

THERAPEUTICS  
DATA COMMONS

# Artificial Intelligence Foundation for Therapeutic Science

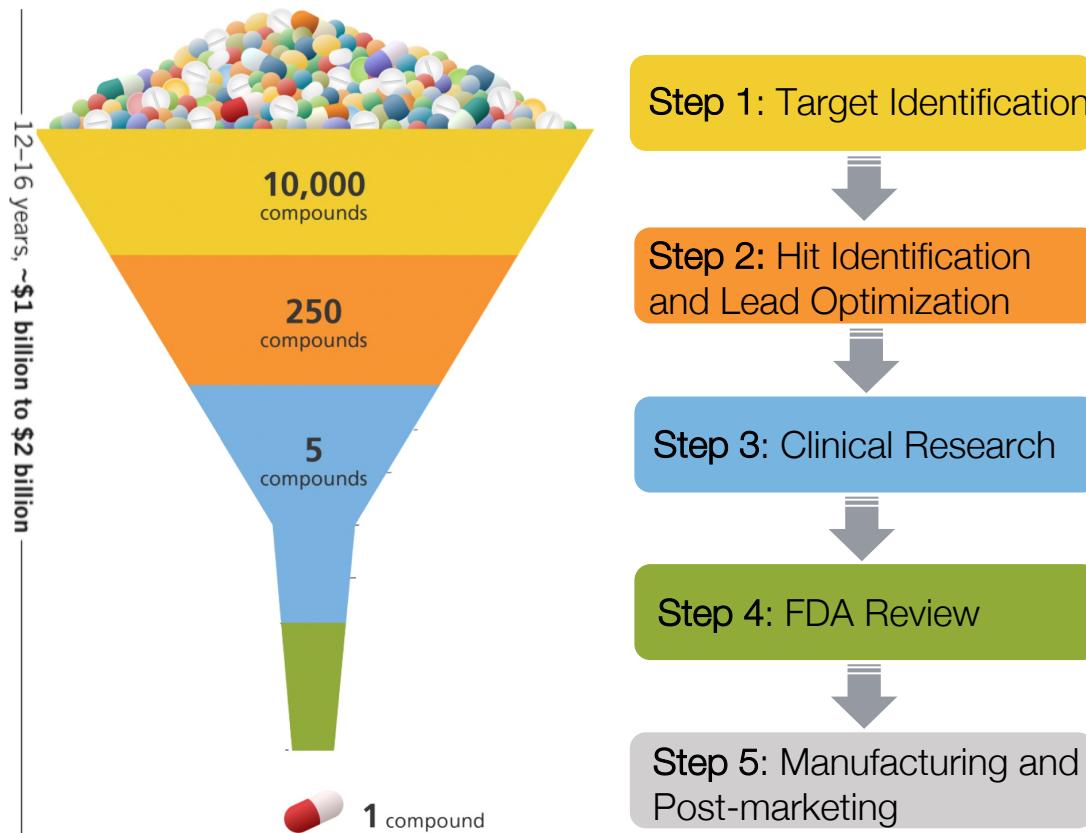
Kexin Huang\*, Tianfan Fu\*, Wenhao Gao\*, Yue Zhao, Yusuf Roohani,  
Jure Leskovec, Connor W. Coley, Cao Xiao, Jimeng Sun, Marinka Zitnik

ACS Fall 2022, Division of Computers in Chemistry

8/22/2022

# Challenges in Drug Discovery & Development

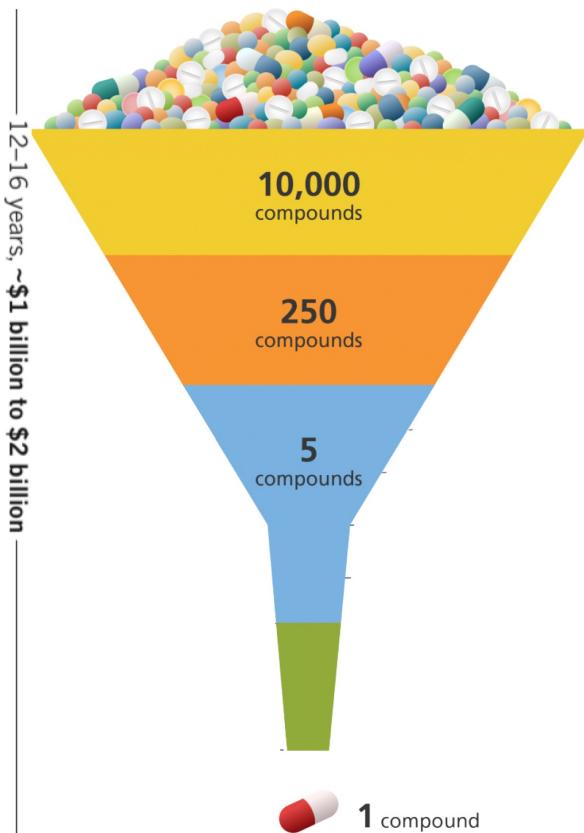
High cost, long time



# Challenges in Drug Discovery & Development

High cost, long time

Various and emerging diseases



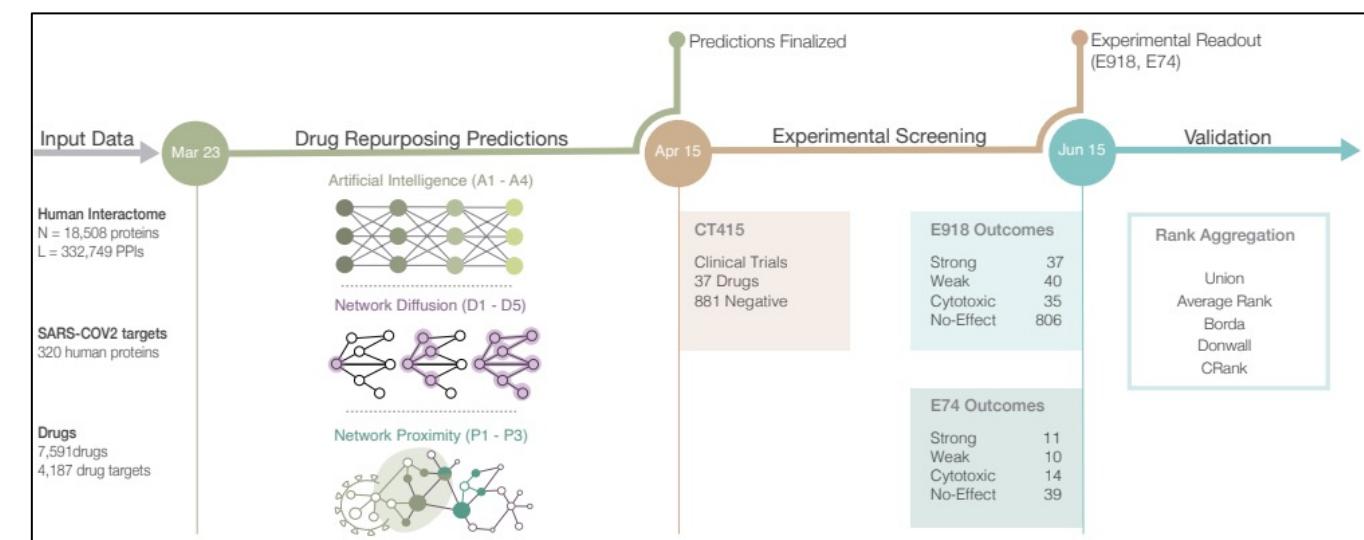
Step 1: Target Identification

Step 2: Hit Identification and Lead Optimization

Step 3: Clinical Research

Step 4: FDA Review

Step 5: Manufacturing and Post-marketing

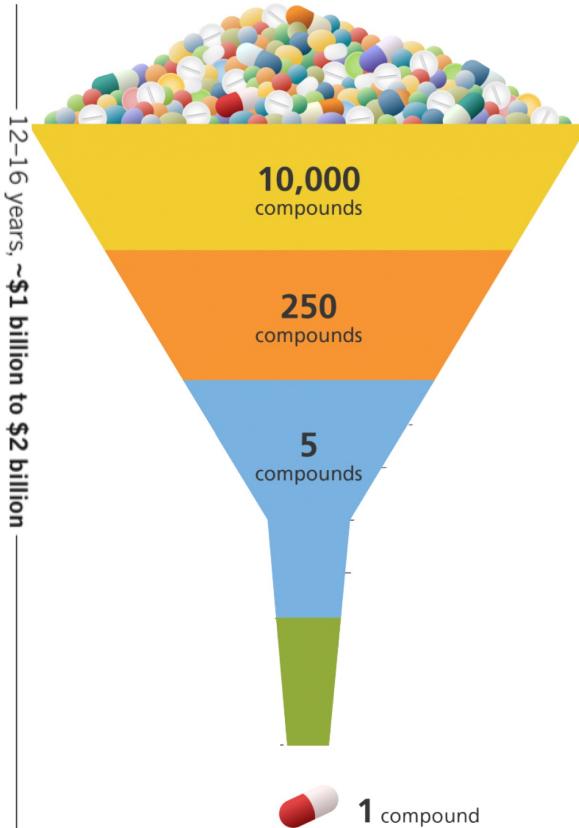


# Challenges in Drug Discovery & Development

High cost, long time

Various and emerging diseases

Abundant molecular modality



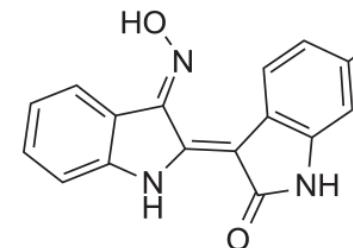
Step 1: Target Identification

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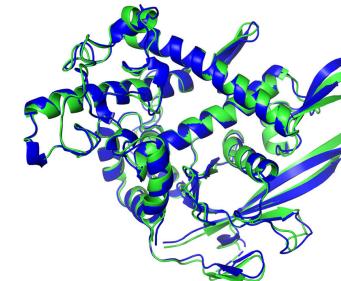
Step 5: Manufacturing and Post-marketing



