Project: Machine Learning Aided Drug Discovery

Drug Candidate Prioritization Using SMILES Data

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Note: Added additional fields of Metrics used at the starting and added some more description on Feature Importance

Intro to Drug Discovery

Drug discovery is a complex and multidisciplinary process aimed at identifying and developing new medications for the treatment of diseases. The goal is to **find compounds that can effectively and safely interact with specific biological targets, such as proteins or enzymes**, to modify their activity and alleviate or cure the associated medical conditions.

The drug discovery process typically involves several stages:

> **Target Identification and Validation** : Researchers identify and validate specific molecular targets that play a key role in a disease. These targets could be proteins, nucleic acids, or other molecules associated with the disease's progression.

> **Hit Generation**: Scientists search for initial compounds, known as "hits," that have the potential to interact with the chosen target. These hits can be derived from various sources, including natural products, existing drugs, or compounds designed through computational methods.

> **Lead Optimization**: Promising hits are further developed and optimized to enhance their efficacy, selectivity, and safety profile. This stage often involves medicinal chemistry, where chemical modifications are made to improve the compound's properties.

> This is followed with PreClinical Testing, Conducting Clinical Trials, Regulatory Approval, and finally Post Marketing Sureillance.

Drug discovery is a lengthy and resource-intensive process, often taking many years and involving collaboration between scientists, researchers, and pharmaceutical companies.

However, what takes the most time are the Hit Generation and Lead Optimization stages. It is very resource intensive for the doctors to maunally go throught thousands of compounds and molecules and determine if they can be a possible lead for further optimization. That is where Machine Learning can dive in and help the process.

How can Machine Learning aid in Drug Discovery

Like mentioned in the previous section, Machine learning can help in the Hit generation phase of the drug discovery process. How can it do so?

It can parse through rows of protein ligand complexes or compounds and their "activity level" to identify the kinds of molecules a protein binds with well and acts. This can help us curate a predictor such that given a molecule whether it can predict how likely it is to bind with a protein. Hence when scientists hypothesize a new molecule, they can, even before chemically making it, check whether it can be effective or not.

Now let us install a few important libraries

Metrics Used

We will be using the following metrics

Accuracy measures the overall correctness of a classification model, computed as the ratio of correct predictions to the total predictions.
Formula: Accuracy = (Number of Correct Predictions) / (Total Number of Predictions)

Balanced Accuracy is designed for imbalanced datasets, is the average accuracy per class, combining sensitivity and specificity.
Formula: Balanced Accuracy = (Sensitivity + Specificity) / 2

ROC AUC (Receiver Operating Characteristic Area Under the Curve) assesses a binary classification model's ability to distinguish between positive and negative classes across varying probability thresholds.
It computes the area under the ROC curve, depicting the true positive rate against the false positive rate.

F1 Score balances precision and recall, provides a singular metric for model performance, especially in scenarios with imbalanced class distributions.
Formula: F1 Score = 2 * (Precision * Recall) / (Precision + Recall)

[A:]

```
!pip install matplotlib==3.5.2
```

```
#instal chembl web service package to deal with data
! pip install chembl_webresource_client
```

Import libraries.

```
# Core
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
# from matplotlib.pyplot.bar_label
import seaborn as sns
from scipy import stats
import glob
import random
import datetime
import plotly.express as px
import plotly.graph_objects as go
import plotly.io as pio

import os
import pickle
# from  datasist.structdata import detect_outliers
from tqdm import tqdm
#chembl Package
from chembl_webresource_client.new_client import new_client
# Core
import numpy as np
import pandas as pd
pd.set_option('display.max_columns', None)
import matplotlib.pyplot as plt
import seaborn as sns; sns.set(rc={'figure.figsize':[7,7]},font_scale=1.2)
from datetime import date,timedelta
from mpl_toolkits.mplot3d import Axes3D
from mpl_toolkits.mplot3d import axes3d
import sklearn
from sklearn.model_selection import StratifiedKFold
from sklearn.model_selection import KFold
from sklearn.preprocessing import LabelEncoder,OneHotEncoder
# Pre Processing
from sklearn.impute import SimpleImputer
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.preprocessing import MinMaxScaler
# Regressors
from sklearn.linear_model import Ridge
from sklearn.linear_model import Lasso
from sklearn.neighbors import KNeighborsRegressor
from sklearn.ensemble import RandomForestRegressor,AdaBoostRegressor
from sklearn.svm import SVR
from sklearn.linear_model import LinearRegression
from sklearn.preprocessing import PolynomialFeatures
from sklearn.linear_model import LogisticRegression
# Error Metrics
from sklearn.metrics import r2_score #r2 square
from sklearn.metrics import mean_absolute_error
from sklearn.metrics import mean_squared_error
from sklearn.metrics import ConfusionMatrixDisplay ,classification_report
from sklearn.metrics import accuracy_score, precision_score,recall_score,f1_score


#classefication
from sklearn.svm import SVC
from sklearn.tree import DecisionTreeClassifier
from sklearn import tree
from sklearn.neighbors import KNeighborsClassifier
from sklearn.linear_model import SGDClassifier #stacstic gradient descent clasifeier
import graphviz
from sklearn.neighbors import KNeighborsClassifier
from sklearn.ensemble import RandomForestClassifier
#crossvalidation
from sklearn.model_selection import cross_val_score
from sklearn.model_selection import LeaveOneOut
from sklearn.metrics import ConfusionMatrixDisplay
#clustring
from sklearn.cluster import KMeans
from sklearn.cluster import AgglomerativeClustering
#hyper parameter tunning
from sklearn.model_selection import GridSearchCV
#pca
from sklearn.decomposition import PCA
#clustring
from sklearn.cluster import KMeans
from warnings import filterwarnings
filterwarnings("ignore")
```

```
seed = 42
np.random.seed =seed
```

📌 Helper Function ⚒

We define 3 handy functions below namely check_duplicate, numerical_plotting, and categorical_plotting.

```
#check duplicate data
def check_duplicate(df):
    if df.duplicated().all():
        return  'There are duplicate Data in Data Frame Nedded To be  removed . '
    else :
        return 'Data Is clean ,No Duplicate Data Found .'

def numerical_plotting(df, col, title, symb):
    fig, ax = plt.subplots(2, 1, sharex=True, figsize=(8,5),gridspec_kw={"height_ratios": (.2, .8)})
    ax[0].set_title(title,fontsize=18)
    sns.boxplot(x=col, data=df, ax=ax[0])
    ax[0].set(yticks=[])
    sns.distplot(df[col],kde=True)
    plt.xticks(rotation=45)
    ax[1].set_xlabel(col, fontsize=16)
    plt.axvline(df[col].mean(), color='darkgreen', linewidth=2.2, label='mean=' + str(np.round(df[col].mean(),1)) + symb)
    plt.axvline(df[col].median(), color='red', linewidth=2.2, label='median='+ str(np.round(df[col].median(),1)) + symb)
    plt.axvline(df[col].mode()[0], color='purple', linewidth=2.2, label='mode='+ str(df[col].mode()[0]) + symb)
    plt.legend(bbox_to_anchor=(1, 1.03), ncol=1, fontsize=17, fancybox=True, shadow=True, frameon=True)
    plt.tight_layout()
    plt.show()

def categorical_plotting(df,col,title):
    fig, ax = plt.subplots(figsize=(10,5))
    ax=sns.countplot(x=col, data=df, palette='flare', order = df[col].value_counts().index)
    ax.set_xticklabels(ax.get_xticklabels(), rotation=45)
    ax.bar_label(ax.containers[0])
    plt.title(title)
    plt.show()
```

📌 About Dataset

ChEMBL is a manually curated database of bioactive molecules with drug-like properties. It is constantly updated and maintained by the larger scintific community. It brings together chemical, bioactivity and genomic data to aid the translation of genomic information into effective new drugs.

This database consists of 629943 biological compounds from 1552 organisms. Since our project focuses on drug discovery for breast cancer we will collect only those rows from it pertaining to the aromatase enzyme.

Breast Cancer

Research shows that Breast Cancer, specifically, the ER positive Breast cancer, effects primarily females above the age of 50. Aromatase is an enzyme occuring in the fat tissue which facilitates the production of estrogen. However, aromatase can malfunction and cause excess prodution of estrogen which is the leading cause of er positive breast cancer. Then curating a drug which can bind to the aromatase enzyme and thus prevent it from converting other hormones to estrogen. Hence these are called aromatase inhibitors.

