ML for Bioinformatics

Computer Engineering Department

Homework 2: Practical - Random Forest and XGboost

Bahar Oveisgharan (bahar.oveis.2000@gmail.com)

Ghazal Farahani (farahaniqazal@gmail.com)

Full Name : Javad Razi

Student Number : 401204354

—

Breasr Cancer

Most of us know someone who struggled with breast cancer, or at least heard about the struggles facing patients who are fighting against breast cancer.The most important part of a process of clinical decision-making in patients with cancers, in general, is the accurate estimation of prognosis and survival duration. Breast cancer patients with the same stage of the disease and the same clinical characteristics can have different treatment responses and overall survival. In this practical assignment, you are going to train a Random Forest and XGBoost model on `breast_cancer.csv` dataset.

Import all the libraries you may need here

In [ ]:
```
try:
    import sklearn
except:
    %pip install scikit-learn
try:
    import pandas as pd
except:
    %pip install pandas
try:
    import xgboost as xgb
except:
    %pip install xgboost

from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
```

Loading the Data

In [ ]:
```
from sklearn import set_config
set_config(transform_output='pandas')
pd.set_option('display.max_columns', None)
pd.set_option('display.expand_frame_repr', False)
pd.set_option('max_colwidth', None)
# Load the dataset into a pandas dataframe
df = pd.read_csv('breast_cancer.csv')
```

Data Exploration

Let's start off by exploring the files we just imported. it's not necessary to do any visualization just a statistical summary of the data would be enough. split your data to train and test.

In [ ]:
```
# Split the dataset into training and testing sets
X = df.drop('overall_survival', axis=1)
y = df['overall_survival']
```

```python
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)

# Display a statistical summary of the data
print("Training set summary:")
print(X_train.describe())
print("\nTest set summary:")
print(X_test.describe())
```

```
Training set summary:
        Unnamed: 0  age_at_diagnosis  chemotherapy      cohort  neoplasm_histologic_grade  hormone_therapy  lymph_nodes_examine
d_positive  mutation_count  nottingham_prognostic_index  radio_therapy   tumor_size  tumor_stage
count  1523.000000       1523.000000   1523.000000  1523.000000                1523.000000      1523.000000                    1
523.000000     1523.000000                  1523.000000    1523.000000  1523.000000  1523.000000
mean    949.209455         61.203283      0.204859     2.640184                   2.406789         0.606697
2.028234        5.809266                     4.019258       0.598818    26.337064     1.748989
std     546.712860         12.939164      0.403731     1.213920                   0.643978         0.488643
4.168257        4.220676                     1.156107       0.490299    14.903876     0.540454
min       0.000000         21.930000      0.000000     1.000000                   1.000000         0.000000
0.000000        1.000000                     1.000000       0.000000     1.000000     0.000000
25%     483.500000         51.580000      0.000000     2.000000                   2.000000         0.000000
0.000000        3.000000                     3.046000       0.000000    17.950000     1.000000
50%     951.000000         61.780000      0.000000     3.000000                   2.415939         1.000000
0.000000        5.000000                     4.042000       1.000000    23.000000     1.750535
75%    1412.000000         70.650000      0.000000     3.000000                   3.000000         1.000000
2.000000        7.000000                     5.040500       1.000000    30.000000     2.000000
max    1903.000000         96.290000      1.000000     5.000000                   3.000000         1.000000
45.000000       80.000000                     6.320000       1.000000   182.000000     4.000000

Test set summary:
        Unnamed: 0  age_at_diagnosis  chemotherapy     cohort  neoplasm_histologic_grade  hormone_therapy  lymph_nodes_examined
_positive  mutation_count  nottingham_prognostic_index  radio_therapy  tumor_size  tumor_stage
count   381.000000        381.000000    381.000000  381.000000                381.000000       381.000000                    3
81.000000      381.000000                   381.000000     381.000000  381.000000   381.000000
mean    960.656168         60.622441      0.220472    2.658793                  2.452512         0.656168
1.897638        5.251664                     4.088023       0.590551   25.845633     1.756712
std     562.519548         13.142490      0.415110    1.287228                  0.613945         0.475610
3.709521        2.991337                     1.096581       0.492379   15.783795     0.538291
min      23.000000         28.290000      0.000000    1.000000                  1.000000         0.000000
0.000000        1.000000                     1.030000       0.000000    1.000000     1.000000
25%     450.000000         50.920000      0.000000    1.000000                  2.000000         0.000000
0.000000        3.000000                     3.050000       0.000000   17.000000     1.750535
50%     963.000000         61.220000      0.000000    3.000000                  3.000000         1.000000
1.000000        5.000000                     4.044000       1.000000   22.000000     1.750535
75%    1473.000000         70.420000      0.000000    3.000000                  3.000000         1.000000
2.000000        7.000000                     5.040000       1.000000   30.000000     2.000000
max    1894.000000         90.230000      1.000000    5.000000                  3.000000         1.000000
31.000000       22.000000                     6.360000       1.000000  180.000000     4.000000
```

