Epileptic Seizure Prediction using EEG signals

A Project Report By

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AIM: The Objective of the project is to solve a current world problem with the help of Machine Learning.

Problem Statement: Epileptic Seizure Prediction using Machine learning to detect and avoid sleep anomalies and convulsion threats.

Analysis:

The project involves comparison of various results obtained via different types of machine learning models. These models are developed and implemented using the famous libraries 'keras' and 'Scikit-learn'. The models used over in the projects are:

- 1. Decision Tree
- 2. KNN classifier
- 3. Naive Bayes
- 4. Random Forest
- 5. SVM
- 6. ANN
- **7. RNN**
- 8. LSTM
- 9. CNN

- 1. Decision Tree: A decision tree is a supervised machine learning algorithm that builds a tree-like model to make decisions or predictions by learning from input data. It splits the data based on different attributes and creates a tree structure where each internal node represents a decision rule and each leaf node represents an outcome.
- **2. KNN** classifier: K-nearest neighbors (KNN) classifier is a supervised learning algorithm that assigns a class label to an input sample based on its K nearest neighbors in the training data. It measures the similarity between instances using distance metrics and assigns the most common class label among the K nearest neighbors to the input sample.
- **3. Naive Bayes:** Naive Bayes is a probabilistic machine learning algorithm that is based on Bayes' theorem. It assumes that the features in the data are conditionally independent of each other given the class label. It calculates the probability of a sample belonging to a particular class based on the feature values and assigns the class label with the highest probability.
- **4. Random Forest:** Random Forest is an ensemble learning method that combines multiple decision trees to create a more robust and accurate model. It generates a set of decision trees by bootstrapping the training data and selecting random subsets of features for each tree. The final prediction is made by aggregating the predictions of all individual trees.
- **5. SVM (Support Vector Machine):** Support Vector Machine is a powerful supervised learning algorithm used for classification and regression tasks. It finds an optimal hyperplane that separates the data points of different classes with the maximum margin. SVM can handle both linear and non-linear data by using different kernel functions.
- **6. ANN (Artificial Neural Network):** Artificial Neural Network is a computational model inspired by the structure and functionality of the human brain. It consists of interconnected nodes or "neurons" organized in layers. ANN can learn and generalize from input data to make predictions or decisions. It is commonly used for various machine learning tasks including classification, regression, and pattern recognition.

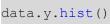
- **7. RNN (Recurrent Neural Network):** Recurrent Neural Network is a type of neural network that is designed to process sequential data. It has connections between the nodes that form a directed cycle, allowing information to be stored and propagated across multiple time steps. RNNs are suitable for tasks such as natural language processing, speech recognition, and time series analysis.
- **8. CNN (Convolutional Neural Network):** Convolutional Neural Network is a deep learning architecture primarily used for image recognition and computer vision tasks. It consists of multiple layers, including convolutional layers that apply filters to input images, pooling layers that downsample the features, and fully connected layers that make predictions. CNNs are capable of automatically learning hierarchical representations of visual data.
- **9. LSTM (Long Short-Term Memory):** Long Short-Term Memory is a specialized type of recurrent neural network architecture. It is designed to overcome the limitation of traditional RNNs in capturing long-term dependencies. LSTM introduces memory cells and gating mechanisms that allow it to selectively store and retrieve information over extended sequences, making it particularly effective in tasks involving long-range dependencies.