📌 Data Collection

In this project we will collect our own data from the database.

First we search for our target protein in the ChemBL database.

Target protein: "Aromatase".

```
#create an object
target = new_client.target
#prepare query for our target protien
target_query = target.search('aromatase')
#convert it to data frame
targets = pd.DataFrame.from_dict(target_query)
targets
```

cross_references	organism	pref_name	score	species_group_flag	target_chembl_
[{'xref_id': 'P11511',					

Since we want to develop an aromatase inhibitor for humans we will choose the organism as Homo Sapiens

```
selected_target = targets.target_chembl_id[0]
selected_target
```

```
'CHEMBL1978'
```

Collect IC50 standard type data

Since we want to collect data curated to the inhibition of aromatase we should focus on those molecules. For this we will use the IC50 measure. Half maximal inhibitory concentration (IC50) is a measure of the potency of a substance in inhibiting a specific biological or biochemical function.

Hence, lower the standard value of IC50 higher the potency of the drug.

```
#retrive biomedical activity of protien
activity = new_client.activity
response = activity.filter(target_chembl_id=selected_target).filter(standard_type="IC50")
```

```
df = pd.DataFrame.from_dict(response)
df.head()
```

	action_type	activity_comment	activity_id	activity_properties	assay_chembl_id
0	None	None	82585	[]	CHEMBL666794
1	None	None	94540	[]	CHEMBL666794
2	None	None	112960	[]	CHEMBL661700
3	None	None	116766	[]	CHEMBL661700
4	None	None	118017	[]	CHEMBL661700

```
df.shape
```

```
(2966, 46)
```

```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 2966 entries, 0 to 2965
Data columns (total 46 columns):
 #   Column                     Non-Null Count  Dtype
---  ------                     --------------  -----
 0   action_type                85 non-null     object
 1   activity_comment           94 non-null     object
 2   activity_id                2966 non-null   int64
 3   activity_properties        2966 non-null   object
 4   assay_chembl_id            2966 non-null   object
 5   assay_description          2966 non-null   object
 6   assay_type                 2966 non-null   object
 7   assay_variant_accession    0 non-null      object
 8   assay_variant_mutation     0 non-null      object
 9   bao_endpoint               2966 non-null   object
 10  bao_format                 2966 non-null   object
 11  bao_label                  2966 non-null   object
 12  canonical_smiles           2966 non-null   object
 13  data_validity_comment      127 non-null    object
 14  data_validity_description  127 non-null    object
 15  document_chembl_id         2966 non-null   object
 16  document_journal           2941 non-null   object
 17  document_year              2966 non-null   int64
 18  ligand_efficiency          2484 non-null   object
 19  molecule_chembl_id         2966 non-null   object
 20  molecule_pref_name         340 non-null    object
```

```
 21  parent_molecule_chembl_id  2966 non-null   object
 22  pchembl_value              2521 non-null   object
 23  potential_duplicate        2966 non-null   int64
 24  qudt_units                 2919 non-null   object
 25  record_id                  2966 non-null   int64
 26  relation                   2890 non-null   object
 27  src_id                     2966 non-null   int64
 28  standard_flag              2966 non-null   int64
 29  standard_relation          2890 non-null   object
 30  standard_text_value        0 non-null      object
 31  standard_type              2966 non-null   object
 32  standard_units             2920 non-null   object
 33  standard_upper_value       0 non-null      object
 34  standard_value             2890 non-null   object
 35  target_chembl_id           2966 non-null   object
 36  target_organism            2966 non-null   object
 37  target_pref_name           2966 non-null   object
 38  target_tax_id              2966 non-null   object
 39  text_value                 0 non-null      object
 40  toid                       0 non-null      object
 41  type                       2966 non-null   object
 42  units                      2735 non-null   object
 43  uo_units                   2920 non-null   object
 44  upper_value                0 non-null      object
 45  value                      2890 non-null   object
dtypes: int64(6), object(40)
memory usage: 1.0+ MB
```

standard value refers to the potency of the drug the lower of its value is the higher of potency of drugs

Data Preprocessing - part 1

- Handel Missing Data
- Data Labeling (binning)

Missing data

```
# check missing Value  in [standard_value,canonical_smiles]
df.isnull().sum().sort_values(ascending=False)[['standard_value','canonical_smiles']]
```

```
standard_value      76
canonical_smiles     0
dtype: int64
```

Canonical Smiles is the Simplified Molecular Line Entry record for each of the compounds. This represents the molecule and Standard Value is the drug effectiveness of Molecule on the Protein.

Lesser the better. Think of it like, lesser concentration but derives the same effect.

```
# i will drop any non value in [standard_value,canonical_smiles]
df2 = df[df['standard_value'].notnull()]
df2
```

	action_type	activity_comment	activity_id	activity_properties	assay_chembl_i
0	None	None	82585	[]	CHEMBL6667
1	None	None	94540	[]	CHEMBL6667
2	None	None	112960	[]	CHEMBL6617
3	None	None	116766	[]	CHEMBL6617
4	None	None	118017	[]	CHEMBL6617
...	...	...	...	...	

```
df2.reset_index(inplace = True)
```

'description': 'relation': '=', 'result_f...

```
df2
```

	index	action_type	activity_comment	activity_id	activity_properties	assay_c
0	0	None	None	82585	[]	CHEM
1	1	None	None	94540	[]	CHEM
2	2	None	None	112960	[]	CHEM
3	3	None	None	116766	[]	CHEM
4	4	None	None	118017	[]	CHEM
...	...	...	...	...	...	
2885	2961	{'action_type': 'INHIBITOR', 'description': 'N...	None	24742461	[{'comments': None, 'relation': '=', 'result_f...	CHEMB
2886	2962	None	None	24783443	[]	CHEMB
2887	2963	{'action_type': 'INHIBITOR', 'description': 'N...	None	24886565	[]	CHEMB
2888	2964	{'action_type': 'INHIBITOR', 'description': 'N...	None	24886566	[]	CHEMB
2889	2965	{'action_type': 'INHIBITOR', 'description': 'N...	None	24886567	[]	CHEMB

2890 rows × 47 columns

Data Labeling

Based on the standard value, we can bin the molecules into active, inactive, and intermediate.

```
bioactivity_class = []
class_number = []
for i in df2.standard_value:
  if float(i) >= 10000:
    bioactivity_class.append("inactive")
    class_number.append(0)
  elif float(i) <= 1000:
    bioactivity_class.append("active")
    class_number.append(1)
  else:
    class_number.append(2)
    bioactivity_class.append("intermediate")
```

Now if we discard the remaining labeling and documentation related columns, we are left with a few columns which we can actually use for training a machine learning model. In that the most important one is canonical_smiles which represents the molecular information.

```
#collect [molecule_chembl_id,standard_value,canonical_smiles,classes] in one data frame
selection = ['molecule_chembl_id','canonical_smiles','standard_value']
df3 = df2[selection]
df3 =pd.concat([df3,pd.Series(bioactivity_class,name='class'), pd.Series(class_number, name='class_number') ],axis=1)
df3
```

	molecule_chembl_id	canonical_smiles	standard_v
0	CHEMBL341591	CC12CCC(O)CC1=CCC1C2CCC2(C)C(CC3CN3)CCC12	7
1	CHEMBL2111947	C[C@]12CC[C@H]3[C@@H](CC=C4C[C@@H](O)CC[C@@]43...	50
2	CHEMBL431859	CCn1c(C(c2ccc(F)cc2)n2ccnc2)c(C)c2cc(Br)ccc21	2
3	CHEMBL113637	CCn1cc(C(c2ccc(F)cc2)n2ccnc2)c2ccccc21	
4	CHEMBL112021	Clc1ccccc1Cn1cc(Cn2ccnc2)c2ccccc21	
...	...	...	
2885	CHEMBL1200374	C=C1C[C@@H]2[C@H](CC[C@]3(C)C(=O)CC[C@@H]23)[C...	
2886	CHEMBL5184829	O=C(Nc1ccc2[nH]ncc2c1)[C@]12ON=C(c3cccnc3)[C@H...	10
2887	CHEMBL5176279	CCOC(=O)Cc1csc(N/N=C/c2ccc3cc(OC)ccc3c2)n1	
2888	CHEMBL5177928	COc1ccc2cc(/C=N/NC3=NC(=O)CS3)ccc2c1	

```
df2.pop('index')
df2.head()
```

