NAME: Aesha Dobariya
NJIT UCID: ad2389
Email Address: ad2389@njit.edu
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Professor: Yasser Abduallah
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Final Project Report

Using SVM, RF and LSTM To Predict Diabetes

2.1 Abstract

Diabetes is a chronic disease with significant global prevalence and health implications, making early and accurate diagnosis critical for effective management. This study explores the application of machine learning and deep learning techniques to predict the likelihood of diabetes based on diagnostic measurements. Specifically, Long Short-Term Memory (LSTM) networks, Support Vector Machines (SVM), and Random Forest classifiers are implemented and compared for predictive performance. The research aims to identify the most effective algorithm for analyzing diagnostic data, thereby providing a reliable tool for early detection. Results are evaluated using standard metrics such as accuracy, precision, recall, and F1-score to assess the models' predictive capabilities. This work contributes to the growing field of artificial intelligence in healthcare by leveraging advanced computational methods for improved disease diagnosis.

2.2 Introduction

Diabetes mellitus is a metabolic disorder characterized by chronic hyperglycemia, posing a significant challenge to public health systems worldwide. Accurate and timely diagnosis is essential to mitigate complications and improve patient outcomes. Traditional diagnostic methods, while effective, can be labor-intensive and subject to human error, creating a need for automated systems that leverage computational methods for better accuracy and efficiency.

Recent advancements in machine learning and deep learning have revolutionized predictive analytics in healthcare, enabling the development of robust diagnostic models. This study integrates traditional machine learning techniques—Support Vector Machines (SVM) and Random Forest—with a deep learning approach, Long Short-Term Memory (LSTM), to predict diabetes based on diagnostic measurements. While SVM and Random Forest are known for their reliability in handling structured data, LSTM networks offer the advantage of modeling sequential dependencies, making them suitable for time-series or sequential diagnostic datasets.

The primary objective of this research is to evaluate and compare the predictive performance of these algorithms, providing insights into their suitability for diabetes prediction. By identifying the most effective computational approach, this study aims to support early detection efforts and contribute to the broader application of artificial intelligence in medical diagnostics.

2.3 Key concepts and principals

1. Diabetes Mellitus: Background

- **Definition**: A chronic metabolic disorder characterized by elevated blood glucose levels (hyperglycemia).
- **Public Health Challenge**: Significant complications such as cardiovascular disease, kidney damage, and neuropathy necessitate early diagnosis and management.
- **Diagnostic Importance**: Accurate and timely detection can mitigate long-term health risks and improve quality of life.

2. The Role of Automated Systems

- **Traditional Diagnostic Limitations**:
  - Labor-intensive procedures.
  - Risk of human error during interpretation.
- **Automated Approaches**: Machine learning (ML) and deep learning (DL) techniques reduce human dependency and enhance diagnostic precision.

3. Machine Learning Techniques

Support Vector Machines (SVM):

- A supervised learning algorithm effective for binary classification tasks.
- Works well with structured data by finding an optimal hyperplane to separate classes.
- Robust in handling small to medium-sized datasets with clear margins.

Random Forest (RF):

- An ensemble learning method using multiple decision trees for classification.
- Handles non-linear relationships and reduces overfitting.
- Known for its interpretability and reliability in structured data analysis.

4. Deep Learning Technique

- **Long Short-Term Memory (LSTM)**:
  - A type of recurrent neural network (RNN) capable of learning long-term dependencies.
  - Suited for sequential or time-series data (e.g., glucose monitoring trends).
  - Offers flexibility in modeling temporal relationships between features.

5. Study Objectives

- **Predictive Performance Evaluation**:
  - Compare the accuracy, precision, recall, F1-score, and other metrics across SVM, RF, and LSTM models.
- **Suitability for Diabetes Prediction**:
  - Assess the trade-offs between traditional ML methods and deep learning approaches.
- **Contribution to Healthcare AI**:
  - Identify the best algorithm for diabetes diagnosis to enhance early detection efforts.

6. Theoretical Framework

- **Supervised Learning**:
  - All three algorithms fall under supervised learning, where models are trained on labeled data (features + outcomes).
- **Feature Importance**:
  - Models like RF inherently offer insights into feature contributions, which are crucial for interpretability in medical diagnostics.
- **Sequential Dependencies**:
  - LSTM excels in cases where temporal patterns or sequential data (e.g., progression of glucose levels) are integral to prediction.