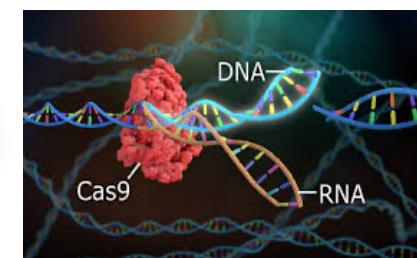
Small molecules



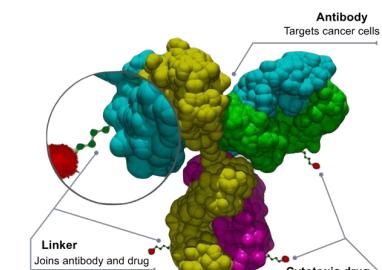
Vaccines



Proteins



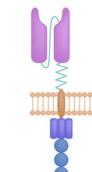
Gene-editing



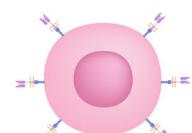
Anti- Nano-bodies



T-cell



CAR



CAR-T

# Data-driven Methods Demonstrated a Clear Impact



MAIN ABOUT PHARMA.AI PIPELINE NEWS & MEDIA CAREERS



ENG 简



## From Start to Phase 1 in 30 Months: AI-discovered and AI-designed Anti-fibrotic Drug Enters Phase I Clinical Trial

2022.02.24



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## News

Recursion is Granted FDA Fast Track Designation for REC-2282 for the Potential Treatment of NF2-Mutated Meningiomas



SALT LAKE CITY, Oct. 7, 2021 /PRNewswire/ -- Recursion (NASDAQ: RXRX), a clinical-stage biotechnology company decoding biology by

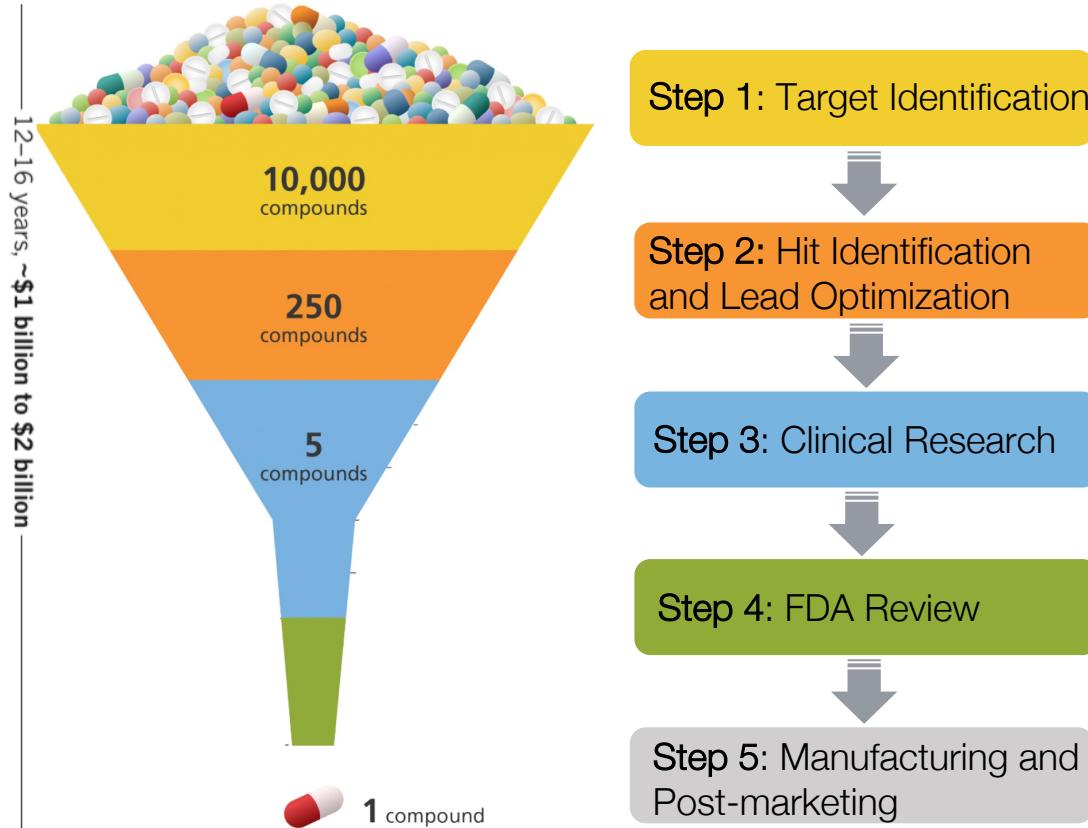


[investors.exscientia.ai/press-releases/](https://investors.exscientia.ai/press-releases/)

<https://insilico.com/phase1>

[ir.recursion.com](http://ir.recursion.com)

