# **Drug Target Identification**

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#### **Problem Statement**



Drug discovery and development pipeline is resource-intensive and time-consuming, which make them a major obstacle for rapid drug development.



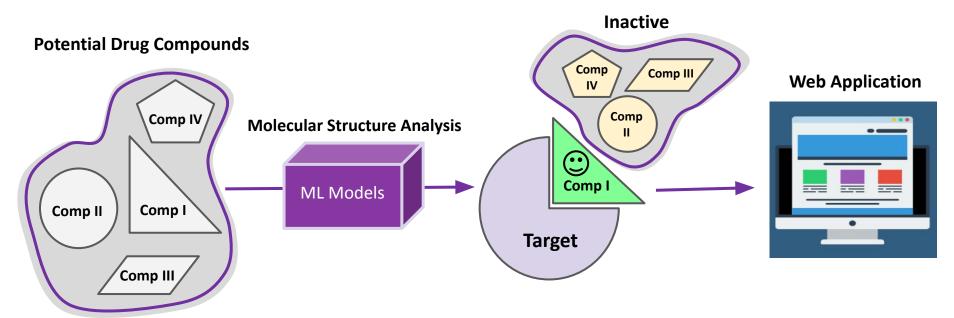
Current challenge is to develop discovery pipelines that can identify promising drug compounds early.



A reliable method that can identify the potential drug compound with respect to its successful clinical translatability is needed.

## **Objectives**

- Create a prototype for identifying potential drug compounds.
- How we did it?



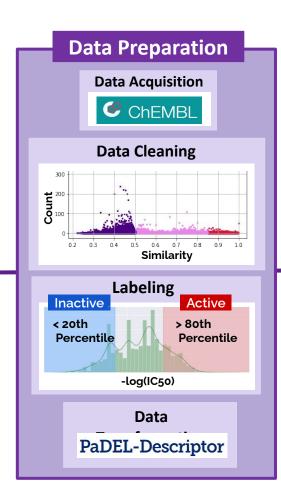
### **Pipeline**

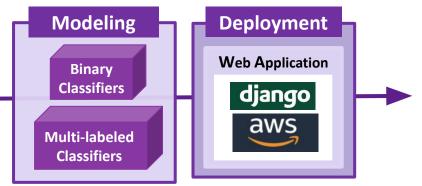
Targets Search

Google Scholar

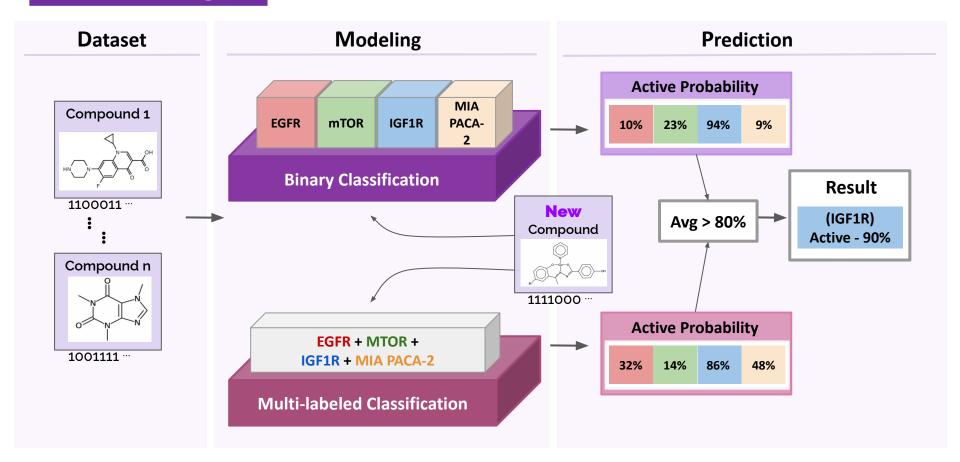
Pub Med.gov

nature





## Modeling



## **Web Application Demo**

## **Appendix**

#### **Preprocessing**

#### **Cleaning**

- Filtered data by
  - standard\_type = 'IC50'
  - standard unit = ['nM', 'uM', 'pM']
  - target\_organism = 'Homo Sapiens'
- Dropped data points with missing standard\_value or canonical\_smiles.
- Converted the standard values to have the same standard unit (nM).