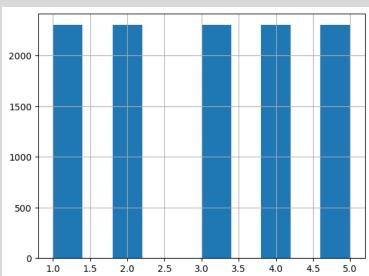
Code:

```
import pandas as pd
import scipy
import matplotlib.pyplot as plt
import numpy as np
from sklearn.utils import shuffle
from sklearn.model selection import GridSearchCV
from sklearn.preprocessing import normalize, StandardScaler
from sklearn.model selection import train test split
from sklearn.pipeline import Pipeline
from sklearn.metrics import accuracy score
from sklearn.model selection import cross validate,
RepeatedStratifiedKFold, GridSearchCV
from sklearn.linear model import LogisticRegression
from sklearn.svm import SVC
from sklearn.neighbors import KNeighborsClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier,
GradientBoostingClassifier
import plotly
import plotly.figure factory as ff
from plotly import tools
from plotly.offline import init notebook mode, iplot
import imblearn
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.metrics import confusion matrix
from keras.layers import Dense, Convolution1D, MaxPool1D, Flatten, Dropout
from keras.layers import Input, LSTM
from keras.models import Model
from tensorflow import keras
from tensorflow.keras import layers
# from keras.layers.normalization import BatchNormalization
from keras.layers import BatchNormalization
import keras
from matplotlib.pyplot import figure
```

```
from keras.callbacks import EarlyStopping, ModelCheckpoint
init notebook mode(connected=True)
pd.set option('display.max columns', 100)
# 응응
# import mne
# import pandas as pd
# import numpy as np
# # Load the .edf file into Python
# raw = mne.io.read raw edf('rsvp 10Hz 02a.edf')
# # Extract the EEG signals
# eeg data = raw.get data()
# # Convert the EEG signals into a pandas DataFrame
# df = pd.DataFrame(np.transpose(eeg data))
# # Save the DataFrame as a .csv file
# df.to csv('sample.csv', index=False)
# 응응
data = pd.read csv("sample.csv")
# 응응
data.head()
# 응응
data.tail()
# 응응
data.shape
# %% [markdown]
# This dataset is a pre processed form of Electroencephalogram (EEG)
signals specifically collected for the sake of predicting Epileptic
seizures. This dataset contains 11500 samples and 180 features, each
feature representing the EEG signal data.
```

```
# %% [markdown]
# ROWS: 11500
# COLUMNS: 180
# %% [markdown]
# The last column contains the category of the 178-dimensional input
vector. y can take values: {1, 2, 3, 4, 5}
# 5 - eyes open, means when they were recording the EEG signal of the
brain the patient had their eyes open
# 4 - eyes closed, means when they were recording the EEG signal the
patient had their eyes closed
# 3 - Yes they identify where the region of the tumor was in the brain and
recording the EEG activity from the healthy brain area
# 2 - They recorder the EEG from the area where the tumor was located
# 1 - Recording of seizure activity All subjects falling in classes 2, 3,
4, and 5 are subjects who did not have epileptic seizure. Only subjects in
class 1 have epileptic seizure.
# 응응
data['y'].value counts()
# %%
```





```
# 응응
plt.figure(figsize=(50,4))
plt.subplot(131)
[plt.plot(data.values[i][1:-1]) for i in range(23)];
  500
 -500
 -1000
 -1500
       Ö
                25
                          50
                                             100
                                                      125
                                                                150
                                                                         175
# %% [markdown]
# As we can see, samples with y label {1} have seizures whereas all other
\{2,3,4,5\} do not have seizures. So this multi-classification task can be
converted to a binary classification task. The first part will cover
binary classification. Later we'll train the models for
multi-classification.
# 응응
dic = \{5: 0, 4: 0, 3: 0, 2: 0, 1: 1\}
data['y'] = data['y'].map(dic)
#Converting this to a binary classification task
# 응응
print(data['y'].value counts())
data.head()
# 응응
data = data.drop('Unnamed', axis = 1)
# 응응
data = shuffle(data)
# 응응
data.describe()
```

```
# 응응
data.info()
# 응응
print('Number of records of Non Epileptic {0} VS Epilepttic
\{1\}'.format(len(data[data['y'] == 0]), len(data[data['y'] == 1])))
