EE769-

Introduction to Machine learning

Report: Classification, Feature Engineering and Deployment of Machine Learning models

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Question:

1. Regression and out-of-distribution prediction:

a. Download the wine quality datasets from https://archive.ics.uci.edu/ml/datasets/Wine+Quality

b. Explore, visualize, and pre-process the data as appropriate. [1]

c. Train, validate varying at least one hyperparameter, and test at least two types of models: [2]

i. Random forest

ii. Support vector regression with RBF kernel

iii. Neural network with single hidden layer (output layer should have linear activation)

d. Search the net about how to determine the importance of each variable, and find the importance in the final models tried. Comment on whether the same variables are important for different models. [1]

e. Test the model for red with data from white and vice versa, and comment on whether the model for red wines is applicable to white wines and versa or not. [1]

2. Classification:

a. Download the data to predict Down syndrome in mice from https://archive.ics.uci.edu/ml/datasets/Mice+Protein+Expression#. The prediction problem is to either predict the genotype (binary) using the gene expression variables from DYRK1A_N to CaNA_N.

b. Explore, visualize, and pre-process the data as appropriate, including developing a strategy to deal with missing variables. You can choose to impute the variable. The recommended way is to use multivariate feature imputation (https://scikit-learn.org/stable/modules/impute.html) [1]

c. Train, validate varying at least one hyperparameter, and test at least two types of models: [2]

i. Random forest

ii. Support vector classification using RBF kernel

iii. Neural network with single hidden layer (output layer should be have softmax activation)

d. See if removing some features systematically will improve your models using recursive feature elimination https://scikit-learn.org/stable/modules/generated/sklearn.feature_selection.RFECV.html). [1]

3. Practice using pre-trained neural networks to extract domain-specific features for new tasks.

a. Read the pytorch tutorial to use a pre-trained "ConvNet as fixed feature extractor" from https://pytorch.org/tutorials/beginner/transfer_learning_tutorial.html and you can ignore "finetuning the ConvNet". Test this code out to see if it runs properly in your environment after eliminating code blocks that you do not need. [1]

b. Write a function that outputs ResNet18 features for a given input image. Extract features for training images (in image_datasets['train']). You should get an Nx512 dimensional array. [1]

c. Compare RBF kernel SVM (do grid search on kernel width and regularization) and random forest (do grid search on max depth and number of trees). Test the final model on test data and show the results -- accuracy and F1 score. [1]

4. Deploy one model from part 1 on a local webserver with a web frontend (e.g. using streamlit). Add some GUI elements, such as sliders for acidity, citrus etc. [2] Most of this should be in the video demo.

CODE:

```
################################################################################################################################

#                                    EE769-INTRODUCTION TO MACHINE LEARNING
#
#                                              ~BY                                                #
#                                               ~SANJAY R                                          #
#                                               ~23M0002                                           #
################################################################################################################################

#                                     REFERENCES:
#                                     [1]. CHATGPT 3.5 LLC
#                                     [2]. https://archive.ics.uci.edu/ml/datasets/Wine+Quality
#                                     [3]. https://archive.ics.uci.edu/ml/datasets/Mice+Protein+Expression
#                                     [4]. https://scikit-learn.org/stable/modules/impute.html
#                                     [5]. https://scikit-learn.org/stable/modules/generated/sklearn.feature_selection.RFECV.html
#                                     [6]. https://pytorch.org/tutorials/beginner/transfer_learning_tutorial.html
#                                     [7]. https://www.youtube.com/watch?v=5XnHlluw-Eo
################################################################################################################################


###Q1
#[1]
# Import necessary libraries
import numpy as np                                  # NumPy for numerical operations
import pandas as pd                                 # Pandas for data manipulation
import matplotlib.pyplot as plt                     # Matplotlib for data visualization
from sklearn.model_selection import train_test_split, GridSearchCV       # functions for data splitting and hyperparameter tuning
```

```
from sklearn.ensemble import RandomForestRegressor                    # Random Forest Regressor model

from sklearn.svm import SVR                                           # Support Vector Regressor model

from sklearn.neural_network import MLPRegressor                       # Multi-layer Perceptron Regressor model

from sklearn.metrics import mean_squared_error                        # function to calculate mean squared error

from sklearn.preprocessing import StandardScaler                      # StandardScaler for feature scaling

from urllib.request import urlretrieve                                # function to download data from a URL

###Q1 a)

# To download the dataset

url = "https://archive.ics.uci.edu/ml/machine-learning-databases/wine-quality/winequality-white.csv"  # URL of the dataset [2]

data_file = "winequality-white.csv"  # Name of the downloaded file to store the dataset

urlretrieve(url, data_file)  # To save it locally


wine_data = pd.read_csv(data_file, delimiter=';')  # Read the dataset into a Pandas DataFrame, specifying the delimiter as ';'

###Q1 b)

# To explore the data

print(wine_data.head())  # Print the first few rows of the dataset to understand its structure

print(wine_data.describe())  # Print summary statistics of the dataset


# For Visualization ...

plt.figure(figsize=(10, 6))  # Set the figure size for the plot

plt.hist(wine_data['quality'], bins=7, edgecolor='black')  # Create a histogram of the 'quality' column

plt.xlabel('Quality')  # Label the x-axis as 'Quality'

plt.ylabel('Count')  # Label the y-axis as 'Count'

plt.title('Distribution of Wine Quality')  # Set the title of the plot

plt.show()  # Display the plot


# To pre-process the data

X = wine_data.drop('quality', axis=1)  # Extract features by dropping the 'quality' column
```

```
y = wine_data['quality']  # Extract target variable


###Q1 c)


X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)  # Split the data into training and testing sets


# Standardize the features

scaler = StandardScaler()  # Initialize a StandardScaler object

X_train_scaled = scaler.fit_transform(X_train)  # Fit and transform the training features

X_test_scaled = scaler.transform(X_test)  # Transform the testing features using the fitted scaler


# Train, validate and test the models

# i) Random Forest

rf_model = RandomForestRegressor(random_state=42)  # Initialize a Random Forest Regressor model [1]

param_grid_rf = {'n_estimators': [50, 100, 150, 200]} # Define hyperparameter grid for Random Forest

grid_search_rf = GridSearchCV(rf_model, param_grid_rf, cv=5, scoring='neg_mean_squared_error') # Initialize GridSearchCV for hyperparameter tuning

grid_search_rf.fit(X_train_scaled, y_train)  # Fit the GridSearchCV object to the training data

best_rf_model = grid_search_rf.best_estimator_  # Get the best Random Forest model from the search

rf_predictions = best_rf_model.predict(X_test_scaled)  # Make predictions on the testing set using the best model

rf_mse = mean_squared_error(y_test, rf_predictions)  # Calculate the mean squared error for Random Forest


# ii) Support Vector Regression with RBF Kernel

svr_model = SVR(kernel='rbf')  # Initialize a Support Vector Regressor model with RBF kernel

param_grid_svr = {'C': [0.1, 1, 10, 100], 'gamma': [0.1, 1, 10]}  # Define hyperparameter grid for SVR

grid_search_svr = GridSearchCV(svr_model, param_grid_svr, cv=5, scoring='neg_mean_squared_error')  # Initialize GridSearchCV for hyperparameter tuning

grid_search_svr.fit(X_train_scaled, y_train)  # Fit the GridSearchCV object to the training data
```

```
best_svr_model = grid_search_svr.best_estimator_  # Get the best SVR model from the search

svr_predictions = best_svr_model.predict(X_test_scaled)  # Make predictions on the testing set using the best model

svr_mse = mean_squared_error(y_test, svr_predictions)  # Calculate the mean squared error for SVR


# iii) Neural Network with Single Hidden Layer

nn_model = MLPRegressor(hidden_layer_sizes=(100,), activation='relu', solver='adam', max_iter=1000)  # Initialize a Neural Network Regressor model with a single hidden layer

nn_model.fit(X_train_scaled, y_train)  # Fit the Neural Network model to the training data

nn_predictions = nn_model.predict(X_test_scaled)  # Make predictions on the testing set

nn_mse = mean_squared_error(y_test, nn_predictions)  # Calculate the mean squared error for Neural Network


# Results

print("Random Forest MSE:", rf_mse)  # Print the mean squared error for Random Forest

print("SVR with RBF Kernel MSE:", svr_mse)  # Print the mean squared error for SVR

print("Neural Network MSE:", nn_mse)  # Print the mean squared error for Neural Network
```

OUTPUT:

ixed acidity	volatile acidity	citric acid	residual sugar	chlorides	\
0	7.0	0.27	0.36	20.7	0.045
1	6.3	0.30	0.34	1.6	0.049
2	8.1	0.28	0.40	6.9	0.050
3	7.2	0.23	0.32	8.5	0.058
4	7.2	0.23	0.32	8.5	0.058

free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	\
0	45.0	170.0	1.0010	3.00	0.45
1	14.0	132.0	0.9940	3.30	0.49
2	30.0	97.0	0.9951	3.26	0.44
3	47.0	186.0	0.9956	3.19	0.40
4	47.0	186.0	0.9956	3.19	0.40