	action_type	activity_comment	activity_id	activity_properties	assay_chembl_id
0	None	None	82585	[]	CHEMBL666794
1	None	None	94540	[]	CHEMBL666794
2	None	None	112960	[]	CHEMBL661700
3	None	None	116766	[]	CHEMBL661700
4	None	None	118017	[]	CHEMBL661700

```
#remove null datata in class
df3 = df3[df3['class'].notnull()]
df3 =df3[df3['standard_value'].notnull()]
df3 =df3[df3['canonical_smiles'].notnull()]
df3
```

	molecule_chembl_id	canonical_smiles	standard_v
0	CHEMBL341591	CC12CCC(O)CC1=CCC1C2CCC2(C)C(CC3CN3)CCC12	7
1	CHEMBL2111947	C[C@]12CC[C@H]3[C@@H](CC=C4C[C@@H](O)CC[C@@]43...	50
2	CHEMBL431859	CCn1c(C(c2ccc(F)cc2)n2ccnc2)c(C)c2cc(Br)ccc21	2
3	CHEMBL113637	CCn1cc(C(c2ccc(F)cc2)n2ccnc2)c2ccccc21	
4	CHEMBL112021	Clc1ccccc1Cn1cc(Cn2ccnc2)c2ccccc21	
...	...	...	
2885	CHEMBL1200374	C=C1C[C@@H]2[C@H](CC[C@]3(C)C(=O)CC[C@@H]23)[C...	
2886	CHEMBL5184829	O=C(Nc1ccc2[nH]ncc2c1)[C@]12ON=C(c3cccnc3)[C@H...	10

Dataset feature Expansion via Lipinski Descriptors.

Since training from a single string column is not much informational, we will also use the Lipinski Descriptors which are based on the molecular sequence and tell us a few key information about it.

- Lipinski Descriptors are used for evaluating the druglikeness of compounds. Such druglikeness is based on the **Absorption, Distribution**, **Metabolism** and **Excretion (ADME)** that is also known as the pharmacokinetic profile. Lipinski analyzed all orally active FDA-approved drugs in the formulation of what is to be known as the Rule-of-Five or Lipinski's Rule.
- Molecular weight < 500 g/mol
- Octanol-water partition coefficient (LogP) < 5
- Hydrogen bond donors < 5
- Hydrogen bond acceptors < 10

```
! pip install rdkit-pypi
```

```
Requirement already satisfied: rdkit-pypi in /usr/local/lib/python3.10/dist-packages (2022.9.5)
Requirement already satisfied: numpy in /usr/local/lib/python3.10/dist-packages (from rdkit-pypi) (1.23.5)
Requirement already satisfied: Pillow in /usr/local/lib/python3.10/dist-packages (from rdkit-pypi) (9.4.0)
```

```
from rdkit import Chem
from rdkit.Chem import Descriptors, Lipinski


new_df = df3.copy()


def lipinski(smiles, verbose=False):

    moldata= []
    for elem in smiles:
        mol=Chem.MolFromSmiles(elem)
        moldata.append(mol)

    baseData= np.arange(1,1)
    i=0
    for mol in moldata:

        desc_MolWt = Descriptors.MolWt(mol)
        desc_MolLogP = Descriptors.MolLogP(mol)
        desc_NumHDonors = Lipinski.NumHDonors(mol)
        desc_NumHAcceptors = Lipinski.NumHAcceptors(mol)

        row = np.array([desc_MolWt,
                        desc_MolLogP,
                        desc_NumHDonors,
                        desc_NumHAcceptors])

        if(i==0):
            baseData=row
        else:
            baseData=np.vstack([baseData, row])
        i=i+1

    columnNames=["MW","LogP","NumHDonors","NumHAcceptors"]
    descriptors = pd.DataFrame(data=baseData,columns=columnNames)
    return descriptors
```

```
df_lipinski = lipinski(new_df.canonical_smiles)
df_lipinski
```

	MW	LogP	NumHDonors	NumHAcceptors
0	329.528	4.28820	2.0	2.0
1	315.501	3.89810	2.0	2.0
2	412.306	5.70542	0.0	3.0
3	319.383	4.63450	0.0	3.0
4	321.811	4.58780	0.0	3.0
...	...	...	...	...
2885	296.410	4.02950	0.0	2.0
2886	373.416	3.11580	2.0	5.0
2887	369.446	3.85650	1.0	7.0
2888	299.355	2.40130	1.0	5.0
2889	285.310	2.65916	0.0	5.0

2890 rows × 4 columns

Merge Lipinski feature columns with our initial dataframe

```
merged_df = pd.concat([df_lipinski,new_df],axis=1)
merged_df
```

	MW	LogP	NumHDonors	NumHAcceptors	molecule_chembl_id	
0	329.528	4.28820	2.0	2.0	CHEMBL341591	CC12CCC(O)CC1
1	315.501	3.89810	2.0	2.0	CHEMBL2111947	C[C@]12
2	412.306	5.70542	0.0	3.0	CHEMBL431859	CCn1c(C(c
3	319.383	4.63450	0.0	3.0	CHEMBL113637	CCn
4	321.811	4.58780	0.0	3.0	CHEMBL112021	(
...	...	...	...	...	...	
2885	296.410	4.02950	0.0	2.0	CHEMBL1200374	
2886	373.416	3.11580	2.0	5.0	CHEMBL5184829	O=C(Nc1cc
2887	369.446	3.85650	1.0	7.0	CHEMBL5176279	CCOC(=O)(
2888	299.355	2.40130	1.0	5.0	CHEMBL5177928	COc1

Remove Null Values from the new columns

```
#delete null column
merged_df =merged_df[merged_df['MW'].notnull()]
merged_df =merged_df[merged_df['LogP'].notnull()]
merged_df =merged_df[merged_df['NumHDonors'].notnull()]
merged_df =merged_df[merged_df['NumHAcceptors'].notnull()]
merged_df
```

	MW	LogP	NumHDonors	NumHAcceptors	molecule_chembl_id	
0	329.528	4.28820	2.0	2.0	CHEMBL341591	CC12CCC(O)CC1
1	315.501	3.89810	2.0	2.0	CHEMBL2111947	C[C@]12

Data Preprocessing - part 2

- Data normalization
- Data Statistics
- Data Analysis & Visualization

Classification dataset

So far we have made the dataset ready for classification task of drug discovery. We will not be using the intermediate class as it is neither exactly acitve or inactive. An alternative approach would be to consider the intermediate range to be inactive as well.

Regression dataset (optional)

Though not necessary, we can perform regression analysis on this dataset as well. We can also use the standard_value as a output column and train regression models to predict its value. However, when we closely look upon the data we see a major problem.

```
merged_df['standard_value'] = pd.to_numeric(merged_df['standard_value'], downcast='float')
merged_df.describe()
```

	MW	LogP	NumHDonors	NumHAcceptors	standard_value	class_num
count	2890.000000	2890.000000	2890.000000	2890.000000	2.890000e+03	2890.000
mean	321.351385	3.657816	0.644983	3.865744	2.173576e+10	1.062
std	93.507497	1.311032	1.044485	1.869571	7.235369e+11	0.703
min	130.078000	-1.402800	0.000000	0.000000	0.000000e+00	0.000
25%	257.333750	2.830815	0.000000	3.000000	1.000000e+02	1.000
50%	306.619500	3.654300	0.000000	3.000000	1.000000e+03	1.000
75%	358.416000	4.415725	1.000000	5.000000	7.370000e+03	2.000
max	914.664000	10.306000	9.000000	15.000000	3.388442e+13	2.000

```
merged_df['standard_value'].plot(kind='kde')
```

```
<AxesSubplot:ylabel='Density'>
```

We can see that the data distribution of IC50 is very sharp. With the 1st quartile, second quartile and the third quartile close to 1000 (10^3) , whereas the maximum is at 10^13. Hence, we won't be able to train a sensible regressor which can accurately predict this value realiably with the limited number of records we have.

Hence, we have to normalize this data.

Data Normalization

- Convert IC50 to pIC50 To allow IC50 data to be more uniformly distributed, we will convert IC50 to the negative logarithmic scale which is essentially -log10(IC50).