# 응응
#Description of Non Epileptic
data[data['y'] == 0].describe().T
# 응응
#Description of Epileptic
data[data['y'] == 1].describe().T
print('Mean VALUE for Epiletic: {}'.format((data[data['y'] ==
1].describe().mean()).mean()))
print('Std VALUE for Epiletic: {}'.format((data[data['y'] ==
1].describe().std()).std()))
print('Totall Mean VALUE for NON Epiletic: {}'.format((data[data['y'] ==
0].describe().mean()).mean()))
print('Totall Std VALUE for NON Epiletic: {}'.format((data[data['y'] ==
0].describe().std()).std()))
# %%
#lists of arrays containing all data without y column
not epileptic = [data[data['y']==0].iloc[:, range(0,
len (data.columns) -1) ].values]
epileptic = [data[data['y']==1].iloc[:, range(0,
len (data.columns) -1) ].values]
#We will create and calculate 2d indicators in order plot data in 2
dimensions;
def indic(data):
```

```
"""Indicators can be different. In our case we use just min and max
values
    Additionally, it can be mean and std or another combination of
indicators"""
    max = np.max(data, axis=1)
    min = np.min(data, axis=1)
    return max, min
x1, y1 = indic(not epileptic)
x2, y2 = indic(epileptic)
fig = plt.figure(figsize=(14,6))
ax1 = fig.add subplot(111)
ax1.scatter(x1, y1, s=10, c='b', label='Not Epiliptic')
ax1.scatter(x2, y2, s=10, c='r', label='Epileptic')
plt.legend(loc='lower left');
plt.show()
 -400
 -600
 -800
 -1000
 -1200
 -1400
 -1600
 -1800
        Not Epiliptic
        Epileptic
                                      1200
                                                        1600
           600
                   800
                            1000
                                               1400
                                                                 1800
                                                                          2000
# 응응
#Epileptic
x,y = indic(data[data['y']==1].iloc[:, range(0,
len(data.columns) -1)].values)
plt.figure(figsize=(14,4))
plt.title('Epileptic')
plt.scatter(x, y, c='r');
```

```
Epileptic
 -250
 -500
 -750
 -1000
 -1250
 -1500
 -1750
                                                           1500
                                                                    1750
                                                                              2000
# 응응
#Not Epileptic
x,y = indic(data[data['y']==0].iloc[:, range(0,
len(data.columns) -1)].values)
plt.figure(figsize=(14,4))
plt.title('NOT Epileptic')
plt.scatter(x, y);
                                        NOT Epileptic
 -200
 -400
 -600
 -800
 -1000
 -1200
                                           1000
                                                            1500
                                                                              2000
# %%
print('Number of records of Non Epileptic {0} VS Epilepttic
\{1\}'.format(len(data[data['y'] == 0]), len(data[data['y'] == 1])))
# %% [markdown]
# ### Removing Outliers
# %%
X = data.drop('y', axis=1)
y = data['y']
df = pd.DataFrame(normalize(X))
```

```
# Initialize the counters for detected and managed outliers
detected outliers = 0
managed outliers = 0
# Loop through each of the 178 explanatory variables and calculate the IQR
and bounds
for col in df.columns[:-1]:
   Q1 = df[col].quantile(0.25)
   Q3 = df[col].quantile(0.75)
   IOR = 03 - 01
   lower bound = Q1 - 1.5 * IQR
   upper bound = Q3 + 1.5 * IQR
    # Identify any data points that fall outside the bounds and either
remove or adjust them
   outliers = (df[col] < lower bound) | (df[col] > upper bound)
   if outliers.any():
        detected outliers += outliers.sum()
        df.loc[outliers, col] = np.nanmedian(df[col])
        managed outliers += outliers.sum()
print(f"Detected {detected outliers} outliers and managed
{managed outliers} outliers.")
# %% [markdown]
# ### Eliminating Imbalance
# %% [markdown]
# As we can see, this dataset is quite imbalanced, so we'll need to
perform balancing techniques. This can be done using the imblearn library
in Python that can create synthetic samples in order to balance out the
data and thus provide us with more accurate results.
# %%
# define oversampling strategy
```

```