# Challenges of AI in Drug Discovery & Development



Step 1: Target Identification



Step 2: Hit Identification  
and Lead Optimization



Step 3: Clinical Research



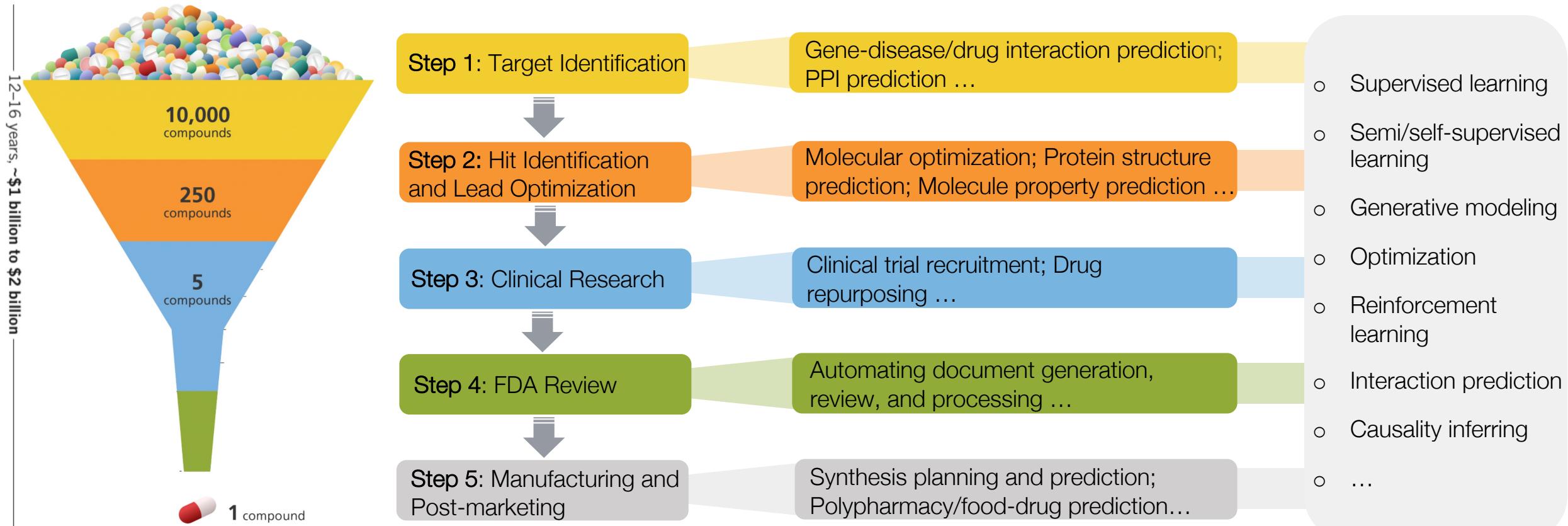
Step 4: FDA Review



Step 5: Manufacturing and  
Post-marketing

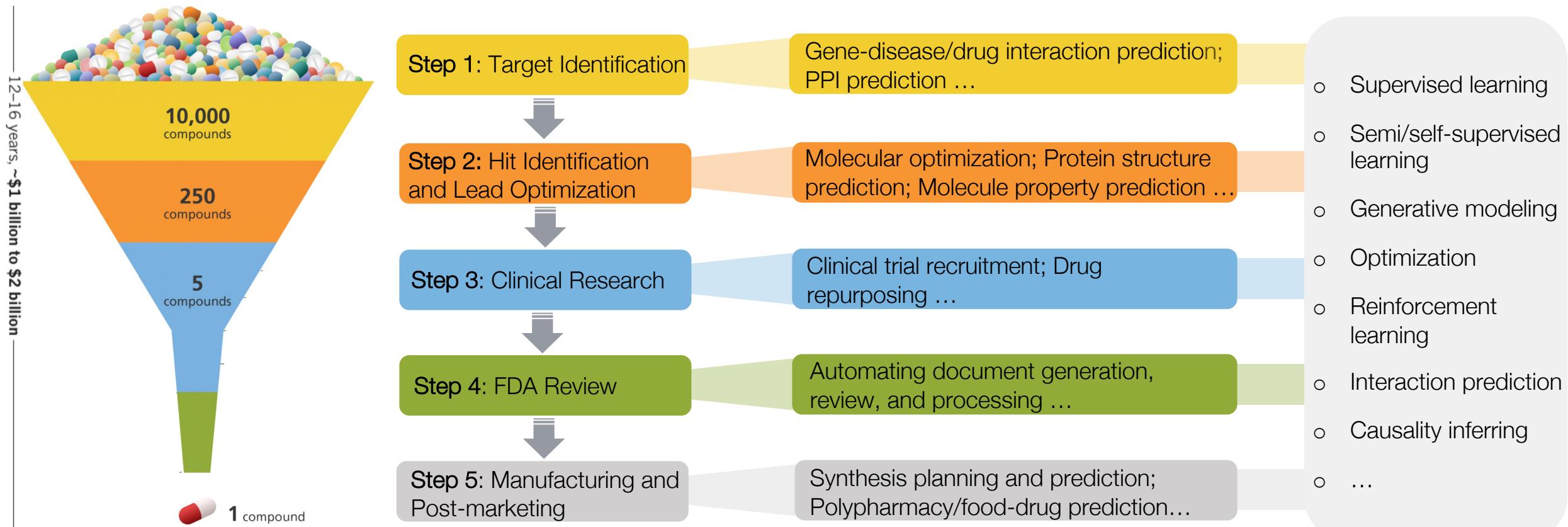
# Challenges of AI in Drug Discovery & Development

- Formulate various tasks as machine-learning-solvable tasks.



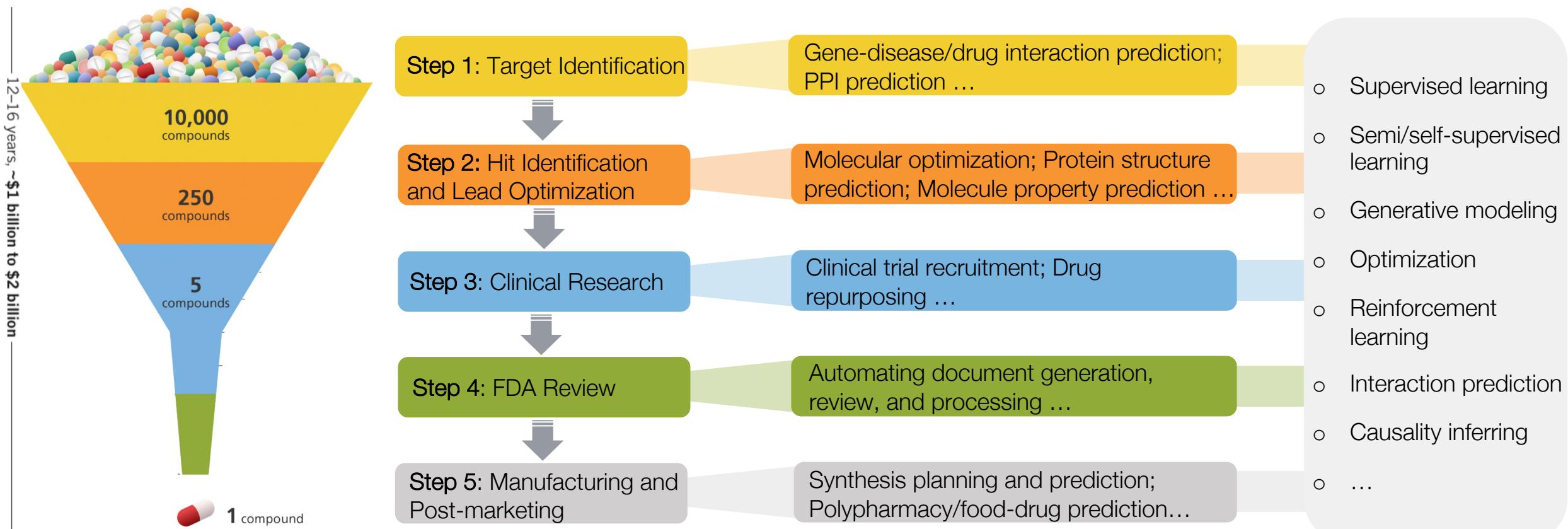
# Challenges of AI in Drug Discovery & Development

- Formulate various tasks as machine-learning-solvable tasks.
- Identify, retrieve, and process datasets of many different types scattered around.



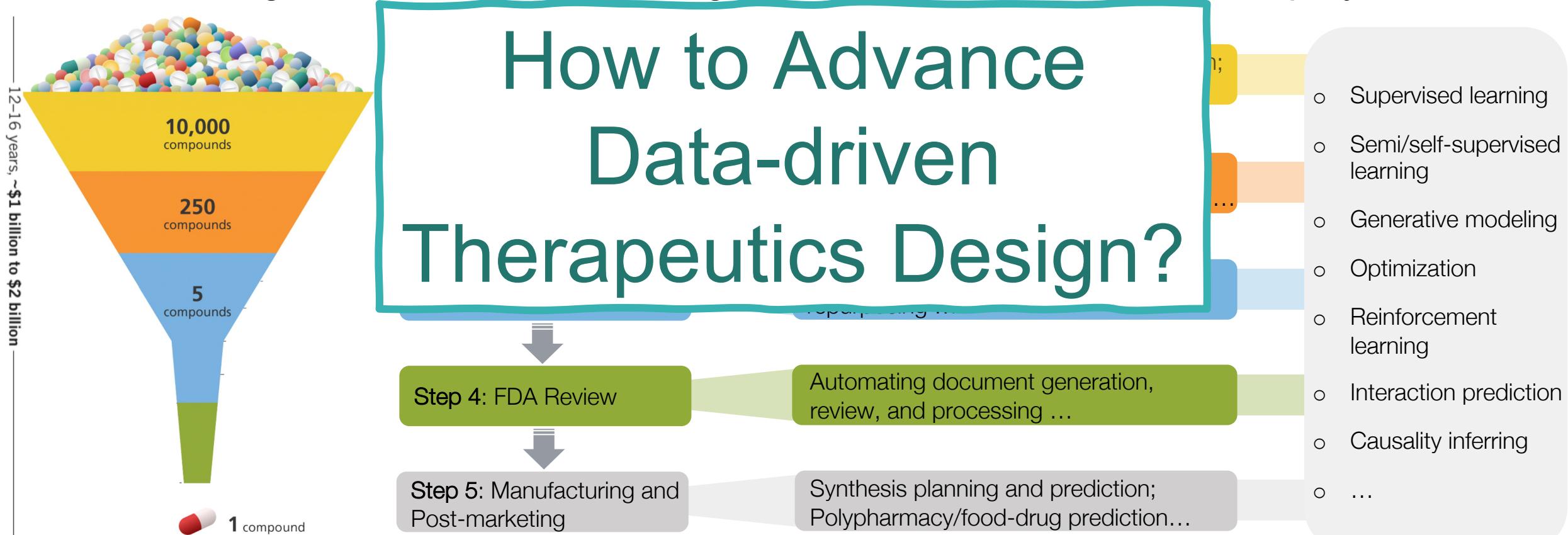
# Challenges of AI in Drug Discovery & Development

- Formulate various tasks as machine-learning-solvable tasks.
- Identify, retrieve, and process datasets of many different types scattered around.
- Assess algorithmic advances to align with real-world and clinical deployment.



# Challenges of AI in Drug Discovery & Development

- Formulate various tasks as machine-learning-solvable tasks.
- Identify, retrieve, and process datasets of many different types scattered around.
- Assess algorithmic advances to align with real-world and clinical deployment.