This custom function pIC50() will accept a DataFrame as input and will:

Take the IC50 values from the standard_value column and converts it from nM to M by multiplying the value by 10 Take the molar value and apply -log10 Delete the standard_value column and create a new pIC50 column

```
def pIC50(input):
    pIC50 = []

    for i in input['standard_value_norm']:
        molar = i*(10**-9) # Converts nM to M
        pIC50.append(-np.log10(molar))

    input['pIC50'] = pIC50
    x = input.drop('standard_value_norm', 1)

    return x
```

```
def norm_value(input):
    norm = []

    for i in input['standard_value'].astype(float):
        if i > 100000000:
          i = 100000000
        norm.append(i)

    input['standard_value_norm'] = norm
    x = input

    return x
```

Convert IC50 to pIC50

```
#apply normalization
df_norm = norm_value(merged_df)
df_norm
```

	MW	LogP	NumHDonors	NumHAcceptors	molecule_chembl_id	
0	329.528	4.28820	2.0	2.0	CHEMBL341591	CC12CCC(O)CC1
1	315.501	3.89810	2.0	2.0	CHEMBL2111947	C[C@]12
2	412.306	5.70542	0.0	3.0	CHEMBL431859	CCn1c(C(c
3	319.383	4.63450	0.0	3.0	CHEMBL113637	CCn
4	321.811	4.58780	0.0	3.0	CHEMBL112021	(
...	...	...	...	...	...	
2885	296.410	4.02950	0.0	2.0	CHEMBL1200374	
2886	373.416	3.11580	2.0	5.0	CHEMBL5184829	O=C(Nc1cc
2887	369.446	3.85650	1.0	7.0	CHEMBL5176279	CCOC(=O)(
2888	299.355	2.40130	1.0	5.0	CHEMBL5177928	COc1

```
#apply pci50 transformation for more data distribution
df_final = pIC50(df_norm)
df_final
```

	MW	LogP	NumHDonors	NumHAcceptors	molecule_chembl_id	
0	329.528	4.28820	2.0	2.0	CHEMBL341591	CC12CCC(O)CC1
1	315.501	3.89810	2.0	2.0	CHEMBL2111947	C[C@]12
2	412.306	5.70542	0.0	3.0	CHEMBL431859	CCn1c(C(c
3	319.383	4.63450	0.0	3.0	CHEMBL113637	CCn
4	321.811	4.58780	0.0	3.0	CHEMBL112021	(
...	...	...	...	...	...	
2885	296.410	4.02950	0.0	2.0	CHEMBL1200374	
2886	373.416	3.11580	2.0	5.0	CHEMBL5184829	O=C(Nc1cc
2887	369.446	3.85650	1.0	7.0	CHEMBL5176279	CCOC(=O)(
2888	299.355	2.40130	1.0	5.0	CHEMBL5177928	COc1

```
df_final.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 2890 entries, 0 to 2889
Data columns (total 10 columns):
 #   Column              Non-Null Count  Dtype  
---  ------              --------------  -----  
 0   MW                  2890 non-null   float64
 1   LogP                2890 non-null   float64
 2   NumHDonors          2890 non-null   float64
 3   NumHAcceptors       2890 non-null   float64
 4   molecule_chembl_id  2890 non-null   object 
 5   canonical_smiles    2890 non-null   object 
 6   standard_value      2890 non-null   float64
 7   class               2890 non-null   object 
 8   class_number        2890 non-null   int64  
 9   pIC50               2890 non-null   float64
dtypes: float64(6), int64(1), object(3)
memory usage: 248.4+ KB
```

```
df_final.describe()
```

	MW	LogP	NumHDonors	NumHAcceptors	standard_value	class_num
count	2890.000000	2890.000000	2890.000000	2890.000000	2.890000e+03	2890.000
mean	321.351385	3.657816	0.644983	3.865744	2.173576e+10	1.062
std	93.507497	1.311032	1.044485	1.869571	7.235369e+11	0.703
min	130.078000	-1.402800	0.000000	0.000000	0.000000e+00	0.000
25%	257.333750	2.830815	0.000000	3.000000	1.000000e+02	1.000
50%	306.619500	3.654300	0.000000	3.000000	1.000000e+03	1.000
75%	358.416000	4.415725	1.000000	5.000000	7.370000e+03	2.000
max	914.664000	10.306000	9.000000	15.000000	3.388442e+13	2.000

Let us remove any undefined data which might have resulted from the log transformation.

```
df_final[df_final['pIC50']== np.inf]
```

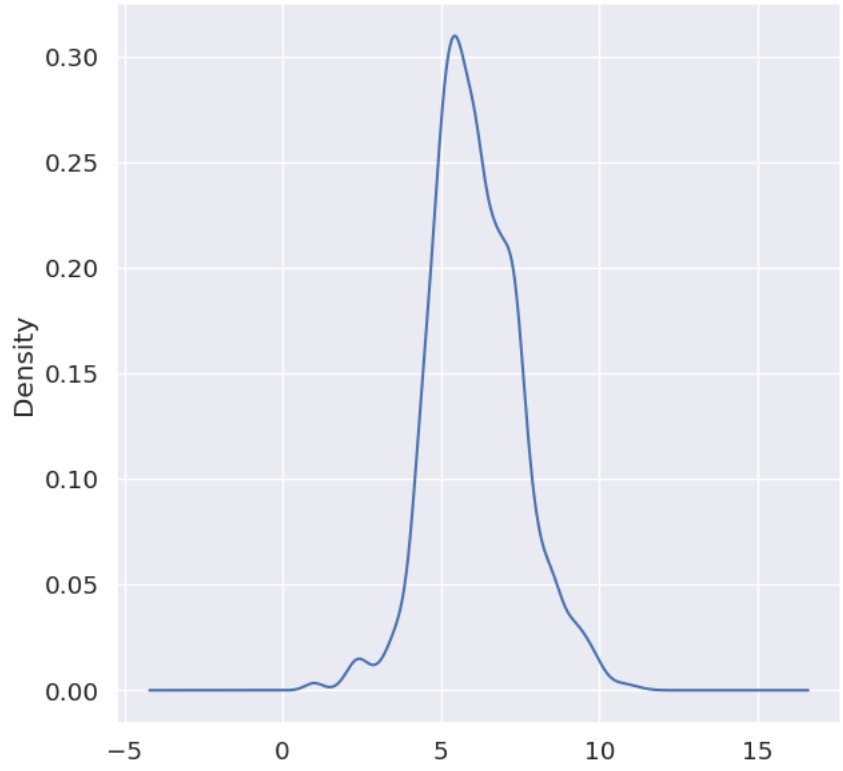
	MW	LogP	NumHDonors	NumHAcceptors	molecule_chembl_id	canonical_

```
#removing infinit value and nan in column Pic50
df_final.replace([np.inf, -np.inf], np.nan,inplace=True)
df_final.dropna(inplace=True)
```

Now let us reexamine the distribution of the output column

```
df_final['pIC50'].plot(kind='kde')
```

```
<AxesSubplot:ylabel='Density'>
```



We can clearly see that this range and distribution of data is much more legible and can be used to train solid regression models.