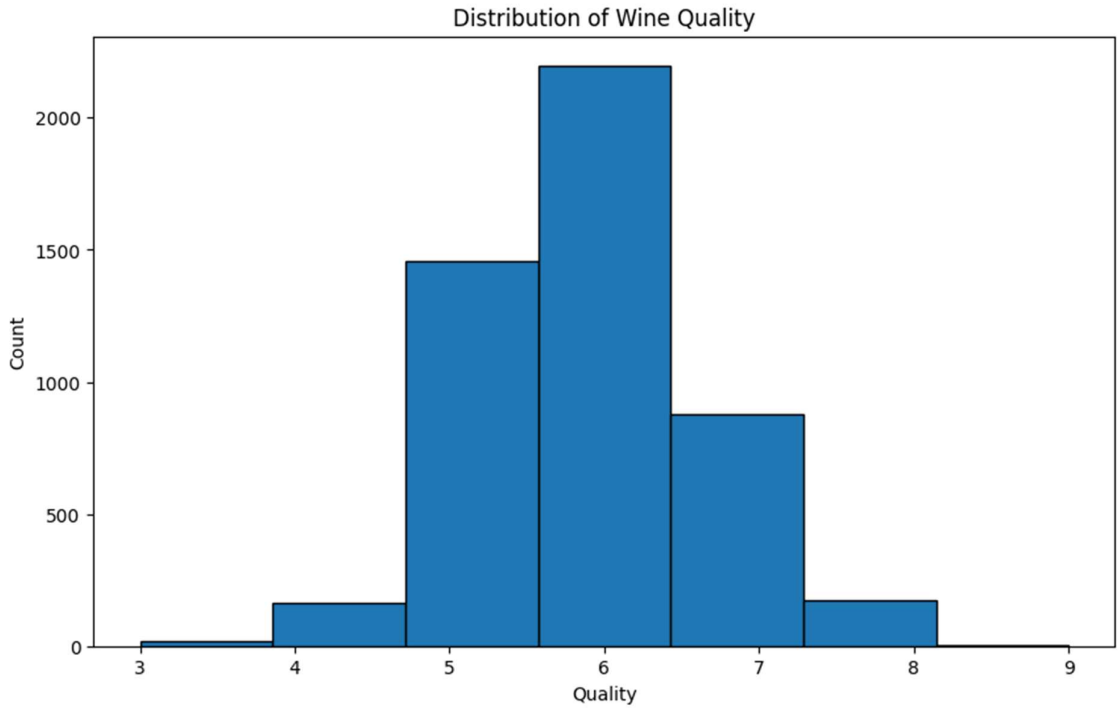
	alcohol	quality
0	8.8	6
1	9.5	6
2	10.1	6
3	9.9	6
4	9.9	6

	fixed acidity	volatile acidity	citric acid	residual sugar	\
count	4898.000000	4898.000000	4898.000000	4898.000000	
mean	6.854788	0.278241	0.334192	6.391415	
std	0.843868	0.100795	0.121020	5.072058	
min	3.800000	0.080000	0.000000	0.600000	
25%	6.300000	0.210000	0.270000	1.700000	
50%	6.800000	0.260000	0.320000	5.200000	
75%	7.300000	0.320000	0.390000	9.900000	
max	14.200000	1.100000	1.660000	65.800000	

	chlorides	free sulfur dioxide	total sulfur dioxide	density	\
count	4898.000000	4898.000000	4898.000000	4898.000000	
mean	0.045772	35.308085	138.360657	0.994027	
std	0.021848	17.007137	42.498065	0.002991	
min	0.009000	2.000000	9.000000	0.987110	
25%	0.036000	23.000000	108.000000	0.991723	
50%	0.043000	34.000000	134.000000	0.993740	
75%	0.050000	46.000000	167.000000	0.996100	
max	0.346000	289.000000	440.000000	1.038980	

	pH	sulphates	alcohol	quality
count	4898.000000	4898.000000	4898.000000	4898.000000
mean	3.188267	0.489847	10.514267	5.877909
std	0.151001	0.114126	1.230621	0.885639
min	2.720000	0.220000	8.000000	3.000000

25%	3.090000	0.410000	9.500000	5.000000
50%	3.180000	0.470000	10.400000	6.000000
75%	3.280000	0.550000	11.400000	6.000000
max	3.820000	1.080000	14.200000	9.000000



To upload winequality files

from google.colab import files

uploaded = files.upload()

Q1 d) **Determination of Importance**

Random Forest:

Random Forest provides a built-in feature importance score based on how much each feature decreases impurity across all trees in the forest. We can access this information through the feature_importances_ attribute of the trained model.

Support Vector Regression (SVR):

SVR does not inherently provide feature importance like Random Forest. However, we can still infer feature importance by examining the coefficients of the support vectors, which indicate the influence of each feature on the model's predictions.

Neural Network:

Neural networks do not have a straightforward way to calculate feature importance. However, we can use techniques such as permutation importance or layer-wise relevance propagation (LRP) to understand the importance of input features.

###Q1 d)

#[1]

```
rf_feature_importance = rf_model.feature_importances_                    # Random Forest Feature Importance


# For SVR Coefficients
svr_coefficients = None
if hasattr(svr_model, 'coef_'):
    svr_coefficients = svr_model.coef_[0]


# For Neural Network Feature Importance (Using Permutation Importance)
from sklearn.inspection import permutation_importance
nn_permutation_importance = permutation_importance(nn_model, X_test_scaled, y_test, n_repeats=10, random_state=42)
nn_feature_importance = nn_permutation_importance.importances_mean


# To create DataFrames for each model's feature importance
rf_feature_importance_df = pd.DataFrame({'Feature': X.columns, 'Random Forest Importance': rf_feature_importance})
if svr_coefficients is not None:
    svr_feature_importance_df = pd.DataFrame({'Feature': X.columns, 'SVR Coefficients': svr_coefficients})
nn_feature_importance_df = pd.DataFrame({'Feature': X.columns, 'Neural Network Importance': nn_feature_importance})
```

```
# To merge all feature importance DataFrames on the 'Feature' column

feature_importance_df = pd.merge(rf_feature_importance_df, nn_feature_importance_df, on='Feature', how='outer')

if svr_coefficients is not None:

    feature_importance_df = pd.merge(feature_importance_df, svr_feature_importance_df, on='Feature', how='outer')


# Print the merged DataFrame

print(feature_importance_df)
```

O/p:

	Feature	Random Forest Importance	Neural Network Importance
0	fixed acidity	0.054148	0.343676
1	volatile acidity	0.113917	0.304700
2	citric acid	0.049815	0.017748
3	residual sugar	0.060430	0.025763
4	chlorides	0.065521	0.031198
5	free sulfur dioxide	0.050250	0.154181
6	total sulfur dioxide	0.077462	0.255654
7	density	0.056422	0.389796
8	pH	0.056519	0.231806
9	sulphates	0.134183	0.125450
10	alcohol	0.281334	0.562540

```
### Q1 e)

#[1]

# Load red wine data

red_data = pd.read_csv("winequality-white.csv", delimiter=";")


# Separate features and target variable for red wine data

X_red = red_data.drop(columns=['quality'])

y_red = red_data['quality']


# Standardize features for red wine data
```

```
X_red_scaled = scaler.transform(X_red)

# Predict using models trained on white wine data
rf_red_pred = rf_model.predict(X_red_scaled)
svr_red_pred = svr_model.predict(X_red_scaled)
nn_red_pred = nn_model.predict(X_red_scaled)

# Evaluate performance on red wine data using the models trained on white wine data
rf_red_rmse = np.sqrt(mean_squared_error(y_red, rf_red_pred))
svr_red_rmse = np.sqrt(mean_squared_error(y_red, svr_red_pred))
nn_red_rmse = np.sqrt(mean_squared_error(y_red, nn_red_pred))

print("Performance of White Wine Models on Red Wine Data:")
print("Random Forest RMSE:", rf_red_rmse)
print("SVR RMSE:", svr_red_rmse)
print("Neural Network RMSE:", nn_red_rmse)
```

O/p:

Performance of White Wine Models on Red Wine Data:

Random Forest RMSE: 0.852017877186941

SVR RMSE: 0.838412404742264

Neural Network RMSE: 1.2177320228448185

Red Data:

Random Forest RMSE: 0.34563525186181604

SVR RMSE: 0.56581312113129

Neural Network RMSE: 0.6794603028660857

White Data:

Random Forest RMSE: 0.852017877186941

SVR RMSE: 0.838412404742264

Neural Network RMSE: 1.2177320228448185

The models from red wine generalize to white wine upto some extent, but the RMSE's are significantly higher and may not be best suited

```
from google.colab import files
uploaded = files.upload()

### Q2 a) & b)
#[1]
import pandas as pd
from sklearn.experimental import enable_iterative_imputer
from sklearn.impute import IterativeImputer
from sklearn.preprocessing import LabelEncoder
import matplotlib.pyplot as plt
import seaborn as sns

# Load the data
url = "https://archive.ics.uci.edu/ml/machine-learning-databases/00342/Data_Cortex_Nuclear.xls"
#[3]
data = pd.read_excel(url)

# Display Properties
print(data.head())
print(data.info())
print(data.describe())

# First few columns of data
columns_to_visualize = data.columns[:10]
for column in columns_to_visualize:
    sns.histplot(data[column])
    plt.title(column)
    plt.show()
```

```
# Pre-processing

# Identification of categorical columns and non-numeric columns
categorical_columns = ['Genotype', 'Treatment', 'Behavior', 'class']
non_numeric_columns = ['MouseID']

# Encode categorical columns
label_encoders = {}
for col in categorical_columns:
    label_encoders[col] = LabelEncoder()
    data[col] = label_encoders[col].fit_transform(data[col])

# Exclude non-numeric columns
data_numeric = data.drop(columns=non_numeric_columns)

# Disable output truncation
from IPython.display import display
pd.set_option('display.max_rows', None)
pd.set_option('display.max_columns', None) # Made just to see all data instead of ..

# Apply multivariate feature imputation #[4]
imputer = IterativeImputer(max_iter=10, random_state=0)
data_imputed_numeric = imputer.fit_transform(data_numeric)

# Convert imputed data back to DataFrame
data_imputed = pd.DataFrame(data_imputed_numeric, columns=data_numeric.columns)

# Verify if missing values have been imputed
print("Missing Values After Imputation:")
print(data_imputed.isnull().sum())
```

```
# Reset display options to default
pd.reset_option('display.max_rows')
pd.reset_option('display.max_columns') # That display is resetted (..)
```