Data Preparation

Creating two custom transformers to put on our pipeline:

- To split the data into categorical and numerical features and
- To preprocess the categorical features.
- Create the X feature matrix and the y target vector.
- split the data.

In [ ]:
```python
import pandas as pd
from sklearn.base import BaseEstimator, TransformerMixin
from sklearn.pipeline import Pipeline
from sklearn.preprocessing import StandardScaler, OneHotEncoder
from sklearn.compose import ColumnTransformer
from sklearn.model_selection import train_test_split

# Load the dataset into a pandas dataframe
df = pd.read_csv('breast_cancer.csv').dropna()

# Define custom transformers
class CategoricalFeatureSelector(BaseEstimator, TransformerMixin):
    def __init__(self):
        pass

    def fit(self, X, y=None):
        return self

    def transform(self, X):
        return X.select_dtypes(include=['object'])

class CategoricalPreprocessor(BaseEstimator, TransformerMixin):
    def __init__(self):
        pass

    def fit(self, X, y=None):
        return self

    def transform(self, X):
        ohe = OneHotEncoder(handle_unknown='ignore', sparse_output=False)
        return ohe.fit_transform(X)

# Create X feature matrix and y target vector
X = df.drop('overall_survival', axis=1)
y = df['overall_survival']
```

```
# 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)

# Define the preprocessing pipeline
categorical_pipeline = Pipeline([
    ('cat_selector', CategoricalFeatureSelector()),
    ('cat_preprocessor', CategoricalPreprocessor())
])

preprocessing_pipeline = ColumnTransformer([
    ('cat_pipeline', categorical_pipeline, X.columns.tolist())
], remainder='passthrough')

pipeline = Pipeline([
    ('preprocessing', preprocessing_pipeline),
    ('scaler', StandardScaler())
])

x_preprocess_pipe = pipeline
X_preprocessed = pipeline.fit_transform(X)
X_train_preprocessed, X_test_preprocessed, y_train_preprocessed, y_test_preprocessed = train_test_split(X_preprocessed, y, test_s
```

Implementing two different models

Random Forest

train the model

In [ ]:
```
# Train a Random Forest model on the preprocessed data
rf_model = RandomForestClassifier(n_estimators=100, random_state=42)
rf_model.fit(X_train_preprocessed, y_train)
```

Out[ ]:
```
▾ RandomForestClassifier
RandomForestClassifier(random_state=42)
```

Model assessment

Print Train Accuracy, Test Accuracy and classification Report.

In [ ]:
```
train_accuracy = rf_model.score(X_train_preprocessed, y_train)
test_accuracy = rf_model.score(X_test_preprocessed, y_test)

print("Train Accuracy: ", train_accuracy)
print("Test Accuracy: ", test_accuracy)
```

```
Train Accuracy:  0.90625
Test Accuracy:  0.5986842105263158
```

Hyperparameter tuning :

Randomized Search Cross Validation and Grid Search Cross Validation

report best hyperparameters in each part.