7. Broader Implications

- **Advancing Predictive Healthcare**:
  - Incorporating ML/DL methods into diagnostics improves efficiency, reduces errors, and ensures consistency.
- **AI in Medicine**:
  - This study reflects the broader integration of artificial intelligence in clinical settings, paving the way for automated and personalized healthcare solutions.

8. Challenges and Considerations

- **Data Quality and Size**:
  - Machine learning models rely on sufficient and high-quality datasets for optimal performance.
- **Model Interpretability**:
  - While SVM and RF are easier to interpret, deep learning models like LSTM may lack transparency, a critical factor in healthcare applications.
- **Computational Resources**:
  - LSTM and other deep learning techniques require more computational power compared to traditional ML methods.

9. Expected Outcomes

- Identification of the most effective model for diabetes prediction.
- Insights into the trade-offs between computational complexity and diagnostic accuracy.
- Support for early diagnosis initiatives to reduce diabetes-related complications

10. Dataset:

- The dataset is downloaded from kegal, the link is given below for referances

https://www.kaggle.com/datasets/uciml/pima-indians-diabetes-database

2.4 Source code

```
import os
import numpy as np
import pandas as pd
from sklearn.model_selection import train_test_split, StratifiedKFold
from sklearn.preprocessing import StandardScaler
from sklearn.metrics import accuracy_score, precision_score, recall_score, f1_score, confusion_matrix
from sklearn.ensemble import RandomForestClassifier
from sklearn.svm import SVC
import tensorflow as tf
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Dense, LSTM, Dropout
import joblib
```

2.4.1 Importing the packages and libraries that are required for the project

```
data = pd.read_csv(r"diabetes.csv")
data.describe()
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	0.471876	33.240885	0.348958
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884160	0.331329	11.760232	0.476951
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.078000	21.000000	0.000000
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.243750	24.000000	0.000000
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.372500	29.000000	0.000000
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	0.626250	41.000000	1.000000
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000	81.000000	1.000000

```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
 #   Column                    Non-Null Count  Dtype
---  ------                    --------------  -----
 0   Pregnancies               768 non-null    int64
 1   Glucose                   768 non-null    int64
 2   BloodPressure             768 non-null    int64
 3   SkinThickness             768 non-null    int64
 4   Insulin                   768 non-null    int64
 5   BMI                       768 non-null    float64
 6   DiabetesPedigreeFunction  768 non-null    float64
 7   Age                       768 non-null    int64
 8   Outcome                   768 non-null    int64
dtypes: float64(2), int64(7)
memory usage: 54.1 KB
```

2.4.2 Loading Data And Preprocessing

```
# Separate features (X) and target (y)
X = data.iloc[:, :-1].values
y = data.iloc[:, -1].values
```

2.4.3 Separating The Dataset into Features and Output label

```python
# Function to calculate metrics
def calculate_metrics(y_test, y_pred):
    cm = confusion_matrix(y_test, y_pred)
    tp, fn, fp, tn = cm.ravel()
    accuracy = accuracy_score(y_test, y_pred)
    precision = precision_score(y_test, y_pred, zero_division=0)
    recall = recall_score(y_test, y_pred)
    f1 = f1_score(y_test, y_pred)

    fpr = fp / (fp + tn) if (fp + tn) > 0 else 0
    fnr = fn / (fn + tp) if (fn + tp) > 0 else 0
    tss = recall - fpr
    hss = (2 * (tp * tn - fp * fn)) / (
        (tp + fn) * (fn + tn) + (tp + fp) * (fp + tn)
    ) if (tp + fn + fp + tn) > 0 else 0

    return {
        "Accuracy": accuracy,
        "Precision": precision,
        "Recall": recall,
        "F1-Score": f1,
        "TSS": tss,
        "HSS": hss,
        "TP": tp,
        "TN": tn,
        "FP": fp,
        "FN": fn,
        "FPR": fpr,
        "FNR": fnr
    }
```

```python
# Results dictionary
results = {
    'Model': [],
    'Fold': [],
    'Accuracy': [],
    'Precision': [],
    'Recall': [],
    'F1-Score': [],
    'TP': [],
    'TN': [],
    'FP': [],
    'FN': [],
    'FPR': [],
    'FNR': [],
    'TSS': [],
    'HSS': []
}
```

2.4.3 matrix calculation

```
# 10-Fold Cross-Validation for Random Forest
skf = StratifiedKFold(n_splits=10, shuffle=True, random_state=42)
fold = 1