O/p:

```
MouseID  DYRK1A_N   ITSN1_N    BDNF_N     NR1_N    NR2A_N    pAKT_N  \
0   309_1  0.503644  0.747193  0.430175  2.816329  5.990152  0.218830
1   309_2  0.514617  0.689064  0.411770  2.789514  5.685038  0.211636
2   309_3  0.509183  0.730247  0.418309  2.687201  5.622059  0.209011
3   309_4  0.442107  0.617076  0.358626  2.466947  4.979503  0.222886
4   309_5  0.434940  0.617430  0.358802  2.365785  4.718679  0.213106

    pBRAF_N  pCAMKII_N   pCREB_N  ...   pCFOS_N     SYP_N  H3AcK18_N  \
0  0.177565   2.373744  0.232224  ...  0.108336  0.427099   0.114783
1  0.172817   2.292150  0.226972  ...  0.104315  0.441581   0.111974
2  0.175722   2.283337  0.230247  ...  0.106219  0.435777   0.111883
3  0.176463   2.152301  0.207004  ...  0.111262  0.391691   0.130405
4  0.173627   2.134014  0.192158  ...  0.110694  0.434154   0.118481

    EGR1_N  H3MeK4_N    CaNA_N Genotype  Treatment  Behavior   class
0  0.131790  0.128186  1.675652   Control  Memantine      C/S  c-CS-m
1  0.135103  0.131119  1.743610   Control  Memantine      C/S  c-CS-m
2  0.133362  0.127431  1.926427   Control  Memantine      C/S  c-CS-m
3  0.147444  0.146901  1.700563   Control  Memantine      C/S  c-CS-m
4  0.140314  0.148380  1.839730   Control  Memantine      C/S  c-CS-m

[5 rows x 82 columns]
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1080 entries, 0 to 1079
Data columns (total 82 columns):
```

#	Column	Non-Null Count	Dtype
0	MouseID	1080 non-null	object
1	DYRK1A_N	1077 non-null	float64
2	ITSN1_N	1077 non-null	float64
3	BDNF_N	1077 non-null	float64
4	NR1_N	1077 non-null	float64
5	NR2A_N	1077 non-null	float64
6	pAKT_N	1077 non-null	float64
7	pBRAF_N	1077 non-null	float64
8	pCAMKII_N	1077 non-null	float64
9	pCREB_N	1077 non-null	float64
10	pELK_N	1077 non-null	float64
11	pERK_N	1077 non-null	float64
12	pJNK_N	1077 non-null	float64
13	PKCA_N	1077 non-null	float64
14	pMEK_N	1077 non-null	float64
15	pNR1_N	1077 non-null	float64
16	pNR2A_N	1077 non-null	float64
17	pNR2B_N	1077 non-null	float64
18	pPKCAB_N	1077 non-null	float64
19	pRSK_N	1077 non-null	float64
20	AKT_N	1077 non-null	float64
21	BRAF_N	1077 non-null	float64
22	CAMKII_N	1077 non-null	float64
23	CREB_N	1077 non-null	float64
24	ELK_N	1062 non-null	float64
25	ERK_N	1077 non-null	float64
26	GSK3B_N	1077 non-null	float64
27	JNK_N	1077 non-null	float64
28	MEK_N	1073 non-null	float64

29 TRKA_N 1077 non-null float64

30 RSK_N 1077 non-null float64

31 APP_N 1077 non-null float64

32 Bcatenin_N 1062 non-null float64

33 SOD1_N 1077 non-null float64

34 MTOR_N 1077 non-null float64

35 P38_N 1077 non-null float64

36 pMTOR_N 1077 non-null float64

37 DSCR1_N 1077 non-null float64

38 AMPKA_N 1077 non-null float64

39 NR2B_N 1077 non-null float64

40 pNUMB_N 1077 non-null float64

41 RAPTOR_N 1077 non-null float64

42 TIAM1_N 1077 non-null float64

43 pP70S6_N 1077 non-null float64

44 NUMB_N 1080 non-null float64

45 P70S6_N 1080 non-null float64

46 pGSK3B_N 1080 non-null float64

47 pPKCG_N 1080 non-null float64

48 CDK5_N 1080 non-null float64

49 S6_N 1080 non-null float64

50 ADARB1_N 1080 non-null float64

51 AcetylH3K9_N 1080 non-null float64

52 RRP1_N 1080 non-null float64

53 BAX_N 1080 non-null float64

54 ARC_N 1080 non-null float64

55 ERBB4_N 1080 non-null float64

56 nNOS_N 1080 non-null float64

57 Tau_N 1080 non-null float64

58 GFAP_N 1080 non-null float64

59 GluR3_N 1080 non-null float64

```
 60  GluR4_N         1080 non-null   float64
 61  IL1B_N          1080 non-null   float64
 62  P3525_N         1080 non-null   float64
 63  pCASP9_N        1080 non-null   float64
 64  PSD95_N         1080 non-null   float64
 65  SNCA_N          1080 non-null   float64
 66  Ubiquitin_N     1080 non-null   float64
 67  pGSK3B_Tyr216_N  1080 non-null   float64
 68  SHH_N           1080 non-null   float64
 69  BAD_N           867 non-null    float64
 70  BCL2_N          795 non-null    float64
 71  pS6_N           1080 non-null   float64
 72  pCFOS_N         1005 non-null   float64
 73  SYP_N           1080 non-null   float64
 74  H3AcK18_N       900 non-null    float64
 75  EGR1_N          870 non-null    float64
 76  H3MeK4_N        810 non-null    float64
 77  CaNA_N          1080 non-null   float64
 78  Genotype        1080 non-null   object
 79  Treatment       1080 non-null   object
 80  Behavior        1080 non-null   object
 81  class           1080 non-null   object
dtypes: float64(77), object(5)
memory usage: 692.0+ KB
None
       DYRK1A_N     ITSN1_N      BDNF_N       NR1_N      NR2A_N  \
count  1077.000000  1077.000000  1077.000000  1077.000000  1077.000000
mean     0.425810    0.617102    0.319088    2.297269    3.843934
std      0.249362    0.251640    0.049383    0.347293    0.933100
min      0.145327    0.245359    0.115181    1.330831    1.737540
25%      0.288121    0.473361    0.287444    2.057411    3.155678
```

50%	0.366378	0.565782	0.316564	2.296546	3.760855
75%	0.487711	0.698032	0.348197	2.528481	4.440011
max	2.516367	2.602662	0.497160	3.757641	8.482553

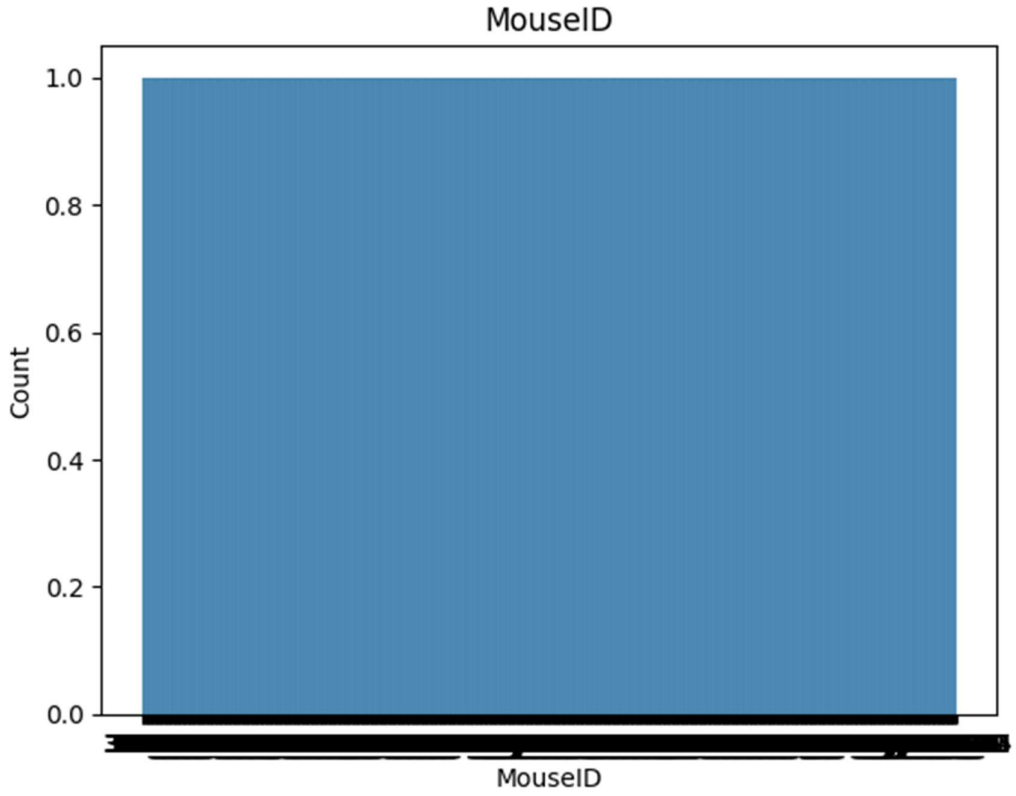
	pAKT_N	pBRAF_N	pCAMKII_N	pCREB_N	pELK_N	... \
count	1077.000000	1077.000000	1077.000000	1077.000000	1077.000000	...
mean	0.233168	0.181846	3.537109	0.212574	1.428682	...
std	0.041634	0.027042	1.295169	0.032587	0.466904	...
min	0.063236	0.064043	1.343998	0.112812	0.429032	...
25%	0.205755	0.164595	2.479834	0.190823	1.203665	...
50%	0.231177	0.182302	3.326520	0.210594	1.355846	...
75%	0.257261	0.197418	4.481940	0.234595	1.561316	...
max	0.539050	0.317066	7.464070	0.306247	6.113347	...