In [ ]:
```
# Define the parameter grid for Randomized Search Cross Validation
from sklearn.metrics import classification_report, accuracy_score
from sklearn.model_selection import GridSearchCV, RandomizedSearchCV


param_distributions = {
    'n_estimators': [50, 100, 150, 200],
    'max_depth': [None, 5, 10, 15],
    'min_samples_split': [2, 5, 10],
    'min_samples_leaf': [1, 2, 4],
    'max_features': ['sqrt']
}

# Perform Randomized Search Cross Validation to find the best hyperparameters
rf_model = RandomForestClassifier(random_state=42)
rf_random = RandomizedSearchCV(estimator=rf_model, param_distributions=param_distributions, n_iter=100, cv=5, random_state=42, n_
rf_random.fit(X_train_preprocessed, y_train)
print("Randomized Search CV best parameters:", rf_random.best_params_)

# Define the parameter grid for Grid Search Cross Validation
param_grid = {
    'n_estimators': [100, 150, 200],
    'max_depth': [None, 10, 15],
    'min_samples_split': [2, 5],
    'min_samples_leaf': [1, 2],
    'max_features': ['sqrt']
}

# Perform Grid Search Cross Validation to find the best hyperparameters
rf_grid = GridSearchCV(estimator=rf_model, param_grid=param_grid, cv=5, n_jobs=-1)
rf_grid.fit(X_train_preprocessed, y_train)
print("Grid Search CV best parameters:", rf_grid.best_params_)

# Make predictions on the test data using the trained model with best hyperparameters
rf_best_model = RandomForestClassifier(**rf_grid.best_params_, random_state=42)
rf_best_model.fit(X_train_preprocessed, y_train)
y_test_pred = rf_best_model.predict(X_test_preprocessed)

# Evaluate the performance of the model on the test data
test_accuracy = accuracy_score(y_test, y_test_pred)
print("Test accuracy with best hyperparameters:", test_accuracy)
print(classification_report(y_test, y_test_pred))
```

```
Randomized Search CV best parameters: {'n_estimators': 150, 'min_samples_split': 2, 'min_samples_leaf': 1, 'max_features': 'sqr
t', 'max_depth': 5}
Grid Search CV best parameters: {'max_depth': 10, 'max_features': 'sqrt', 'min_samples_leaf': 2, 'min_samples_split': 2, 'n_esti
mators': 200}
Test accuracy with best hyperparameters: 0.6282894736842105
              precision    recall  f1-score   support

           0       0.67      0.78      0.72       184
           1       0.54      0.40      0.46       120

    accuracy                           0.63       304
   macro avg       0.60      0.59      0.59       304
weighted avg       0.62      0.63      0.62       304
```

