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LECTURE:	Fall25-CS634 Data Mining

Data Mining: Final Term Project Report

Topic: A Comparative Analysis of Machine Learning Models for Diabetes Prediction.

1. Introduction:

Early prediction of diabetes is one of the biggest challenges in healthcare, as it allows doctors to identify high risk patients and offer timely care. Machine leaning therefore makes the process more efficient by learning the pattern from medical data to assist in classifying a person as either likely to have diabetes or not.

In this project, I focused on building and comparing different machine learning models to perform binary classification, with each patient belonging to one of two categories. 0 - Non-diabetic or 1 – Diabetic. Binary classification forms an important aspect in medical applications as decisions between two classes can have a direct implication in diagnosis, treatment planning, and patient monitoring. I implemented the Pima Indians Diabetes dataset, which consists of several health-related measurements including glucose level, BMI, Insulin, age and blood pressure. These features are common indicators used in diabetes screenings. To understand how various types of algorithms perform on this dataset, I implemented and compared three models: Random Forest - the necessary ensemble-based algorithm, Support Vector Machine (SVM) is a classic machine learning classifier and Long Short-Term Memory (LSTM) - a deep learning model.

All models were evaluated by 10-fold stratified cross-validation along with a wide range of performance metrics. The objective of this project is to analyze how classical machine learning, ensemble methods, and deep learning differ in terms of accuracy, consistency, and overall predictive capability related to diabetes classification.

2. Dataset

2.1 Dataset Name and Source:

For this project, I have used the Pima Indians Diabetes Dataset, which is very popular for medical predictions or any kind of binary classification problem. The dataset consists of diagnostic measurements collected from adult female patients of Pima Indian descent.
Dataset link: https://www.kaggle.com/datasets/uciml/pima-indians-diabetes-database.

2.2 Dataset Description:

The dataset contains 400 patient records and a total of 9 attributes. Eight of these represent medical predictor variables, and the final attribute represents the target in binary form.

Features(X):Pregnancies,Glucose,BloodPressure,SkinThickness,Insulin,BMI,DiabetesPedigreeFunction, Age

Target Variable (y): 0 - non-diabetic, 1 – Diabetic. This makes the problem a binary classification task.

2.3 Class Distribution:

The dataset is moderately imbalanced:152 diabetic cases (38%), 248 non-diabetic cases (62%) Because of this imbalance, performance metrics such as Balanced Accuracy, TSS, and HSS are especially important for evaluating the models**.**

2.4 Preprocessing Steps:

Preprocessing of the dataset consisted of the following steps to ensure clean and reliable input for model training:

a) **Handling Invalid Zero Values:** Some of the medical features contain impossible zero values in real clinical settings, such as Glucose = 0. These were regarded as missing values and subject to median imputation. This was done for: Glucose, Blood Pressure, Skin Thickness, Insulin, BMI.

b) **Feature and Label Splitting:**

X = the eight medical predictor features

Y = Outcome column

c) **Stratified Train/Test Split:** A stratified split was used to keep the same class proportions of the original dataset in both the training and testing sets.

d) **Standardization:** All features were standardized using StandardScaler, which normalizes the data by removing the mean and scaling to unit variance. This step helps improve model performance, especially for SVM and neural networks.

2.5 Why this dataset was chosen:

- Widely used for research on predicting diabetes.
- It is small and computationally efficient for 10-fold cross-validation
- It contains clinically meaningful features.
- It is ideal for comparing classical ML, ensemble models, and deep learning approaches side by side.

3. Project Overview:

The project proposes the development and comparison of several machine learning models for the prediction of diabetes using the Pima Indians Diabetes dataset. In general, the workflow is divided into three key stages: data preprocessing, model implementation, and performance evaluation. Each stage plays an important role in the preparation of the dataset, training models, and analyzing their behavior.

3.1 Data Preprocessing

The dataset was cleaned and prepared before training the models by taking care of quality input. The preprocessing step involved:

- Handling invalid zero values in medical features using median imputation
- Separating features and labels
- Applying StandardScaler to normalize all numerical attributes
- Using stratified sampling to maintain class balance during splitting.

3.2 Model Implementation and Optimization

For the project, three different models were developed and optimized:

a) Random Forest Classifier:

- An ensemble learning algorithm with a tree-based structure.
- Hyperparameters tuned using GridSearchCV
- Parameters optimized: n_estimators, min_samples_split

b) Support Vector Machine (SVM):

- A classic machine learning model
- Uses a linear kernel for this dataset
- The regularization parameter C was optimized by using grid search.

c) Long Short-Term Memory Network:

- A deep learning model using recurrent neural networks
- Architecture: One LSTM layer with 64 units, Sigmoid-activated dense output layer, Binary cross-entropy loss and Adam optimizer.

3.3 Performance Analysis and Comparison

- 10-fold cross-validation ensures equal evaluation across the dataset.
- Calculating the manual metrics in detail: TP, TN, FP, FN, Accuracy, Recall, Precision, F1, Balanced Accuracy, TSS, HSS, and Error Rate.
- ROC and AUC analysis for discriminative performance.
- Brier Score to assess probability calibration.

4. Algorithms Overview:

In this project, three machine learning algorithms were evaluated: Random Forest, SVM, and LSTM. This was done to gather an understanding of the performance of different modeling approaches to diabetes prediction problem. These represent three distinct categories of machine learning: ensemble methods, classical machine learning, and deep learning.

Random Forest is an ensemble-based algorithm that constructs multiple decision trees during training and combines their outputs to give the final prediction. Each tree is trained using a randomly selected subset of data and features, which is known as bootstrap sampling. This randomness reduces overfitting, improves model stability, and allows the Random Forest to capture non-linear patterns within the data. Given that the Pima Diabetes dataset contains several interacting medical features, Random Forest is very suitable for this problem. In this project, some important hyperparameters such as the number of trees (n_estimators) and the minimum number of samples required to split a node (min_samples_split) were fine-tuned using GridSearchCV to improve predictive accuracy.

Support Vector Machine is one of the classic algorithms in machine learning, the goal of which is to find the optimal hyperplane that will serve as the best separator between the two classes, namely diabetic and non-diabetic patients. The SVM is thus able to implement robust generalization, even with limited data, by maximizing the margin between the two classes. Thus, this model works rather well when the data are approximately linearly separable. Fortunately, this characteristic holds true for this dataset. A linear kernel was implemented for this project, while the regularization parameter C was tuned within the model to balance the trade-off between maximizing the margin and minimizing the classification error.

Long Short-Term Memory (LSTM) is a type of RNN specifically designed to learn long-term dependencies using memory cells and gating. While LSTMs have traditionally been used with sequential or time-series data, they are still able to model complex relationships between non-sequential features by learning internal representations of the data. The LSTM model implemented for this project uses a single layer LSTM containing 64 units, with a dense output layer that utilizes sigmoid activation, allowing for binary classification. It was trained on binary cross-entropy loss with the Adam optimizer. The use of LSTM here allows the comparison of deep learning against machine learning on this dataset. A holisticness three algorithms provide a holistic comparison across classical ML, ensemble learning, and deep learning. Their dissimilarities in structure and learning capability help indicate which type of models perform best for medical prediction tasks like diabetes classification.

5. Technical Implementation Details:

a) Data Processing Pipeline
- Missing value imputation
- Feature standardization
- Train-test splitting

b) Model Training Framework
- Cross-validation implementation
- Hyperparameter optimization
- Performance metric calculation

c) Evaluation System
- Comprehensive metrics calculation
- ROC curve generation
- Statistical analysis of results

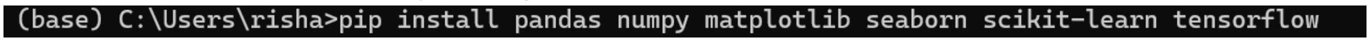
Tutorial to run the .py file in your device

Prerequisites:

- Make sure the Datasets (CSV files) are in same directory.
- The Naming convention should be same as it is in the zip file/ folder/ GitHub.
- The Dataset consists of 400 records; hence it may take a while to process.
- Make sure the python environment is set up beforehand.

Step 1: Set up the Environments.

- Ensure you have installed Python on your system.
- Install the required Libraries by running.



```
(base) C:\Users\risha>pip install pandas numpy matplotlib seaborn scikit-learn tensorflow
```

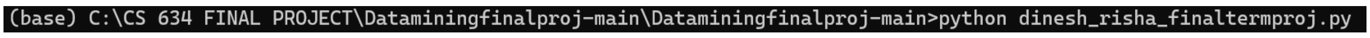
Step 2: Prepare the data files.

Make sure you have the following CSV files are in the same directory and with same naming convention as the script. **“**pima_diabetes_400**”**
Note: *The Dataset is taken from Pima Indian Healthcare system.*

Step 3: Run the program.

- Check if the Python file is saved as, e.g.: dinesh_risha_Final_Term_Project.py.
- Open a terminal or command prompt.
- Navigate to the directory containing the Python file and CSV files, Type Command: Cd /d

  “Path of the file”
- Run the script by entering:



```
(base) C:\CS 634 FINAL PROJECT\Dataminingfinalproj-main\Dataminingfinalproj-main>python dinesh_risha_finaltermproj.py
```

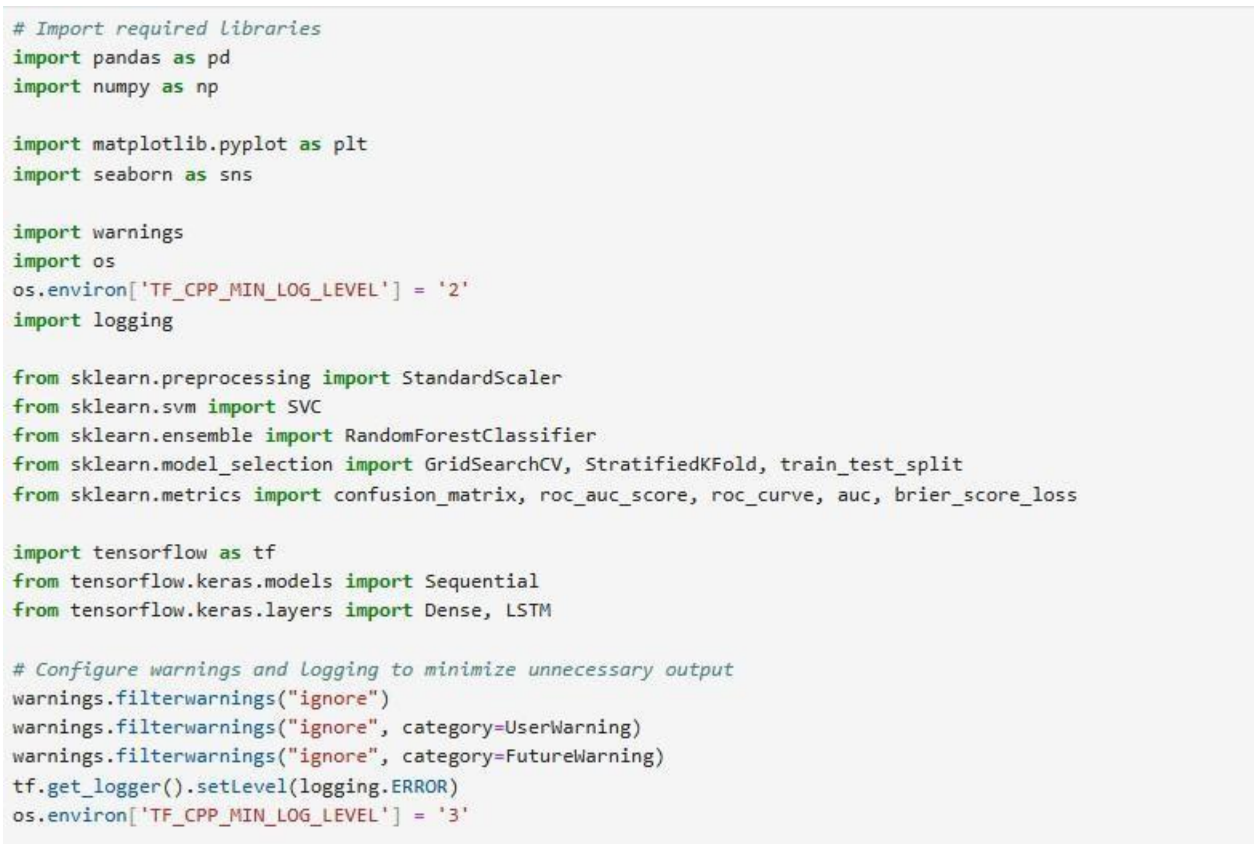
6. Implementation of Code:

6.1 Importing the packages and libraries that are required for the project.

This cell imports the necessary libraries:

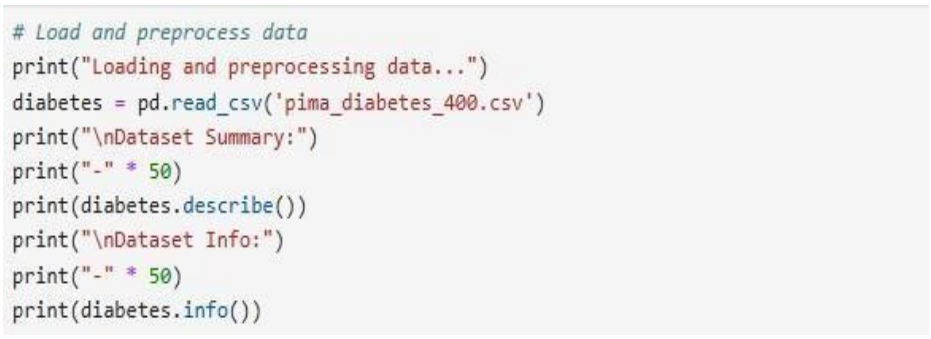
- Basic Data Processing and Analysis: pandas, numpy.
- Visualization Libraries: matplotlib, seaborn.
- Warning Suppression
- Scikit-learn Components: StandardScaler, SVC, RandomForestClassifier, GridSearchCV, StratifiedKFold, train_test_split, confusion_matrix, roc_auc_score, roc_curve, auc, brier_score_loss..