Data statistics and Null checks

```
df_smiles = df_final # for later reference
df_final.describe()
```

	MW	LogP	NumHDonors	NumHAcceptors	standard_value	class_num
count	2889.000000	2889.000000	2889.000000	2889.000000	2.889000e+03	2889.000
mean	321.384293	3.658169	0.645206	3.866044	2.174328e+10	1.062
std	93.506945	1.311121	1.044597	1.869825	7.236620e+11	0.704
min	130.078000	-1.402800	0.000000	0.000000	4.000000e-03	0.000
25%	257.336000	2.833260	0.000000	3.000000	1.000000e+02	1.000
50%	306.793000	3.654300	0.000000	3.000000	1.000000e+03	1.000
75%	358.416000	4.416900	1.000000	5.000000	7.370000e+03	2.000
max	914.664000	10.306000	9.000000	15.000000	3.388442e+13	2.000

```
#check duplicate data
check_duplicate(df_final)
```

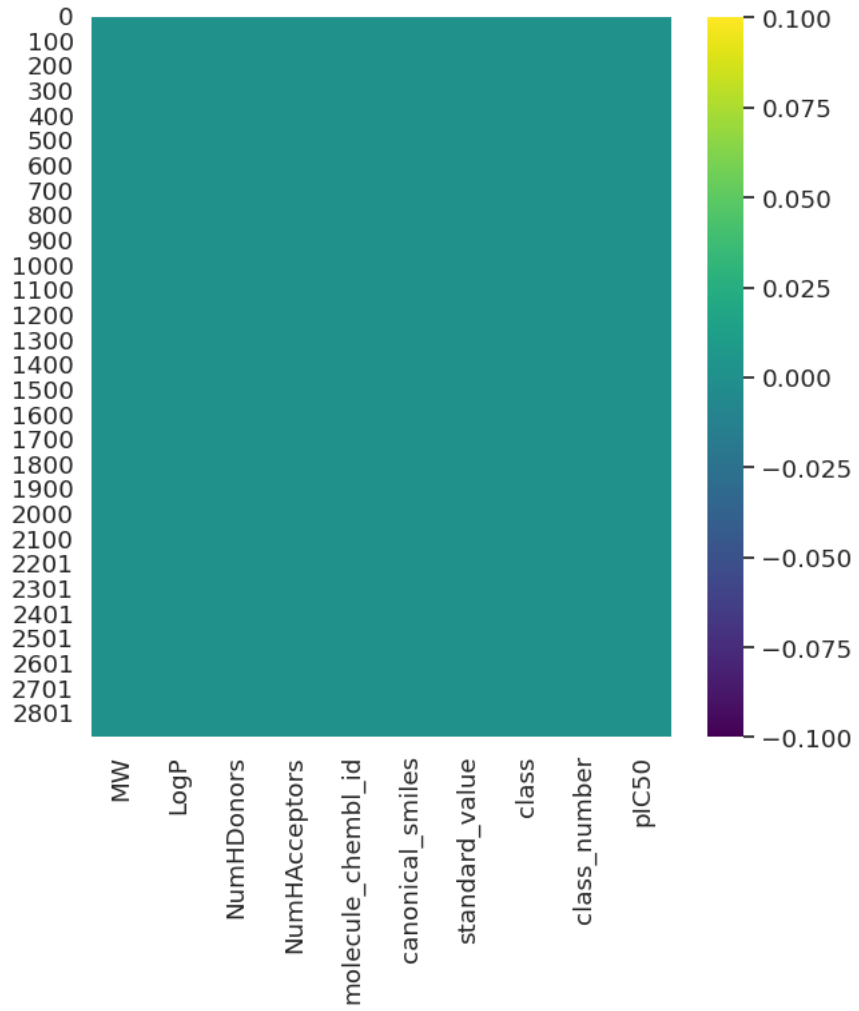
```
'Data Is clean ,No Duplicate Data Found .'
```

```
# check missing Value
df_final.isnull().sum().sort_values(ascending=False)
```

```
MW                  0
LogP                0
NumHDonors          0
NumHAcceptors       0
molecule_chembl_id  0
canonical_smiles    0
standard_value      0
class               0
class_number        0
pIC50               0
dtype: int64
```

```
cols =df_final.columns
sns.heatmap(df_final[cols].isnull(), cmap='viridis')
```

```
<AxesSubplot:>
```



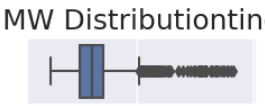
Data Analaysis & Visualization

Now let us further analyse through visualizations the individual columns in order to check for any skewed data or any outliers.

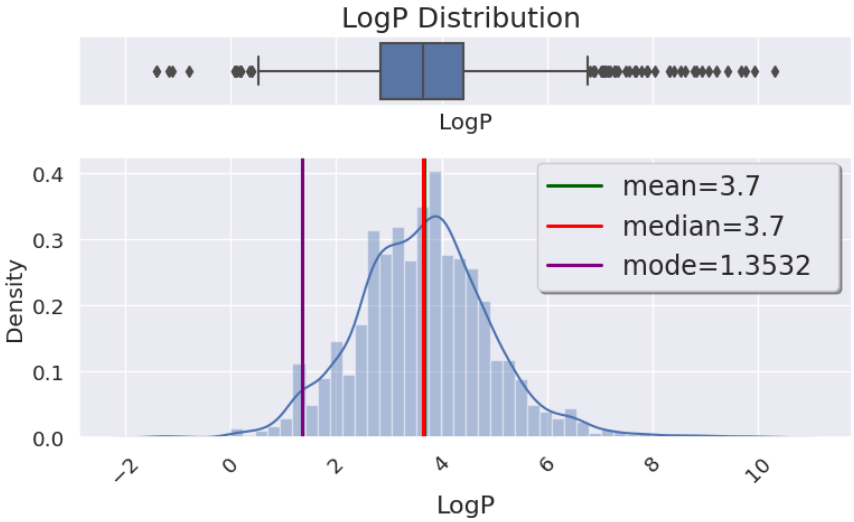
Distplots for Numerical Values

For the numeric columns from our dataset we can extract the mean, median, and mode apart from the boxplot and data density distribution w.r.t respective columns.

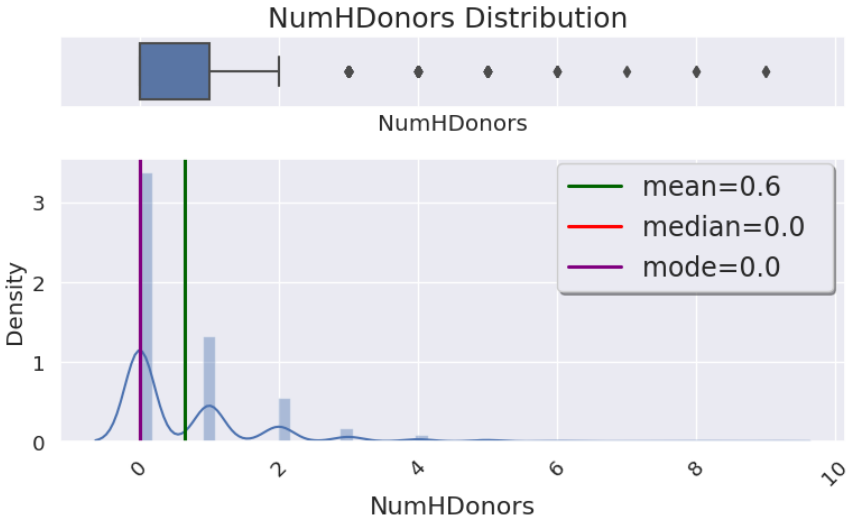
```
numerical_plotting(df_final,'MW','MW Distributionting','  ')
```



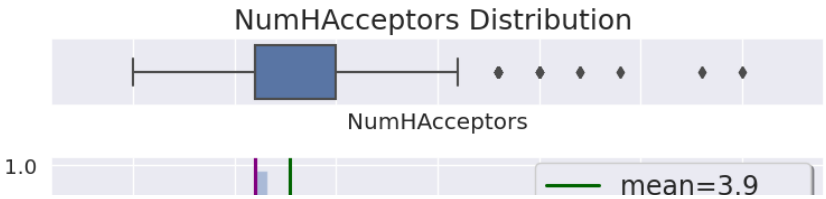

```
numerical_plotting(df_final,'LogP','LogP Distribution ','  ')
```




```
numerical_plotting(df_final,'NumHDonors','NumHDonors Distribution ','  ')
```

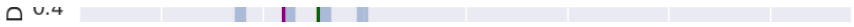



```
numerical_plotting(df_final,'NumHAcceptors','NumHAcceptors Distribution ','  ')
```