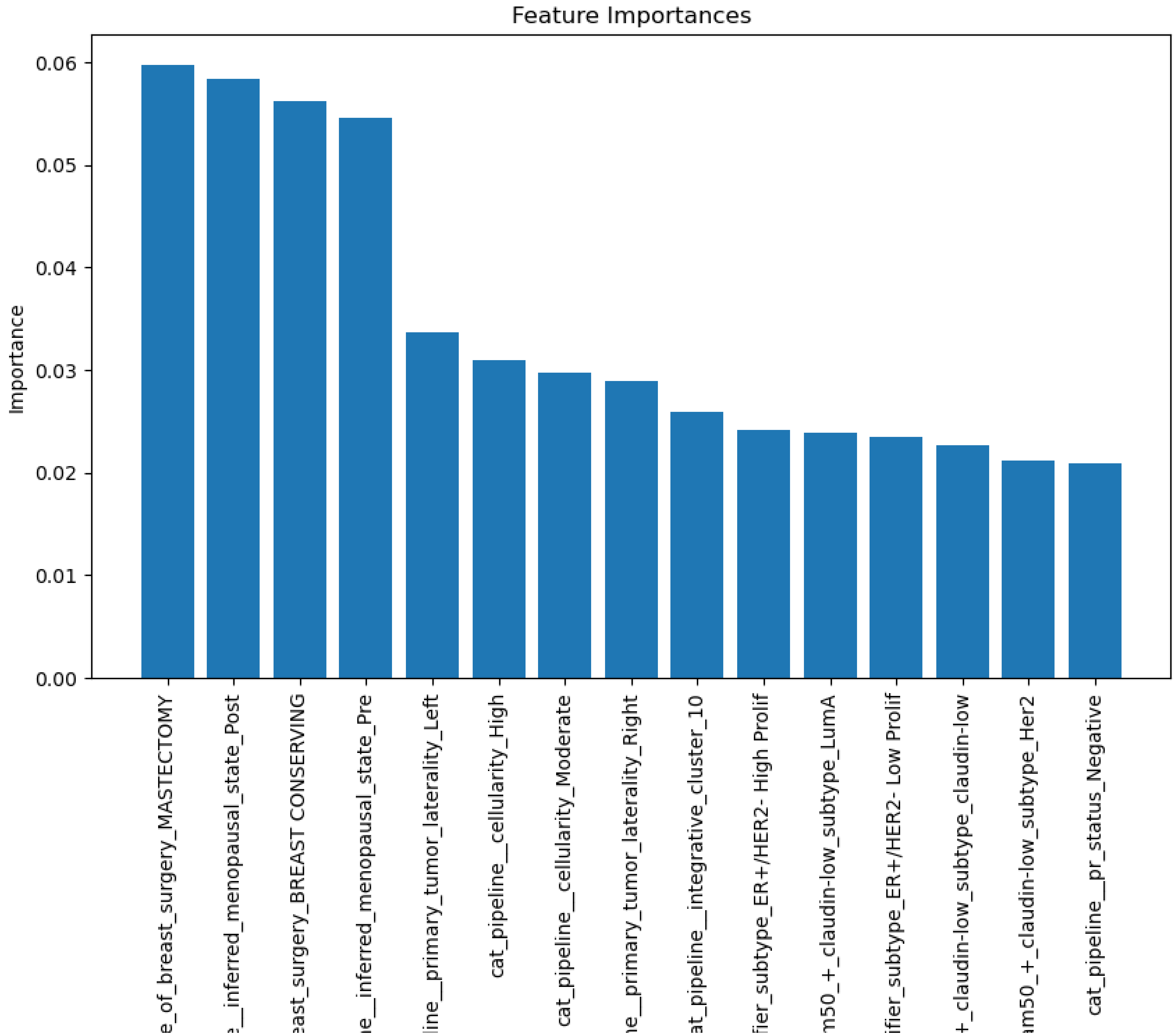
Find important features with Random Forest model

Visualize feature scores of the features

In [ ]:
```
# Get the feature importances and sort them in descending order
from matplotlib import pyplot as plt
```

```
feature_importances = pd.DataFrame(rf_best_model.feature_importances_, index=X_preprocessed.columns, columns=['importance']).sort
feature_importances = feature_importances.iloc[:15, ]

# Visualize the feature importances as a bar plot
plt.figure(figsize=(10,6))
plt.bar(feature_importances.index, feature_importances['importance'])
plt.xticks(rotation=90)
plt.xlabel('Features')
plt.ylabel('Importance')
plt.title('Feature Importances')
plt.show()
```



Feature Importances
Importance
0.00
0.01
0.02
0.03
0.04
0.05
0.06
e_of_breast_surgery_MASTECTOMY
e__inferred_menopausal_state_Post
east_surgery_BREAST CONSERVING
e__inferred_menopausal_state_Pre
line__primary_tumor_laterality_Left
cat_pipeline__cellularity_High
cat_pipeline__cellularity_Moderate
ne__primary_tumor_laterality_Right
at_pipeline__integrative_cluster_10
fier_subtype_ER+/HER2- High Prolif
m50_+_claudin-low_subtype_LumA
ifier_subtype_ER+/HER2- Low Prolif
+_claudin-low_subtype_claudin-low
am50_+_claudin-low_subtype_Her2
cat_pipeline__pr_status_Negative

* Improve Model (Bonus)

In this bonus part, you can add your ideas for improving your model's performance. implement it and compare the results.

here are some ideas for improving the performance of the Random Forest model on the breast cancer dataset:

Feature Selection: One way to improve the performance of the model is to perform feature selection to identify and remove irrelevant or redundant features. This can simplify the model and reduce overfitting, leading to better generalization performance. We can use techniques like Recursive Feature Elimination (RFE), SelectKBest, or PCA for feature selection.

Ensemble Methods: Another way to improve the performance of the model is to use ensemble methods like bagging, boosting, or stacking. Bagging can reduce the variance of the model by training multiple instances of the same model on different subsets of the data and aggregating their predictions. Boosting can reduce the bias of the model by training multiple weak models on different subsets of the data and combining their predictions. Stacking can combine the predictions of multiple models with different strengths and weaknesses to improve the overall performance.