- TensorFlow and Environment Settings: Sequential, Dense, LSTM

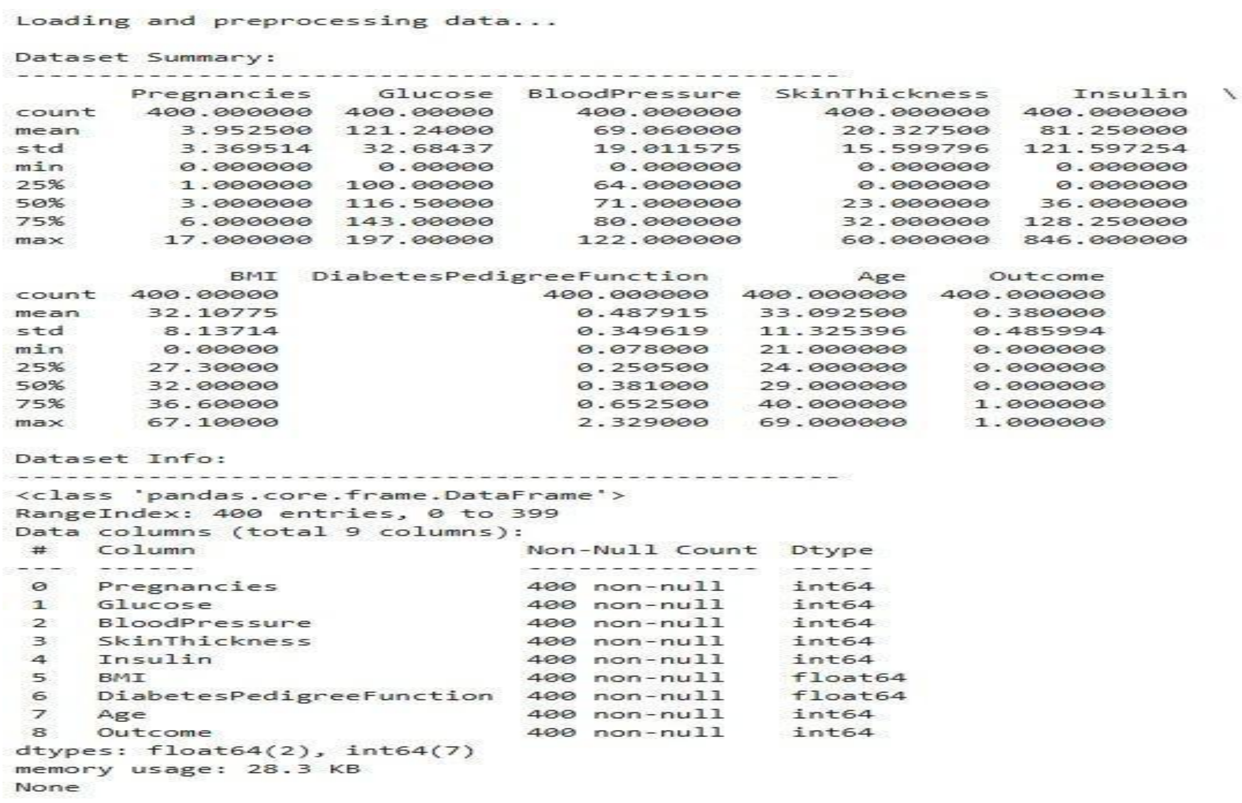


```python
# Import required libraries
import pandas as pd
import numpy as np

import matplotlib.pyplot as plt
import seaborn as sns

import warnings
import os
os.environ['TF_CPP_MIN_LOG_LEVEL'] = '2'
import logging

from sklearn.preprocessing import StandardScaler
from sklearn.svm import SVC
from sklearn.ensemble import RandomForestClassifier
from sklearn.model_selection import GridSearchCV, StratifiedKFold, train_test_split
from sklearn.metrics import confusion_matrix, roc_auc_score, roc_curve, auc, brier_score_loss

import tensorflow as tf
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Dense, LSTM

# Configure warnings and logging to minimize unnecessary output
warnings.filterwarnings("ignore")
warnings.filterwarnings("ignore", category=UserWarning)
warnings.filterwarnings("ignore", category=FutureWarning)
tf.get_logger().setLevel(logging.ERROR)
os.environ['TF_CPP_MIN_LOG_LEVEL'] = '3'
```

6.2 Data Loading and Processing: Loads the diabetes dataset from 'pima_diabetes_400.csv' and creates a pandas Data Frame for data manipulation.

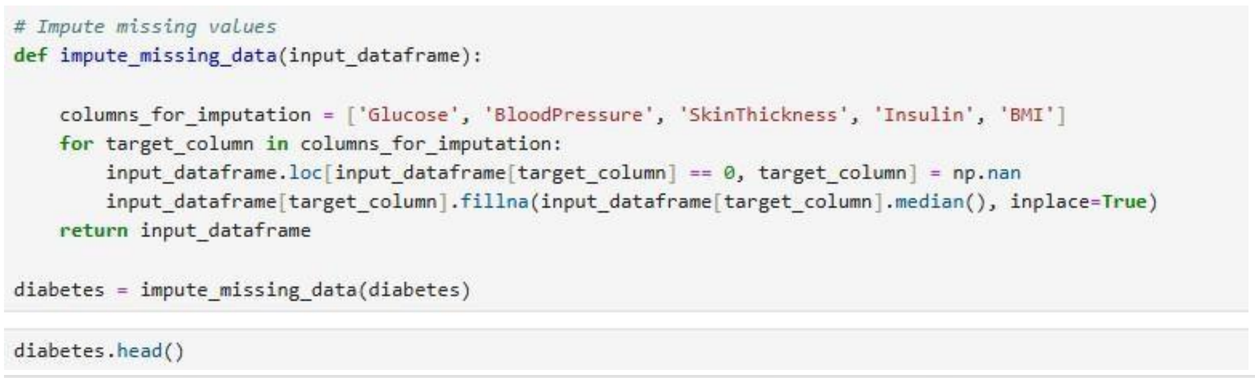


```python
# Load and preprocess data
print("Loading and preprocessing data...")
diabetes = pd.read_csv('pima_diabetes_400.csv')
print("\nDataset Summary:")
print("-" * 50)
print(diabetes.describe())
print("\nDataset Info:")
print("-" * 50)
print(diabetes.info())
```



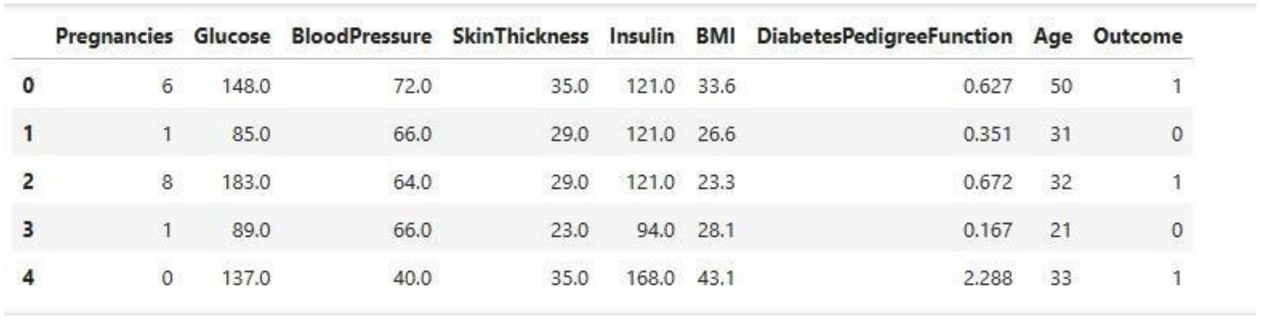
```
Loading and preprocessing data...

Dataset Summary:
--------------------------------------------------
       Pregnancies    Glucose  BloodPressure  SkinThickness     Insulin  \
count   400.000000  400.00000     400.000000     400.000000  400.000000
mean      3.952500  121.24000      69.060000      20.327500   81.250000
std       3.369514   32.68437      19.011575      15.599796  121.597254
min       0.000000    0.00000       0.000000       0.000000    0.000000
25%       1.000000  100.00000      64.000000       0.000000    0.000000
50%       3.000000  116.50000      71.000000      23.000000   36.000000
75%       6.000000  143.00000      80.000000      32.000000  128.250000
max      17.000000  197.00000     122.000000      60.000000  846.000000

             BMI  DiabetesPedigreeFunction         Age     Outcome
count  400.00000                400.000000  400.000000  400.000000
mean    32.10775                  0.487915   33.092500    0.380000
std      8.13714                  0.349619   11.325396    0.485994
min      0.00000                  0.078000   21.000000    0.000000
25%     27.30000                  0.250500   24.000000    0.000000
50%     32.00000                  0.381000   29.000000    0.000000
75%     36.60000                  0.652500   40.000000    1.000000
max     67.10000                  2.329000   69.000000    1.000000

Dataset Info:
--------------------------------------------------
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 400 entries, 0 to 399
Data columns (total 9 columns):
 #   Column                    Non-Null Count  Dtype
---  ------                    --------------  -----
 0   Pregnancies               400 non-null    int64
 1   Glucose                   400 non-null    int64
 2   BloodPressure             400 non-null    int64
 3   SkinThickness             400 non-null    int64
 4   Insulin                   400 non-null    int64
 5   BMI                       400 non-null    float64
 6   DiabetesPedigreeFunction  400 non-null    float64
 7   Age                       400 non-null    int64
 8   Outcome                   400 non-null    int64
dtypes: float64(2), int64(7)
memory usage: 28.3 KB
None
```

6.3 Missing Value Imputation Function: The function handles missing values in medical measurements that are incorrectly recorded as zeros in the diabetes dataset. Since medical measurements like glucose or blood pressure cannot be zero in living patients, these values are treated as missing data and replaced with meaningful estimates.



```
# Impute missing values
def impute_missing_data(input_dataframe):

    columns_for_imputation = ['Glucose', 'BloodPressure', 'SkinThickness', 'Insulin', 'BMI']
    for target_column in columns_for_imputation:
        input_dataframe.loc[input_dataframe[target_column] == 0, target_column] = np.nan
        input_dataframe[target_column].fillna(input_dataframe[target_column].median(), inplace=True)
    return input_dataframe

diabetes = impute_missing_data(diabetes)
```

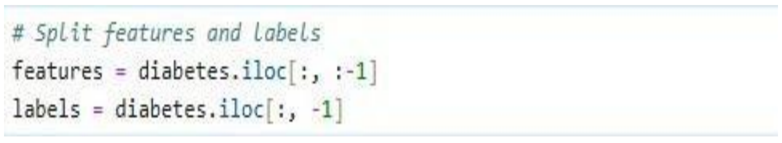
```
diabetes.head()
```



	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148.0	72.0	35.0	121.0	33.6	0.627	50	1
1	1	85.0	66.0	29.0	121.0	26.6	0.351	31	0
2	8	183.0	64.0	29.0	121.0	23.3	0.672	32	1
3	1	89.0	66.0	23.0	94.0	28.1	0.167	21	0
4	0	137.0	40.0	35.0	168.0	43.1	2.288	33	1

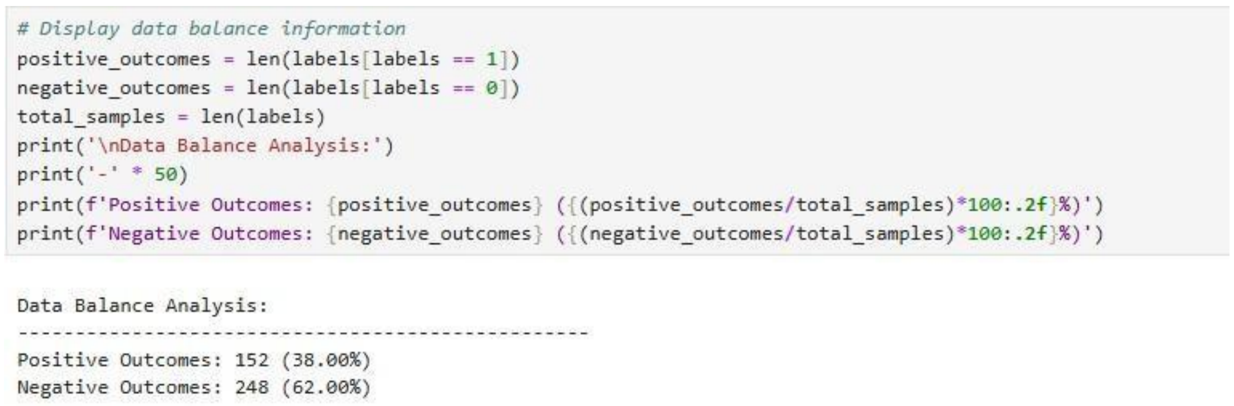
6.4 Features and Label Splitting: The code separates the diabetes dataset into two components:

Features (X): Input variables used to make predictions and Labels (y): Target variable to be predicted



```
# Split features and labels
features = diabetes.iloc[:, :-1]
labels = diabetes.iloc[:, -1]
```

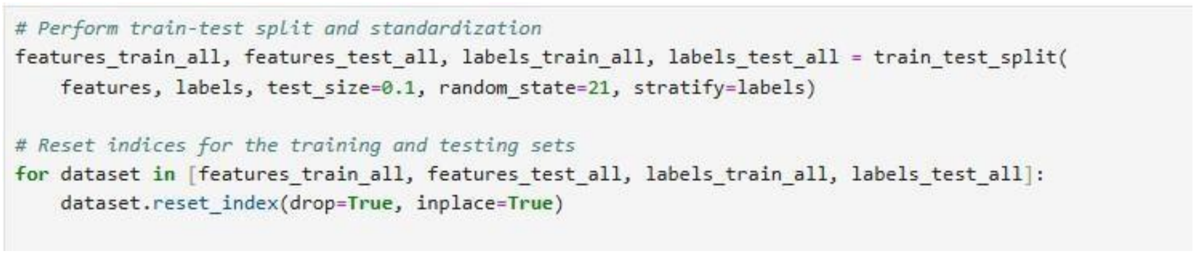
6.5 Data Balance Information :



```
# Display data balance information
positive_outcomes = len(labels[labels == 1])
negative_outcomes = len(labels[labels == 0])
total_samples = len(labels)
print('\nData Balance Analysis:')
print('-' * 50)
print(f'Positive Outcomes: {positive_outcomes} ({(positive_outcomes/total_samples)*100:.2f}%)')
print(f'Negative Outcomes: {negative_outcomes} ({(negative_outcomes/total_samples)*100:.2f}%)')
```

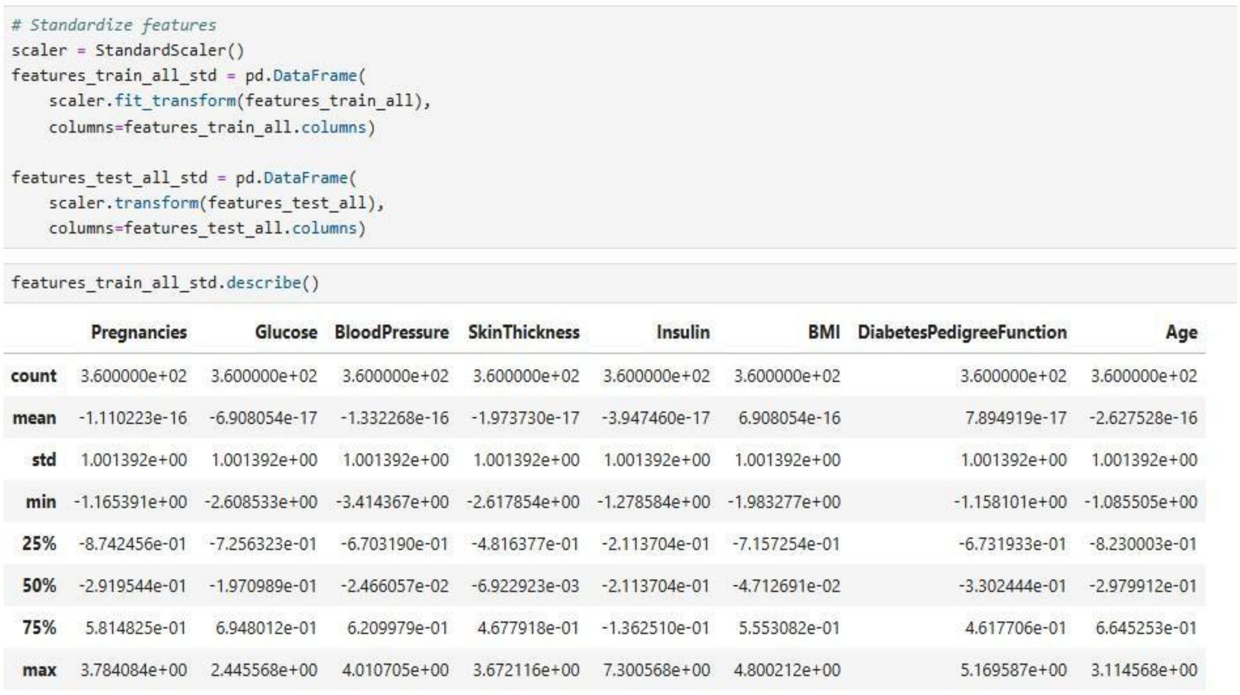
```
Data Balance Analysis:
--------------------------------------------------
Positive Outcomes: 152 (38.00%)
Negative Outcomes: 248 (62.00%)
```

6.6 Train Test Split: The code splits the dataset into training and testing sets while maintaining the class distribution of the target variable.



```python
# Perform train-test split and standardization
features_train_all, features_test_all, labels_train_all, labels_test_all = train_test_split(
    features, labels, test_size=0.1, random_state=21, stratify=labels)

# Reset indices for the training and testing sets
for dataset in [features_train_all, features_test_all, labels_train_all, labels_test_all]:
    dataset.reset_index(drop=True, inplace=True)
```

6.7 Feature Standardization: The code standardizes feature values by removing the mean and scaling to unit variance, which is essential for machine learning algorithms to perform optimally.



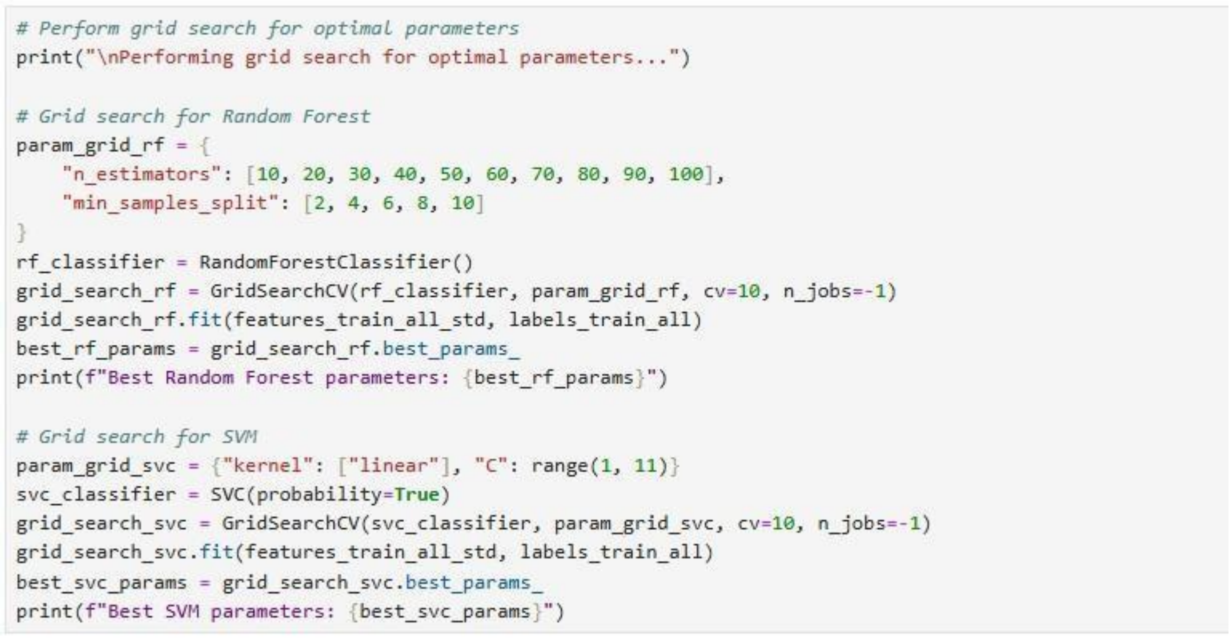
```python
# Standardize features
scaler = StandardScaler()
features_train_all_std = pd.DataFrame(
    scaler.fit_transform(features_train_all),
    columns=features_train_all.columns)

features_test_all_std = pd.DataFrame(
    scaler.transform(features_test_all),
    columns=features_test_all.columns)
```

```python
features_train_all_std.describe()
```

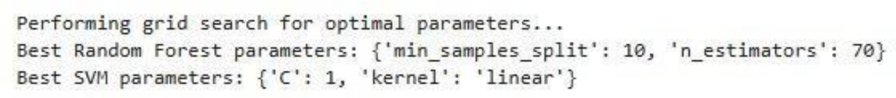
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age
count	3.600000e+02	3.600000e+02	3.600000e+02	3.600000e+02	3.600000e+02	3.600000e+02	3.600000e+02	3.600000e+02
mean	-1.110223e-16	-6.908054e-17	-1.332268e-16	-1.973730e-17	-3.947460e-17	6.908054e-16	7.894919e-17	-2.627528e-16
std	1.001392e+00	1.001392e+00	1.001392e+00	1.001392e+00	1.001392e+00	1.001392e+00	1.001392e+00	1.001392e+00
min	-1.165391e+00	-2.608533e+00	-3.414367e+00	-2.617854e+00	-1.278584e+00	-1.983277e+00	-1.158101e+00	-1.085505e+00
25%	-8.742456e-01	-7.256323e-01	-6.703190e-01	-4.816377e-01	-2.113704e-01	-7.157254e-01	-6.731933e-01	-8.230003e-01
50%	-2.919544e-01	-1.970989e-01	-2.466057e-02	-6.922923e-03	-2.113704e-01	-4.712691e-02	-3.302444e-01	-2.979912e-01
75%	5.814825e-01	6.948012e-01	6.209979e-01	4.677918e-01	-1.362510e-01	5.553082e-01	4.617706e-01	6.645253e-01
max	3.784084e+00	2.445568e+00	4.010705e+00	3.672116e+00	7.300568e+00	4.800212e+00	5.169587e+00	3.114568e+00

6.8 Hyperparameter Optimization:

- Implements a hyperparameter optimization process for Random Forest and Support Vector Machine (SVM) classifiers in a diabetes prediction system.
- The primary objective is to identify the optimal configuration of model parameters that maximize prediction performance while maintaining computational efficiency.
- The optimization process employs GridSearchCV from scikit-learn to perform an exhaustive search over specified parameter ranges.



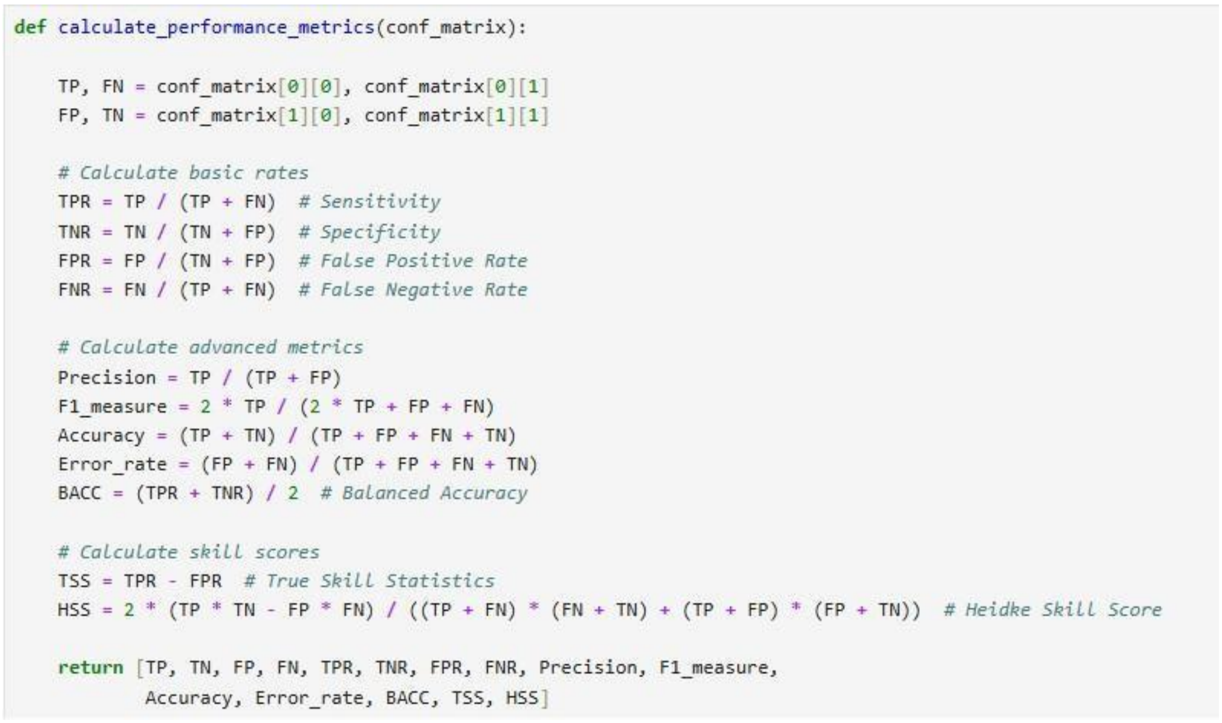
```python
# Perform grid search for optimal parameters
print("\nPerforming grid search for optimal parameters...")

# Grid search for Random Forest
param_grid_rf = {
    "n_estimators": [10, 20, 30, 40, 50, 60, 70, 80, 90, 100],
    "min_samples_split": [2, 4, 6, 8, 10]
}
rf_classifier = RandomForestClassifier()
grid_search_rf = GridSearchCV(rf_classifier, param_grid_rf, cv=10, n_jobs=-1)
grid_search_rf.fit(features_train_all_std, labels_train_all)
best_rf_params = grid_search_rf.best_params_
print(f"Best Random Forest parameters: {best_rf_params}")

# Grid search for SVM
param_grid_svc = {"kernel": ["linear"], "C": range(1, 11)}
svc_classifier = SVC(probability=True)
grid_search_svc = GridSearchCV(svc_classifier, param_grid_svc, cv=10, n_jobs=-1)
grid_search_svc.fit(features_train_all_std, labels_train_all)
best_svc_params = grid_search_svc.best_params_
print(f"Best SVM parameters: {best_svc_params}")
```



```
Performing grid search for optimal parameters...
Best Random Forest parameters: {'min_samples_split': 10, 'n_estimators': 70}
Best SVM parameters: {'C': 1, 'kernel': 'linear'}
```