#### Labeling

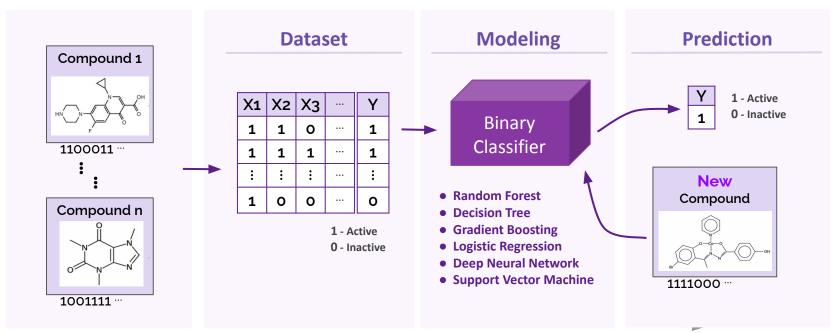
- Standardized IC50 to pIC50 to avoid skewed distribution.
- Checked the standard values at different percentiles to determine the cutoff values for labeling.

#### **Transformation**

■ Used PaDEL descriptor to transform the SMILE notations into rule-based Pubchem Fingerprints.

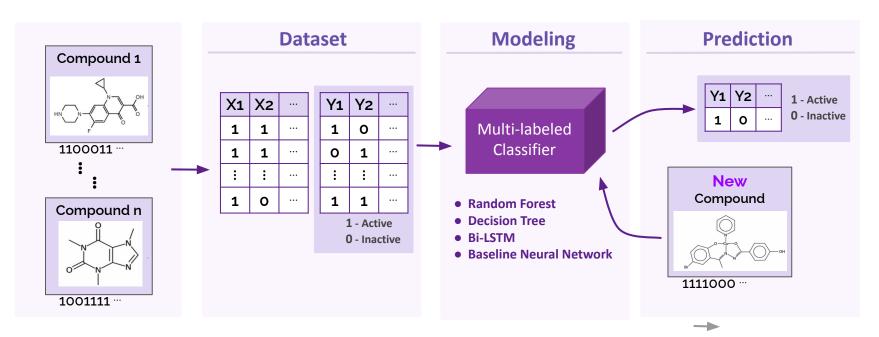
#### Modeling - Binary Classifiers

Build models on each selected target to identify the bioactivity of candidate compounds.

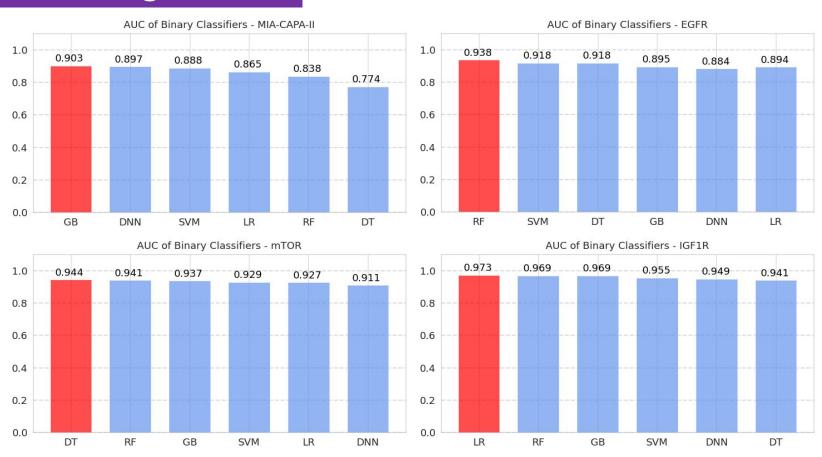


#### Modeling - Multi-labeled Classifiers

Build models on all selected target to identify the bioactivity of candidate compounds.



## Modeling - Results



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