oversample =
imblearn.over sampling.RandomOverSampler(sampling_strategy='minority')
# fit and apply the transform
X, y = oversample.fit resample(data.drop('y', axis=1), data['y'])
X.shape, y.shape
# 응응
print('Number of records of Non Epileptic {0} VS Epilepttic
{1}'.format(len(y == True), len(y == False)))
# %% [markdown]
# Now the data is balanced as number of records for epileptic as well as
non epileptic are equal (18400) Before it was 2300 by 9200
# %% [markdown]
# ### Normalizing
# 응응
# X = data.drop('y', axis=1)
# y = data['y']
normalized df = pd.DataFrame(normalize(X))
normalized df
# 응응
normalized df['y'] = y
print('Normalized Totall Mean VALUE for Epiletic:
{}'.format((normalized df[normalized df['y'] ==
1].describe().mean()).mean()))
print('Normalized Totall Std VALUE for Epiletic:
{}'.format((normalized df[normalized df['y'] ==
1].describe().std()).std()))
print('Normalized Totall Mean VALUE for NOT Epiletic:
{}'.format((normalized df[normalized df['y'] ==
0].describe().mean()).mean()))
```

```
print('Normalized Totall Std VALUE for NOT Epiletic:
{}'.format((normalized df[normalized df['y'] ==
0].describe().std()).std()))
# %% [markdown]
# #### Splitting data
# 응응
X = normalized df.drop('y', axis=1)
y = normalized df['y']
X train, X test, y train, y test = train test split(X, y, test size=.3,
random state=42)
# Split the training set into training and validation sets
X train, X val, y train, y val = train test split(X train, y train,
test size=0.2, random state=42)
# 응응
#Check the shapes after splitting
he = X train, X test, y train, y test
[arr.shape for arr in he]
# %% [markdown]
# ### Testing on Models
# %% [markdown]
# 1. Decision Tree
# 응응
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import confusion matrix
from sklearn.metrics import accuracy score
from sklearn.metrics import classification report
dtree model = DecisionTreeClassifier(max depth =
None, min_samples_split=2, criterion='entropy').fit(X train,
y train.values.ravel())
```

```
dtree predictions = dtree model.predict(X test)
#accuracy = DecisionTreeClassifier.score(X test, y test)
#print(accuracy)
# creating a confusion matrix
cm = confusion matrix(y test, dtree predictions)
print(classification report(y test, dtree predictions))
accuracy = accuracy score(y test, dtree predictions)
print("Accuracy:", accuracy)
# %% [markdown]
# 2. KNN classifier
# 응응
from sklearn.neighbors import KNeighborsClassifier
knn = KNeighborsClassifier(n_neighbors = 3).fit(X train,
y train.values.ravel())
knn predictions = knn.predict(X test)
cm = confusion matrix(y test, knn predictions)
print(classification report(y test,knn predictions))
accuracy knn = accuracy score(y test, knn predictions)
print(accuracy knn)
# %% [markdown]
# 3. Naive Bayes Classifier
# 응응
# training a Naive Bayes classifier
from sklearn.naive bayes import GaussianNB
gnb = GaussianNB(var_smoothing=1e-09).fit(X_train, y_train.values.ravel())
gnb predictions = gnb.predict(X test)
# accuracy on X test
accuracy = gnb.score(X test, y test)
print(accuracy)
```

```
# creating a confusion matrix
cm = confusion matrix(y test, gnb predictions)
print('Accuracy: ${cm}')
print(classification report(y test, gnb predictions))
# %% [markdown]
# 4. Random Forest Classifier
# 응응
from sklearn.ensemble import RandomForestClassifier
import sklearn.metrics as metrics
clf4 = RandomForestClassifier(random state=42, n estimators=10)
clf4.fit(X train, y train.values.ravel())
y pred4 = clf4.predict(X test)
Acc2 = metrics.accuracy score(y test, y pred4)
print (Acc2)
cm = confusion matrix(y test, y pred4)
print('Accuracy: ${cm}')
print(classification report(y test, y pred4))
# 응응
from sklearn.svm import SVC
# 응응
model = SVC(kernel= 'rbf')
model.fit(X train, y train)
# 응응
predictions = model.predict(X test)
# 응응
print("Accuracy:", metrics.accuracy score(y test, predictions))
print("Precision:", metrics.precision score(y test, predictions))
print("Recall:", metrics.recall score(y test, predictions))
# %% [markdown]
# ### Creating an Artificial Neural Network
```

```
# 응응
import tensorflow as tf
from keras.models import Sequential
from keras.utils import np utils