6.9 Classification Metrics Calculator:

- This function calculates classification performance metrics from a binary confusion matrix.
- It is designed for evaluating binary classification models in machine learning applications.
- The metrics provided help assess model performance across different aspects including accuracy, precision, recall, and various skill scores, enabling thorough model evaluation and comparison

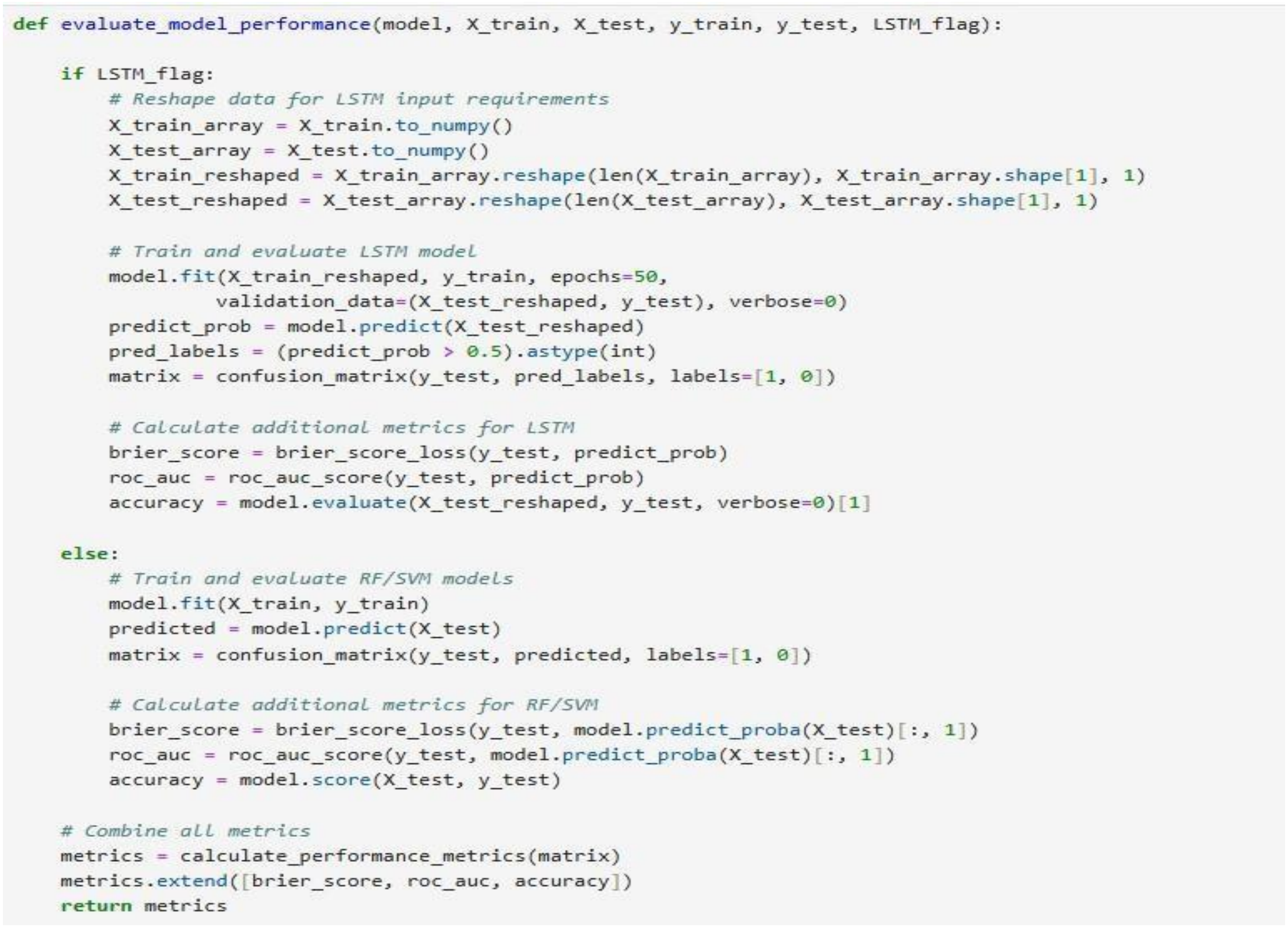


```python
def calculate_performance_metrics(conf_matrix):

    TP, FN = conf_matrix[0][0], conf_matrix[0][1]
    FP, TN = conf_matrix[1][0], conf_matrix[1][1]

    # Calculate basic rates
    TPR = TP / (TP + FN)  # Sensitivity
    TNR = TN / (TN + FP)  # Specificity
    FPR = FP / (TN + FP)  # False Positive Rate
    FNR = FN / (TP + FN)  # False Negative Rate

    # Calculate advanced metrics
    Precision = TP / (TP + FP)
    F1_measure = 2 * TP / (2 * TP + FP + FN)
    Accuracy = (TP + TN) / (TP + FP + FN + TN)
    Error_rate = (FP + FN) / (TP + FP + FN + TN)
    BACC = (TPR + TNR) / 2  # Balanced Accuracy

    # Calculate skill scores
    TSS = TPR - FPR  # True Skill Statistics
    HSS = 2 * (TP * TN - FP * FN) / ((TP + FN) * (FN + TN) + (TP + FP) * (FP + TN))  # Heidke Skill Score

    return [TP, TN, FP, FN, TPR, TNR, FPR, FNR, Precision, F1_measure,
            Accuracy, Error_rate, BACC, TSS, HSS]
```

6.10 Model Evaluation Function:

- Trains a machine learning model and evaluates its performance using multiple metrics.
- This function handles both standard ML models and LSTM neural networks, performing appropriate preprocessing and evaluation for each type.

- The function supports binary classification tasks and provides evaluation metrics including confusion matrix- based metrics, ROC-AUC, and Brier score.



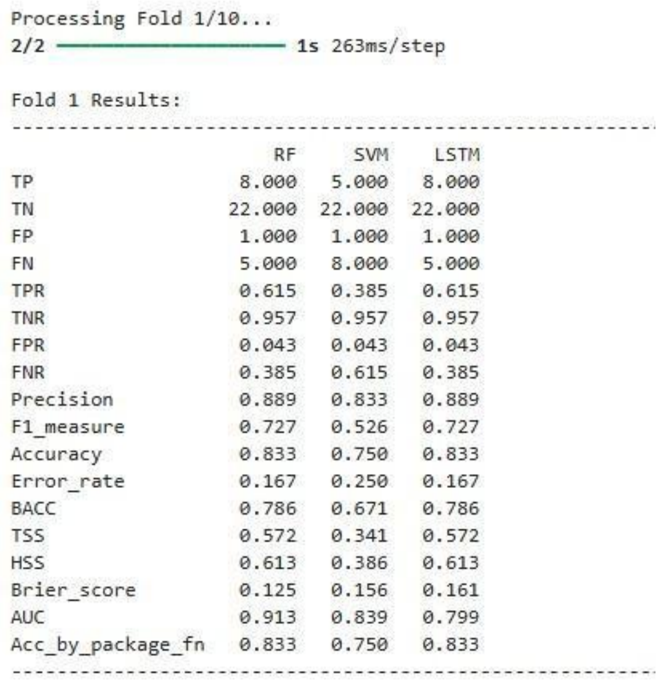
```
def evaluate_model_performance(model, X_train, X_test, y_train, y_test, LSTM_flag):

    if LSTM_flag:
        # Reshape data for LSTM input requirements
        X_train_array = X_train.to_numpy()
        X_test_array = X_test.to_numpy()
        X_train_reshaped = X_train_array.reshape(len(X_train_array), X_train_array.shape[1], 1)
        X_test_reshaped = X_test_array.reshape(len(X_test_array), X_test_array.shape[1], 1)

        # Train and evaluate LSTM model
        model.fit(X_train_reshaped, y_train, epochs=50,
                  validation_data=(X_test_reshaped, y_test), verbose=0)
        predict_prob = model.predict(X_test_reshaped)
        pred_labels = (predict_prob > 0.5).astype(int)
        matrix = confusion_matrix(y_test, pred_labels, labels=[1, 0])

        # Calculate additional metrics for LSTM
        brier_score = brier_score_loss(y_test, predict_prob)
        roc_auc = roc_auc_score(y_test, predict_prob)
        accuracy = model.evaluate(X_test_reshaped, y_test, verbose=0)[1]

    else:
        # Train and evaluate RF/SVM models
        model.fit(X_train, y_train)
        predicted = model.predict(X_test)
        matrix = confusion_matrix(y_test, predicted, labels=[1, 0])

        # Calculate additional metrics for RF/SVM
        brier_score = brier_score_loss(y_test, model.predict_proba(X_test)[:, 1])
        roc_auc = roc_auc_score(y_test, model.predict_proba(X_test)[:, 1])
        accuracy = model.score(X_test, y_test)

    # Combine all metrics
    metrics = calculate_performance_metrics(matrix)
    metrics.extend([brier_score, roc_auc, accuracy])
    return metrics
```

6.11 Cross Validation Function:

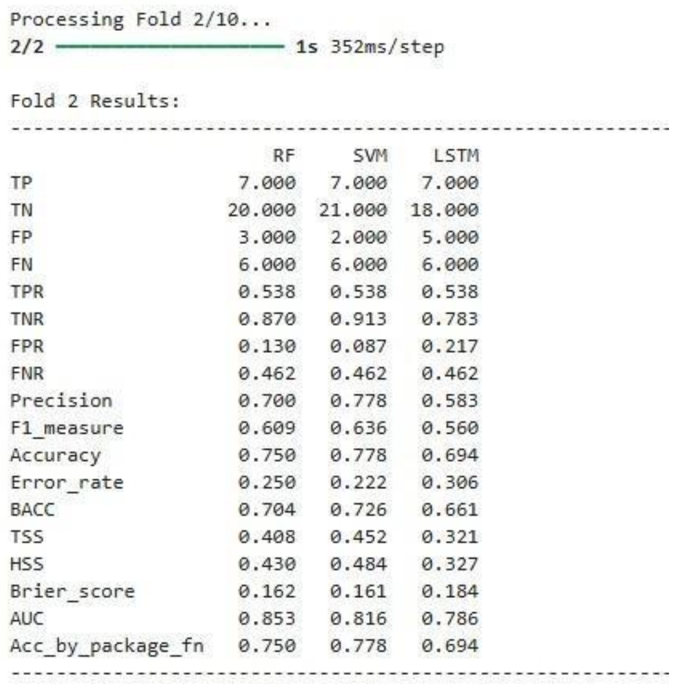
- Function for performing stratified k-fold cross-validation across multiple models simultaneously.
- Supports both traditional ML models and deep learning models (LSTM), handling all necessary preprocessing and metric collection.
- It also provides progress tracking, error handling, and detailed performance metrics for model comparison and evaluation.

```python
# Initialize cross-validation
cv_stratified = StratifiedKFold(n_splits=10, shuffle=True, random_state=21)
metrics_lists = {
    'RF': [],
    'SVM': [],
    'LSTM': []
}

# Initialize best_models which helps in maintaining the best performing model for each algorithm
best_models = {
    'RF': None,
    'SVM': None,
    'LSTM': None
}

def run_single_fold(fold_num, train_idx, test_idx):
    global best_models  # Add this line to access global variable
    print(f"\nProcessing Fold {fold_num + 1}/10...")

    # Split data for current fold
    features_train = features_train_all_std.iloc[train_idx]
    features_test = features_train_all_std.iloc[test_idx]
    labels_train = labels_train_all.iloc[train_idx]
    labels_test = labels_train_all.iloc[test_idx]

    # Initialize models
    models = {
        'RF': RandomForestClassifier(**best_rf_params),
        'SVM': SVC(**best_svc_params, probability=True),
        'LSTM': Sequential([
            LSTM(64, activation='relu', input_shape=(8, 1), return_sequences=False),
            Dense(1, activation='sigmoid')
        ])
    }

    # Compile LSTM
    models['LSTM'].compile(loss='binary_crossentropy', optimizer='adam', metrics=['accuracy'])

    # Train and evaluate each model
    current_fold_metrics = {}
    for name, model in models.items():
        #print(f"Training {name}...", end=' ')
        metrics = evaluate_model_performance(
            model, features_train, features_test,
            labels_train, labels_test,
            name == 'LSTM'
        )
        metrics_lists[name].append(metrics)
        current_fold_metrics[name] = metrics

        # Update best model if this fold's accuracy is better
        if best_models[name] is None or metrics[10] > best_models[name]['accuracy']:  # metrics[10] is accuracy
            best_models[name] = {
                'model': model,
                'accuracy': metrics[10]
            }
        #print("Done")

    # Display current fold metrics
    metric_columns = ['TP', 'TN', 'FP', 'FN', 'TPR', 'TNR', 'FPR', 'FNR',
                      'Precision', 'F1_measure', 'Accuracy', 'Error_rate', 'BACC',
                      'TSS', 'HSS', 'Brier_score', 'AUC', 'Acc_by_package_fn']

    df = pd.DataFrame(current_fold_metrics, index=metric_columns)
    print(f"\nFold {fold_num + 1} Results:")
    print("-" * 100)
    print(df.round(3).to_string())
    print("-" * 100)

    return current_fold_metrics
```