# Random Forest Classifier (Cross-validation)
rf_model = RandomForestClassifier(random_state=42)
for train_index, test_index in skf.split(X, y):
    X_train, X_test = X[train_index], X[test_index]
    y_train, y_test = y[train_index], y[test_index]

    rf_model.fit(X_train, y_train)
    y_pred = rf_model.predict(X_test)

    metrics = calculate_metrics(y_test, y_pred)
    for metric, value in metrics.items():
        results[metric].append(value)
    results['Model'].append('Random Forest')
    results['Fold'].append(fold)
    fold += 1
```

2.4.4 Random forest algorithm

```
# Standardize data for LSTM and SVM
scaler = StandardScaler()
X_scaled = scaler.fit_transform(X)

# Train-Test Split for LSTM and SVM
X_train, X_test, y_train, y_test = train_test_split(X_scaled, y, test_size=0.2, random_state=42, stratify=y)
```

```
# LSTM Model
X_train_lstm = X_train.reshape(X_train.shape[0], X_train.shape[1], 1)
X_test_lstm = X_test.reshape(X_test.shape[0], X_test.shape[1], 1)

lstm_model = Sequential([
    LSTM(64, activation='tanh', input_shape=(X_train_lstm.shape[1], 1)),
    Dropout(0.2),
    Dense(32, activation='relu'),
    Dropout(0.2),
    Dense(1, activation='sigmoid')
])
lstm_model.compile(optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])
lstm_model.fit(X_train_lstm, y_train, epochs=50, batch_size=32, verbose=0)
y_pred_lstm = (lstm_model.predict(X_test_lstm) > 0.5).astype(int)
metrics = calculate_metrics(y_test, y_pred_lstm)
for metric, value in metrics.items():
    results[metric].append(value)
results['Model'].append('LSTM')
results['Fold'].append('N/A')  # LSTM doesn't use cross-validation
```

2.4.5 LSTM

```python
# SVM Model
svm_model = SVC(kernel='linear', random_state=42)
svm_model.fit(X_train, y_train)
y_pred_svm = svm_model.predict(X_test)
metrics = calculate_metrics(y_test, y_pred_svm)
for metric, value in metrics.items():
    results[metric].append(value)
results['Model'].append('SVM')
results['Fold'].append('N/A')  # SVM doesn't use cross-validation
```

2.4.6 SVM

```python
# Convert results to DataFrame
results_df = pd.DataFrame(results)

# Print the results
print(results_df)
```

2.4.7 printing result

```python
# Plot Confusion Matrices
def plot_confusion_matrix(y_test, y_pred, title):
    cm = confusion_matrix(y_test, y_pred)
    plt.figure(figsize=(6, 4))
    sns.heatmap(cm, annot=True, fmt='d', cmap='Blues', xticklabels=['No', 'Yes'], yticklabels=['No', 'Yes'])
    plt.title(f'{title} - Confusion Matrix')
    plt.xlabel('Predicted')
    plt.ylabel('Actual')
    plt.show()

# Plot for each model
plot_confusion_matrix(y_test, rf_model.predict(X_test), 'Random Forest')
plot_confusion_matrix(y_test, y_pred_svm, 'SVM')
plot_confusion_matrix(y_test, y_pred_lstm, 'LSTM')
```

2.4.8 graphical representation of all the algorithms

```python
# Calculate average metrics for each model and compare
average_metrics = results_df.groupby('Model').mean(numeric_only=True)

# Compare models based on average metrics
comparison = {
    "Model": [],
    "Average Accuracy": [],
    "Average F1-Score": [],
    "Average TSS": [],
    "Average HSS": []
}

for model in average_metrics.index:
    comparison["Model"].append(model)
    comparison["Average Accuracy"].append(average_metrics.loc[model, "Accuracy"])
    comparison["Average F1-Score"].append(average_metrics.loc[model, "F1-Score"])
    comparison["Average TSS"].append(average_metrics.loc[model, "TSS"])
    comparison["Average HSS"].append(average_metrics.loc[model, "HSS"])

comparison_df = pd.DataFrame(comparison)

# Print model comparison
print("\nModel Comparison:")
print(comparison_df)

# Identify the best model based on Average Accuracy
best_model_row = comparison_df.loc[comparison_df['Average Accuracy'].idxmax()]
best_model_name = best_model_row['Model']
best_model_accuracy = best_model_row['Average Accuracy']