from keras.layers import Dense, Activation
# %% [markdown]
# Defining the model
# 응응
model = Sequential()
# 응응
# Add a dense layer with 10 neurons and ReLU activation function as the
input layer
model.add(Dense(256, input dim=X train.shape[1], activation='LeakyReLU'))
model.add(Dense(128, input dim=X train.shape[1], activation='LeakyReLU'))
model.add(Dense(128, input dim=X train.shape[1], activation='LeakyReLU'))
model.add(Dense(64, input_dim=X train.shape[1], activation='LeakyReLU'))
model.add(Dense(32, input dim=X train.shape[1], activation='LeakyReLU'))
model.add(Dense(32, input dim=X train.shape[1], activation='LeakyReLU'))
model.add(Dense(32, input dim=X train.shape[1], activation='LeakyReLU'))
model.add(Dense(16, input dim=X train.shape[1], activation='LeakyReLU'))
model.add(Dense(16, input dim=X train.shape[1], activation='LeakyReLU'))
model.add(Dense(8, input_dim=X train.shape[1], activation='LeakyReLU'))
model.add(Dense(5, input dim=X train.shape[1], activation='LeakyReLU'))
# Add a dense layer with 1 neuron and sigmoid activation function as the
output layer
model.add(Dense(1, activation='softmax'))
# Compile the model
model.compile(loss='binary crossentropy', optimizer='SGD',
metrics=['accuracy'])
# Train the model on the training data
model.fit(X train, y train, epochs=50, batch size=32, verbose=1)
# Evaluate the model on the test data
test loss, test accuracy = model.evaluate(X test, y test, verbose=0)
```

```
print("Test loss:", test loss)
print("Test accuracy:", test accuracy)
# %%
model.summary()
# %% [markdown]
# ### Parallel Implementation of Support Vector Machine
# %% [markdown]
# This parallel implementation will be done using the JobLIB library in
python and sklearn for SVM. This will speed up the training of the model.
# 응응
from sklearn.svm import SVC
from sklearn.model selection import train test split
from sklearn.metrics import accuracy score
from joblib import Parallel, delayed
# %%
def train svm(X train subset, y train subset, X test, y test):
   clf = SVC(kernel='rbf')
    clf.fit(X train subset, y train subset)
   y pred = clf.predict(X test)
   return accuracy score (y test, y pred)
# 응응
n cores = 2 # number of CPU cores to use
accuracies = Parallel(n jobs=n cores)(
   delayed(train svm)(X train subset, y train subset, X test, y test)
    for X train subset, y train subset in zip(np.array split(X train,
n cores), np.array split(y train, n cores))
# 응응
mean accuracy = np.mean(accuracies)
print(f"Mean accuracy: {mean accuracy}")
```

```
# %% [markdown]
# ### ANN
# 응응
from keras.models import Sequential
from keras.layers import Dense, Dropout
num features = X train.shape[1]
# Define the model
model = Sequential()
model.add(Dense(64, activation='relu', input_shape=(num features,)))
model.add(Dropout(0.5))
model.add(Dense(32, activation='relu'))
model.add(Dropout(0.5))
model.add(Dense(1, activation='sigmoid'))
# Compile the model
model.compile(loss='binary crossentropy', optimizer='adam',
metrics=['accuracy'])
# Train the model
model.fit(X train, y train, epochs=500, batch size=32,
validation_data=(X val, y val))
# Evaluate the model on the test set
loss, accuracy = model.evaluate(X test, y test)
print('Test accuracy:', accuracy)
# %% [markdown]
# ## Recurrent Neural Network
# %%
import numpy as np
from keras.models import Sequential
from keras.layers import Dense, SimpleRNN
# Define hyperparameters
seq length = 10
```

```
input dim = 32
hidden units = 64
# Generate some sample data
x train = np.random.rand(100, seq length, input dim)
y train = np.random.randint(0, 2, size=(100,))
# Define RNN model
model = Sequential()
model.add(SimpleRNN(units=hidden units, input shape=(seq length,
input dim)))
model.add(Dense(units=1, activation='sigmoid'))
# Compile model
model.compile(loss='binary crossentropy', optimizer='adam',
metrics=['accuracy'])
# Train model
model.fit(x train, y train, epochs=10, batch_size=32)
# Generate some sample test data
x \text{ test} = \text{np.random.rand}(50, \text{ seq length, input dim})
y test = np.random.randint(0, 2, size=(50,))
# Evaluate model on test data
loss, accuracy = model.evaluate(x test, y test)
print(accuracy)