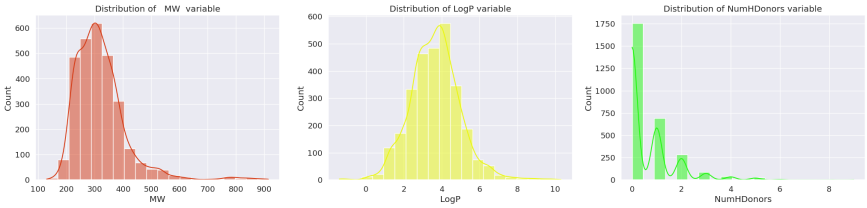


Histograms for Categorical values

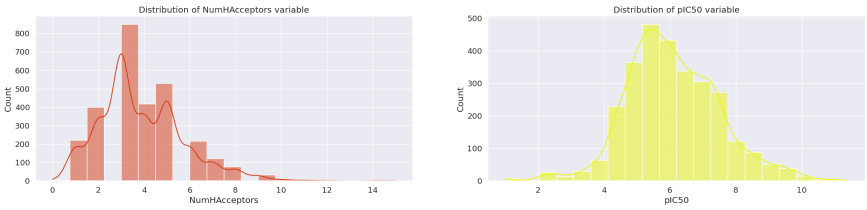
And for the categorical values from the dataset we will plot the histograms for respective columns.



```
fig, axes = plt.subplots(1, 3, figsize = (25, 5))
ax = axes.flatten()
sns.histplot(ax = axes[0], x = df_final["MW"], bins = 20, kde = True, color = "#D63913").set(title = "Distribution of   MW  variable");
sns.histplot(ax = axes[1], x = df_final["LogP"], bins = 20, kde = True, color = "#EAF90E").set(title = "Distribution of LogP variable");
sns.histplot(ax = axes[2], x = df_final["NumHDonors"], bins = 20, kde = True, color = "#20F90E").set(title = "Distribution of NumHDonors
```




```
fig, axes = plt.subplots(1, 2, figsize = (25, 5))
ax = axes.flatten()
sns.histplot(ax = axes[0], x = df_final["NumHAcceptors"], bins = 20, kde = True, color = "#D63913").set(title = "Distribution of NumHAc
sns.histplot(ax = axes[1], x = df_final["pIC50"], bins = 20, kde = True, color = "#EAF90E").set(title = "Distribution of pIC50 variable'
```

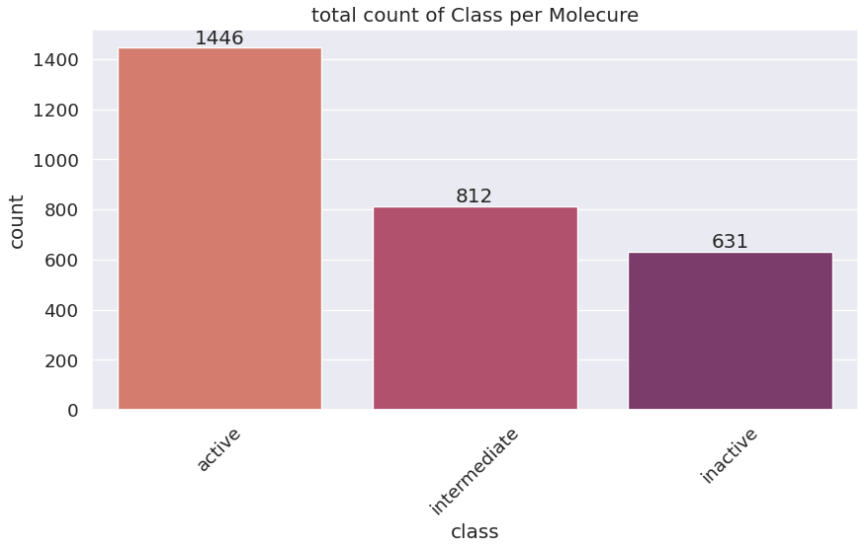


From the above analysis we get to know that each of the columns are not highly skewed and that our classifiers and regressors can work on them. However, we have to explore class-wise distribution or boxplots of the columns in order to see the variety in the distribution of data across the columns which can be learned by our ml models.

Count Plot

Based on the below distribution we will model our problem such that active class is active class, and we will consider both intermediate and inactive classes as inactive classes for a simpler and more balanced class distribution.

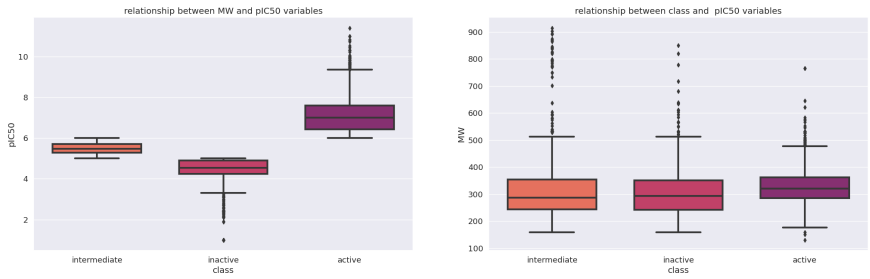
```
categorical_plotting(df_final,'class','total count of Class per Molecure')
```



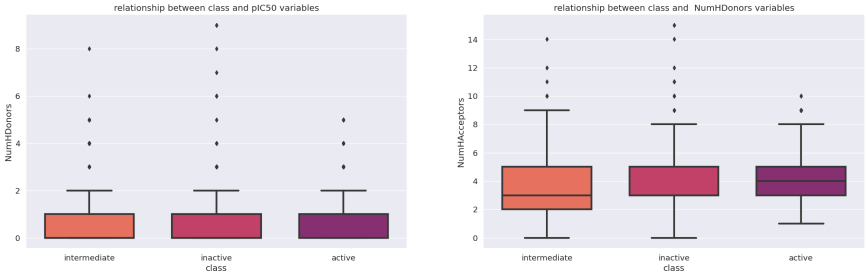
In the above plots we explored the individual column's data distribution. However, it is also important to explore the class wise data distribution in columns.

Class segregated Box Plots

```
fig, axes = plt.subplots(1, 2, figsize = (25, 7))

sns.boxplot(ax = axes[0], x = "class", y = "pIC50", data = df_final, width = 0.7, orient = "v", fliersize = 5,
            saturation = 1, linewidth = 3,palette='flare');
axes[1].set_title("relationship between class and  pIC50 variables");

sns.boxplot(ax = axes[1], x = "class", y = "MW", data = df_final, width = 0.7, orient = "v", fliersize = 5,
            saturation = 1, linewidth = 3,palette='flare')
axes[0].set_title("relationship between MW and pIC50 variables");
```



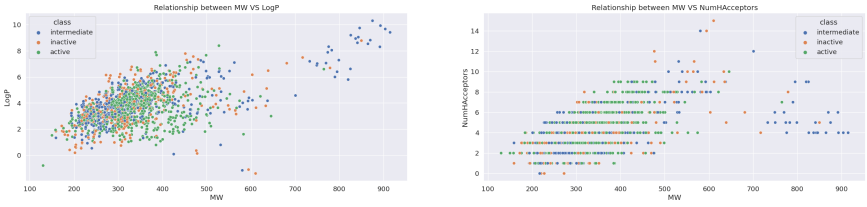
```
fig, axes = plt.subplots(1, 2, figsize = (25, 7))

sns.boxplot(ax = axes[0], x = "class", y = "NumHDonors", data = df_final, width = 0.7, orient = "v", fliersize = 5,
            saturation = 1, linewidth = 3,palette='flare');
axes[1].set_title("relationship between class and  NumHDonors variables");

sns.boxplot(ax = axes[1], x = "class", y = "NumHAcceptors", data = df_final, width = 0.7, orient = "v", fliersize = 5,
            saturation = 1, linewidth = 3,palette='flare')
axes[0].set_title("relationship between class and pIC50 variables");
```



Scatter Plot

Scatter Plot to explore any significant relationship between the variables

```
fig, axes = plt.subplots(1, 2, figsize = (30, 6))
axes = axes.flatten()
sns.scatterplot(ax = axes[0], x = "MW", y = "LogP", data = df_final, color = "#000000",hue='class',
                ).set(title = "Relationship between MW VS LogP");

sns.scatterplot(ax = axes[1], x = "MW", y = "NumHAcceptors", data = df_final,hue='class',
                color = "#E9F709").set(title = "Relationship between MW VS NumHAcceptors");
```




```
df_final.corr()
```

	MW	LogP	NumHDonors	NumHAcceptors	standard_value	class
MW	1.000000	0.514570	0.346487	0.584111	-0.004997	C
LogP	0.514570	1.000000	-0.042298	-0.208555	-0.013055	C

Key Takeaways

From the above analysis we can see that no high degree of multi collinearity exists.

But some positive corrolation exists between Molecular Weight, NumHAcceptors, and LogP (solubility).

Additianally, as we explore the box plots of the input features, we see that many of the box plots are of similar range and mean. Expecially, columns such as NumHDonors and NumHAcceptors.