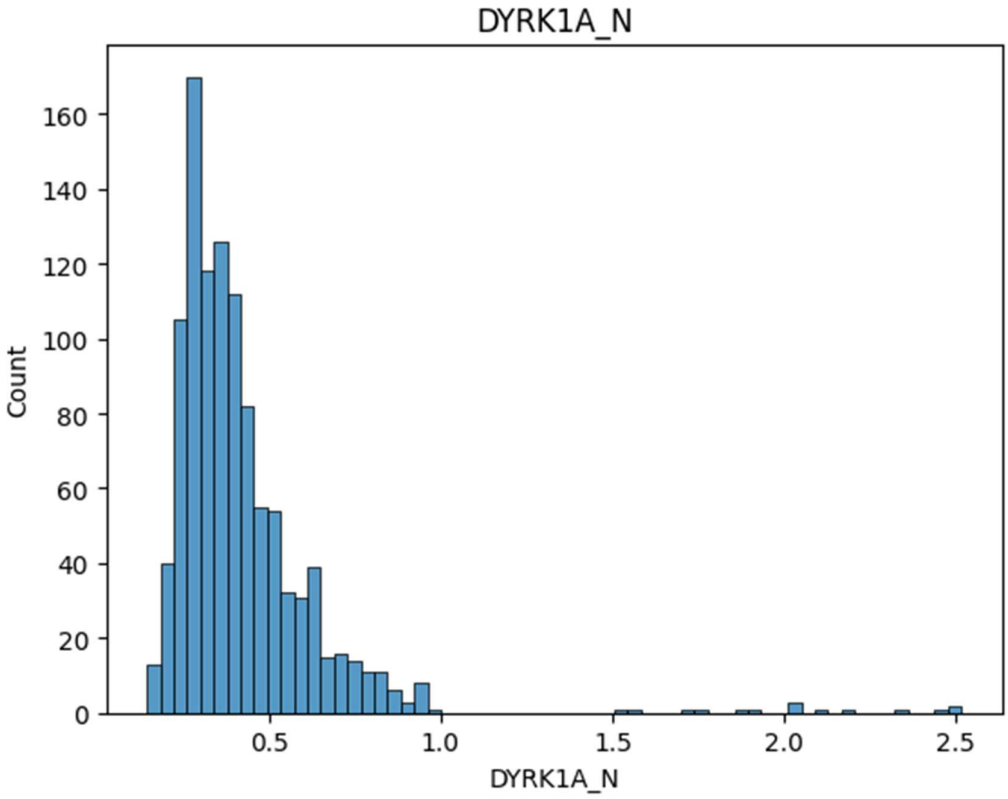
	SHH_N	BAD_N	BCL2_N	pS6_N	pCFOS_N \
count	1080.000000	867.000000	795.000000	1080.000000	1005.000000
mean	0.226676	0.157914	0.134762	0.121521	0.131053
std	0.028989	0.029537	0.027417	0.014276	0.023863
min	0.155869	0.088305	0.080657	0.067254	0.085419
25%	0.206395	0.136424	0.115554	0.110839	0.113506
50%	0.224000	0.152313	0.129468	0.121626	0.126523
75%	0.241655	0.174017	0.148235	0.131955	0.143652
max	0.358289	0.282016	0.261506	0.158748	0.256529

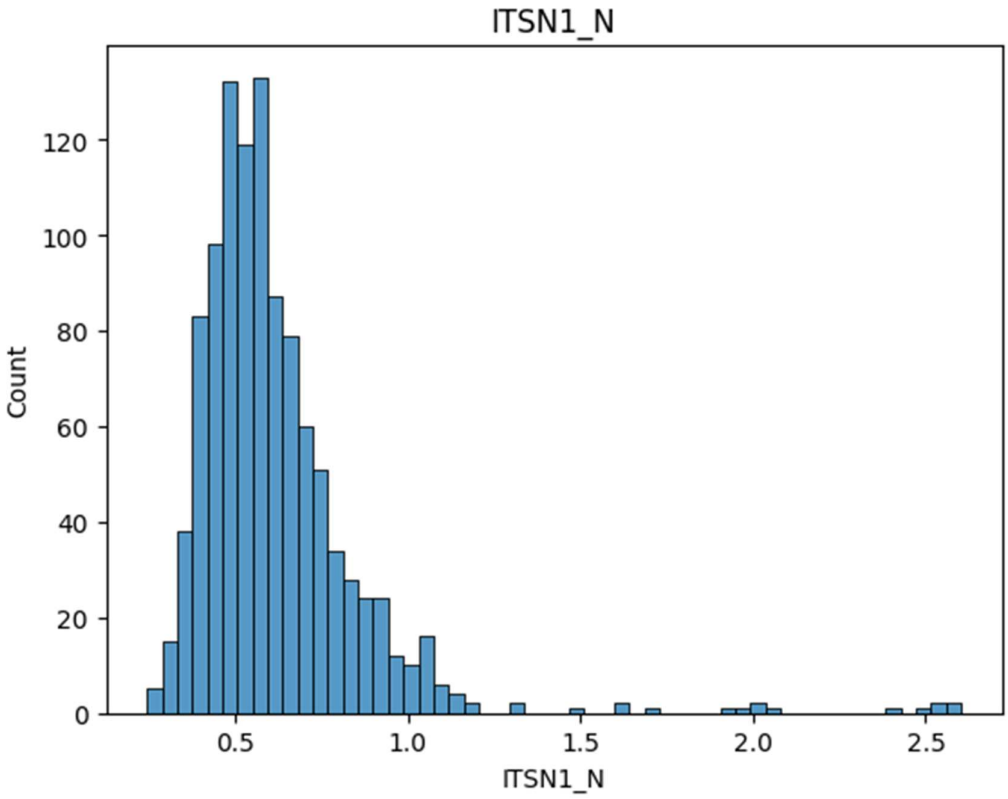
	SYP_N	H3AcK18_N	EGR1_N	H3MeK4_N	CaNA_N
count	1080.000000	900.000000	870.000000	810.000000	1080.000000
mean	0.446073	0.169609	0.183135	0.205440	1.337784
std	0.066432	0.059402	0.040406	0.055514	0.317126
min	0.258626	0.079691	0.105537	0.101787	0.586479
25%	0.398082	0.125848	0.155121	0.165143	1.081423
50%	0.448459	0.158240	0.174935	0.193994	1.317441

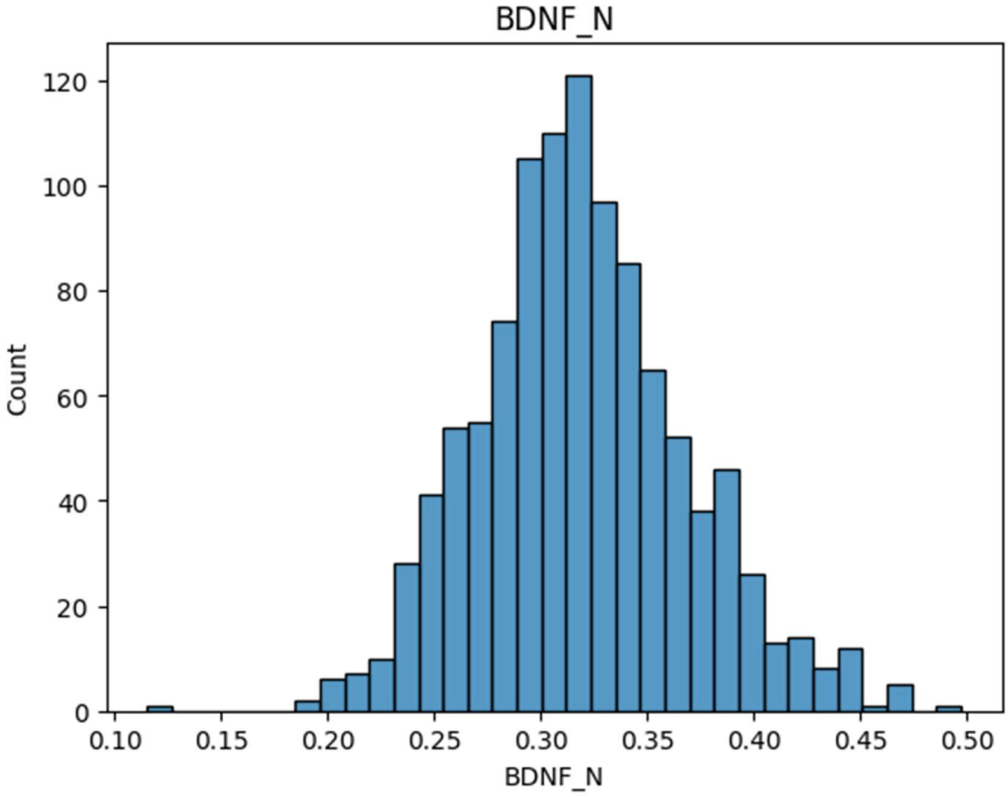
75%	0.490773	0.197876	0.204542	0.235215	1.585824
max	0.759588	0.479763	0.360692	0.413903	2.129791