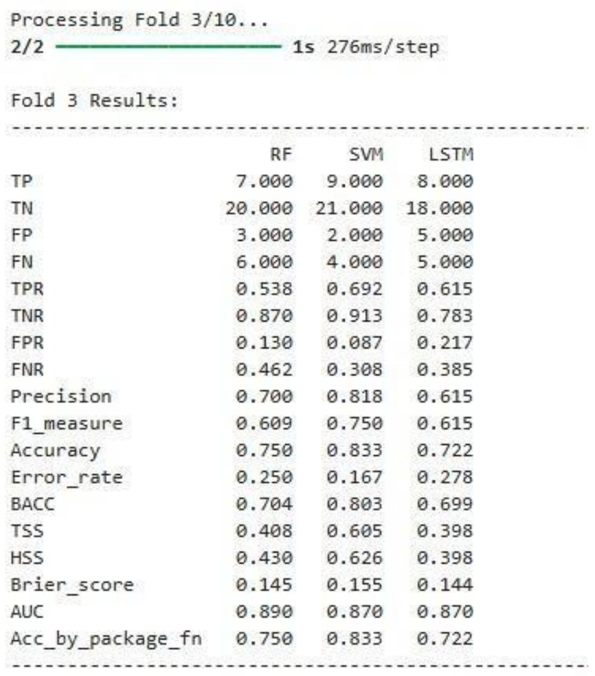
```python
# Displays the result of each fold
for fold_num, (train_idx, test_idx) in enumerate(cv_stratified.split(features_train_all_std, labels_train_all)):
    fold_metrics = run_single_fold(fold_num, train_idx, test_idx)
```



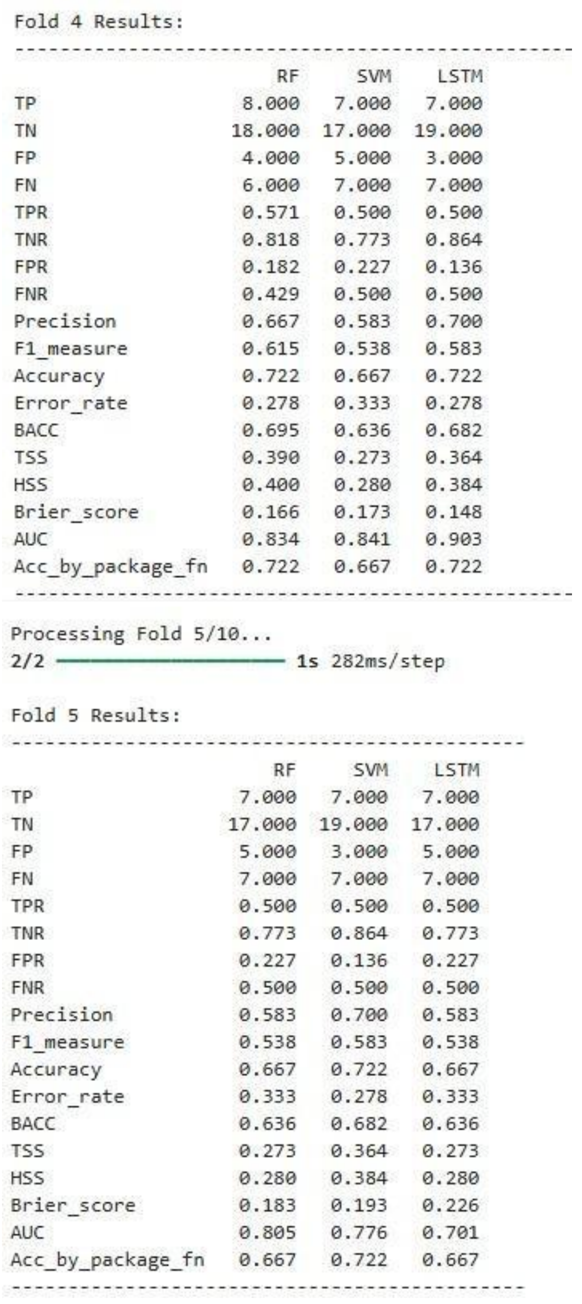
```
Processing Fold 1/10...
2/2 ━━━━━━━━━━━━━━━━━━━━ 1s 263ms/step

Fold 1 Results:
----------------------------------------------------------
                      RF     SVM    LSTM
TP                 8.000   5.000   8.000
TN                22.000  22.000  22.000
FP                 1.000   1.000   1.000
FN                 5.000   8.000   5.000
TPR                0.615   0.385   0.615
TNR                0.957   0.957   0.957
FPR                0.043   0.043   0.043
FNR                0.385   0.615   0.385
Precision          0.889   0.833   0.889
F1_measure         0.727   0.526   0.727
Accuracy           0.833   0.750   0.833
Error_rate         0.167   0.250   0.167
BACC               0.786   0.671   0.786
TSS                0.572   0.341   0.572
HSS                0.613   0.386   0.613
Brier_score        0.125   0.156   0.161
AUC                0.913   0.839   0.799
Acc_by_package_fn  0.833   0.750   0.833
----------------------------------------------------------
```



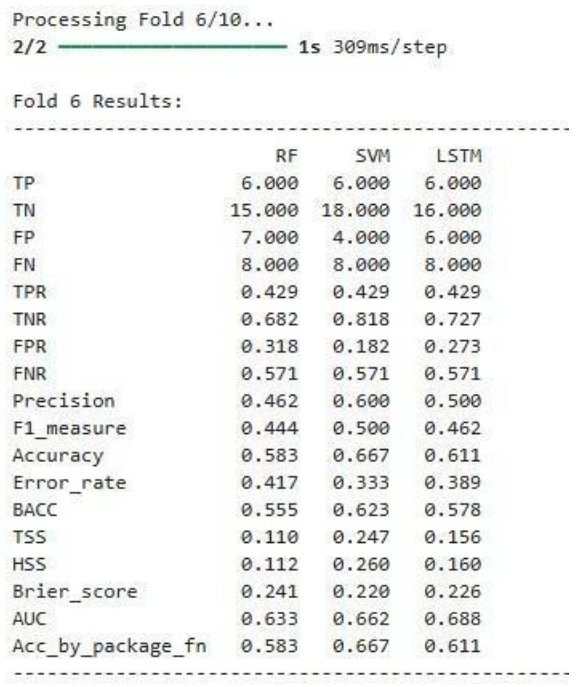
```
Processing Fold 2/10...
2/2 ━━━━━━━━━━━━━━━━━━━━ 1s 352ms/step

Fold 2 Results:
----------------------------------------------------------
                      RF     SVM    LSTM
TP                 7.000   7.000   7.000
TN                20.000  21.000  18.000
FP                 3.000   2.000   5.000
FN                 6.000   6.000   6.000
TPR                0.538   0.538   0.538
TNR                0.870   0.913   0.783
FPR                0.130   0.087   0.217
FNR                0.462   0.462   0.462
Precision          0.700   0.778   0.583
F1_measure         0.609   0.636   0.560
Accuracy           0.750   0.778   0.694
Error_rate         0.250   0.222   0.306
BACC               0.704   0.726   0.661
TSS                0.408   0.452   0.321
HSS                0.430   0.484   0.327
Brier_score        0.162   0.161   0.184
AUC                0.853   0.816   0.786
Acc_by_package_fn  0.750   0.778   0.694
----------------------------------------------------------
```



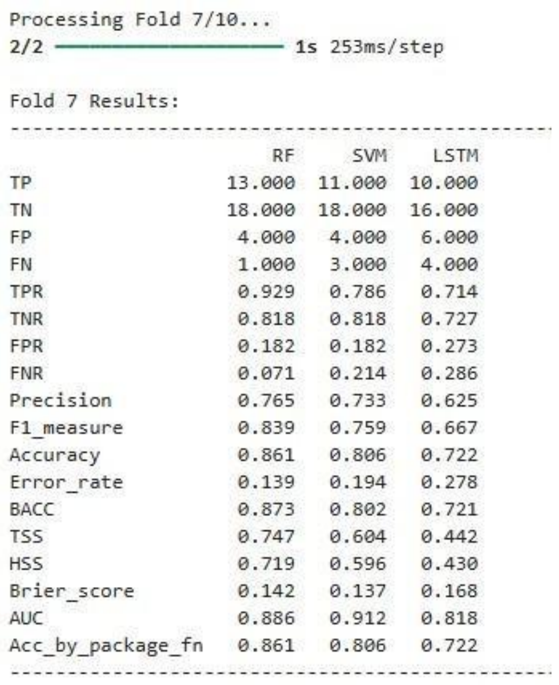
```
Processing Fold 3/10...
2/2 ━━━━━━━━━━━━━━━━━━━━ 1s 276ms/step

Fold 3 Results:
---------------------------------------------------
                      RF     SVM    LSTM
TP                 7.000   9.000   8.000
TN                20.000  21.000  18.000
FP                 3.000   2.000   5.000
FN                 6.000   4.000   5.000
TPR                0.538   0.692   0.615
TNR                0.870   0.913   0.783
FPR                0.130   0.087   0.217
FNR                0.462   0.308   0.385
Precision          0.700   0.818   0.615
F1_measure         0.609   0.750   0.615
Accuracy           0.750   0.833   0.722
Error_rate         0.250   0.167   0.278
BACC               0.704   0.803   0.699
TSS                0.408   0.605   0.398
HSS                0.430   0.626   0.398
Brier_score        0.145   0.155   0.144
AUC                0.890   0.870   0.870
Acc_by_package_fn  0.750   0.833   0.722
---------------------------------------------------
```



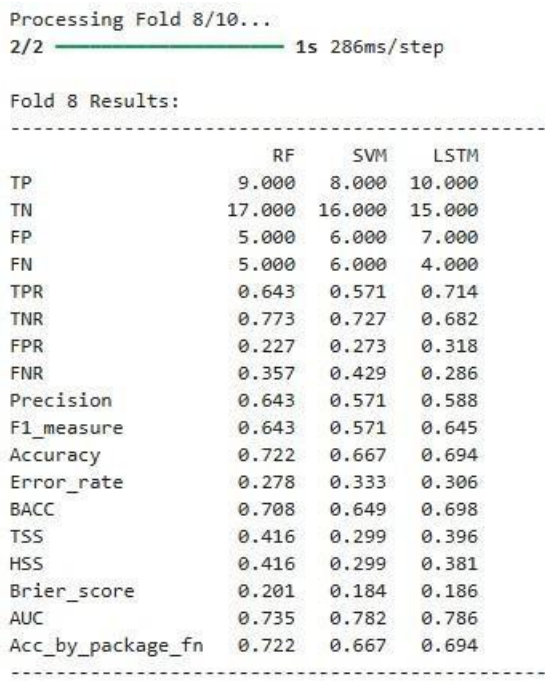
```
Fold 4 Results:
--------------------------------------------------
                     RF      SVM     LSTM
TP                 8.000    7.000    7.000
TN                18.000   17.000   19.000
FP                 4.000    5.000    3.000
FN                 6.000    7.000    7.000
TPR                0.571    0.500    0.500
TNR                0.818    0.773    0.864
FPR                0.182    0.227    0.136
FNR                0.429    0.500    0.500
Precision          0.667    0.583    0.700
F1_measure         0.615    0.538    0.583
Accuracy           0.722    0.667    0.722
Error_rate         0.278    0.333    0.278
BACC               0.695    0.636    0.682
TSS                0.390    0.273    0.364
HSS                0.400    0.280    0.384
Brier_score        0.166    0.173    0.148
AUC                0.834    0.841    0.903
Acc_by_package_fn  0.722    0.667    0.722
--------------------------------------------------

Processing Fold 5/10...
2/2 ━━━━━━━━━━━━━━━━━━━━ 1s 282ms/step

Fold 5 Results:
---------------------------------------------
                     RF      SVM     LSTM
TP                 7.000    7.000    7.000
TN                17.000   19.000   17.000
FP                 5.000    3.000    5.000
FN                 7.000    7.000    7.000
TPR                0.500    0.500    0.500
TNR                0.773    0.864    0.773
FPR                0.227    0.136    0.227
FNR                0.500    0.500    0.500
Precision          0.583    0.700    0.583
F1_measure         0.538    0.583    0.538
Accuracy           0.667    0.722    0.667
Error_rate         0.333    0.278    0.333
BACC               0.636    0.682    0.636
TSS                0.273    0.364    0.273
HSS                0.280    0.384    0.280
Brier_score        0.183    0.193    0.226
AUC                0.805    0.776    0.701
Acc_by_package_fn  0.667    0.722    0.667
---------------------------------------------
```