Hence this conclusion steers us in the direction to check if we can accumulate more features from molecular sequence in the form of molecular descriptors.

This will give our model a richer context to help differentiate between active and inactive classes and also in regression prediction of the pIC50 values.

📌Enter PaDEL Descriptor!

Apart from the above 5 molecular descriptors mentioned above such as Molecular Weight, Solubility etc, there are a wide range of molecular descriptors used in cheminformatics and computational chemistry. These descriptors provide a quantitative representation of the structural and physicochemical properties of chemical compounds. PaDEL descriptors are particularly useful in the field of quantitative structure-activity relationship (QSAR) studies, where the goal is to correlate the chemical structure of a compound with its biological or chemical activity.

So given a molecular structure, such as in the form of SMILES data. We can derieve these molecular descriptors including but not limited to

- Number of Atoms
- Number of Bonds
- Radius of Gyration (RG): A measure of the spatial distribution of atoms in a molecule.
- Electron Affinity (EA): The energy change when an electron is added to a neutral atom or molecule.
- Molecular Polarizability (MP): A measure of how easily the electron cloud of a molecule can be distorted by an external electric field.
- Number of Amine Groups (NOAM): The count of amine functional groups in the molecule.

4.1 | Download Padel Descriptor

- it is software to calculate molecular descriptors, which are numerical values that can be used to characterize the properties of a molecule

```
! wget https://github.com/dataprofessor/bioinformatics/raw/master/padel.zip
! wget https://github.com/dataprofessor/bioinformatics/raw/master/padel.sh
```

```
! unzip padel.zip -y
```

4.2 | Calculate Molecure Descriptor

```
selection = ['canonical_smiles','molecule_chembl_id' ]
df3_selection = df_final[selection]
df3_selection.to_csv('molecule.smi', sep='\t', index=False, header=False)
```

```
! cat 'molecule.smi' | head -5
```

```
CC12CCC(O)CC1=CCC1C2CCC2(C)C(CC3CN3)CCC12       CHEMBL341591
C[C@]12CC[C@H]3[C@@H](CC=C4C[C@@H](O)CC[C@@]43C)[C@@H]1CC[C@@H]2[C@H]1CN1       CHEMBL2111947
CCn1c(C(c2ccc(F)cc2)n2ccnc2)c(C)c2cc(Br)ccc21   CHEMBL431859
CCn1cc(C(c2ccc(F)cc2)n2ccnc2)c2ccccc21  CHEMBL113637
Clc1ccccc1Cn1cc(Cn2ccnc2)c2ccccc21      CHEMBL112021
```

```
! cat 'molecule.smi' | wc -l
```

```
2889
```

```
#start calculation
! bash padel.sh
```

```
! cat padel.sh
```

```
java -Xms1G -Xmx1G -Djava.awt.headless=true -jar ./PaDEL-Descriptor/PaDEL-Descriptor.jar -removesalt -standardizenitro -fingerprints
```

```
#prepare x matrix
df_x = pd.read_csv('/content/descriptors_output.csv')
df_x
```

	Name	PubchemFP0	PubchemFP1	PubchemFP2	PubchemFP3	PubchemFP4	Pul
0	CHEMBL113637	1	1	1	0	0	
1	CHEMBL112021	1	1	1	0	0	
2	CHEMBL111868	1	1	0	0	0	
3	CHEMBL41761	1	1	1	0	0	
4	CHEMBL431859	1	1	1	0	0	
...	...	...	...	...	...	...	
2884	CHEMBL1200374	1	1	1	0	0	
2885	CHEMBL5176279	1	1	1	0	0	
2886	CHEMBL1444	1	1	0	0	0	
2887	CHEMBL5184829	1	1	1	0	0	
2888	CHEMBL5177928	1	1	0	0	0	

2889 rows × 882 columns

📌 Data Preperation & spliting

```
df_x= df_x.drop(['Name'], axis=True)
df_x
```

	PubchemFP0	PubchemFP1	PubchemFP2	PubchemFP3	PubchemFP4	PubchemFP5	Pubchem
0	1	1	1	0	0	0	
1	1	1	1	0	0	0	
2	1	1	0	0	0	0	
3	1	1	1	0	0	0	
4	1	1	1	0	0	0	
...	...	...	...	...	...	...	
2884	1	1	1	0	0	0	
2885	1	1	1	0	0	0	
2886	1	1	0	0	0	0	
2887	1	1	1	0	0	0	
2888	1	1	0	0	0	0	

2889 rows × 881 columns

```
#get y axis that from df_final column (pci)
df_y = df_final['class']
df_y
```

```
0       intermediate
1           inactive
2             active
3             active
4             active
            ...
2885          active
2886        inactive
2887          active
2888          active
2889          active
Name: class, Length: 2889, dtype: object
```

```
#printing shape of our data set
df_x.shape, df_y.shape
```

```
((2889, 881), (2889,))
```

```
final =pd.concat([df_x,df_y, df_final['pIC50'] ],axis=1)
final
```

	PubchemFP0	PubchemFP1	PubchemFP2	PubchemFP3	PubchemFP4	PubchemFP5	Pubchem
0	1.0	1.0	1.0	0.0	0.0	0.0	
1	1.0	1.0	1.0	0.0	0.0	0.0	
2	1.0	1.0	0.0	0.0	0.0	0.0	
3	1.0	1.0	1.0	0.0	0.0	0.0	
4	1.0	1.0	1.0	0.0	0.0	0.0	
...	...	...	...	...	...	...	
2885	1.0	1.0	1.0	0.0	0.0	0.0	
2886	1.0	1.0	0.0	0.0	0.0	0.0	
2887	1.0	1.0	1.0	0.0	0.0	0.0	
2888	1.0	1.0	0.0	0.0	0.0	0.0	
2889	NaN	NaN	NaN	NaN	NaN	NaN	N

2890 rows × 883 columns

```
final.dropna(inplace=True)
```

```
final
```

	PubchemFP0	PubchemFP1	PubchemFP2	PubchemFP3	PubchemFP4	PubchemFP5	Pubchem
0	1.0	1.0	1.0	0.0	0.0	0.0	
1	1.0	1.0	1.0	0.0	0.0	0.0	
2	1.0	1.0	0.0	0.0	0.0	0.0	
3	1.0	1.0	1.0	0.0	0.0	0.0	
4	1.0	1.0	1.0	0.0	0.0	0.0	
...	...	...	...	...	...	...	
2884	1.0	1.0	1.0	0.0	0.0	0.0	
2885	1.0	1.0	1.0	0.0	0.0	0.0	
2886	1.0	1.0	0.0	0.0	0.0	0.0	
2887	1.0	1.0	1.0	0.0	0.0	0.0	
2888	1.0	1.0	0.0	0.0	0.0	0.0	

2888 rows × 883 columns

```
print(final.columns)
```

```
Index(['PubchemFP0', 'PubchemFP1', 'PubchemFP2', 'PubchemFP3', 'PubchemFP4',
       'PubchemFP5', 'PubchemFP6', 'PubchemFP7', 'PubchemFP8', 'PubchemFP9',
       ...
       'PubchemFP873', 'PubchemFP874', 'PubchemFP875', 'PubchemFP876',
       'PubchemFP877', 'PubchemFP878', 'PubchemFP879', 'PubchemFP880', 'class',
       'pIC50'],
      dtype='object', length=883)
```

```
x = final.drop(['class', 'pIC50'], axis=True)
y = final['class']
```

```
final.columns
```

```
Index(['PubchemFP0', 'PubchemFP1', 'PubchemFP2', 'PubchemFP3', 'PubchemFP4',
       'PubchemFP5', 'PubchemFP6', 'PubchemFP7', 'PubchemFP8', 'PubchemFP9',
       ...
       'PubchemFP873', 'PubchemFP874', 'PubchemFP875', 'PubchemFP876',
       'PubchemFP877', 'PubchemFP878', 'PubchemFP879', 'PubchemFP880', 'class',
```

```
           'pIC50'],
          dtype='object', length=883)
```

```
# x.fillna(0, inplace=True)
```

```
check_nan = final.isna().values.any()
check_nan
```

```
     False
```

```
x.shape
```

```
     (2888, 881)
```

```
y.shape
```

```
     (2888,)
```

