solution: formalize as a link prediction task by concatenating KGs with a special **same as** relation between mapped entities (see <u>arxiv:1906.02390</u>, <u>arxiv:1911.08936</u>)

* caveat: specialized models often perform superior

Future: PyKEEN already packages most common EA benchmarking datasets for evaluation



Image from Zhu et al., 2017 https://www.ijcai.org/proceedings/2017/0595.pdf

Inductive Link Prediction and NodePiece

Problem: Previous knowledge graph embedding models could only be trained and applied in the *transductive* setting

Motivation: Want to apply KGEMs to entities outside of training graph => we need to move from *transductive* to *inductive* models



Inductive Link Prediction and NodePiece

NodePiece: moves beyond "shallow embeddings" and uses a combination of compositional strategies:

- Anchor or relation tokenization
- Degree, page rank, personal page rank searcher
- MLP, DeepSet, or arbitrary aggregator
- Inductive out-of-the-box any new node can be tokenized with a fixed-size vocabulary

Implementation: NodePiece is now available in PyKEEN along with a generalized training and evaluation workflow for inductive datasets



Inductive Link Prediction Challenge

More Problems:

- New models can train under inductive link prediction scenario
- Meaningful benchmarks (especially for biomedicine) aren't available

Solution: We implemented an algorithm for generating inductive link prediction benchmarks and made two based on Wikidata

Future: apply to biomedical knowledge graphs (e.g., using chemical similarity for induction)

Model	MRR	H@100	H@10	H@5	H@3	H@1	AMRI
InductiveNodePieceGNN	0.0705	0.374	0.1458	0.0990	0.0730	0.0319	0.682
InductiveNodePiece	0.0651	0.287	0.1246	0.0809	0.0542	0.0373	0.646

Baseline Results for Comparison

Language Models and KGE Models

- PyKEEN wraps P transformers (e.g., BERT) as representations for two tasks:
 - Improve a language model with explicit structured knowledge from a KG
 - Improve a KGE model with implicit unstructured knowledge in a language model
- Simple method for enabling inductive link prediction using entity labels
- See more: <u>https://pykeen.readthedocs.io/en/stable/t</u> <u>utorial/representations.html#label-based</u>

```
from pykeen.datasets import get_dataset
from pykeen.models import ERModel
from pykeen.nn.representation import (
    LabelBasedTransformerRepresentation.
from pykeen.pipeline import pipeline
dataset = get_dataset(dataset="Nations")
entity representations = LabelBasedTransformerRepresentation.from triples factory(
    triples factory=dataset.training,
result = pipeline(
    dataset=dataset.
    model=ERModel.
    model kwarqs=dict(
        interaction="ermlpe",
        interaction_kwargs=dict(
            embedding_dim=entity_representations.embedding_dim,
        ),
        entity representations=entity representations.
        relation representations kwargs=dict(
            shape=entity representations.shape,
        ),
    ),
    training kwargs=dict(
        num epochs=1,
    ),
```

Alternate KGEM Software



Wrapping Up

- Chat with us on the issue tracker for new features or support
- Join us! We can provide mentorship.
- Implement your next KGE model with PyKEEN
- Use PyKEEN in your downstream tasks







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