# 응응
X train.shape, X test.shape
# 응응
y train.shape
# %% [markdown]
# ### Defining a Convolutional Network
# 응응
def evaluate model(history, X_test, y_test, model):
```

```
scores = model.evaluate((X test), y test, verbose=0)
   print("Accuracy: %.2f%%" % (scores[1]*100))
   print(history)
   fig1, ax acc = plt.subplots()
   plt.plot(history.history['accuracy'])
   plt.plot(history.history['val accuracy'])
   plt.xlabel('Epoch')
   plt.ylabel('Accuracy')
   plt.title('Model - Accuracy')
   plt.legend(['Training', 'Validation'], loc='lower right')
   plt.show()
   fig2, ax loss = plt.subplots()
   plt.xlabel('Epoch')
   plt.ylabel('Loss')
   plt.title('Model - Loss')
   plt.legend(['Training', 'Validation'], loc='upper right')
   plt.plot(history.history['loss'])
   plt.plot(history.history['val loss'])
   plt.show()
   target names=['1','2', '3']
   y true=[]
   for element in y test:
        y true.append(np.argmax(element))
   prediction proba=model.predict(X test)
   prediction=np.argmax(prediction proba,axis=1)
   cnf matrix = confusion matrix(y true, prediction)
# 응응
def network CNN(X train, y train):
   im shape=(X train.shape[1],1)
   inputs cnn=Input(shape=(im shape), name='inputs cnn')
   conv1d 1 = layers.Conv1D(filters=32, kernel size=6)(inputs cnn)
   batch normalization = BatchNormalization()(conv1d 1)
   max pooling1d = layers.MaxPooling1D( 2,
padding='same') (batch normalization)
   conv1d 2 = layers.Conv1D(filters=64, kernel size=3) (max pooling1d)
   batch normalization 1 = BatchNormalization()(conv1d 2)
```

```
max pooling1d 1 = layers.MaxPooling1D(2,
padding='same') (batch normalization 1)
    flatten = Flatten() (max pooling1d 1)
    dense = Dense(32) (flatten)
    dense 1 = Dense(16) (dense)
   main output = Dense(2)(dense 1)
    model1 = Model(inputs= inputs cnn, outputs=main output)
   model1.compile(optimizer='adam',
loss='sparse categorical crossentropy',metrics = ['accuracy'])
   return (model1)
# 응응
model1 = network CNN(X train, y train)
print(model1.summary())
# %%
save path = './tmp/checkpoint 1'
model checkpoint callback = keras.callbacks.ModelCheckpoint(
   filepath=save path,
   save weights only=True,
   monitor='val accuracy',
   mode='max',
    save best only=True)
history = model1.fit(X train, y train,epochs=100, batch size=32,
validation data=(X val, y val), callbacks=[model checkpoint callback])
# 응응
X train.shape , y train.shape
# 응응
evaluate model(history, X test, y test, model1)
y pred=model1.predict(X test)
# 응응
model1.load weights(save path)
evaluate model(history, X test, y test, model1)
# %% [markdown]
```

```
# ### Bidirectional LSTM
# 응응
def network LSTM(X_train,y_train):
    im shape=(X train.shape[1],1)
    inputs lstm=Input(shape=(im shape), name='inputs lstm')
    dense = Dense(units=32, activation='relu', name='dense')(inputs lstm)
    lstm = layers.Bidirectional(LSTM(units=128, name='lstm'))(dense)
    dropout = Dropout(0.3)(lstm)
   batch normalization =
BatchNormalization(name='batch normalization')(dropout)
    dense 1 = Dense(units=64, activation='relu',
name='dense 1') (batch normalization)
    dropout 2 = Dropout(0.3, name='dropout 2')(dense 1)
   batch normalization 1 =
BatchNormalization(name='batch normalization 1')(dropout 2)
    main output = Dense(units=2,
activation='softmax') (batch normalization 1)
    model = Model(inputs= inputs lstm, outputs=main output)
    model.compile(optimizer='adam',
loss='sparse categorical crossentropy',metrics = ['accuracy'])
   return (model)
# 응응
model2 = network LSTM(X train, y train)
print(model2.summary())
# 응응
# Training Bidirectional LSTM model
# Saving model at highest validation accuracy
save path = './tmp/checkpoint 2'
model checkpoint callback = keras.callbacks.ModelCheckpoint(
   filepath=save path,
    save weights only=True,
   monitor='val accuracy',
   mode='max',
    save best only=True)
```

```
history2 = model2.fit(X_train, y_train,epochs=50, batch_size=32,
validation_data=(X_val,y_val), callbacks=[model_checkpoint_callback])

# %%
evaluate_model(history2, X_test, y_test, model2)

# %%
model2.load_weights(save_path)
evaluate_model(history2, X_test, y_test, model2)
```