# Add a line to print which model is best
best_model_summary = f"\nThe best model for this dataset based on Average Accuracy is: {best_model_name} with an Accuracy of {best_model_accuracy:.4f}."
print(best_model_summary)
```

2.4.9 comparison of all the algorithms

```python
# Visualizing Metric Comparison
average_metrics = results_df.groupby('Model').mean(numeric_only=True)

average_metrics.plot(kind='bar', figsize=(12, 6), title="Average Metrics per Model")
plt.ylabel("Score")
plt.xticks(rotation=45)
plt.show()
```

2.4.10 graphically visualization of all the algorithms

SAVING MODELS

```python
# Save models
joblib.dump(rf_model, os.path.join(output_dir, "rf_model.pkl"))
lstm_model.save(os.path.join(output_dir, "lstm_model.h5"))
joblib.dump(svm_model, os.path.join(output_dir, "svm_model.pkl"))

print("Models saved as 'rf_model.pkl', 'lstm_model.h5', and 'svm_model.pkl'")
```

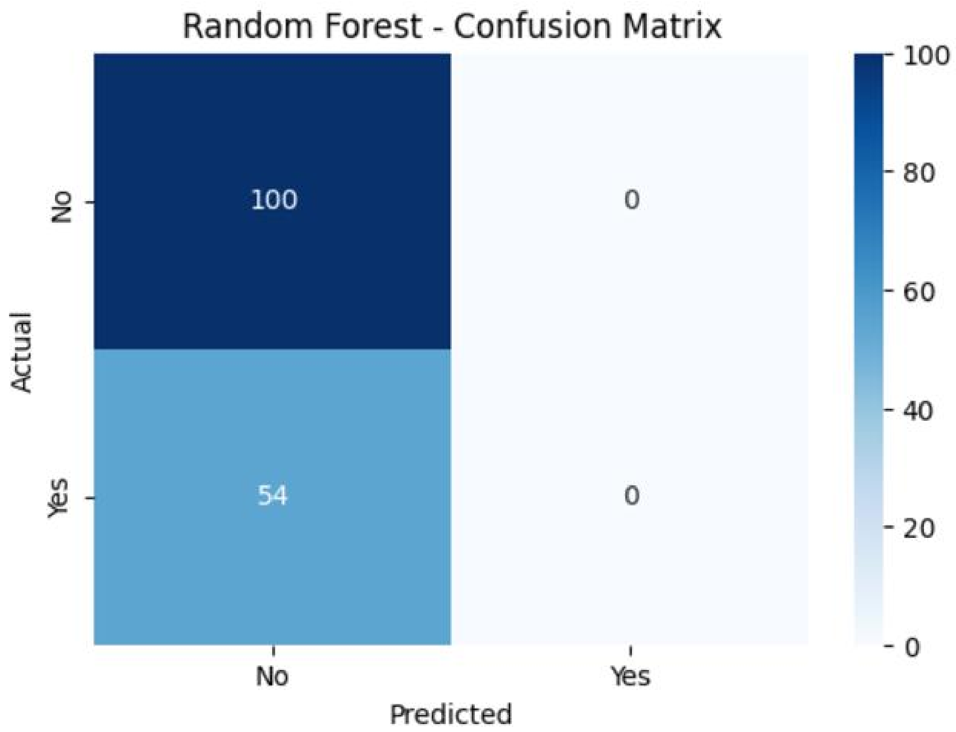
2.4.11 saving models

2.5 OUTPUT

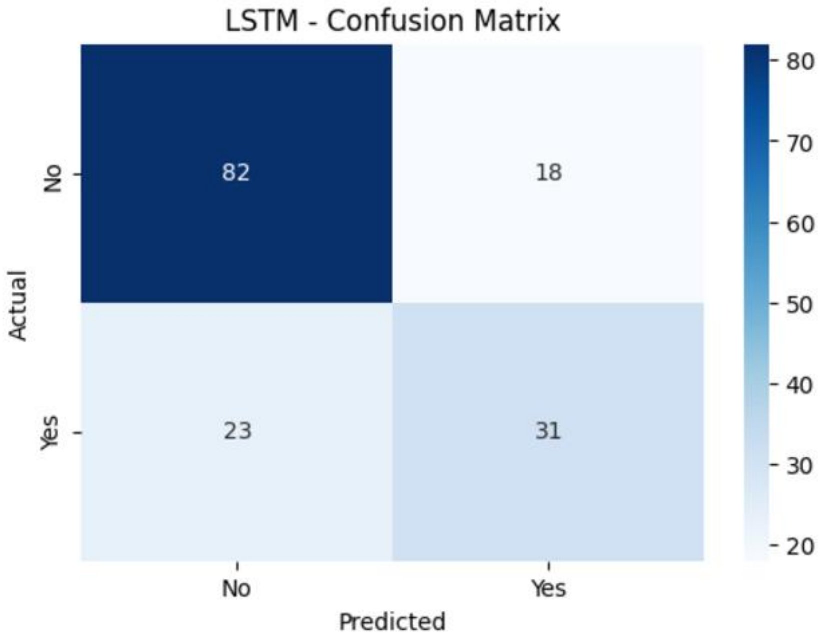
```
C:\Users\DELL\AppData\Roaming\Python\Python311\site-packages\keras\src\layers\rnn\rnn.py:204: UserWarning: Do not pass an `input_shape`/`input_dim` argum
ent to a layer. When using Sequential models, prefer using an `Input(shape)` object as the first layer in the model instead.
  super().__init__(**kwargs)