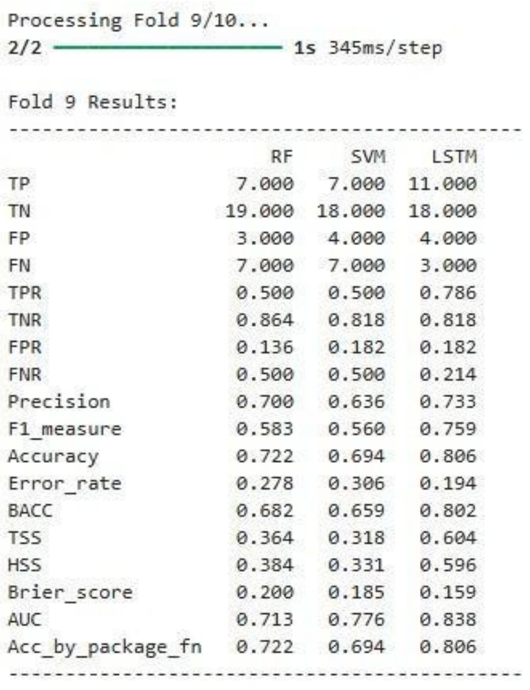
```
Processing Fold 6/10...
2/2 ━━━━━━━━━━━━━━━━━━━━ 1s 309ms/step

Fold 6 Results:
--------------------------------------------------
                      RF      SVM     LSTM
TP                 6.000    6.000    6.000
TN                15.000   18.000   16.000
FP                 7.000    4.000    6.000
FN                 8.000    8.000    8.000
TPR                0.429    0.429    0.429
TNR                0.682    0.818    0.727
FPR                0.318    0.182    0.273
FNR                0.571    0.571    0.571
Precision          0.462    0.600    0.500
F1_measure         0.444    0.500    0.462
Accuracy           0.583    0.667    0.611
Error_rate         0.417    0.333    0.389
BACC               0.555    0.623    0.578
TSS                0.110    0.247    0.156
HSS                0.112    0.260    0.160
Brier_score        0.241    0.220    0.226
AUC                0.633    0.662    0.688
Acc_by_package_fn  0.583    0.667    0.611
--------------------------------------------------
```



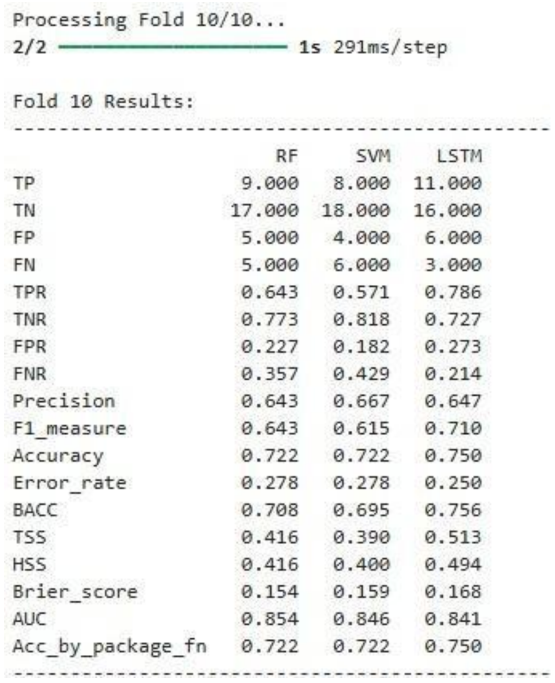
```
Processing Fold 7/10...
2/2 ━━━━━━━━━━━━━━━━━━━━ 1s 253ms/step

Fold 7 Results:
--------------------------------------------------
                      RF      SVM     LSTM
TP                13.000   11.000   10.000
TN                18.000   18.000   16.000
FP                 4.000    4.000    6.000
FN                 1.000    3.000    4.000
TPR                0.929    0.786    0.714
TNR                0.818    0.818    0.727
FPR                0.182    0.182    0.273
FNR                0.071    0.214    0.286
Precision          0.765    0.733    0.625
F1_measure         0.839    0.759    0.667
Accuracy           0.861    0.806    0.722
Error_rate         0.139    0.194    0.278
BACC               0.873    0.802    0.721
TSS                0.747    0.604    0.442
HSS                0.719    0.596    0.430
Brier_score        0.142    0.137    0.168
AUC                0.886    0.912    0.818
Acc_by_package_fn  0.861    0.806    0.722
--------------------------------------------------
```



```
Processing Fold 8/10...
2/2 ━━━━━━━━━━━━━━━━━━━━ 1s 286ms/step

Fold 8 Results:
-----------------------------------------------
                      RF     SVM    LSTM
TP                 9.000   8.000  10.000
TN                17.000  16.000  15.000
FP                 5.000   6.000   7.000
FN                 5.000   6.000   4.000
TPR                0.643   0.571   0.714
TNR                0.773   0.727   0.682
FPR                0.227   0.273   0.318
FNR                0.357   0.429   0.286
Precision          0.643   0.571   0.588
F1_measure         0.643   0.571   0.645
Accuracy           0.722   0.667   0.694
Error_rate         0.278   0.333   0.306
BACC               0.708   0.649   0.698
TSS                0.416   0.299   0.396
HSS                0.416   0.299   0.381
Brier_score        0.201   0.184   0.186
AUC                0.735   0.782   0.786
Acc_by_package_fn  0.722   0.667   0.694
-----------------------------------------------
```

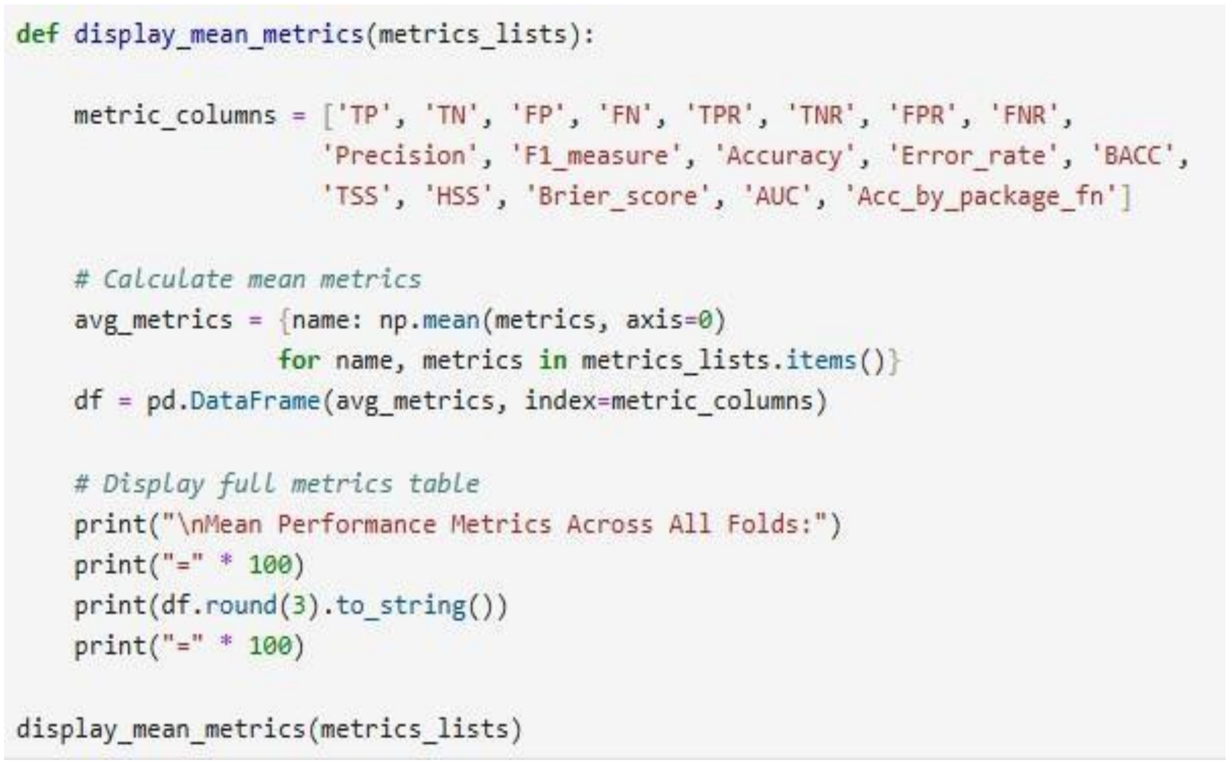


```
Processing Fold 9/10...
2/2 ━━━━━━━━━━━━━━━━━━━━ 1s 345ms/step

Fold 9 Results:
---------------------------------------------
                      RF     SVM    LSTM
TP                 7.000   7.000  11.000
TN                19.000  18.000  18.000
FP                 3.000   4.000   4.000
FN                 7.000   7.000   3.000
TPR                0.500   0.500   0.786
TNR                0.864   0.818   0.818
FPR                0.136   0.182   0.182
FNR                0.500   0.500   0.214
Precision          0.700   0.636   0.733
F1_measure         0.583   0.560   0.759
Accuracy           0.722   0.694   0.806
Error_rate         0.278   0.306   0.194
BACC               0.682   0.659   0.802
TSS                0.364   0.318   0.604
HSS                0.384   0.331   0.596
Brier_score        0.200   0.185   0.159
AUC                0.713   0.776   0.838
Acc_by_package_fn  0.722   0.694   0.806
---------------------------------------------
```

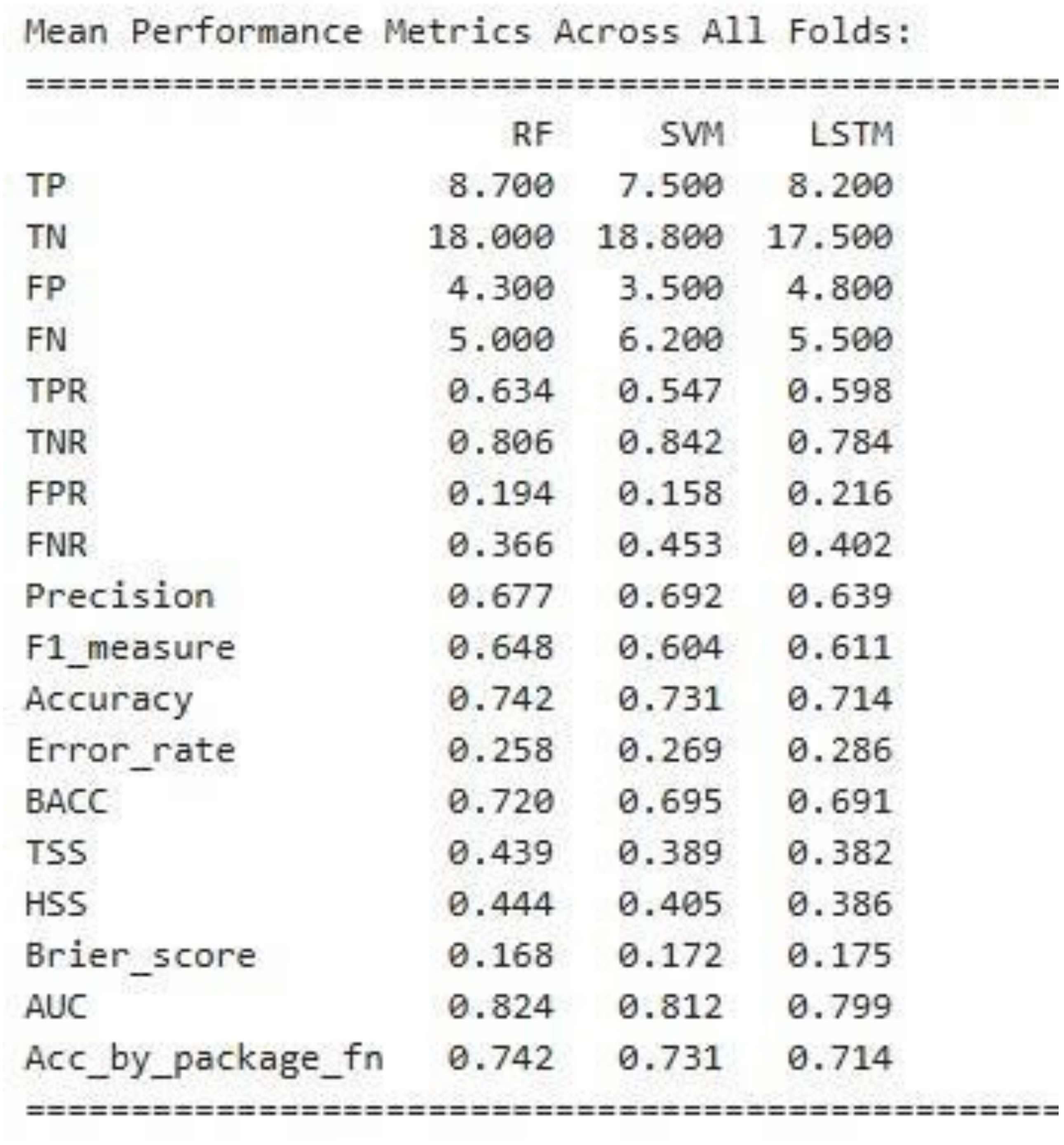


```
Processing Fold 10/10...
2/2 ━━━━━━━━━━━━━━━━━━━━ 1s 291ms/step

Fold 10 Results:
-----------------------------------------------
                      RF     SVM    LSTM
TP                 9.000   8.000  11.000
TN                17.000  18.000  16.000
FP                 5.000   4.000   6.000
FN                 5.000   6.000   3.000
TPR                0.643   0.571   0.786
TNR                0.773   0.818   0.727
FPR                0.227   0.182   0.273
FNR                0.357   0.429   0.214
Precision          0.643   0.667   0.647
F1_measure         0.643   0.615   0.710
Accuracy           0.722   0.722   0.750
Error_rate         0.278   0.278   0.250
BACC               0.708   0.695   0.756
TSS                0.416   0.390   0.513
HSS                0.416   0.400   0.494
Brier_score        0.154   0.159   0.168
AUC                0.854   0.846   0.841
Acc_by_package_fn  0.722   0.722   0.750
-----------------------------------------------
```