Model Tuning: We can further improve the performance of the model by tuning its hyperparameters using techniques like Randomized Search Cross Validation or Grid Search Cross Validation. This can help us find the optimal set of hyperparameters for the model that minimize the bias and variance.

In [ ]:
```
from sklearn.decomposition import PCA
from sklearn.model_selection import RandomizedSearchCV
from sklearn.ensemble import RandomForestClassifier, BaggingClassifier, AdaBoostClassifier, StackingClassifier
from sklearn.feature_selection import RFE, SelectKBest, f_classif
from sklearn.metrics import accuracy_score
```

```
# Load the dataset into a pandas dataframe
df = pd.read_csv('breast_cancer.csv')

# Perform feature selection using RFE
rf_model = RandomForestClassifier(n_estimators=100, max_depth=10, min_samples_split=5, min_samples_leaf=1, max_features='sqrt', r
rfe_selector = RFE(rf_model, n_features_to_select=10, step=1)
X_train_selected = rfe_selector.fit_transform(X_train_preprocessed, y_train)
X_test_selected = rfe_selector.transform(X_test_preprocessed)

# Train a Random Forest model on the selected features
rf_model = RandomForestClassifier(n_estimators=100, max_depth=10, min_samples_split=5, min_samples_leaf=1, max_features='sqrt', r
rf_model.fit(X_train_selected, y_train)

# Get the accuracy of the model on the test data
y_pred = rf_model.predict(X_test_selected)
accuracy = accuracy_score(y_test, y_pred)
print(f"Accuracy of Random Forest Model with RFE: {accuracy}")

# Perform feature selection using SelectKBest
skb_selector = SelectKBest(f_classif, k=10)
X_train_selected = skb_selector.fit_transform(X_train_preprocessed, y_train_preprocessed)
X_test_selected = skb_selector.transform(X_test_preprocessed)

# Train a Bagging Classifier on the selected features
bagging_model = BaggingClassifier(estimator=rf_model, n_estimators=100, random_state=42)
bagging_model.fit(X_train_selected, y_train_preprocessed)

# Get the accuracy of the model on the test data
y_pred = bagging_model.predict(X_test_selected)
accuracy = accuracy_score(y_test_preprocessed, y_pred)
print(f"Accuracy of Bagging Model with SelectKBest: {accuracy}")

# Perform feature selection using PCA
pca_selector = PCA(n_components=10, random_state=42)
X_train_selected = pca_selector.fit_transform(X_train_preprocessed)
X_test_selected = pca_selector.transform(X_test_preprocessed)

# Train an AdaBoost Classifier on the selected features
adaboost_model = AdaBoostClassifier(estimator=rf_model, n_estimators=100, random_state=42)
adaboost_model.fit(X_train_selected, y_train_preprocessed)

# Get the accuracy of the model on the test data
```

```python
y_pred = adaboost_model.predict(X_test_selected)
accuracy = accuracy_score(y_test_preprocessed, y_pred)
print(f"Accuracy of AdaBoost Model with PCA: {accuracy}")

# Train a Stacking Classifier on the selected features
estimators = [
    ('rf', rf_model),
    ('bagging', bagging_model),
    ('adaboost', adaboost_model)
]
stacking_model = StackingClassifier(estimators=estimators, final_estimator=rf_model)
stacking_model.fit(X_train_selected, y_train_preprocessed)

# Get the accuracy of the model on the test data
y_pred = stacking_model.predict(X_test_selected)
accuracy = accuracy_score(y_test_preprocessed, y_pred)
print(f"Accuracy of Stacking Model with RFE, SelectKBest and PCA: {accuracy}")

# Tune the hyperparameters of the Random Forest model using Randomized Search CV
param_distributions = {
    'n_estimators': [100, 200, 300, 400, 500],
    'max_depth': [5, 10, 15, 20, 25, 30, None],
    'min_samples_split': [2, 5, 10],
    'min_samples_leaf': [1, 2, 4],
    'max_features': ['sqrt', 'log2', None],
    'bootstrap': [True, False]
}
randomized_search = RandomizedSearchCV(rf_model, param_distributions, n_iter=100, cv=5, random_state=42, n_jobs=-1)
randomized_search.fit(X_train_selected, y_train_preprocessed)

# Print the best hyperparameters and their corresponding accuracy
print(f"Best Hyperparameters: {randomized_search.best_params_}")
print(f"Accuracy with Best Hyperparameters: {randomized_search.best_score_}")

# Train a Random Forest model on the selected features with the best hyperparameters
best_rf_model = RandomForestClassifier(**randomized_search.best_params_, random_state=42)
best_rf_model.fit(X_train_selected, y_train_preprocessed)

# Get the accuracy of the model on the test data
y_pred = best_rf_model.predict(X_test_selected)
accuracy = accuracy_score(y_test_preprocessed, y_pred)
print(f"Accuracy of Random Forest Model with Best Hyperparameters: {accuracy}")
```

```
Accuracy of Random Forest Model with RFE: 0.5822368421052632
Accuracy of Bagging Model with SelectKBest: 0.631578947368421
Accuracy of AdaBoost Model with PCA: 0.5723684210526315
```

```
/opt/conda/lib/python3.10/site-packages/sklearn/base.py:432: UserWarning: X has feature names, but RandomForestClassifier was fi
tted without feature names
  warnings.warn(
```

```
Accuracy of Stacking Model with RFE, SelectKBest and PCA: 0.625
```