# Therapeutics Data Commons



THERAPEUTICS  
DATA COMMONS

Website: <https://tdcommons.ai> (or QR code)



Paper: <https://arxiv.org/abs/2102.09548>

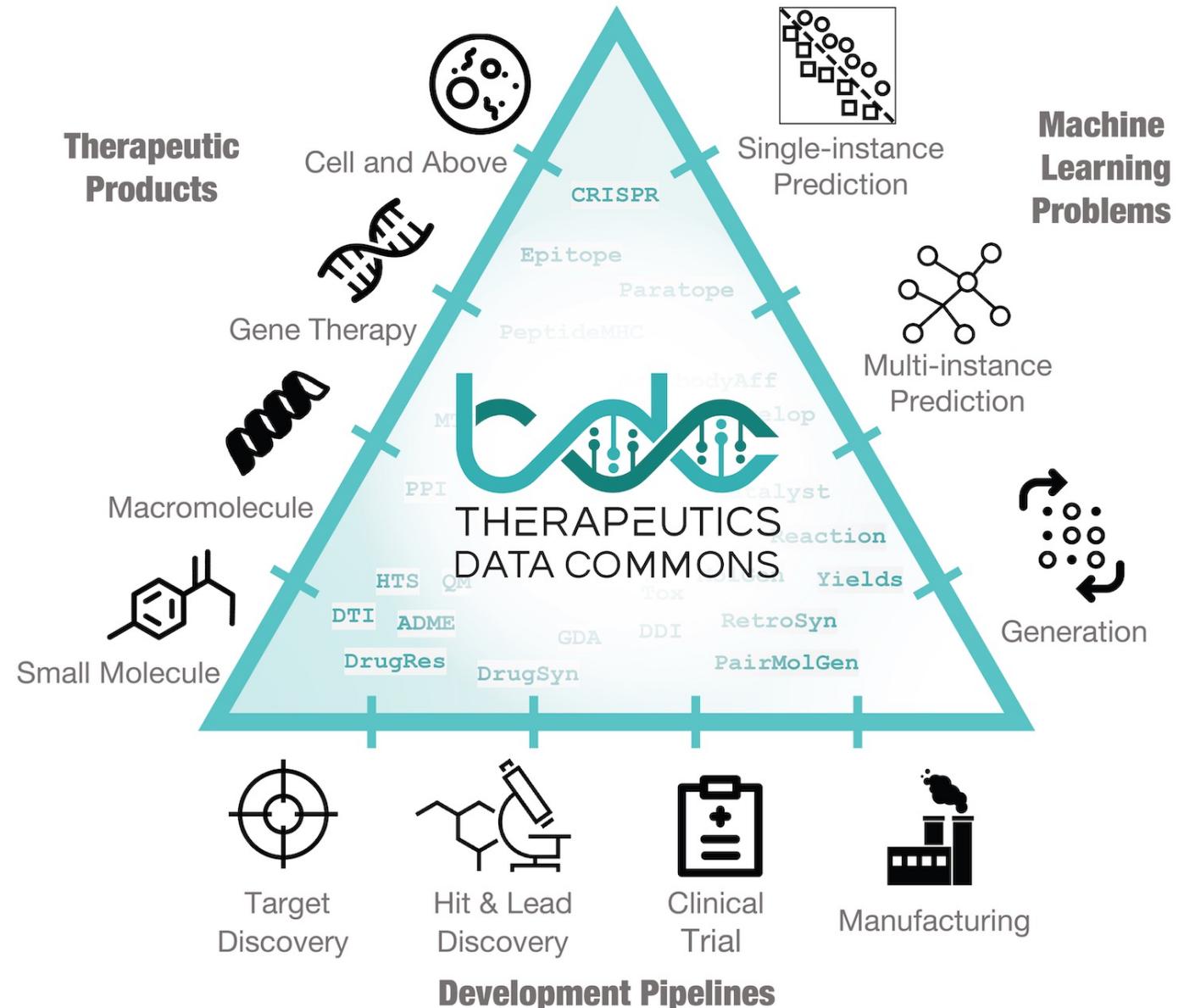
Github: <https://github.com/mims-harvard/TDC>



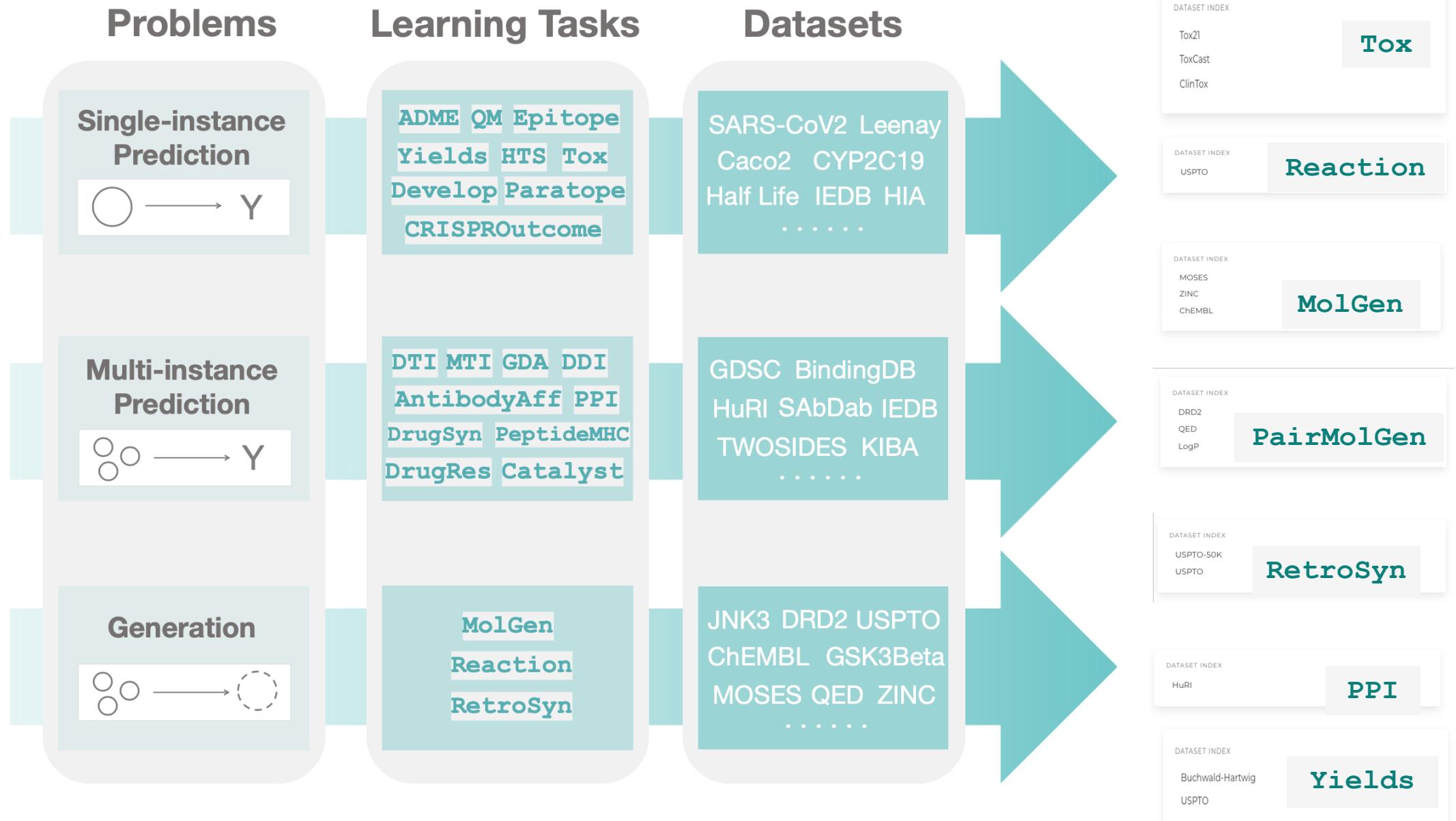
**Facilitate algorithmic and scientific advance  
in therapeutics**



# Wide Range of Therapeutic Modalities and Pipeline



# Three-Tier Design



# Unified, Light-weighted and User-friendly

```
pip install PyTDC
```



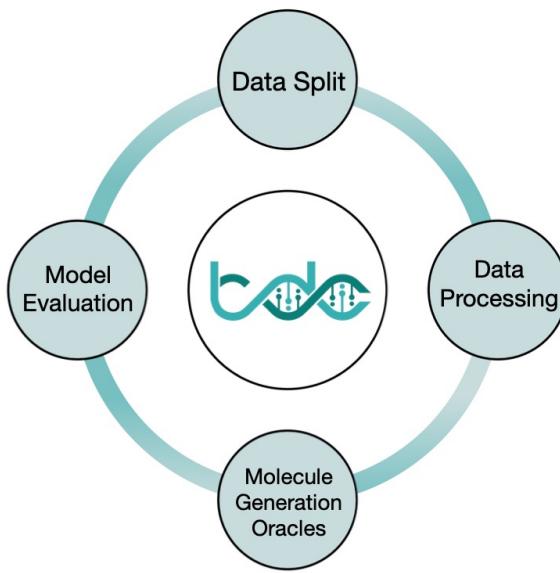
## 3 Lines of Code

The core TDC library uses minimum packages thus is installed hassle-free. Data loaders are simplified so that you can get access to ML-ready datasets within only 3 lines of code.

A screenshot of a Jupyter Notebook interface. It shows two code cells, each starting with 'In [ ]:' followed by a text input field. The first cell's input field is highlighted with a green border. Below the cells is a large, light-gray rectangular area representing the output pane.

