

# ChemicalX

## **Deep Learning For Drug Pair Scoring**

EN104 - Advanced Deep Learning 2024

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# The Team



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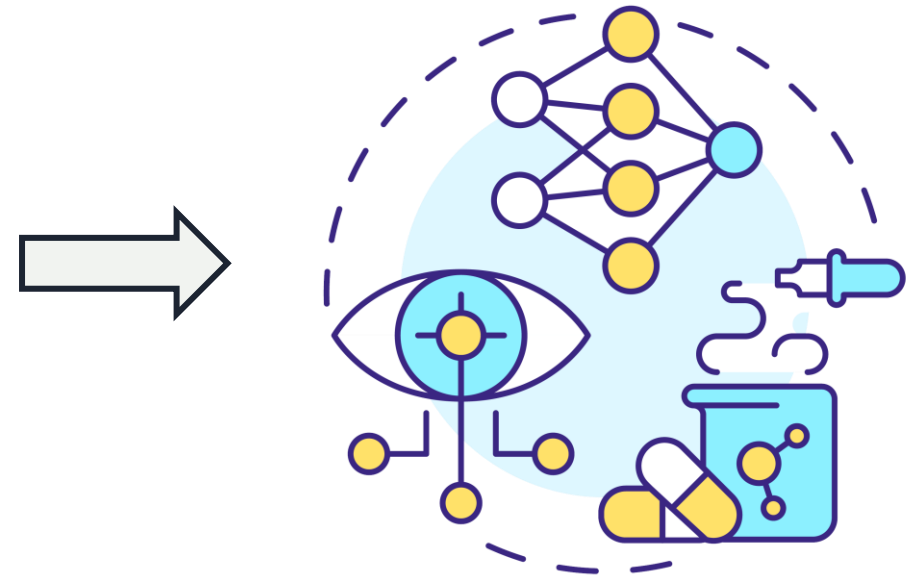
# The Problem : Drug Pair Scoring

+ Status Quo :



Weeks/Months/Years

+ Goal :