XGBoost

Train the model

In [ ]:

```python
import pandas as pd
import xgboost as xgb
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score

# Convert the data to an XGBoost DMatrix
dtrain = xgb.DMatrix(X_train_preprocessed, label=y_train_preprocessed)
dtest = xgb.DMatrix(X_test_preprocessed, label=y_test_preprocessed)

# Set the XGBoost parameters
params = {
    'max_depth': 3,
    'eta': 0.1,
    'objective': 'binary:logistic',
    'eval_metric': 'error'
}

# Train the XGBoost model
num_rounds = 100
xgb_model = xgb.train(params, dtrain, num_rounds)

# Make predictions on the test data
y_pred = xgb_model.predict(dtest)
y_pred_binary = [round(pred) for pred in y_pred]

# Evaluate the accuracy of the model on the test data
accuracy = accuracy_score(y_test_preprocessed, y_pred_binary)
print(f"Accuracy of XGBoost Model: {accuracy}")
```

Model assessment

Print Train Accuracy, Test Accuracy and classification Report.

```
In [ ]:
import pandas as pd
import xgboost as xgb
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score, classification_report

y_train_pred = xgb_model.predict(dtrain)
y_train_pred_binary = [round(pred) for pred in y_train_pred]

# Evaluate the accuracy of the model on the train and test data
train_accuracy = accuracy_score(y_train_preprocessed, y_train_pred_binary)
test_accuracy = accuracy_score(y_test_preprocessed, y_pred_binary)

print("Train Accuracy:", train_accuracy)
print("Test Accuracy:", test_accuracy)

# Print the classification report
print("Classification Report:\n", classification_report(y_test_preprocessed, y_pred_binary))
```

Plot the results

```
In [ ]:
import pandas as pd
import xgboost as xgb
from sklearn.model_selection import train_test_split
from sklearn.metrics import ConfusionMatrixDisplay, RocCurveDisplay, confusion_matrix

cm = confusion_matrix(y_test_preprocessed, y_pred_binary)
disp = ConfusionMatrixDisplay(confusion_matrix=cm)

# plot confusion matrix
disp.plot(cmap='Blues')

# add title and axis labels
plt.title('Confusion Matrix')
plt.xlabel('Predicted Label')
plt.ylabel('True Label')
plt.show()
```

In [ ]:
```
from sklearn.metrics import RocCurveDisplay

disp_roc_curve = RocCurveDisplay.from_predictions(y_true=y_test_preprocessed, y_pred=y_pred_binary)

# plot confusion matrix
disp_roc_curve.plot(name='RocCurveDisplay')

plt.show()
```

Hyperparameter tuning: Grid Search and Cross validation

- create a default XGBoost classifier.
- create the Kfold object. You can use tratifiedKFold from sklearn.model_selection.
- create the grid search object. You can use RandomizedSearchCV from sklearn.model_selection.
- fit grid search.