# TDC has more than Datasets

- Ecosystem of tools, leaderboards, and community resources, including data functions, strategies for systematic model evaluation, meaningful data splits, data processors, and molecule generation oracles



## Model performance evaluators

| FUNCTION INDEX   |
|--|
| Regression Metric  |
| Mean Squared Error (MSE)   |
| Mean Absolute Error (MAE)  |
| Coefficient of Determination ( $R^2$ )                           |
| Binary Classification Metric                                     |
| Area Under the Receiver Operating Characteristic Curve (ROC-AUC) |
| Area Under the Precision-Recall Curve (PR-AUC)                   |
| Accuracy Metric  |
| Precision  |
| Recall   |
| F1 Score   |
| Multi-class Classification Metric                                |
| Micro-F1, Micro-Precision, Micro-Recall, Accuracy                |
| Macro-F1   |
| Cohen's Kappa (Kappa)  |
| Token-level Classification Metric                                |
| Average ROC-AUC  |

## Meaningful data splits

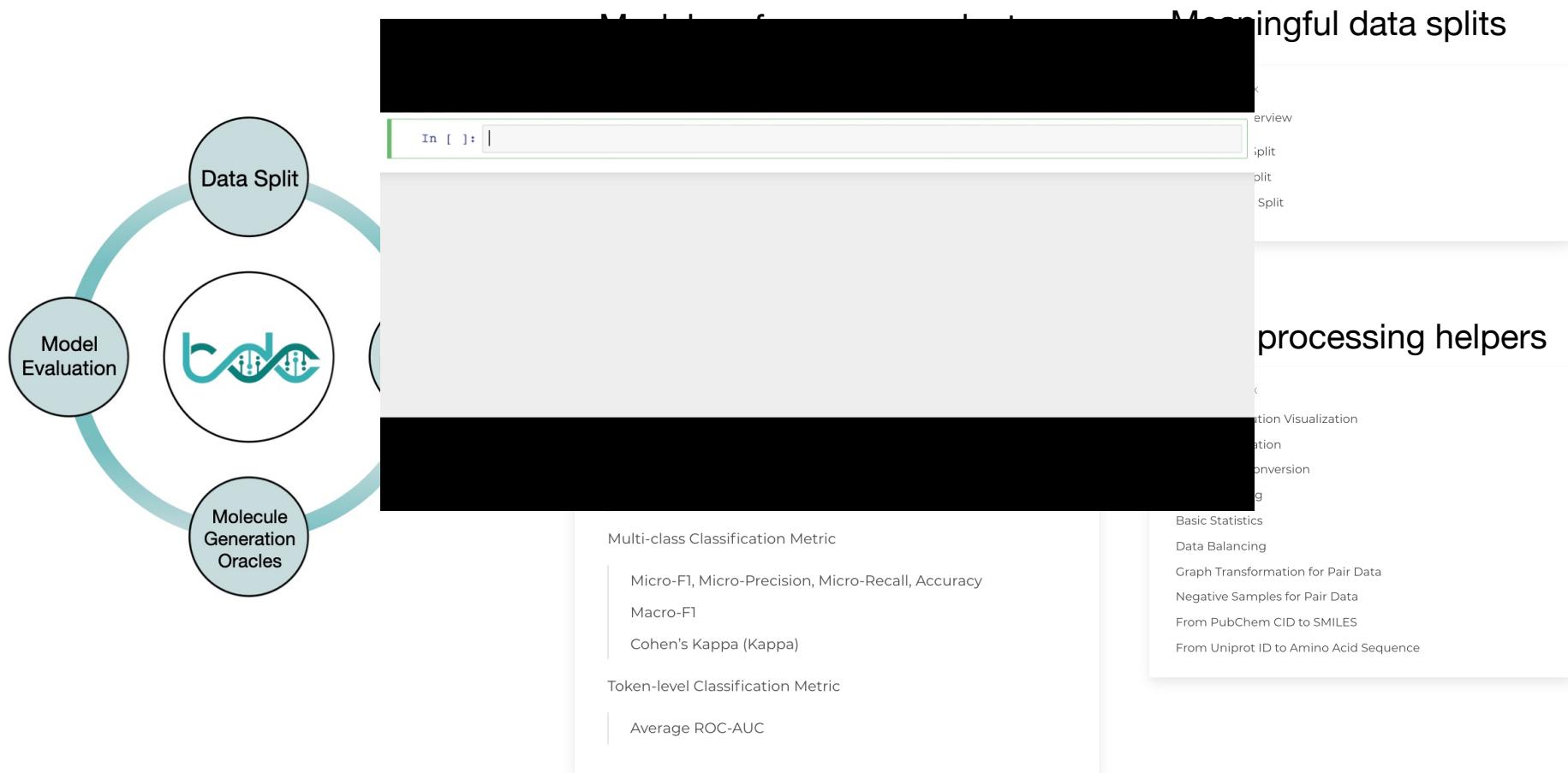
| FUNCTION INDEX      |
|---------------------|
| Data Split Overview |
| Random Split        |
| Scaffold Split      |
| Cold-Start Split    |

## Data processing helpers

| FUNCTION INDEX                         |
|--|
| Label Distribution Visualization       |
| Label Binarization                     |
| Label Units Conversion                 |
| Label Meaning                          |
| Basic Statistics                       |
| Data Balancing                         |
| Graph Transformation for Pair Data     |
| Negative Samples for Pair Data         |
| From PubChem CID to SMILES             |
| From Uniprot ID to Amino Acid Sequence |

# TDC has more than Datasets

- Ecosystem of tools, leaderboards, and community resources, including data functions, strategies for systematic model evaluation, meaningful data splits, data processors, and molecule generation oracles



# Benchmarks and Leaderboards



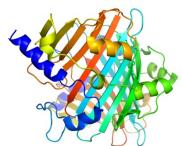
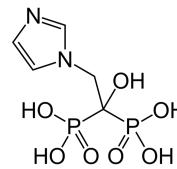
Team 1

▪

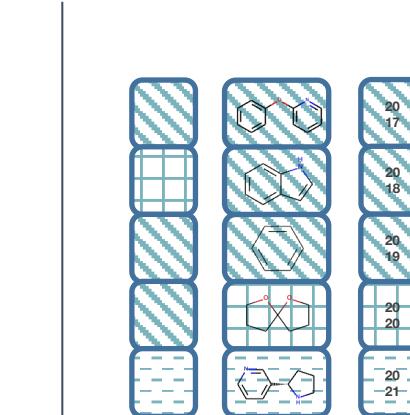


Team N

TDC benchmark provides a dataset, a dataset split, and performance metrics to evaluate AI/ML models



TDC Dataset



TDC.Split

Synthesizability  
Diversity  
Novelty  
Top Docking Score  
% Pass Mol Filters  
AUPRC  
AUROC  
MSE  
...  
TDC.Evaluator

TDC.BenchmarkGroup

# Benchmarks and Leaderboards

Loading TDC  
benchmark class



```
from tdc.benchmark_group import admet_group
group = admet_group(path = 'data/')
benchmark = group.get('Caco2_Wang')
```

Get ML-ready  
train/val/test data



```
predictions = {}
name = benchmark['name']
train_val, test = benchmark['train_val'], benchmark['test']
```

Train your model



```
## --- train your model --- ##
```

Return ready to  
submit metrics



```
predictions[name] = y_pred
group.evaluate(predictions)
# {'caco2_wang': {'mae': 0.234}}
```

# Benchmarks and Leaderboards

Loading TDC  
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## --- train your model ---