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 52ms/step
WARNING:absl:You are saving your model as an HDF5 file via `model.save()` or `keras.saving.save_model(model)`. This file format is considered legacy. We
recommend using instead the native Keras format, e.g. `model.save('my_model.keras')` or `keras.saving.save_model(model, 'my_model.keras')`.
            Model Fold  Accuracy  Precision    Recall  F1-Score  TP  TN  FP  \
0   Random Forest    1  0.805195   0.730769  0.703704  0.716981  43  19   8
1   Random Forest    2  0.753247   0.700000  0.518519  0.595745  44  14  13
2   Random Forest    3  0.714286   0.608696  0.518519  0.560000  41  14  13
3   Random Forest    4  0.870130   0.904762  0.703704  0.791667  48  19   8
4   Random Forest    5  0.792208   0.761905  0.592593  0.666667  45  16  11
5   Random Forest    6  0.727273   0.636364  0.518519  0.571429  42  14  13
6   Random Forest    7  0.753247   0.681818  0.555556  0.612245  43  15  12
7   Random Forest    8  0.766234   0.666667  0.666667  0.666667  41  18   9
8   Random Forest    9  0.789474   0.678571  0.730769  0.703704  41  19   7
9   Random Forest   10  0.723684   0.619048  0.500000  0.553191  42  13  13
10           LSTM  N/A  0.701299   0.580000  0.537037  0.557692  79  29  25
11            SVM  N/A  0.720779   0.622222  0.518519  0.565657  83  28  26