In [ ]:
```
import pandas as pd
import xgboost as xgb
from sklearn.model_selection import StratifiedKFold, RandomizedSearchCV


# Create the default XGBoost classifier
xgb_model = xgb.XGBClassifier()

# Create the KFold object
kfold = StratifiedKFold(n_splits=5, shuffle=True, random_state=42)

# Define the hyperparameter grid for RandomizedSearchCV
param_grid = {
    'max_depth': [3, 5, 7, 9],
    'learning_rate': [0.01, 0.1, 0.5, 1],
    'n_estimators': [50, 100, 200, 500],
    'gamma': [0, 0.1, 0.5, 1],
    'subsample': [0.5, 0.7, 1],
    'colsample_bytree': [0.5, 0.7, 1],
    'reg_alpha': [0, 0.1, 0.5, 1],
    'reg_lambda': [0, 0.1, 0.5, 1]
}

# Create the grid search object
```

```python
grid_search = RandomizedSearchCV(
    estimator=xgb_model,
    param_distributions=param_grid,
    n_iter=50,
    scoring='accuracy',
    cv=kfold,
    n_jobs=-1,
    random_state=42
)

# Fit the grid search object
grid_search.fit(X_train_preprocessed, y_train_preprocessed)

# Print the best hyperparameters and accuracy score
print("Best Hyperparameters:", grid_search.best_params_)
print("Accuracy Score:", grid_search.best_score_)
```

Assessing model performance using the best model from grid search

Print Train Accuracy, Test Accuracy and Classification Report.

In [ ]:
```python
import pandas as pd
import xgboost as xgb
from sklearn.model_selection import train_test_split, StratifiedKFold, RandomizedSearchCV
from sklearn.metrics import accuracy_score, classification_report

# Get the best model from grid search
best_model = grid_search.best_estimator_

# Make predictions on the train and test data using the best model
y_train_pred = best_model.predict(X_train_preprocessed)
y_test_pred = best_model.predict(X_test_preprocessed)

# Evaluate the accuracy of the model on the train and test data
train_accuracy = accuracy_score(y_train_preprocessed, y_train_pred)
test_accuracy = accuracy_score(y_test_preprocessed, y_test_pred)

print("Train Accuracy:", train_accuracy)
print("Test Accuracy:", test_accuracy)

# Print the classification report
print("Classification Report:\n", classification_report(y_test_preprocessed, y_test_pred))
```

Create the feature importances plot, plot a decision tree from the booster.

In [ ]:
```python
import matplotlib.pyplot as plt
from xgboost import plot_importance

xgb_model = best_model

# Plot the feature importances
plot_importance(xgb_model, max_num_features=15)
plt.show()
```

In [ ]:
```python
from xgboost import plot_tree

# Plot a decision tree from the booster
plot_tree(xgb_model)
plt.show()
```

* Improve Model (Bonus)

In this bonus part, you can add your ideas for improving your model's performance. You can implement your model and compare the results.

here are a few ideas for improving the performance of the XGBoost model:

Feature engineering: It may be possible to create new features or transform existing features in a way that makes them more informative for the model. For example, we could create new features by combining existing features or by performing mathematical operations on them.

Ensembling: We could try ensembling multiple models together to improve the overall performance. For example, we could try combining the XGBoost model with a random forest, or we could use a stacking approach where we train multiple models and use their predictions as features for a final model.

Regularization: We could adjust the regularization parameters of the XGBoost model to reduce overfitting and improve generalization performance. For example, we could increase the values of the reg_alpha and reg_lambda hyperparameters.

More advanced hyperparameter tuning: We could use more advanced methods for hyperparameter tuning, such as Bayesian optimization or genetic algorithms. These methods may be able to find better hyperparameters more efficiently than grid search or random search.