predictions[name] = y_pred
group.evaluate(predictions)
# {'caco2_wang': {'mae': 0.234}}
```

The screenshot shows the TDC DRD3 Leaderboard page. At the top, it displays a 'Docking Target Summary' for 'TDC.DRD3' which targets 'Tremor, Schizophrenia'. Below this is a section titled 'Leaderboard: Models Make at Most 5000 Oracle Calls' containing the following table:

| Rank | Model        | Contact    | Link          | #Params   | Top100↓         | Top10↓          | Top1↓           | Diver.↑       | Novel.↑       | %Pass↑        | Top 1-P↓        | M↓             | Molecules            |
|------|--------------|------------|---------------|-----------|-----------------|-----------------|-----------------|---------------|---------------|---------------|-----------------|----------------|----------------------|
| -    | Best-in-data | -          | -             | -         | -12,080         | -12,590         | -12,800         | 0.864         | -             | 0.780         | -11,700         | 5,100          | <a href="#">Link</a> |
| 1    | Graph-GA     | Tianfan Fu | GitHub, Paper | 0         | -14,811 ± 0,413 | -15,930 ± 0,336 | -16,533 ± 0,309 | 0,626 ± 0,092 | 1,000 ± 0,000 | 0,393 ± 0,308 | -14,267 ± 0,450 | 9,669 ± 0,468  | <a href="#">Link</a> |
| 2    | SMILES-LSTM  | Tianfan Fu | GitHub, Paper | 3,149,000 | -13,017 ± 0,385 | -14,030 ± 0,421 | -14,533 ± 0,525 | 0,740 ± 0,056 | 1,000 ± 0,000 | 0,257 ± 0,013 | -12,533 ± 0,403 | 5,826 ± 1,908  | <a href="#">Link</a> |
| 3    | GCPN         | Tianfan Fu | GitHub, Paper | 17,600    | -10,045 ± 0,226 | -11,483 ± 0,581 | -12,300 ± 0,993 | 0,922 ± 0,002 | 1,000 ± 0,000 | 0,167 ± 0,045 | -9,367 ± 0,170  | 10,000 ± 0,000 | <a href="#">Link</a> |
| 4    | MARS         | Tianfan Fu | GitHub, Paper | 153,000   | -9,509 ± 0,035  | -10,693 ± 0,172 | -11,433 ± 0,450 | 0,873 ± 0,002 | 1,000 ± 0,000 | 0,527 ± 0,087 | -9,000 ± 0,082  | 7,073 ± 0,798  | <a href="#">Link</a> |
| 5    | MolDQN       | Tianfan Fu | GitHub, Paper | 2,694,800 | -8,236 ± 0,089  | -9,348 ± 0,188  | -9,990 ± 0,194  | 0,893 ± 0,005 | 1,000 ± 0,000 | 0,023 ± 0,012 | -7,980 ± 0,112  | 10,000 ± 0,000 | <a href="#">Link</a> |

↓: The lower/higher, the better. Click ↓ to sort based on the specific column.

\* Rank is based on Top 100 average docking scores.

\*\* Novelty is calculated against the ZINC training dataset.

Below this is another section titled 'Leaderboard: Models Make at Most 1000 Oracle Calls' containing the following table:

| Rank | Model        | Contact    | Link          | #Params   | Top100↓         | Top10↓          | Top1↓           | Diver.↑       | Novel.↑       | %Pass↑        | Top 1-P↓        | M↓            | Molecules            |
|------|--------------|------------|---------------|-----------|-----------------|-----------------|-----------------|---------------|---------------|---------------|-----------------|---------------|----------------------|
| -    | Best-in-data | -          | -             | -         | -12,080         | -12,590         | -12,800         | 0.864         | -             | 0.780         | -11,700         | 5,100         | <a href="#">Link</a> |
| 1    | Graph-GA     | Tianfan Fu | GitHub, Paper | 0         | -11,224 ± 0,484 | -12,400 ± 0,782 | -13,233 ± 0,713 | 0,815 ± 0,046 | 1,000 ± 0,000 | 0,777 ± 0,096 | -10,600 ± 0,374 | 7,695 ± 0,909 | <a href="#">Link</a> |
| 2    | SMILES-LSTM  | Tianfan Fu | GitHub, Paper | 3,149,000 | -9,971 ± 0,115  | -11,163 ± 0,141 | -11,967 ± 0,205 | 0,871 ± 0,004 | 1,000 ± 0,000 | 0,777 ± 0,026 | -9,367 ± 0,094  | 4,818 ± 0,541 | <a href="#">Link</a> |
| 3    | GCPN         |            |               |           |                 |                 |                 |               |               |               |                 | 0 ± 0         | <a href="#">Link</a> |

[https://tdcommons.ai/  
benchmark/overview/](https://tdcommons.ai/benchmark/overview/)



# Benchmarks and Leaderboards

- Scaffold split
- No single method has the best performance across the board!

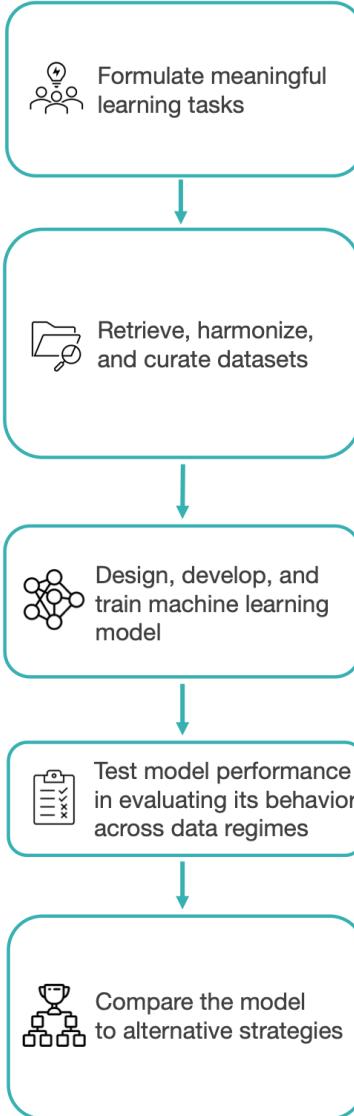
| Raw Feature Type         |           | Expert-Curated Methods |                    | SMILES             | Molecular Graph-Based Methods (state-of-the-Art in ML) |                    |                    |                     |                    |  |
|--------------------------|-----------|------------------------|--------------------|--------------------|--|--------------------|--------------------|---------------------|--------------------|--|
| Dataset                  | Metric    | Morgan [31]            | RDKit2D [24]       | CNN [18]           | NeuralFP [7]   | GCN [23]           | AttentiveFP [43]   | AttrMasking [16]    | ContextPred [16]   |  |
|                          | # Params. | 1477K                  | 633K               | 227K               | 480K   | 192K               | 301K               | 2067K               | 2067K              |  |
| <b>TDC.Caco2</b> (↓)     | MAE       | 0.908±0.060            | <b>0.393±0.024</b> | 0.446±0.036        | 0.530±0.102  | 0.599±0.104        | <b>0.401±0.032</b> | 0.546±0.052         | 0.502±0.036        |  |
| <b>TDC.HIA</b> (↑)       | AUROC     | 0.807±0.072            | <b>0.972±0.008</b> | 0.869±0.026        | 0.943±0.014  | 0.936±0.024        | <b>0.974±0.007</b> | <b>0.978±0.006</b>  | 0.975±0.004        |  |
| <b>TDC.Pgp</b> (↑)       | AUROC     | 0.880±0.006            | <b>0.918±0.007</b> | 0.908±0.012        | 0.902±0.020  | 0.895±0.021        | 0.892±0.012        | <b>0.929±0.006</b>  | 0.923±0.005        |  |