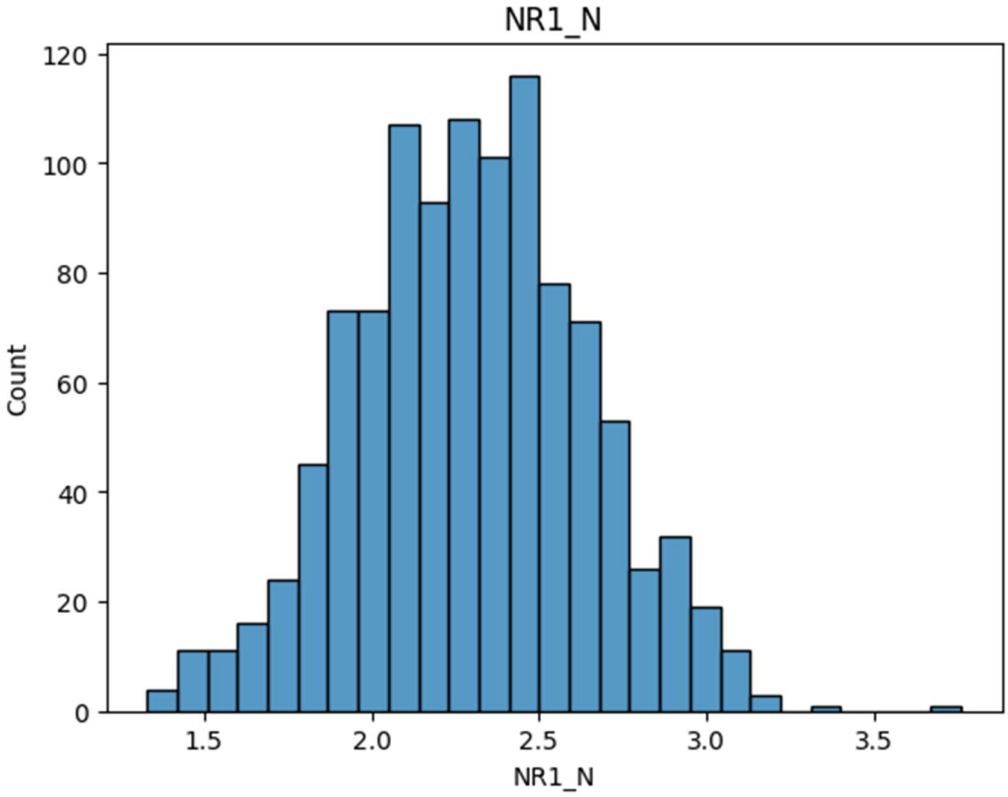
[8 rows x 77 columns]