6.12 Calculate Average: Calculates the average from all the folds and provides proper metrics to compare.

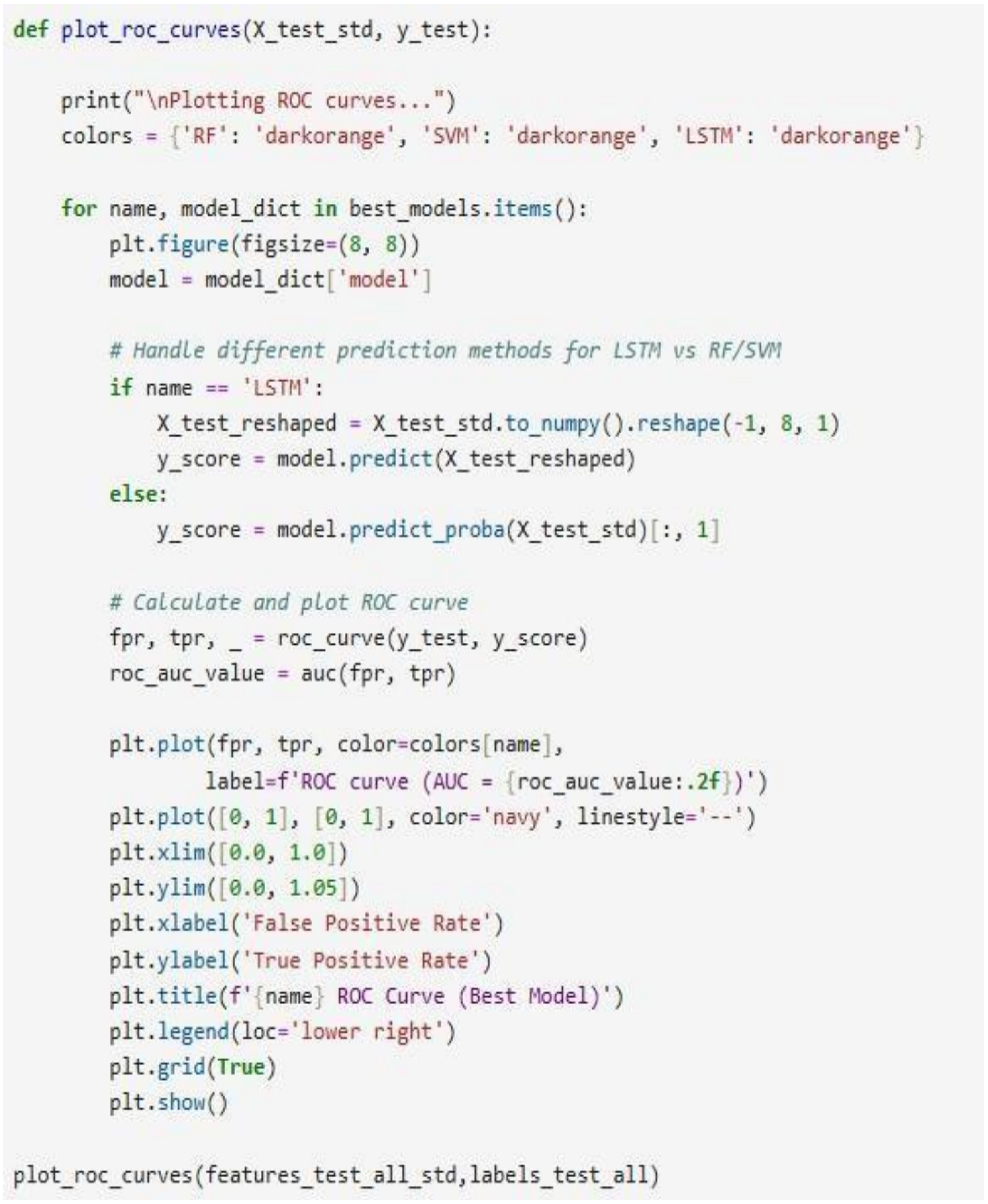


```python
def display_mean_metrics(metrics_lists):

    metric_columns = ['TP', 'TN', 'FP', 'FN', 'TPR', 'TNR', 'FPR', 'FNR',
                      'Precision', 'F1_measure', 'Accuracy', 'Error_rate', 'BACC',
                      'TSS', 'HSS', 'Brier_score', 'AUC', 'Acc_by_package_fn']

    # Calculate mean metrics
    avg_metrics = {name: np.mean(metrics, axis=0)
                  for name, metrics in metrics_lists.items()}
    df = pd.DataFrame(avg_metrics, index=metric_columns)

    # Display full metrics table
    print("\nMean Performance Metrics Across All Folds:")
    print("=" * 100)
    print(df.round(3).to_string())
    print("=" * 100)

display_mean_metrics(metrics_lists)
```



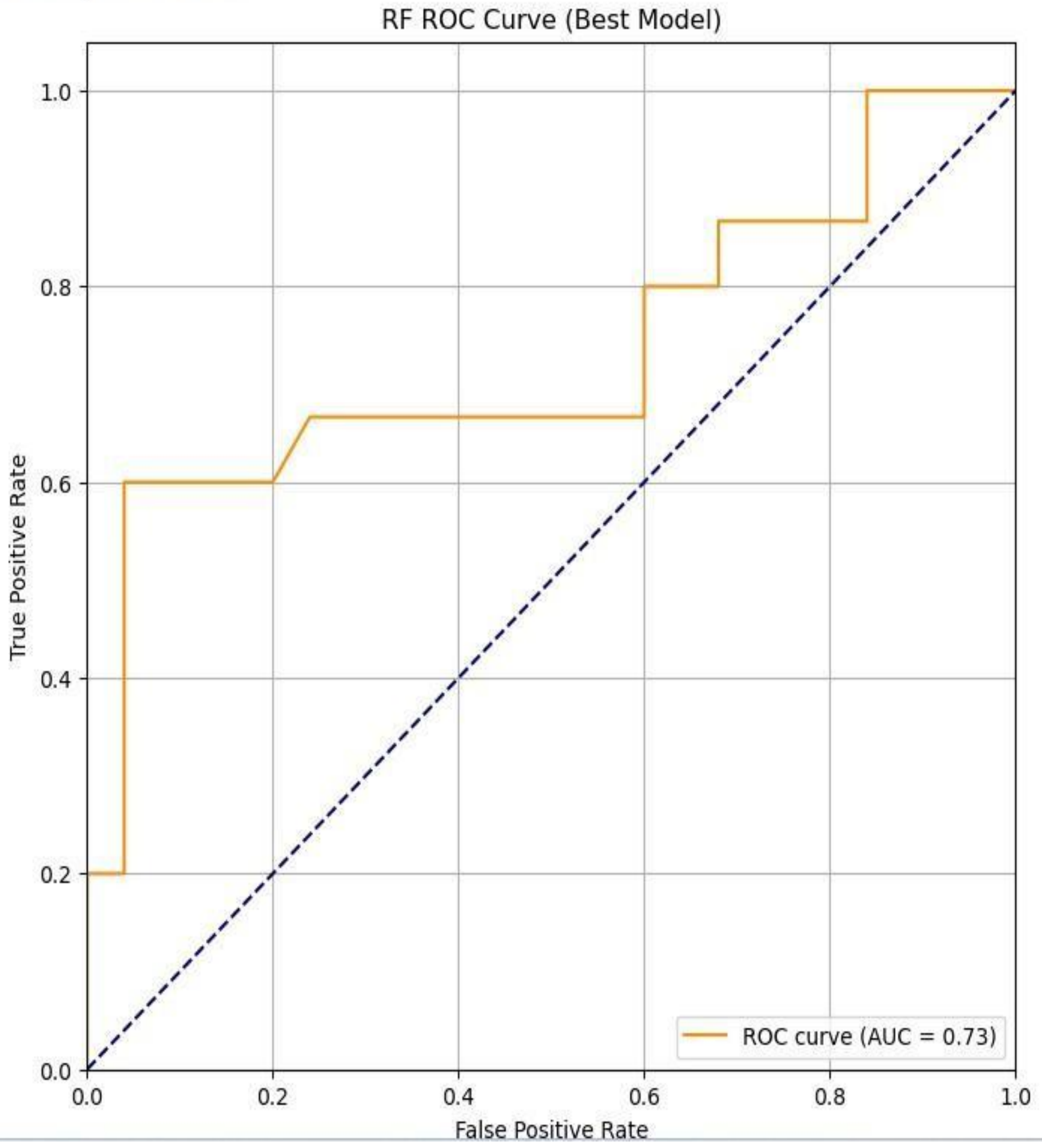
```
Mean Performance Metrics Across All Folds:
==================================================
                        RF     SVM    LSTM
TP                   8.700   7.500   8.200
TN                  18.000  18.800  17.500
FP                   4.300   3.500   4.800
FN                   5.000   6.200   5.500
TPR                  0.634   0.547   0.598
TNR                  0.806   0.842   0.784
FPR                  0.194   0.158   0.216
FNR                  0.366   0.453   0.402
Precision            0.677   0.692   0.639
F1_measure           0.648   0.604   0.611
Accuracy             0.742   0.731   0.714
Error_rate           0.258   0.269   0.286
BACC                 0.720   0.695   0.691
TSS                  0.439   0.389   0.382
HSS                  0.444   0.405   0.386
Brier_score          0.168   0.172   0.175
AUC                  0.824   0.812   0.799
Acc_by_package_fn    0.742   0.731   0.714
==================================================
```

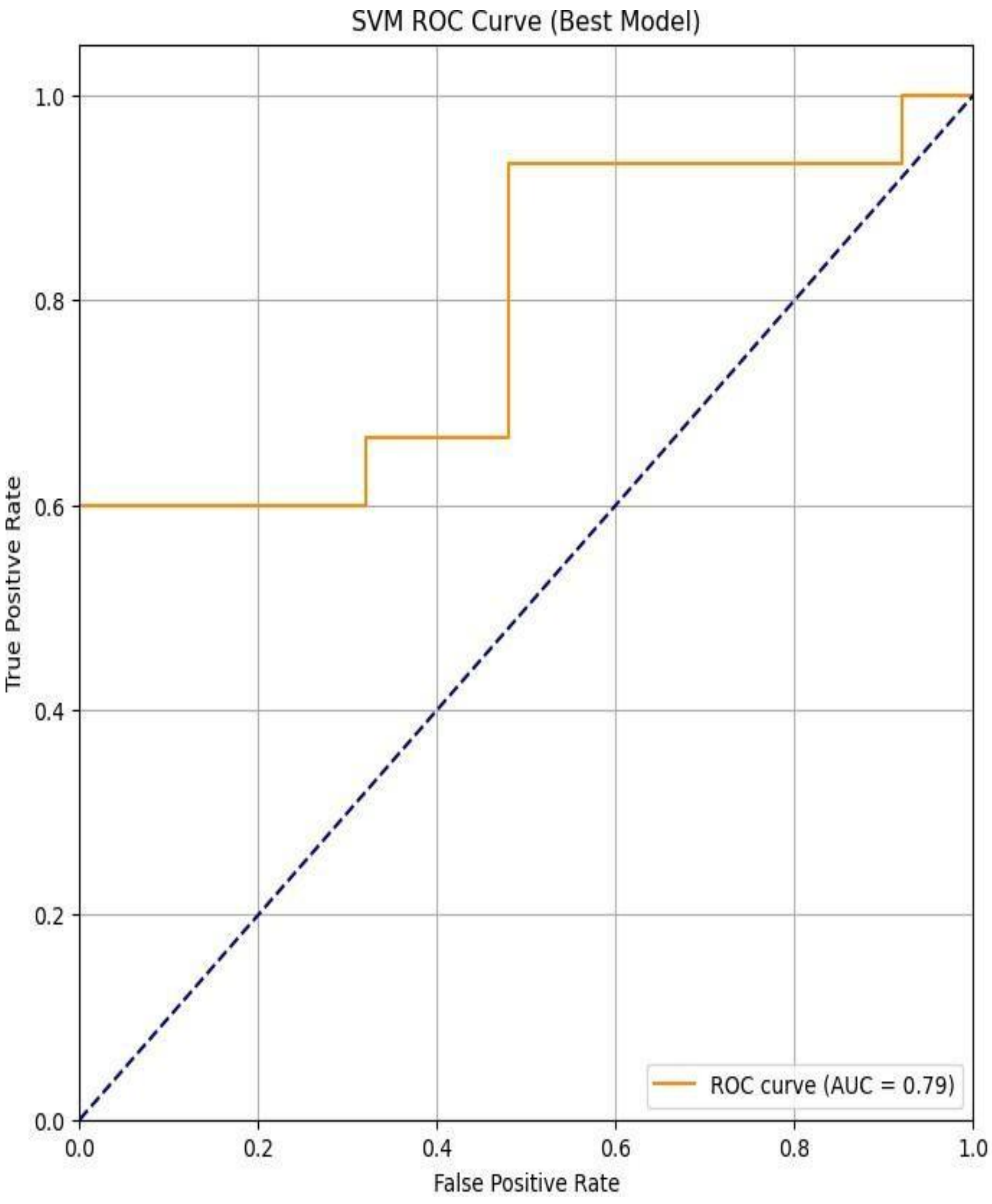
6.13 Evaluating the performance of various algorithms by comparing their ROC curves and AUC scores on the test dataset.