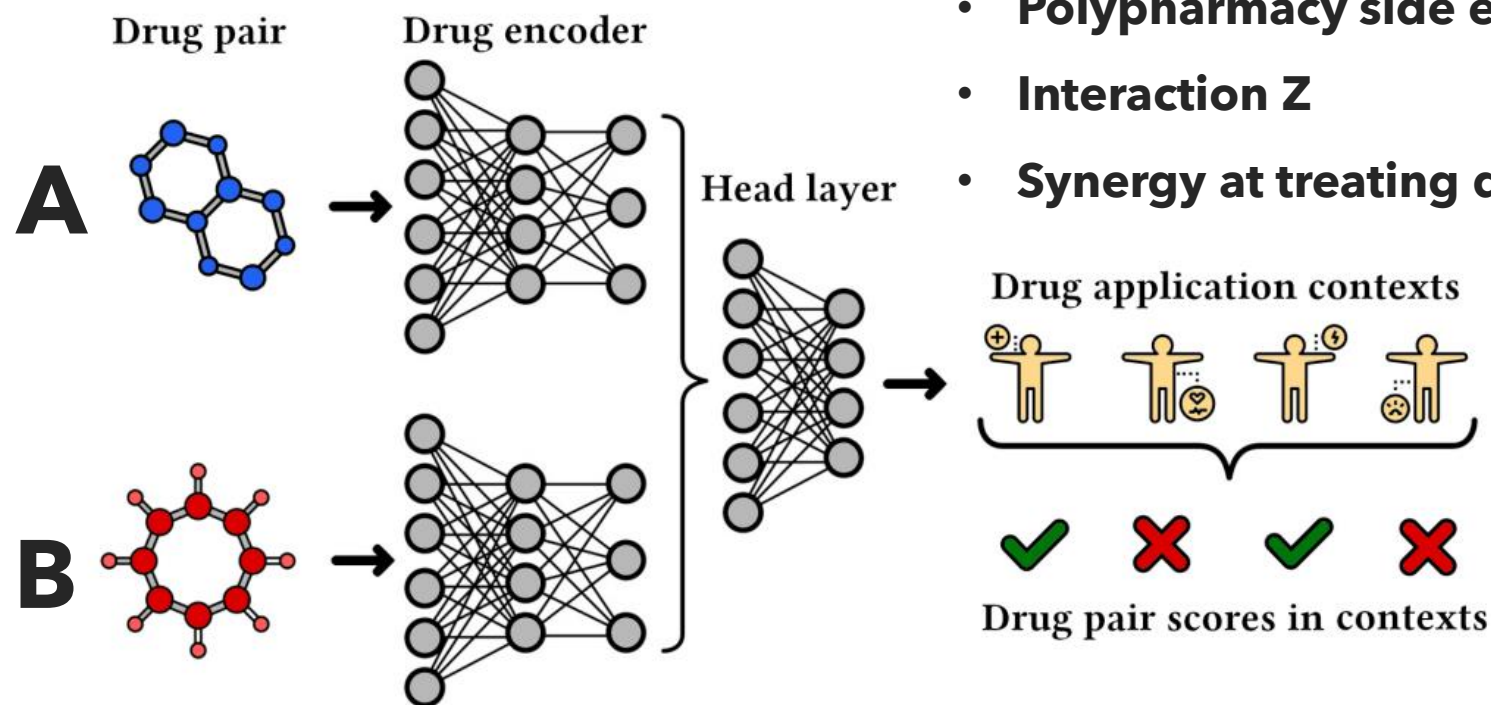
Minutes/Hours/Days

# Drug Pair Scoring



- **Drug-Drug Interaction**
- **Polypharmacy**
- **Drug Synergy**

# Model Architecture



Probability Of :

- Polypharmacy side effect Z
- Interaction Z
- Synergy at treating disease Z

## **Main Requirements:**

Python 3+



PyTorch



PyTorch Geometric



TorchDrug

# Datasets

Dataset	Task
TWOSIDES [44]	Polypharmacy
Drugbank DDI [41]	Interaction
DrugComb [51, 52]	Synergy
DrugCombDB [28]	Synergy
OncolyPharm [21]	Synergy

*Image Source: ChemicalX Paper*

# Preprocessed Data Structure

## FeatureSet:

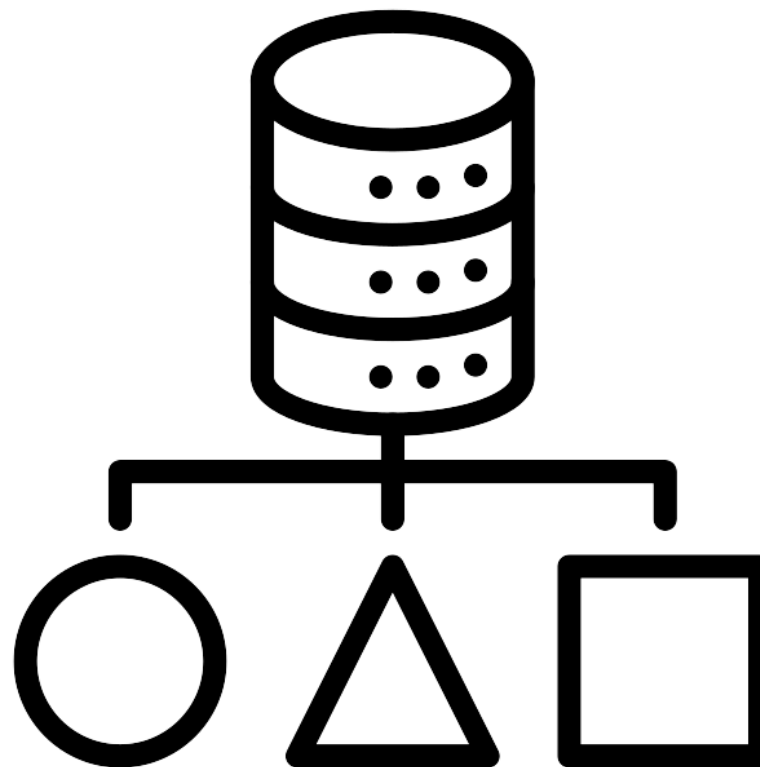
- 256 dimensional hashed Morgan fingerprints for each drug from SMILES.
- TorchDrug Molecular Graph

## ContextSet:

- An encoded context, either a biological aspect such as a cancer cell or another chemical compound.