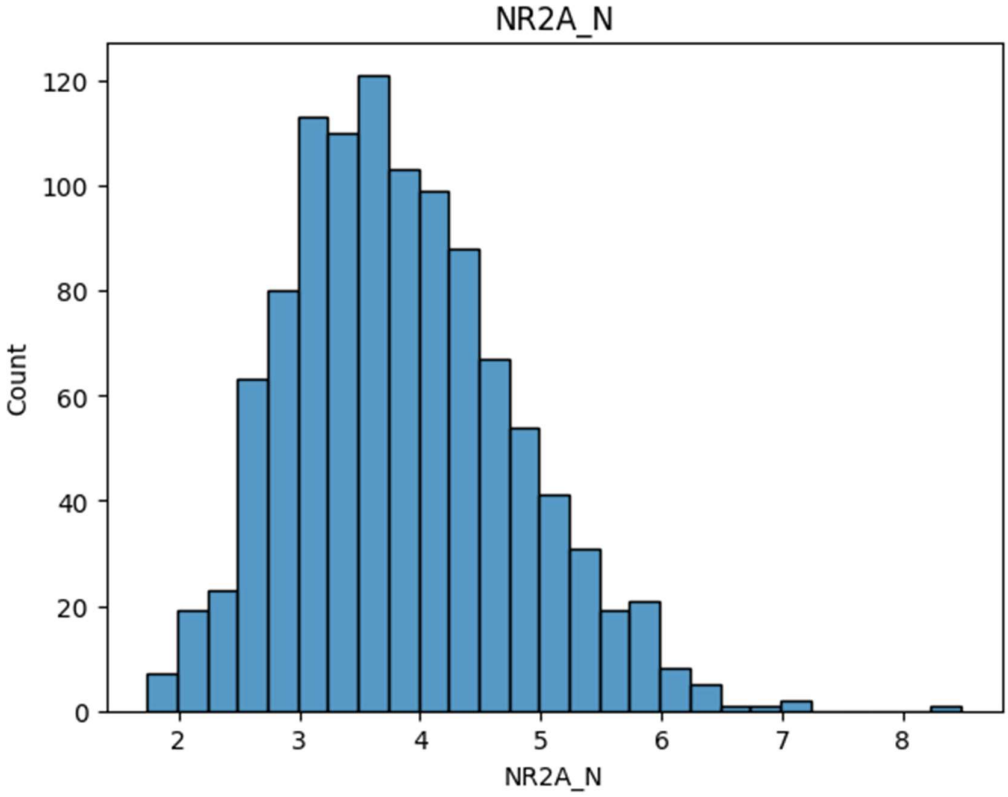


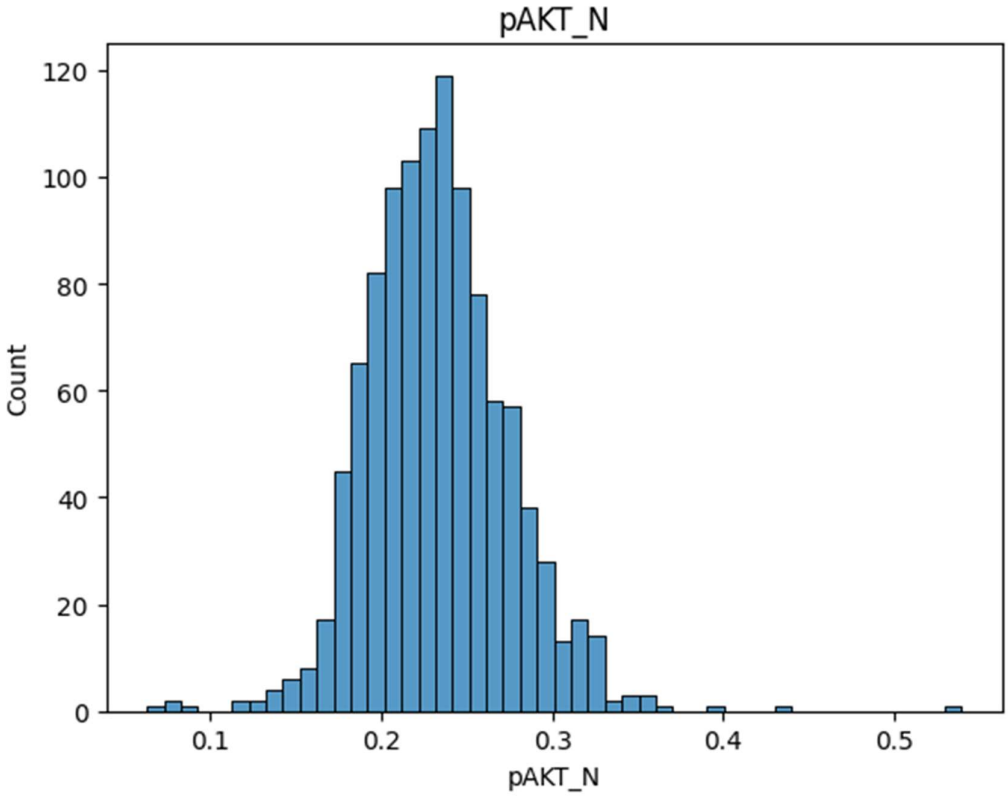

DYRK1A_N
Count
0
20
40
60
80
100
120
140
160
0.5
1.0
1.5
2.0
2.5
DYRK1A_N

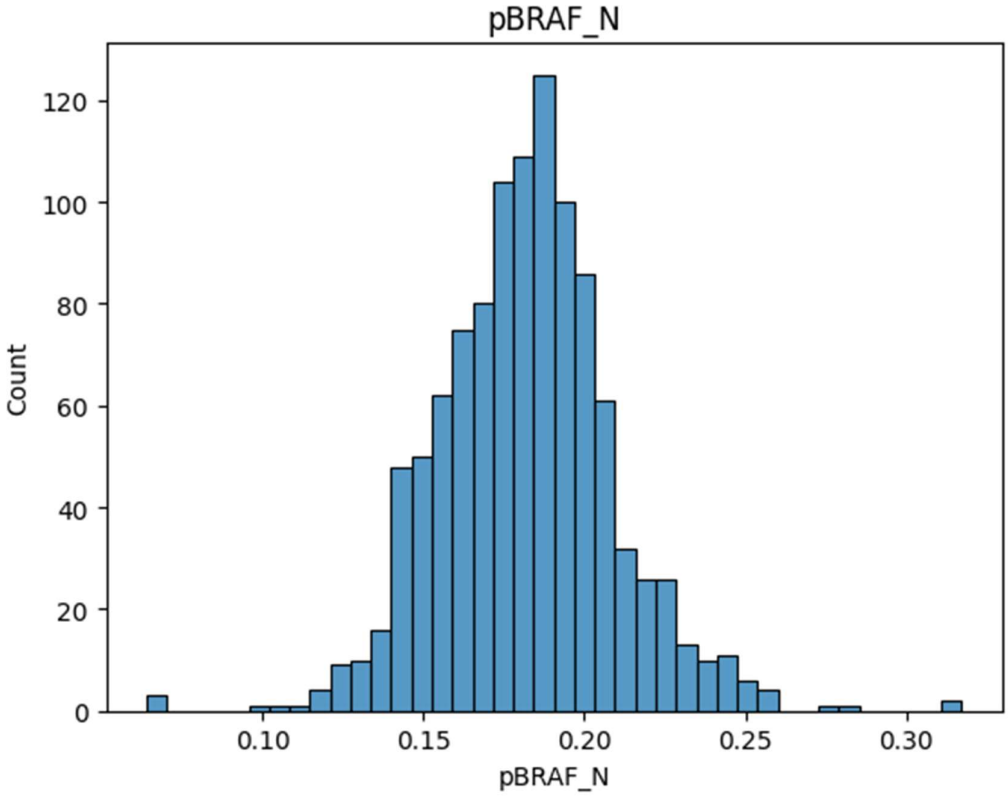

ITSN1_N
Count
0
20
40
60
80
100
120
0.5
1.0
1.5
2.0
2.5
ITSN1_N

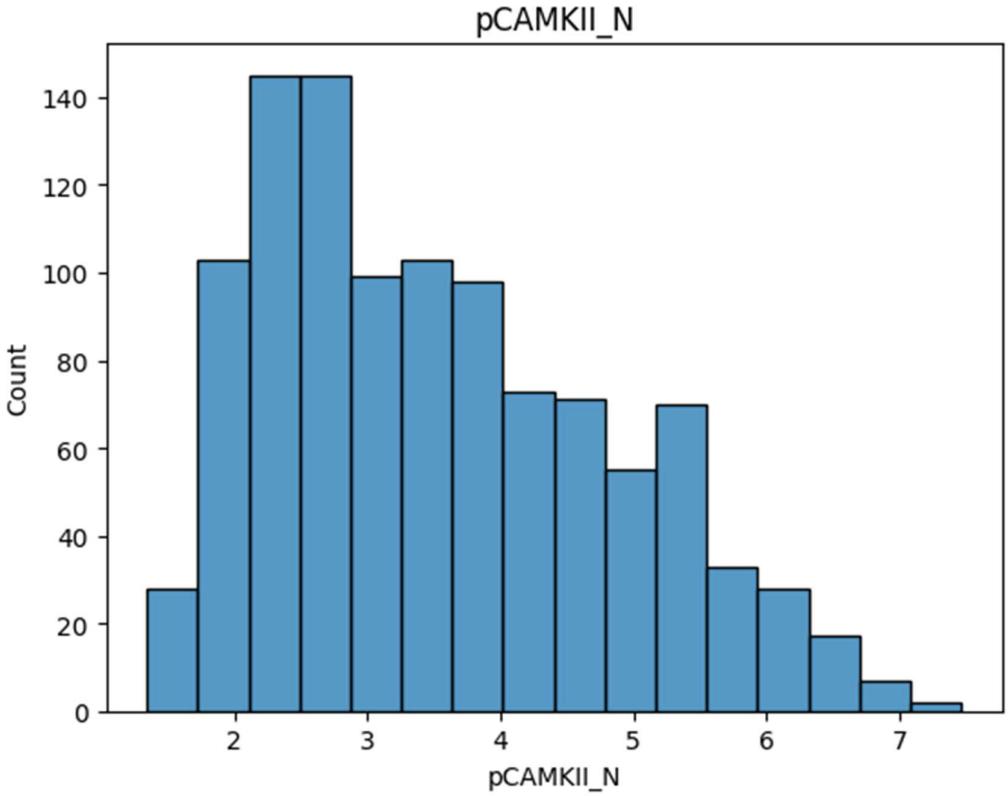

BDNF_N
Count
BDNF_N
0
20
40
60
80
100
120
0.10
0.15
0.20
0.25
0.30
0.35
0.40
0.45
0.50

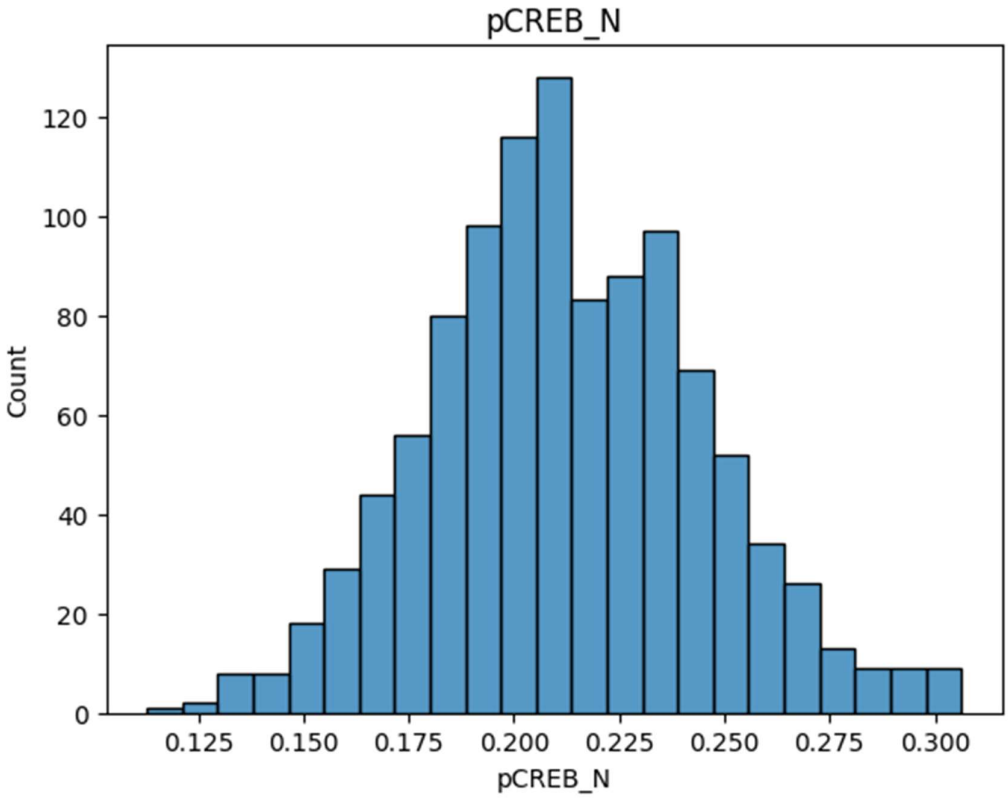

NR1_N
Count
NR1_N
0
20
40
60
80
100
120
1.5
2.0
2.5
3.0
3.5


NR2A_N
Count
NR2A_N
0
20
40
60
80
100
120
2
3
4
5
6
7
8


pAKT_N
Count
pAKT_N
0
20
40
60
80
100
120
0.1
0.2
0.3
0.4
0.5


pBRAF_N
Count
0
20
40
60
80
100
120
0.10
0.15
0.20
0.25
0.30
pBRAF_N


pCAMKII_N
Count
0
20
40
60
80
100
120
140
2
3
4
5
6
7
pCAMKII_N



Missing Values After Imputation:

DYRK1A_N 0

ITSN1_N 0

BDNF_N 0

NR1_N 0

NR2A_N 0

pAKT_N 0

pBRAF_N 0

pCAMKII_N 0

pCREB_N 0

pELK_N 0

pERK_N 0

pJNK_N 0

PKCA_N 0

pMEK_N 0

pNR1_N 0

pNR2A_N 0

pNR2B_N 0

pPKCAB_N 0

pRSK_N 0

AKT_N 0

BRAF_N 0

CAMKII_N 0

CREB_N 0

ELK_N 0

ERK_N 0

GSK3B_N 0

JNK_N 0

MEK_N 0

TRKA_N 0

RSK_N 0

APP_N 0

Bcatenin_N 0

SOD1_N 0

MTOR_N 0

P38_N 0

pMTOR_N 0

DSCR1_N 0

AMPKA_N 0

NR2B_N 0

pNUMB_N 0

RAPTOR_N 0

TIAM1_N 0

pP70S6_N 0

NUMB_N 0

P70S6_N 0

pGSK3B_N 0

pPKCG_N 0

CDK5_N 0

S6_N 0

ADARB1_N 0

AcetylH3K9_N 0

RRP1_N 0

BAX_N 0

ARC_N 0

ERBB4_N 0

nNOS_N 0

Tau_N 0

GFAP_N 0

GluR3_N 0

GluR4_N 0

IL1B_N 0

P3525_N 0

pCASP9_N 0

PSD95_N 0

SNCA_N 0

Ubiquitin_N 0

pGSK3B_Tyr216_N 0

SHH_N 0

BAD_N 0

BCL2_N 0

pS6_N 0

pCFOS_N 0

SYP_N 0

H3AcK18_N 0

EGR1_N 0

H3MeK4_N 0

CaNA_N 0

```
Genotype          0
Treatment         0
Behavior          0
class             0


###Q2 c)
#[1]
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.svm import SVC
from sklearn.neural_network import MLPClassifier
from sklearn.metrics import accuracy_score

# To split the data into training, validation, and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)
X_train, X_val, y_train, y_val = train_test_split(X_train, y_train, test_size=0.2, random_state=42)

# To train and validate the models
# i) Random Forest with hyperparameter tuning
rf_model = RandomForestClassifier(n_estimators=100, random_state=42)  # Default
hyperparameters
rf_model.fit(X_train, y_train)
rf_val_predictions = rf_model.predict(X_val)
rf_val_accuracy = accuracy_score(y_val, rf_val_predictions)
print("Random Forest Validation Accuracy:", rf_val_accuracy)

# ii) Support Vector Classification (SVC) with RBF kernel
svc_model = SVC(kernel='rbf', random_state=42)  # Default hyperparameters
svc_model.fit(X_train, y_train)
svc_val_predictions = svc_model.predict(X_val)
svc_val_accuracy = accuracy_score(y_val, svc_val_predictions)
```

```
print("SVC Validation Accuracy:", svc_val_accuracy)


# iii) Neural Network with single hidden layer and softmax activation
nn_model = MLPClassifier(hidden_layer_sizes=(100,), activation='relu', solver='adam',
                         alpha=0.0001, batch_size='auto', learning_rate='constant',
                         learning_rate_init=0.001, max_iter=200, random_state=42)
nn_model.fit(X_train, y_train)
nn_val_predictions = nn_model.predict(X_val)
nn_val_accuracy = accuracy_score(y_val, nn_val_predictions)
print("Neural Network Validation Accuracy:", nn_val_accuracy)


# To evaluate the model:


# Highest validation accuracy
best_model = max([(rf_val_accuracy, rf_model), (svc_val_accuracy, svc_model), (nn_val_accuracy,
nn_model)])
print("Best Model Validation Accuracy:", best_model[0])
best_model = best_model[1]


# Test the selected model
test_predictions = best_model.predict(X_test)
test_accuracy = accuracy_score(y_test, test_predictions)
print("Test Accuracy of the Best Model:", test_accuracy)
```

O/p:

```
Random Forest Validation Accuracy: 0.6670918367346939
SVC Validation Accuracy: 0.4502551020408163
Neural Network Validation Accuracy: 0.4846938775510204
Best Model Validation Accuracy: 0.6670918367346939
Test Accuracy of the Best Model: 0.673469387755102
```

```
###Q2 d)
#[1]
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.svm import SVC
from sklearn.neural_network import MLPClassifier
from sklearn.metrics import accuracy_score
from sklearn.feature_selection import RFECV
import pandas as pd

# To split the data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)

# To define RFECV for Random Forest #[5]
rfecv_rf = RFECV(estimator=RandomForestClassifier(n_estimators=100, random_state=42), cv=3,
n_jobs=-1)
rfecv_rf.fit(X_train, y_train)
selected_features_rf = X_train.columns[rfecv_rf.support_]

# To define RFECV for SVC with linear kernel
rfecv_svc = RFECV(estimator=SVC(kernel='linear', random_state=42), cv=3, n_jobs=-1)
rfecv_svc.fit(X_train, y_train)
selected_features_svc = X_train.columns[rfecv_svc.support_]

print("Selected Features for Random Forest:", selected_features_rf)
print("Selected Features for SVC with linear kernel:", selected_features_svc)
O/p:
Selected Features for Random Forest: Index(['volatile acidity', 'citric acid', 'residual sugar', 'chlorides',
      'free sulfur dioxide', 'total sulfur dioxide', 'density', 'pH',
      'alcohol'],
     dtype='object')
```

```
Selected Features for SVC with linear kernel: Index(['fixed acidity', 'volatile acidity', 'citric acid',
'residual sugar',
       'chlorides', 'free sulfur dioxide', 'total sulfur dioxide', 'density',
       'pH', 'sulphates', 'alcohol'],
      dtype='object')


#To upload Q3 data
from google.colab import files
uploaded = files.upload()


#Q3 a)
#[1]
import torch
import torch.nn as nn
import torch.optim as optim
from torch.optim import lr_scheduler
import torchvision
from torchvision import datasets, models, transforms
import os
import time
import copy
import tempfile

# Define the train_model function
def train_model(model, criterion, optimizer, scheduler, num_epochs=25):
    since = time.time()

    # Create a temporary directory to save training checkpoints
    with tempfile.TemporaryDirectory() as tempdir:
        best_model_params_path = os.path.join(tempdir, 'best_model_params.pt')
```

```
torch.save(model.state_dict(), best_model_params_path)
best_acc = 0.0

for epoch in range(num_epochs):
    print(f'Epoch {epoch}/{num_epochs - 1}')
    print('-' * 10)

    # Each epoch has a training and validation phase
    for phase in ['train', 'val']:
        if phase == 'train':
            model.train()  # Set model to training mode
        else:
            model.eval()   # Set model to evaluate mode

        running_loss = 0.0
        running_corrects = 0

        # Iterate over data.
        for inputs, labels in dataloaders[phase]:
            inputs = inputs.to(device)
            labels = labels.to(device)

            # zero the parameter gradients
            optimizer.zero_grad()

            # forward
            # track history if only in train
            with torch.set_grad_enabled(phase == 'train'):
                outputs = model(inputs)
                _, preds = torch.max(outputs, 1)
                loss = criterion(outputs, labels)
```

```
                # backward + optimize only if in training phase
                if phase == 'train':
                    loss.backward()
                    optimizer.step()

                # statistics
                running_loss += loss.item() * inputs.size(0)
                running_corrects += torch.sum(preds == labels.data)
            if phase == 'train':
                scheduler.step()

            epoch_loss = running_loss / dataset_sizes[phase]
            epoch_acc = running_corrects.double() / dataset_sizes[phase]

            print(f'{phase} Loss: {epoch_loss:.4f} Acc: {epoch_acc:.4f}')

            # deep copy the model
            if phase == 'val' and epoch_acc > best_acc:
                best_acc = epoch_acc
                torch.save(model.state_dict(), best_model_params_path)

        time_elapsed = time.time() - since
        print(f'Training complete in {time_elapsed // 60:.0f}m {time_elapsed % 60:.0f}s')
        print(f'Best val Acc: {best_acc:4f}')

        # load best model weights
        model.load_state_dict(torch.load(best_model_params_path))
    return model

# Define the data directory
```

```
data_dir = '/content/hymenoptera_data'

# Define the data transforms
data_transforms = {
    'train': transforms.Compose([
        transforms.RandomResizedCrop(224),
        transforms.RandomHorizontalFlip(),
        transforms.ToTensor(),
        transforms.Normalize([0.485, 0.456, 0.406], [0.229, 0.224, 0.225])
    ]),
    'val': transforms.Compose([
        transforms.Resize(256),
        transforms.CenterCrop(224),
        transforms.ToTensor(),
        transforms.Normalize([0.485, 0.456, 0.406], [0.229, 0.224, 0.225])
    ]),
}

# Create data loaders
image_datasets = {x: datasets.ImageFolder(os.path.join(data_dir, x), data_transforms[x]) for x in ['train', 'val']}
dataloaders = {x: torch.utils.data.DataLoader(image_datasets[x], batch_size=4, shuffle=True, num_workers=4) for x in ['train', 'val']}
dataset_sizes = {x: len(image_datasets[x]) for x in ['train', 'val']}
class_names = image_datasets['train'].classes

model_conv = torchvision.models.resnet18(pretrained=True)
for param in model_conv.parameters():
    param.requires_grad = False

# Parameters of newly constructed modules have requires_grad=True by default
num_ftrs = model_conv.fc.in_features
```

```
model_conv.fc = nn.Linear(num_ftrs, 2)

device = torch.device("cuda:0" if torch.cuda.is_available() else "cpu")

print("Using device:", device)


# Define loss function, optimizer, and scheduler

criterion = nn.CrossEntropyLoss()

optimizer_conv = optim.SGD(model_conv.fc.parameters(), lr=0.001, momentum=0.9)

exp_lr_scheduler = lr_scheduler.StepLR(optimizer_conv, step_size=7, gamma=0.1)


# Train the model

model_conv = model_conv.to(device)

model_conv = train_model(model_conv, criterion, optimizer_conv, exp_lr_scheduler,
num_epochs=25)
```