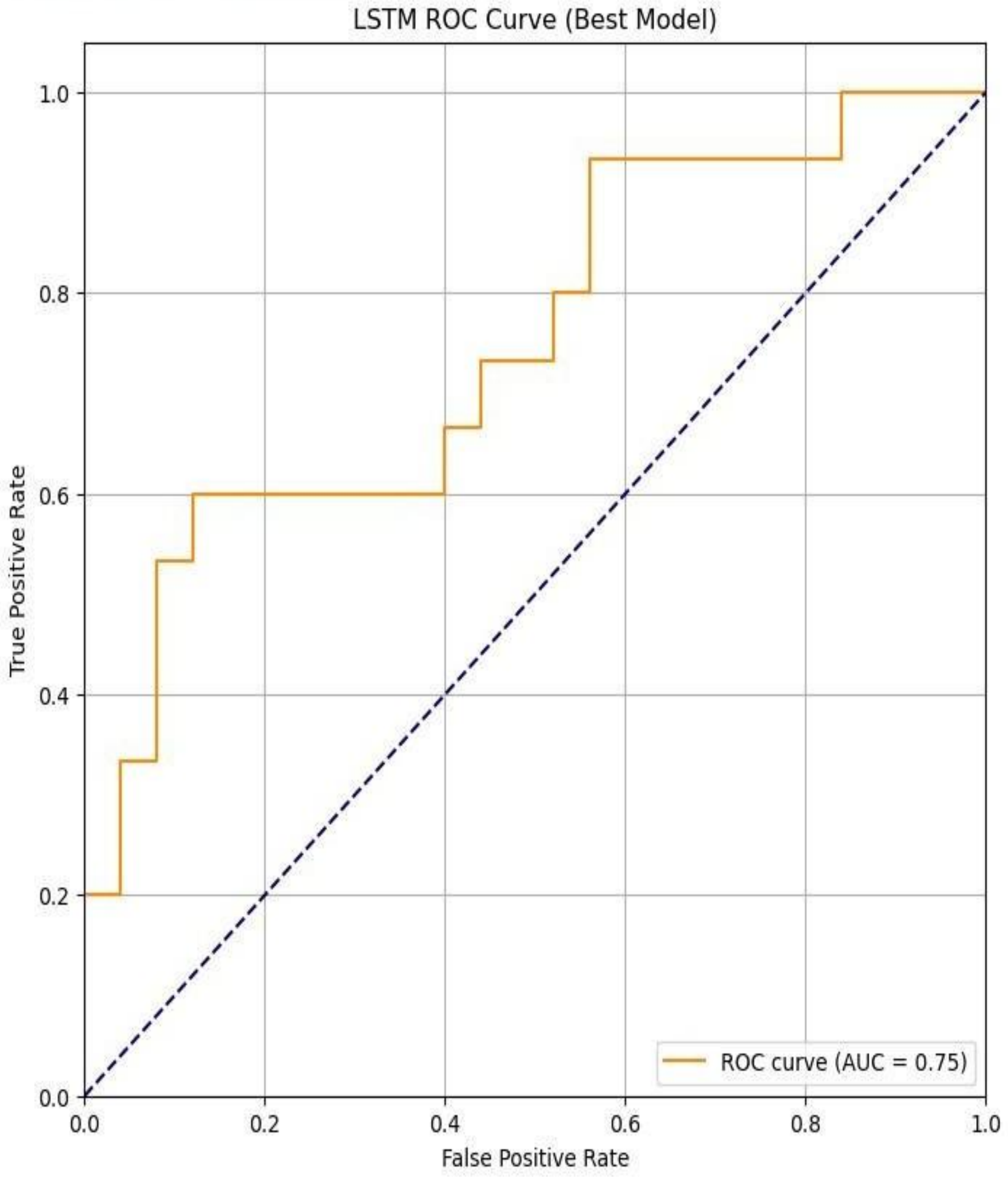
```python
def plot_roc_curves(X_test_std, y_test):

    print("\nPlotting ROC curves...")
    colors = {'RF': 'darkorange', 'SVM': 'darkorange', 'LSTM': 'darkorange'}

    for name, model_dict in best_models.items():
        plt.figure(figsize=(8, 8))
        model = model_dict['model']

        # Handle different prediction methods for LSTM vs RF/SVM
        if name == 'LSTM':
            X_test_reshaped = X_test_std.to_numpy().reshape(-1, 8, 1)
            y_score = model.predict(X_test_reshaped)
        else:
            y_score = model.predict_proba(X_test_std)[:, 1]

        # Calculate and plot ROC curve
        fpr, tpr, _ = roc_curve(y_test, y_score)
        roc_auc_value = auc(fpr, tpr)

        plt.plot(fpr, tpr, color=colors[name],
                 label=f'ROC curve (AUC = {roc_auc_value:.2f})')
        plt.plot([0, 1], [0, 1], color='navy', linestyle='--')
        plt.xlim([0.0, 1.0])
        plt.ylim([0.0, 1.05])
        plt.xlabel('False Positive Rate')
        plt.ylabel('True Positive Rate')
        plt.title(f'{name} ROC Curve (Best Model)')
        plt.legend(loc='lower right')
        plt.grid(True)
        plt.show()

plot_roc_curves(features_test_all_std,labels_test_all)
```

```
Plotting ROC curves...
```

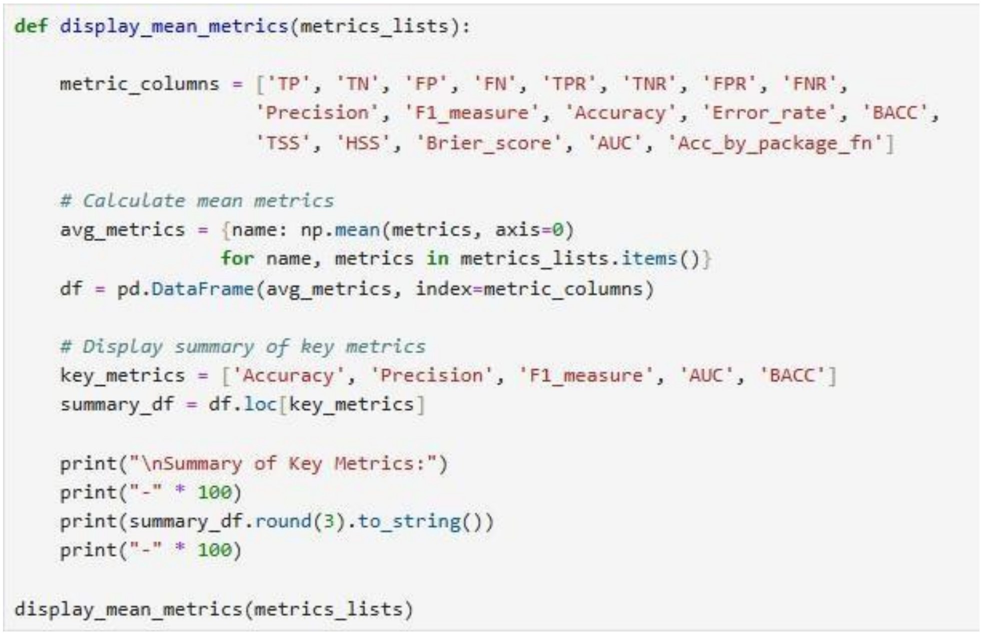



SVM ROC Curve (Best Model)
True Positive Rate
False Positive Rate
0.0
0.2
0.4
0.6
0.8
1.0
ROC curve (AUC = 0.79)

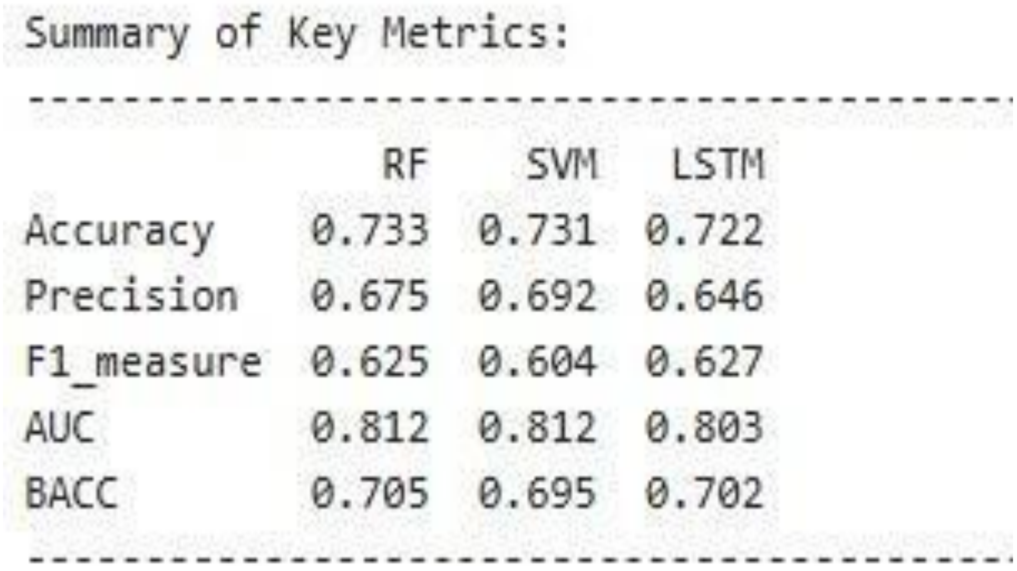
```
2/2 ━━━━━━━━━━━━━━━━━━━━ 0s 15ms/step
```



6.14 Summary of Key Metrics:



```
def display_mean_metrics(metrics_lists):

    metric_columns = ['TP', 'TN', 'FP', 'FN', 'TPR', 'TNR', 'FPR', 'FNR',
                      'Precision', 'F1_measure', 'Accuracy', 'Error_rate', 'BACC',
                      'TSS', 'HSS', 'Brier_score', 'AUC', 'Acc_by_package_fn']

    # Calculate mean metrics
    avg_metrics = {name: np.mean(metrics, axis=0)
                   for name, metrics in metrics_lists.items()}
    df = pd.DataFrame(avg_metrics, index=metric_columns)

    # Display summary of key metrics
    key_metrics = ['Accuracy', 'Precision', 'F1_measure', 'AUC', 'BACC']
    summary_df = df.loc[key_metrics]

    print("\nSummary of Key Metrics:")
    print("-" * 100)
    print(summary_df.round(3).to_string())
    print("-" * 100)

display_mean_metrics(metrics_lists)
```



```
Summary of Key Metrics:
---------------------------------------
               RF    SVM   LSTM
Accuracy    0.733  0.731  0.722
Precision   0.675  0.692  0.646
F1_measure  0.625  0.604  0.627
AUC         0.812  0.812  0.803
BACC        0.705  0.695  0.702
---------------------------------------
```

7. Discussion:

From the three models tested, The Random Forest classifier performed best overall. It generally yielded a higher accuracy for all 10 folds and showed the best balance between precision and recall. The balanced accuracy, about 0.71, shows that it did identify the diabetic and non-diabetic cases without biases toward either class. The ROC curve also rose faster and appeared much smoother compared to the SVM and LSTM which means more stable and reliable predictions.

During the project, I faced a few challenges, especially handing invalid zero values in the dataset and reshaping data for the LSTM model. The training time for LSTM was also noticeably longer. Standardization of features helped in enhancing model performance along GridSearchCV tuning across all algorithms.

8. Conclusions:

During the project, a larger dataset such as SMOTE might help balance the classes and could enhance the performance especially for LSTM. Overall, the Random Forest model proved to be the most practical and dependable in this diabetes prediction task. Overall, the result reflects Random Forest, SVM and LSTM all performed well the prediction of diabetes, but Random Forest was the best choice. It yielded the best balance of accuracy, stability and computational efficiency in all 10 folds. SVM ran second, but its recall and balanced accuracy were slightly lower. Thus, the LSTM model was competitive, though it required a longer time to train and did not give superior results in comparison with traditional machine-learning models on this dataset.

The project also showed how proper preprocessing, hyperparameter tuning, and cross validation are rather important to get reliable results. There was a big difference depending on the algorithm choice and the evaluation method helped to point out strengths and weaknesses of each model. In the case of this dataset, Random Forest proved to be the most practical and effective model for predictions of diabetes.

9. References:

- Pima Indians Diabetes Dataset - UCI Machine Learning Repository - https://archive.ics.uci.edu/ml/datasets/pima+indians+diabetes
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- Seaborn Documentation - https://seaborn.pydata.org/
- CS 634 – Data Mining Course Notes, New Jersey Institute of Technology, Fall 2025.

10. GitHub Link: https://github.com/Risha-20/final_project_rrr62