| <b>TDC.Bioav</b> (↑)     | AUROC     | 0.581±0.086            | <b>0.672±0.021</b> | 0.613±0.013        | 0.632±0.036  | 0.566±0.115        | 0.632±0.039        | 0.577±0.087         | 0.671±0.026        |  |
| <b>TDC.Lipo</b> (↓)      | MAE       | 0.701±0.009            | <b>0.574±0.017</b> | 0.743±0.020        | 0.563±0.023  | <b>0.541±0.011</b> | 0.572±0.007        | 0.547±0.024         | <b>0.535±0.012</b> |  |
| <b>TDC.AqSol</b> (↓)     | MAE       | 1.203±0.019            | <b>0.827±0.047</b> | 1.023±0.023        | 0.947±0.016  | 0.907±0.020        | <b>0.776±0.008</b> | 1.026±0.020         | 1.040±0.045        |  |
| <b>TDC.BBB</b> (↑)       | AUROC     | 0.823±0.015            | <b>0.889±0.016</b> | 0.781±0.030        | 0.836±0.009  | 0.842±0.016        | 0.855±0.011        | 0.892±0.012         | <b>0.897±0.004</b> |  |
| <b>TDC.PPBR</b> (↓)      | MAE       | 12.848±0.362           | <b>9.994±0.319</b> | 11.106±0.358       | <b>9.292±0.384</b>                                     | 10.194±0.373       | <b>9.373±0.335</b> | <b>10.075±0.202</b> | 9.445±0.224        |  |
| <b>TDC.VD</b> (↑)        | Spearman  | 0.493±0.011            | <b>0.561±0.025</b> | 0.226±0.114        | 0.258±0.162  | 0.457±0.050        | 0.241±0.145        | <b>0.559±0.019</b>  | 0.485±0.092        |  |
| <b>TDC.CYP2D6-I</b> (↑)  | AUPRC     | 0.587±0.011            | 0.616±0.007        | 0.544±0.053        | 0.627±0.009  | 0.616±0.020        | 0.646±0.014        | <b>0.721±0.009</b>  | <b>0.739±0.005</b> |  |
| <b>TDC.CYP3A4-I</b> (↑)  | AUPRC     | 0.827±0.009            | 0.829±0.007        | 0.821±0.003        | 0.849±0.004  | 0.840±0.010        | <b>0.851±0.006</b> | <b>0.902±0.002</b>  | <b>0.904±0.002</b> |  |
| <b>TDC.CYP2C9-I</b> (↑)  | AUPRC     | 0.715±0.004            | 0.742±0.006        | 0.713±0.006        | 0.739±0.010  | 0.735±0.004        | 0.749±0.004        | <b>0.829±0.003</b>  | <b>0.839±0.003</b> |  |
| <b>TDC.CYP2D6-S</b> (↑)  | AUPRC     | 0.671±0.066            | 0.677±0.047        | 0.485±0.037        | 0.572±0.062  | 0.617±0.039        | 0.574±0.030        | <b>0.704±0.028</b>  | <b>0.736±0.024</b> |  |
| <b>TDC.CYP3A4-S</b> (↑)  | AUROC     | 0.633±0.013            | <b>0.639±0.012</b> | <b>0.662±0.031</b> | 0.578±0.020  | 0.590±0.023        | 0.576±0.025        | <b>0.582±0.021</b>  | 0.609±0.025        |  |
| <b>TDC.CYP2C9-S</b> (↑)  | AUPRC     | 0.380±0.015            | 0.360±0.040        | 0.367±0.059        | 0.359±0.059  | 0.344±0.051        | 0.375±0.032        | <b>0.381±0.045</b>  | <b>0.392±0.026</b> |  |
| <b>TDC.Half_Life</b> (↑) | Spearman  | <b>0.329±0.083</b>     | 0.184±0.111        | 0.038±0.138        | 0.177±0.165  | <b>0.239±0.100</b> | 0.085±0.068        | 0.151±0.068         | 0.129±0.114        |  |
| <b>TDC.CL-Micro</b> (↑)  | Spearman  | 0.492±0.020            | <b>0.586±0.014</b> | 0.252±0.116        | 0.529±0.015  | 0.532±0.033        | 0.365±0.055        | <b>0.585±0.034</b>  | 0.578±0.007        |  |
| <b>TDC.CL-Hepa</b> (↑)   | Spearman  | 0.272±0.068            | 0.382±0.007        | 0.235±0.021        | 0.401±0.037  | 0.366±0.063        | 0.289±0.022        | <b>0.413±0.028</b>  | <b>0.439±0.026</b> |  |
| <b>TDC.hERG</b> (↑)      | AUROC     | 0.736±0.023            | <b>0.841±0.020</b> | 0.754±0.037        | 0.722±0.034  | 0.738±0.038        | 0.825±0.007        | 0.778±0.046         | 0.756±0.023        |  |
| <b>TDC.AMES</b> (↑)      | AUROC     | 0.794±0.008            | 0.823±0.011        | 0.776±0.015        | 0.823±0.006  | 0.818±0.010        | 0.814±0.008        | <b>0.842±0.008</b>  | 0.837±0.009        |  |
| <b>TDC.DILI</b> (↑)      | AUROC     | 0.832±0.021            | 0.875±0.019        | 0.792±0.016        | 0.851±0.026  | 0.859±0.033        | <b>0.886±0.015</b> | <b>0.919±0.008</b>  | 0.861±0.018        |  |
| <b>TDC.LD50</b> (↓)      | MAE       | 0.649±0.019            | <b>0.678±0.003</b> | 0.675±0.011        | 0.667±0.020  | 0.649±0.026        | 0.678±0.012        | <b>0.685±0.025</b>  | 0.669±0.030        |  |



# TDC Serves the Whole Lifecycle



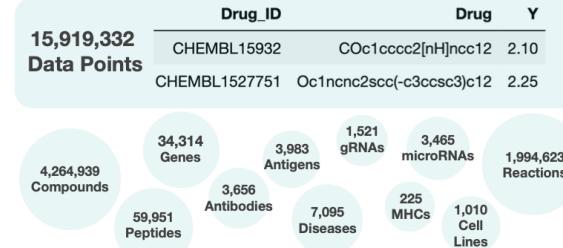
## Lifecycle of Therapeutics Machine Learning



## 22 Learning Tasks



## 66 AI/ML-Ready Datasets



## TDC Data Functions

- 5 Realistic TDC Data Splits Functions
- 17 TDC Molecule Generation Oracles
- 11 TDC Data Processing Helpers

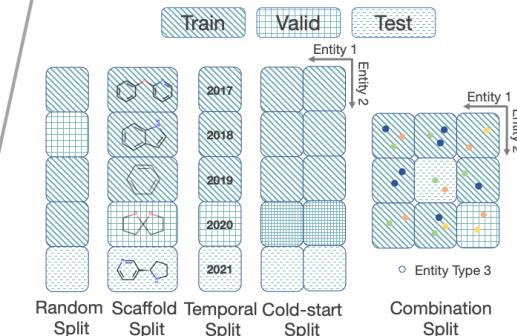
## 23 TDC Evaluator Functions

- |                        |                     |
|------------------------|---------------------|
| Regression: 6 Metrics  | Binary: 8 Metrics   |
| Multi-class: 3 Metrics | Molecule: 6 Metrics |

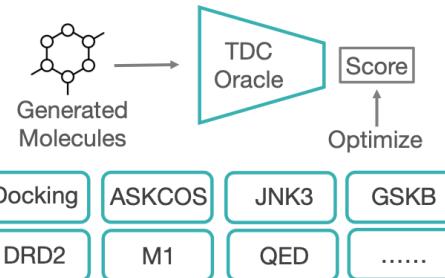
## TDC Leaderboards

- |  |
|--|
| 22 ADMET Group Benchmarks                      |
| 5 Drug Combination Group Benchmarks            |
| 1 Docking Score Molecule Generation Benchmark  |
| 1 Drug-target Binding Generalization Benchmark |

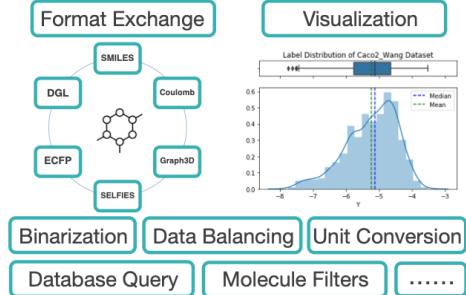
## TDC Data Split Functions



## TDC Molecule Generation Oracles

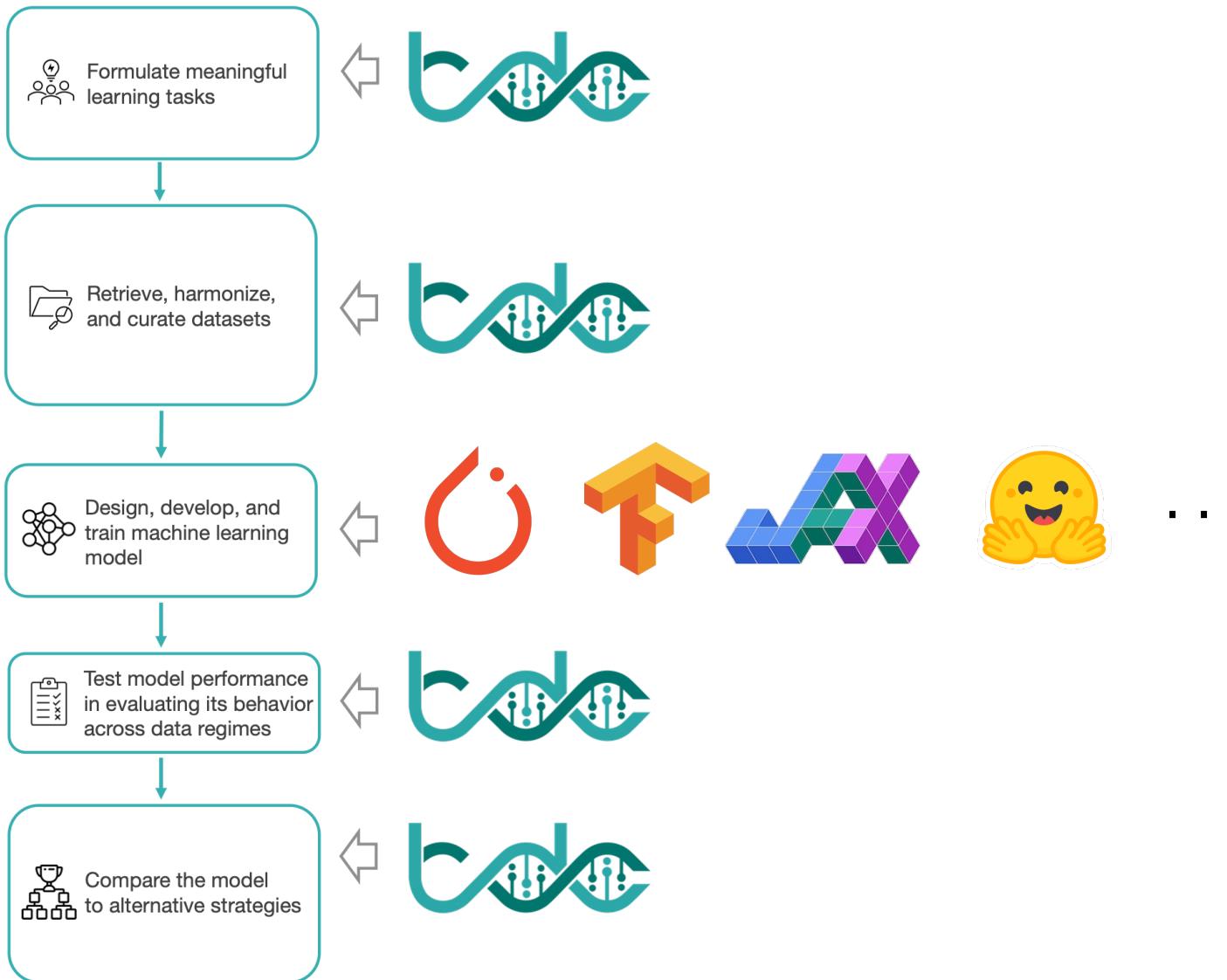


## TDC Data Processing Helpers



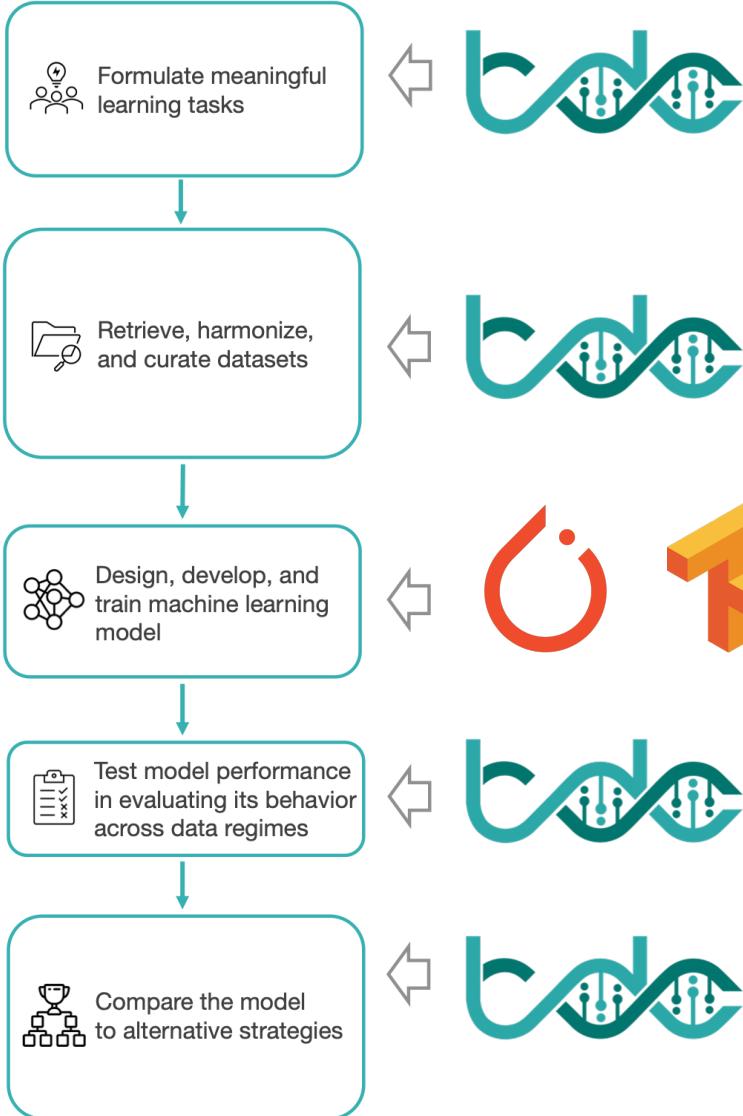
# And Innovation!

Lifecycle of Therapeutics  
Machine Learning



# And Innovation!

Lifecycle of Therapeutics  
Machine Learning



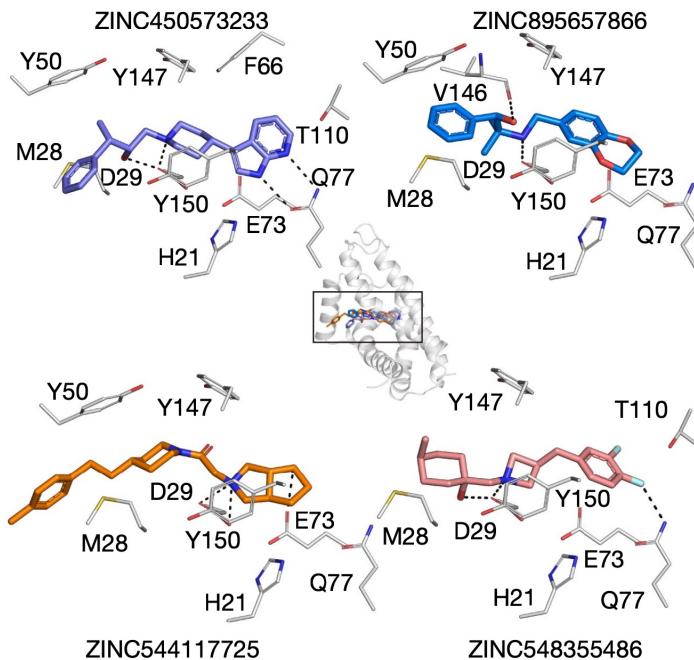
Not just a low-code implementation of existing models!