    FN       FPR   FNR       TSS       HSS
0    7  0.296296  0.14  0.407407  0.568547
1    6  0.481481  0.12  0.037037  0.423789
2    9  0.481481  0.18  0.037037  0.350460
3    2  0.296296  0.04  0.407407  0.699454
4    5  0.407407  0.10  0.185185  0.519126
5    8  0.481481  0.16  0.037037  0.374468
6    7  0.444444  0.14  0.111111  0.434043
7    9  0.333333  0.18  0.333333  0.486667
8    9  0.269231  0.18  0.461538  0.540785
9    8  0.500000  0.16  0.000000  0.356452
10  21  0.462963  0.21  0.074074  0.332705
11  17  0.481481  0.17  0.037037  0.362411
```

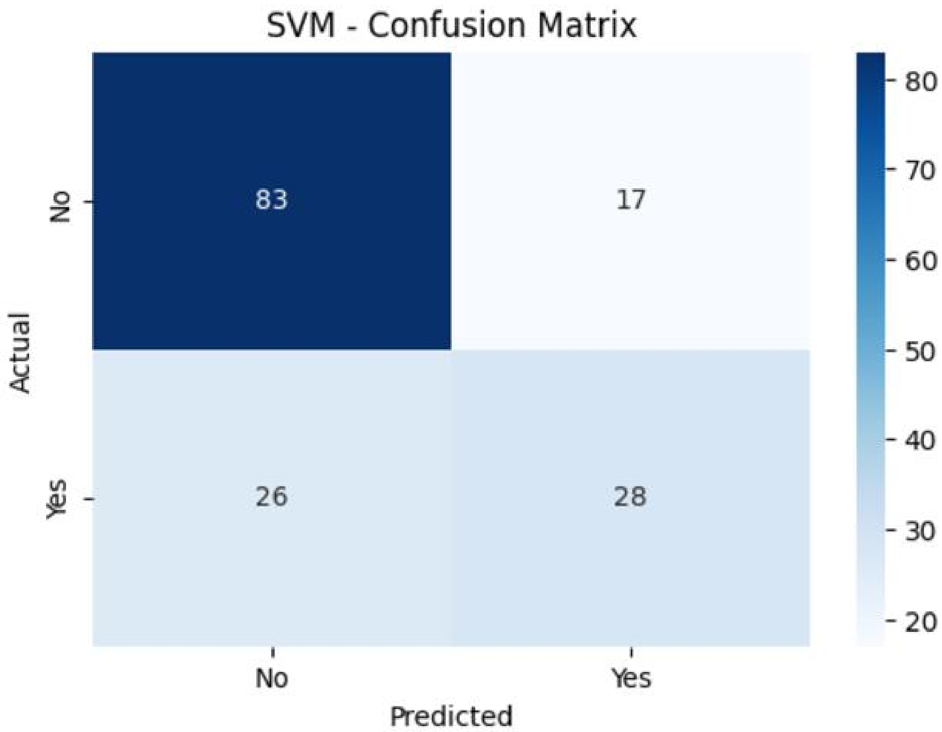
2.5.1 matrix calculation



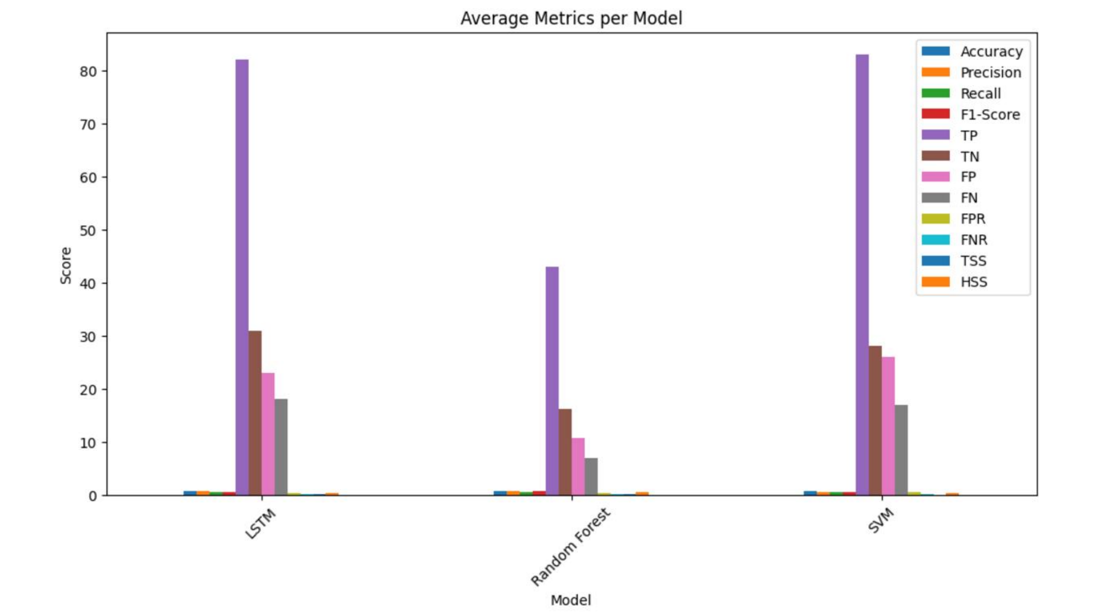
2.5.2 confusion metrix for random forest



2.5.3 confusion metrix for LSTM



2.5.4 confusion metrix for SVM



2.5.5 average metrix per model

```
Model Comparison:
           Model  Average Accuracy  Average F1-Score  Average TSS  Average HSS
0           LSTM          0.701299          0.557692     0.074074     0.332705
1  Random Forest          0.769498          0.643829     0.201709     0.475379
2            SVM          0.720779          0.565657     0.037037     0.362411

The best model for this dataset based on Average Accuracy is: Random Forest with an Accuracy of 0.7695.
Models saved as 'rf_model.pkl', 'lstm_model.h5', and 'svm_model.pkl'
```

2.5.6 matrix comparison based on average of accuracy

2.6 Other:

The source code (.py file) and data sets (.csv files) will be attached to the zip file.

2.7 Link to Git Repository:

https://github.com/ad2389/DM_finalproject