CONTRIBUTIONS:

- 1. Rushil Shivade
- 2. Chirag Kathoye

OUTPUT:

On a comparative study of these models, we get the following results:

Model	Accuracy	Error	
1. Decision Tree	87.71 %	12.29 %	
2. KNN Classifier	91.83 %	8.17 %	
3. Naive Bayes	60.52 %	39.48 %	
4. Random Forest	94.14 %	5.86 %	
5. SVM	86.64 %	13.36 %	
6. ANN	49.58 %	50.42 %	
7. RNN	43.99 %	56.01 %	
8. LSTM	96.85 %	3.15 %	
9. CNN	53.42 %	46.58 %	

1. Decision Tree

[]					
	precision	recall	f1-score	support	
0	0.94	0.80	0.86	2754	
1	0.82	0.95	0.88	2766	
accuracy			0.87	5520	
accuracy	0.88	0.87	0.87 0.87	5520	
macro avg					
weighted avg	0.88	0.87	0.87	5520	
Accuracy: 0.8739130434782608					

2. KNN

[]	pr Inc(acc.				
		precision	recall	f1-score	support
	0	0.92	0.88	0.90	2754
	1	0.88	0.93	0.90	2766
	accuracy			0.90	5520
	macro avg	0.90	0.90	0.90	5520
	weighted avg	0.90	0.90	0.90	5520
	0.90217391304	34783			

3. Naive Bayes

[]						
•••	0.5907608695652173 Accuracy: \${cm}					
		precision	recall	f1-score	support	
	0	0.60	0.54	0.57	2754	
	1	0.58	0.65	0.61	2766	
	accuracy			0.59	5520	
	macro avg	0.59	0.59	0.59	5520	
	weighted avg	0.59	0.59	0.59	5520	

4. Random Forest

```
0.9380434782608695
Accuracy: ${cm}
              precision recall f1-score
                                              support
                   0.94
                             0.94
                                       0.94
           0
                                                 2754
           1
                   0.94
                            0.94
                                       0.94
                                                 2766
                                       0.94
                                                 5520
    accuracy
   macro avg
                                       0.94
                  0.94
                            0.94
                                                 5520
weighted avg
                   0.94
                            0.94
                                       0.94
                                                 5520
```

5. SVM

```
mean_accuracy = np.mean(accuracies)
    print(f"Mean accuracy: {mean_accuracy}")

[ ]

... Mean accuracy: 0.8603260869565217
```

6. ANN

```
Epoch 13/500
...
Epoch 500/500
322/322 [============] - 1s 2ms/step - loss: 0.1931 - accuracy: 0.9236 - val_loss: 0.3889 - val_accuracy: 0.8901
173/173 [============] - 0s 1ms/step - loss: 0.4431 - accuracy: 0.8842
Test accuracy: 0.884239137172699
Output is truncated. View as a scrollable element or open in a text editor. Adjust cell output settings...
```

7. RNN

8. CNN

```
model1.load_weights(save_path)
evaluate_model(history,X_test,y_test,model1)

... Accuracy: 53.42%
<keras.callbacks.History object at 0x000001EC52AA1AB0>

Model - Accuracy

Model - Accuracy
```

9. LSTM

```
model2.load_weights(save_path)
    evaluate_model(history2,X_test,y_test,model2)

... Accuracy: 96.85%
    <keras.callbacks.History object at 0x0000001EC5CA24640>

// Model - Accuracy
```

GRAPHS:

Graphs of Accuracy and Loss for LSTM (giving highest accuracy)