Remove Low Variance Features

One important aspect of dealing with PaDEL descriptors is that it has a huge number of descriptors. 880 to be precise. Hence it can be the case that for our particular dataset some of the descriptors might not provide much value. As in they might all be 0 or all 1. Hence we can eliminate those rows.

```
from sklearn.feature_selection import VarianceThreshold
selection = VarianceThreshold(threshold=(.8 * (1 - .8)))
x = selection.fit_transform(x)
```

```
x.shape
```

```
     (2888, 152)
```

```
y
```

```
     0       intermediate
     1           inactive
     2             active
     3             active
     4             active
                  ...
     2884          active
     2885          active
     2886        inactive
     2887          active
     2888          active
     Name: class, Length: 2888, dtype: object
```

```
y_classification = [ 1 if i=='active' else 0 for i in y]
y_regression = final['pIC50']
```

Split into training and Testing Data

```
# print(y.shape)
x_train ,x_test ,y_train,y_test = train_test_split(x,y_classification,test_size=.2,random_state=42,shuffle=True)
```

```
! pip install lazypredict
```

```
one=0
zero=0
for i in y_classification:
  if i==0:
    zero+=1
  else:
    one+=1
print(one, zero)
```

```
     1445 1443
```

Model Training and Testing

Classification

We will use the lazy predict library which has an array of classifiers and regressors and with just one call it trains all of the classifiers so we can perform through experimentation.

Classification!

```
import lazypredict
from lazypredict.Supervised import LazyRegressor, LazyClassifier

# Defines and builds the lazy regressor
clf = LazyClassifier(verbose=0,ignore_warnings=True, custom_metric=None)
models_train,predictions_train = clf.fit(x_train, x_train, y_train, y_train)
models_test,predictions_test = clf.fit(x_train, x_test, y_train, y_test)
```

```
100%|██████████| 29/29 [00:17<00:00,  1.65it/s]
[LightGBM] [Info] Number of positive: 1154, number of negative: 1156
[LightGBM] [Info] Auto-choosing row-wise multi-threading, the overhead of testing was 0.000554 seconds.
You can set `force_row_wise=true` to remove the overhead.
And if memory is not enough, you can set `force_col_wise=true`.
[LightGBM] [Info] Total Bins 456
[LightGBM] [Info] Number of data points in the train set: 2310, number of used features: 152
[LightGBM] [Info] [binary:BoostFromScore]: pavg=0.499567 -> initscore=-0.001732
[LightGBM] [Info] Start training from score -0.001732
'tuple' object has no attribute '__name__'
Invalid Classifier(s)
100%|██████████| 29/29 [00:10<00:00,  2.74it/s][LightGBM] [Info] Number of positive: 1154, number of negative: 1156
[LightGBM] [Info] Auto-choosing row-wise multi-threading, the overhead of testing was 0.000540 seconds.
You can set `force_row_wise=true` to remove the overhead.
And if memory is not enough, you can set `force_col_wise=true`.
[LightGBM] [Info] Total Bins 456
[LightGBM] [Info] Number of data points in the train set: 2310, number of used features: 152
[LightGBM] [Info] [binary:BoostFromScore]: pavg=0.499567 -> initscore=-0.001732
[LightGBM] [Info] Start training from score -0.001732
```

```
# Performance table of the training set (90% subset)
predictions_train
```

Model	Accuracy	Balanced Accuracy	ROC AUC	F1 Score	Time Taken
RandomForestClassifier	0.85	0.85	0.85	0.85	0.58
LabelSpreading	0.85	0.85	0.85	0.85	0.40
DecisionTreeClassifier	0.85	0.85	0.85	0.85	0.08
ExtraTreeClassifier	0.85	0.85	0.85	0.85	0.05

```
predictions_test
```

Model	Accuracy	Balanced Accuracy	ROC AUC	F1 Score	Time Taken
SVC	0.69	0.69	0.69	0.69	0.70
ExtraTreeClassifier	0.69	0.69	0.69	0.68	0.03
RandomForestClassifier	0.68	0.68	0.68	0.68	0.53
DecisionTreeClassifier	0.68	0.68	0.68	0.68	0.07
LabelPropagation	0.68	0.68	0.68	0.68	0.21
NuSVC	0.68	0.68	0.68	0.68	0.75
LabelSpreading	0.68	0.68	0.68	0.67	0.27
BaggingClassifier	0.68	0.68	0.68	0.68	0.24
ExtraTreesClassifier	0.67	0.68	0.68	0.67	0.50
LogisticRegression	0.67	0.67	0.67	0.67	0.10
SGDClassifier	0.67	0.67	0.67	0.67	0.16
XGBClassifier	0.67	0.67	0.67	0.67	0.25
GaussianNB	0.67	0.67	0.67	0.67	0.03
AdaBoostClassifier	0.67	0.67	0.67	0.67	0.41
CalibratedClassifierCV	0.66	0.66	0.66	0.66	4.09
RidgeClassifierCV	0.66	0.66	0.66	0.66	0.18
NearestCentroid	0.66	0.66	0.66	0.66	0.13
BernoulliNB	0.66	0.66	0.66	0.66	0.03
LinearSVC	0.66	0.66	0.66	0.66	1.01
KNeighborsClassifier	0.66	0.66	0.66	0.66	0.06
LGBMClassifier	0.65	0.65	0.65	0.65	0.18
RidgeClassifier	0.65	0.65	0.65	0.65	0.09
LinearDiscriminantAnalysis	0.65	0.65	0.65	0.65	0.17
Perceptron	0.65	0.64	0.64	0.64	0.05
PassiveAggressiveClassifier	0.61	0.61	0.61	0.61	0.05
QuadraticDiscriminantAnalysis	0.57	0.57	0.57	0.49	0.16
DummyClassifier	0.50	0.50	0.50	0.33	0.04

Code for optional regression analysis

```
# x_train ,x_test ,y_train,y_test = train_test_split(x,y_regression,test_size=.2,random_state=42,shuffle=True)

# import lazypredict
# from lazypredict.Supervised import LazyRegressor

# # Defines and builds the lazy regressor
# clf = LazyRegressor(verbose=0,ignore_warnings=True, custom_metric=None)
# models_train,predictions_train = clf.fit(x_train, x_train, y_train, y_train)
# models_test,predictions_test = clf.fit(x_train, x_test, y_train, y_test)


# predictions_train


# predictions_test
```

Further Optimization doesn't Imporve this much

Feature Importance of Padel Descriptors

In chemical compounds, their structure and its constituents are the major determining factor in its properties and its bonding with other compounds.

The above descriptors, though are many, can't be fully representitive of the molecule's interactive capabilities.

Hence they cannot be solely used as features.

We need a different Approach to this problem

Improve preformance by Utilizing Molecular Fingerprinting and Graph Convolutional Model!

Why is it better?

Molecular fingerprints encode properties of small molecules and assess their similarities computationally through bit string comparisons. Now since these fingerprints are strings they have the advantage of being more abstract.

In the below step we will utilize the deepchem library to curate the molecular fingerprints of our input data using their ConvMolFeaturizer and then utilize the Graph Convolutional Model which will then capitalize on these fingerprints to help classify Drug activity on our aromatase enzyme.

```
df_smiles
```

	MW	LogP	NumHDonors	NumHAcceptors	molecule_chembl_id	
0	329.53	4.29	2.00	2.00	CHEMBL341591	CC12CCC(O)CC1=CC
1	315.50	3.90	2.00	2.00	CHEMBL2111947	C[C@]12CC[(
2	412.31	5.71	0.00	3.00	CHEMBL431859	CCn1c(C(c2ccc
3	319.38	4.63	0.00	3.00	CHEMBL113637	CCn1cc(
4	321.81	4.59	0.00	3.00	CHEMBL112021	Clc1(
...	...	...	...	...	...	
2885	296.41	4.03	0.00	2.00	CHEMBL1200374	(CC[
2886	373.42	3.12	2.00	5.00	CHEMBL5184829	O=C(Nc1ccc2[n
2887	369.45	3.86	1.00	7.00	CHEMBL5176279	CCOC(=O)Cc1c
2888	299.36	2.40	1.00	5.00	CHEMBL5177928	COc1ccc2

```
X = df_smiles['canonical_smiles'].to_numpy(dtype=str)
y = [ 1 if x=='active' else 0 for x in df_smiles['class']]
```