O/p:

```
Using device: cpu

Epoch 0/24

----------

train Loss: 0.6313 Acc: 0.6475

val Loss: 0.6627 Acc: 0.6667

Epoch 1/24

----------

train Loss: 0.5014 Acc: 0.7377

val Loss: 0.2704 Acc: 0.8693

Epoch 2/24

----------

train Loss: 0.3800 Acc: 0.8279

val Loss: 0.1457 Acc: 0.9608

Epoch 3/24

----------

train Loss: 0.4044 Acc: 0.8279
```

val Loss: 0.2639 Acc: 0.9020

Epoch 4/24

---

train Loss: 0.6080 Acc: 0.7459

val Loss: 0.1721 Acc: 0.9412

Epoch 5/24

---

train Loss: 0.3964 Acc: 0.8320

val Loss: 0.1621 Acc: 0.9346

Epoch 6/24

---

train Loss: 0.5903 Acc: 0.7541

val Loss: 0.1882 Acc: 0.9412

Epoch 7/24

---

train Loss: 0.3531 Acc: 0.8197

val Loss: 0.1865 Acc: 0.9281

Epoch 8/24

---

train Loss: 0.3653 Acc: 0.8238

val Loss: 0.1608 Acc: 0.9412

Epoch 9/24

---

train Loss: 0.3515 Acc: 0.8443

val Loss: 0.1560 Acc: 0.9542

Epoch 10/24

---

train Loss: 0.3369 Acc: 0.8484

val Loss: 0.1691 Acc: 0.9412

Epoch 11/24

---

train Loss: 0.3930 Acc: 0.8320

val Loss: 0.1498 Acc: 0.9477

Epoch 12/24

---

train Loss: 0.3977 Acc: 0.8320

val Loss: 0.1525 Acc: 0.9477

Epoch 13/24

---

train Loss: 0.3188 Acc: 0.8730

val Loss: 0.1535 Acc: 0.9477

Epoch 14/24

---

train Loss: 0.3808 Acc: 0.8525

val Loss: 0.1571 Acc: 0.9477

Epoch 15/24

---

train Loss: 0.3249 Acc: 0.8320

val Loss: 0.1689 Acc: 0.9412

Epoch 16/24

---

train Loss: 0.3497 Acc: 0.8443

val Loss: 0.1553 Acc: 0.9412

Epoch 17/24

---

train Loss: 0.3696 Acc: 0.8279

val Loss: 0.1514 Acc: 0.9477

Epoch 18/24

---

train Loss: 0.2849 Acc: 0.8689

val Loss: 0.1645 Acc: 0.9477

Epoch 19/24

---

train Loss: 0.3222 Acc: 0.8648

val Loss: 0.1473 Acc: 0.9412

Epoch 20/24

---

train Loss: 0.3219 Acc: 0.8484

val Loss: 0.1646 Acc: 0.9477

Epoch 21/24

---

train Loss: 0.2955 Acc: 0.8811

val Loss: 0.1736 Acc: 0.9477

Epoch 22/24

---

train Loss: 0.3562 Acc: 0.8361

val Loss: 0.1662 Acc: 0.9542

Epoch 23/24

---

train Loss: 0.3215 Acc: 0.8648

val Loss: 0.1650 Acc: 0.9477

Epoch 24/24

---

train Loss: 0.3115 Acc: 0.8648

val Loss: 0.1531 Acc: 0.9477

Training complete in 17m 5s

Best val Acc: 0.960784

Q3 b)

#[1]

import torch

import torch.nn as nn

import torchvision.models as models

```
import torchvision.transforms as transforms
from torchvision import datasets
import numpy as np

def extract_features(model, dataloader):
    model.eval()  # Set the model to evaluation mode
    features_list = []

    with torch.no_grad():  # Disable gradient calculation
        for inputs, labels in dataloader:
            inputs = inputs.to(device)
            features = model(inputs)  # Forward pass to get the features
            features_list.append(features.cpu().numpy())  # Convert features to numpy array and append
to the list

    return np.concatenate(features_list)  # Concatenate the feature arrays into a single array

# Defining the data transforms
data_transforms = transforms.Compose([
    transforms.Resize(256),
    transforms.CenterCrop(224),
    transforms.ToTensor(),
    transforms.Normalize(mean=[0.485, 0.456, 0.406], std=[0.229, 0.224, 0.225])
])

# To create a dataset using the training images
train_dataset = datasets.ImageFolder('/content/hymenoptera_data/train',
transform=data_transforms)

# Create a data loader for the training dataset
train_dataloader = torch.utils.data.DataLoader(train_dataset, batch_size=4, shuffle=False)
```

```
# Load the pre-trained ResNet18 model
model = models.resnet18(pretrained=True)

# Remove the last fully connected layer
model = nn.Sequential(*list(model.children())[:-1])

# Send the model to the appropriate device
device = torch.device("cuda:0" if torch.cuda.is_available() else "cpu")
model = model.to(device)

# Extract features for training images
train_features = extract_features(model, train_dataloader)

print("Size of extracted features array:", train_features.shape)
```

O/p: Size of extracted features array: (244, 512, 1, 1)

Q3 c)

```
#[1]
from sklearn.model_selection import GridSearchCV
from sklearn.ensemble import RandomForestClassifier
from sklearn.svm import SVC
from sklearn.metrics import accuracy_score, f1_score
from sklearn.model_selection import train_test_split

# Split the data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(train_features, train_dataset.targets, test_size=0.2,
random_state=42)

# Define the parameter grids for grid search
svm_param_grid = {
    'C': [0.1, 1, 10],
```

```
    'gamma': [0.1, 1, 10]
}

rf_param_grid = {
    'n_estimators': [50, 100, 150],
    'max_depth': [None, 10, 20]
}

# Flatten the features
X_train_flattened = X_train.reshape(X_train.shape[0], -1)
X_test_flattened = X_test.reshape(X_test.shape[0], -1)

# Perform grid search for SVM
svm_grid_search = GridSearchCV(SVC(kernel='rbf'), svm_param_grid, cv=3)
svm_grid_search.fit(X_train_flattened, y_train)

# Perform grid search for Random Forest
rf_grid_search = GridSearchCV(RandomForestClassifier(), rf_param_grid, cv=3)
rf_grid_search.fit(X_train_flattened, y_train)

# Get the best models from grid search
best_svm_model = svm_grid_search.best_estimator_
best_rf_model = rf_grid_search.best_estimator_

# Evaluate the models on the test data
svm_pred = best_svm_model.predict(X_test_flattened)
rf_pred = best_rf_model.predict(X_test_flattened)

svm_accuracy = accuracy_score(y_test, svm_pred)
svm_f1_score = f1_score(y_test, svm_pred, average='macro')
```

```
rf_accuracy = accuracy_score(y_test, rf_pred)
rf_f1_score = f1_score(y_test, rf_pred, average='macro')

print("SVM - Accuracy:", svm_accuracy, "F1 Score:", svm_f1_score)
print("Random Forest - Accuracy:", rf_accuracy, "F1 Score:", rf_f1_score)
```

O/P:

SVM - Accuracy: 0.4489795918367347 F1 Score: 0.30985915492957744

Random Forest - Accuracy: 0.9183673469387755 F1 Score: 0.9175084175084175

```
!pip install streamlit
```

###Q4

```
import streamlit as st
import pandas as pd
from sklearn.externals import joblib

# Load the trained regression model
model = joblib.load('wine_quality_regression_model.pkl')

# Define the GUI elements
st.title('Wine Quality Predictor')
st.write('Enter the following attributes to predict the wine quality:')

fixed_acidity = st.slider('Fixed Acidity', min_value=4.0, max_value=16.0, value=8.0, step=0.1)
volatile_acidity = st.slider('Volatile Acidity', min_value=0.0, max_value=2.0, value=0.5, step=0.01)
citric_acid = st.slider('Citric Acid', min_value=0.0, max_value=1.0, value=0.5, step=0.01)
residual_sugar = st.slider('Residual Sugar', min_value=0.0, max_value=16.0, value=8.0, step=0.1)
chlorides = st.slider('Chlorides', min_value=0.0, max_value=1.0, value=0.08, step=0.01)
free_sulfur_dioxide = st.slider('Free Sulfur Dioxide', min_value=1, max_value=72, value=36, step=1)
```

```
total_sulfur_dioxide = st.slider('Total Sulfur Dioxide', min_value=6, max_value=289, value=144, step=1)

density = st.slider('Density', min_value=0.0, max_value=2.0, value=1.0, step=0.001)

pH = st.slider('pH', min_value=2.0, max_value=5.0, value=3.0, step=0.01)

sulphates = st.slider('Sulphates', min_value=0.0, max_value=2.0, value=0.5, step=0.01)

alcohol = st.slider('Alcohol', min_value=8.0, max_value=15.0, value=10.0, step=0.1)


# Handle prediction

if st.button('Predict'):

    # Create a DataFrame with the input data

    data = {

        'fixed acidity': [fixed_acidity],

        'volatile acidity': [volatile_acidity],

        'citric acid': [citric_acid],

        'residual sugar': [residual_sugar],

        'chlorides': [chlorides],

        'free sulfur dioxide': [free_sulfur_dioxide],

        'total sulfur dioxide': [total_sulfur_dioxide],

        'density': [density],

        'pH': [pH],

        'sulphates': [sulphates],

        'alcohol': [alcohol]

    }

    input_df = pd.DataFrame(data)


    # Make prediction

    prediction = model.predict(input_df)[0]


    st.write(f'Predicted wine quality: {prediction}')
```