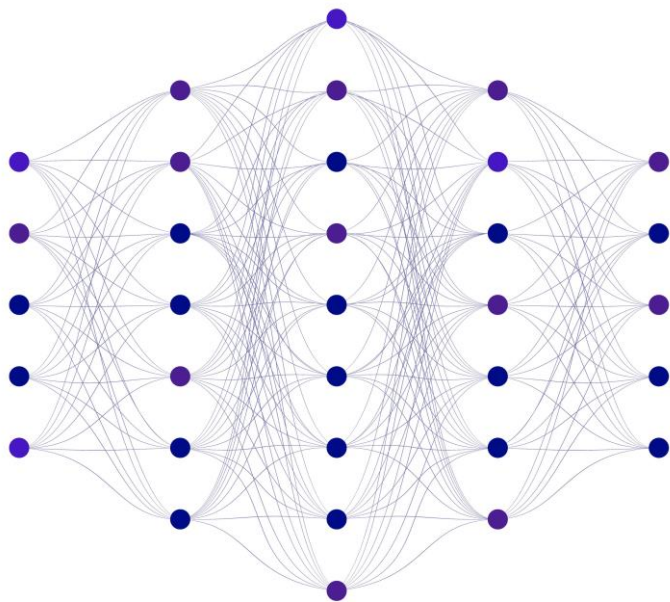
## Labeled Tripple :

- Identifiers for each drug in separate columns, with a classification label in 3<sup>rd</sup> column.





# Models



Model	Year	Domain	Encoder
DeepDDI [41]	2018	Interaction	Feedforward
DeepSynergy [37]	2018	Synergy	Feedforward
MHCADDI [9]	2019	Polypharmacy	GAT
MR-GNN [50]	2019	Interaction	GCN
CASTER [22]	2019	Interaction	Feedforward
SSI-DDI [34]	2020	Interaction	GAT
EPGCN-DS [43]	2020	Interaction	GCN
DeepDrug [4]	2020	Interaction	GCN
GCN-BMP [7]	2020	Interaction	GCN
DeepDDS [47]	2021	Synergy	GCN or GAT
MatchMaker [3]	2021	Synergy	Feedforward

*Image Source: ChemicalX Paper*

# Utilities

**Abstractions  
provided include:**

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**Dataloader**

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**BatchGenerator**

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**Model Pipeline for  
Training/Inference**

## Sample Code: Batch Generator

```
1 from chemicalx.data import DrugCombDB, BatchGenerator
2
3 loader = DrugCombDB()
4
5 context_set = loader.get_context_features()
6 drug_set = loader.get_drug_features()
7 triples = loader.get_labeled_triples()
8
9 train, test = triples.train_test_split(train_size=0.5)
10
11 generator = BatchGenerator(batch_size=1024,
12                             context_features=True,
13                             drug_features=True,
14                             drug_molecules=False,
15                             context_feature_set=context_set,
16                             drug_feature_set=drug_set,
17                             labeled_triples=train)
```

# Sample Code: Regular Training

---

```
1
2 import torch
3 from chemicalx.models import DeepSynergy
4
5 model = DeepSynergy(context_channels=112,
6                     drug_channels=256)
7
8 optimizer = torch.optim.Adam(model.parameters())
9 model.train()
10 loss = torch.nn.BCELoss()
11
12 for batch in generator:
13     optimizer.zero_grad()
14     prediction = model(batch.context_features,
15                       batch.drug_features_left,
16                       batch.drug_features_right)
17     loss_value = loss(prediction, batch.labels)
18     loss_value.backward()
19     optimizer.step()
```

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*Image Source: ChemicalX Paper*

# Sample Code: Pipeline Training

```
from chemicalx import pipeline
from chemicalx.models import DeepSynergy
from chemicalx.data import DrugCombDB

model = DeepSynergy(context_channels=112, drug_channels=256)
dataset = DrugCombDB()

results = pipeline(
    dataset=dataset,
    model=model,
    # Data arguments
    batch_size=5120,
    context_features=True,
    drug_features=True,
    drug_molecules=False,
    # Training arguments
    epochs=100,
)

# Outputs information about the AUC-ROC, etc. to the console.
results.summarize()

# Save the model, losses, evaluation, and other metadata.
results.save("/content/test_results/")
```

# Sample Code: Inference

---

```
1 import pandas as pd
2
3 model.eval()
4 generator.labeled_triples = test
5
6 predictions = []
7 for batch in generator:
8     prediction = model(batch.context_features,
9                        batch.drug_features_left,
10                       batch.drug_features_right)
11     prediction = prediction.detach().cpu().numpy()
12     identifiers = batch.identifiers
13     identifiers["prediction"] = prediction
14     predictions.append(identifiers)
15 predictions = pd.concat(predictions)
```

*Image Source: ChemicalX Paper*