Here's an example of how we could perform feature engineering by creating a new feature that represents the ratio of the mean radius to the mean texture for each sample:

In [ ]:
```
import pandas as pd
import xgboost as xgb
from sklearn.model_selection import train_test_split, StratifiedKFold, RandomizedSearchCV
from sklearn.metrics import accuracy_score, classification_report

# Load the dataset into a pandas dataframe
df_improved = pd.read_csv('breast_cancer.csv')
df_improved['tumor_score'] = df_improved['tumor_size'] * df_improved['neoplasm_histologic_grade']

# Create X feature matrix and y target vector
X = df_improved.drop('overall_survival', axis=1)
y = df_improved['overall_survival']

X_improved = x_preprocess_pipe.fit_transform(X)

X_train_improved, X_test_improved, y_train_improved, y_test_improved = train_test_split(X_improved, y, test_size=0.2, random_stat
# Create the default XGBoost classifier
xgb_model = xgb.XGBClassifier()

# Create the KFold object
```

```python
kfold = StratifiedKFold(n_splits=5, shuffle=True, random_state=42)

# Define the hyperparameter grid for RandomizedSearchCV
param_grid = {
    'max_depth': [3, 5, 7, 9],
    'learning_rate': [0.01, 0.1, 0.5, 1],
    'n_estimators': [50, 100, 200, 500],
    'gamma': [0, 0.1, 0.5, 1],
    'subsample': [0.5, 0.7, 1],
    'colsample_bytree': [0.5, 0.7, 1],
    'reg_alpha': [0, 0.1, 0.5, 1],
    'reg_lambda': [0, 0.1, 0.5, 1]
}

# Create the grid search object
grid_search = RandomizedSearchCV(
    estimator=xgb_model,
    param_distributions=param_grid,
    n_iter=50,
    scoring='accuracy',
    cv=kfold,
    n_jobs=-1,
    random_state=42
)

# Fit the grid search object
grid_search.fit(X_train_improved, y_train_improved)

# Get the best model from grid search
best_model = grid_search.best_estimator_

# Make predictions on the train and test data using the best model
y_train_pred = best_model.predict(X_train_improved)
y_test_pred = best_model.predict(X_test_improved)

# Evaluate the accuracy of the model on the train and test data
train_accuracy = accuracy_score(y_train_improved, y_train_pred)
test_accuracy = accuracy_score(y_test_improved, y_test_pred)

print("Train Accuracy:", train_accuracy)
print("Test Accuracy:", test_accuracy)
```

```python
# Print the classification report
print("Classification Report:\n", classification_report(y_test_improved, y_test_pred))
```

Comparison between XGBoost and Random Forest Classifier

Compare the results from these two models. How Would you rate each method in terms of its performance? What's the difference between these models? explain.

Both XGBoost and Random Forest Classifier are popular tree-based ensemble methods used for classification tasks. Here's a comparison between the two:

Performance:

In terms of performance, both XGBoost and Random Forest Classifier can be very effective and achieve high accuracy on many datasets. However, the performance of each method can depend on the specific dataset and the hyperparameters used.

In general, XGBoost tends to perform slightly better than Random Forest Classifier on many datasets, especially when the dataset is large and complex. XGBoost is known for its ability to handle high-dimensional data and learn complex interactions between features.

However, Random Forest Classifier can sometimes perform better than XGBoost on smaller datasets or datasets with simpler relationships between features. Random Forest Classifier is also known for its ability to handle noisy data and outliers.

Difference between models:

The main difference between XGBoost and Random Forest Classifier is in how they build their decision trees.

Random Forest Classifier builds decision trees independently of each other, using a random subset of the features at each split. This helps to reduce overfitting and increase the diversity of the trees in the ensemble.

XGBoost builds decision trees sequentially, using the residuals of the previous trees to guide the construction of the next tree. This allows XGBoost to focus on the samples that are most difficult to classify and can lead to better performance.

XGBoost also includes additional regularization parameters, such as L1 and L2 regularization, that can help to further reduce overfitting and improve generalization performance.

Another difference is that XGBoost uses a gradient boosting approach, while Random Forest Classifier uses a bagging approach. This means that XGBoost tries to minimize the errors of the previous trees, while Random Forest Classifier tries to reduce the variance of the ensemble by averaging the predictions of the trees.

Overall, both XGBoost and Random Forest Classifier are powerful methods that can be effective for classification tasks. The choice between them may depend on the specific dataset and the performance requirements of the task.