```
from torchdrug import core, models, tasks, utils  
  
model = models.GIN(input_dim=dataset.node_feature_dim,  
                    hidden_dims=[256, 256, 256, 256],  
                    short_cut=True, batch_norm=True, concat_hidden=True)  
task = tasks.PropertyPrediction(model, task=dataset.tasks,  
                                 criterion="bce", metric=("auprc", "auroc"))  
  
import deepchem as dc  
from deepchem.models.graph_models import GraphConvModel
```

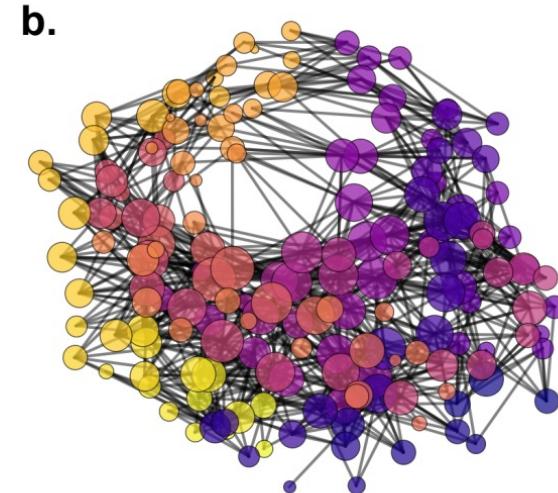
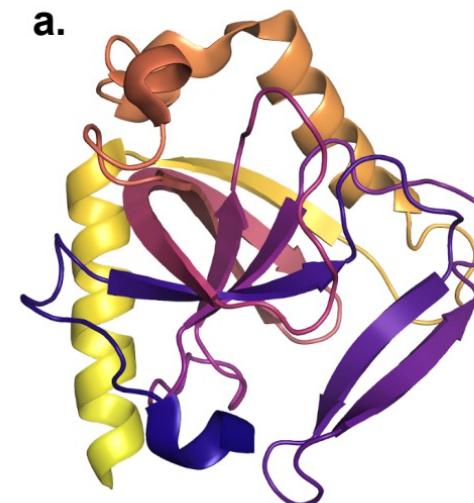


# More Coming Soon

- 3D pocket molecule generation datasets.
- 3D representation convertor
- Protein representation with Graphein
- ....



Pocket-based 3D molecular generation



Protein graphs representation

# Slack Channel for Users

Screenshot of the Slack interface for the TDC team's users channel.

The sidebar shows the following channels:

- Threads
- All DMs
- Mentions & reactions
- Saved items
- Slack Connect
- More
- Starred
- # announce
- # feature-request
- # job-posting
- # new-member** (selected)
- # random
- Channels
- core
- core-team
- tdc-dev
- + Add channels
- Direct messages
- Slackbot
- Kexin you
- Bharath Ramsundar
- Gökce Uluđođan
- new-member

The main channel view for the #new-member channel shows the following:

- A header with the channel name and a "New member" button.
- A message from AI NeuroCare (@Kadi Liis Saar) on Thursday, August 5th:

YouTube  
AI NeuroCare  
Unleash The Digital Healer in You! If Anyone Saved A Life, It Would Be As If He Saved The Life of All Mankind Coaching Clinicians About; Digital Health AI in Healthcare Value based Care Neurology

AI Newsletter.aineurocare.com  
AI NeuroCare - Learn with me!  
AI In HealthCare, Digital Health, Value-based Care, Neurology
- A message from Haoran Liu (@Haoran Liu) on Saturday, August 14th:

Kadi Liis Saar 3:06 AM  
Hi everyone, Just came across this group! My background is in experimental biophysical chemistry and I am now developing various computational approaches, including ML-based methods, for modelling biomolecular interactions. My work is mostly academic but I also work with a drug development startup.  
I wondered if people in this group were keen for a virtual meetup, maybe with some speed-dating element?

Haoran Liu 8:47 AM  
Howdy! Wonderful work by TDC! I am Haoran Liu, a first year PhD student in Texas A&M majoring in Computer Science. Prior to TAMU, I graduated from Waseda University, Japan. My current research topic focus on Deep Graph Learning+BioMed, including molecule/RNA/DNA structure prediction/generation. I don't have any Biology background but I am very interested in all kind of therapeutics science topics. Welcome to discussion and collaboration in AI+Bio!
- A message input field for "#new-member".

**#new-member:** introduce and connect  
**#announce:** update from TDC team  
**#feature-request:** discuss new features  
**#job-posting:** sharing relevant positions

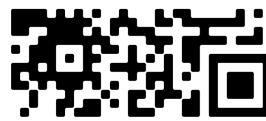


[tinyurl.com/tdc-slack](https://tinyurl.com/tdc-slack)



# TDC is an Open Science Initiative!

<https://tdcommons.ai>



- We welcome contributions from valuable therapeutic problems posing to data deposit and adding functions.



Kexin Huang



Tianfan Fu



Wenhao Gao



Marinka Zitnik

Therapeutics Data Commons  
Machine Learning Datasets and Tasks for Therapeutics

Therapeutics Data Commons (TDC) is the first unifying framework to systematically access and evaluate machine learning across the entire range of therapeutics. Therapeutics machine learning is an exciting field with incredible opportunities for expansion, innovation, and impact. The collection of curated datasets, learning tasks, and benchmarks in TDC serves as a meeting point for domain and machine learning scientists. We envision that TDC can considerably accelerate machine-learning model development, validation and transition into biomedical and clinical implementation.



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