

Experiment No.4
AI for disease Prognosis
Date of Performance: 16/08/2024
Date of Submission: 11/09/2024

Aim: To perform AI for prognosis of a diseases

Objective: The objective of this experiment is to develop an AI-powered disease prognosis system that employs advanced machine learning algorithms, specifically convolutional neural networks (CNNs) for medical imaging and recurrent neural networks (RNNs) for time series data.

Theory:

The objective of using AI for the prognosis of diseases is to improve the accuracy and effectiveness of disease prediction, allowing for earlier and more precise diagnoses and treatment. AI can be a valuable tool in healthcare for a variety of purposes related to disease prognosis:

Early Detection: Detect diseases or medical conditions at an earlier stage when treatment is more effective, potentially saving lives and reducing the severity of the disease's impact.

Risk Assessment: Assess an individual's risk of developing a particular disease based on a range of factors, such as genetics, lifestyle, and medical history.

Personalized Medicine: Tailor treatment plans to individual patients based on their unique characteristics and needs, improving the effectiveness of treatments and reducing side effects.

Predictive Analytics: Use historical patient data to predict disease outcomes and recommend appropriate interventions or treatments.

Resource Allocation: Optimize healthcare resource allocation by identifying patients at higher risk and allocating resources accordingly. This can be especially important in resource-constrained healthcare systems.

Patient Engagement: Engage patients in their own healthcare by providing them with personalized health insights and recommendations.

Reducing Healthcare Costs: Improve the efficiency of healthcare systems by reducing unnecessary tests and treatments through more accurate prognosis and diagnosis.

Research and Drug Development: Assist researchers in identifying potential drug candidates or treatment strategies based on AI analysis of disease pathways and patient data.

Public Health Planning: Help public health officials and organizations plan for disease outbreaks, resource allocation, and prevention strategies.

Chronic Disease Management: Aid in the management of chronic diseases by providing ongoing monitoring and early warnings of potential complications.

Telemedicine: Enable remote monitoring and diagnosis, particularly in underserved or remote areas.

Quality of Life Improvement: Enhance the quality of life for patients by enabling proactive and preventive healthcare rather than just reactive treatment.

In summary, the primary objective of using AI for disease prognosis is to improve healthcare outcomes, reduce costs, and enhance the overall quality of care by providing more accurate, personalized, and timely information to healthcare providers, researchers, and patients. AI has the potential to transform the healthcare industry by making disease prognosis and management more data-driven and patient-centric.

Code: -

```
File Edit Selection View Go Run Search
AIHC_Epdt_Apynb X
C:\Users> Ana3\Downloads> AIHC_Epdt_Apynb> AI for disease Prognosis
+ Code + Markdown Run All Clear All Outputs Outline Python 3.11.8

AI for disease Prognosis

!pip install tensorflow
!pip install numpy
!pip install pandas
!pip install matplotlib

tensorflow is already satisfied: tensorflow in /usr/local/lib/python3.10/site-packages (2.17.0)
absl-py==1.8.0 is already satisfied: absl-py in /usr/local/lib/python3.10/site-packages (from tensorflow) (1.8.0)
astor==0.6.0 is already satisfied: astor in /usr/local/lib/python3.10/site-packages (from tensorflow) (0.6.0)
flatbuffers==23.5.26 is already satisfied: flatbuffers in /usr/local/lib/python3.10/site-packages (from tensorflow) (23.5.26)
gast==0.5.4 is already satisfied: gast in /usr/local/lib/python3.10/site-packages (from tensorflow) (0.5.4)
google-pasta==0.2.1 is already satisfied: google-pasta in /usr/local/lib/python3.10/site-packages (from tensorflow) (0.2.1)
h5py==3.10.0 is already satisfied: h5py in /usr/local/lib/python3.10/site-packages (from tensorflow) (3.10.0)
libclang==13.0.0 is already satisfied: libclang in /usr/local/lib/python3.10/site-packages (from tensorflow) (13.0.0)
ml-dtypes==0.5.0 is already satisfied: ml-dtypes in /usr/local/lib/python3.10/site-packages (from tensorflow) (0.5.0)
opt-einsum==3.3.0 is already satisfied: opt-einsum in /usr/local/lib/python3.10/site-packages (from tensorflow) (3.3.0)
packaging is already satisfied: packaging in /usr/local/lib/python3.10/site-packages (from tensorflow) (24.1)
protobuf==4.21.8 is already satisfied: protobuf in /usr/local/lib/python3.10/site-packages (from tensorflow) (4.21.8)
requests==2.31.0 is already satisfied: requests in /usr/local/lib/python3.10/site-packages (from tensorflow) (2.31.0)
setuptools is already satisfied: setuptools in /usr/local/lib/python3.10/site-packages (from tensorflow) (71.0.4)
six==1.16.0 is already satisfied: six in /usr/local/lib/python3.10/site-packages (from tensorflow) (1.16.0)
termcolor==2.3.0 is already satisfied: termcolor in /usr/local/lib/python3.10/site-packages (from tensorflow) (2.3.0)
typing-extensions==4.6.0 is already satisfied: typing-extensions in /usr/local/lib/python3.10/site-packages (from tensorflow) (4.6.0)
urllib3==2.1.0 is already satisfied: urllib3 in /usr/local/lib/python3.10/site-packages (from tensorflow) (2.1.0)
grpcio==2.6.1 is already satisfied: grpcio in /usr/local/lib/python3.10/site-packages (from tensorflow) (2.6.1)
```

```
File Edit Selection View Go Run Search
AIHC_Epdt_Apynb X
C:\Users> Ana3\Downloads> AIHC_Epdt_Apynb> AI for disease Prognosis
+ Code + Markdown Run All Clear All Outputs Outline Python 3.11.8

# Training set
train_generator = train_datagen.flow_from_directory(
    dataset_dir, # Path to the folder containing "COVID" and "NORMAL"
    target_size=(128, 128), # Resize images
    batch_size=32,
    class_mode='binary', # Binary classification (COVID or NORMAL)
    subset='training' # Use this subset for training
)

Found 260 Images belonging to 2 classes.

# Validation set
validation_generator = train_datagen.flow_from_directory(
    dataset_dir,
    target_size=(128, 128),
    batch_size=32,
    class_mode='binary',
    subset='validation' # Use this subset for validation
)

Found 64 Images belonging to 2 classes.

import tensorflow as tf
```

```

File Edit Selection View Go Run ... Search
AHM_Epi_Applb X
C:\Users> Ana > Downloads > AHM_Epi_Applb > AI for disease prognosis
+ Code + Markdown | Run All | Clear All Outputs | Outline ... Python 3.11.9

import tensorflow as tf

# Build CNN model
cnn_model = tf.keras.models.Sequential()

cnn_model.add(tf.keras.layers.Conv2D(32, (3, 3), activation='relu', input_shape=(128, 128, 3)))
cnn_model.add(tf.keras.layers.MaxPooling2D((2, 2)))
cnn_model.add(tf.keras.layers.Conv2D(64, (3, 3), activation='relu'))
cnn_model.add(tf.keras.layers.MaxPooling2D((2, 2)))
cnn_model.add(tf.keras.layers.Conv2D(128, (3, 3), activation='relu'))
cnn_model.add(tf.keras.layers.MaxPooling2D((2, 2)))

cnn_model.add(tf.keras.layers.Flatten())
cnn_model.add(tf.keras.layers.Dense(128, activation='relu'))
cnn_model.add(tf.keras.layers.Dropout(0.5)) # To prevent overfitting
cnn_model.add(tf.keras.layers.Dense(1, activation='sigmoid')) # Binary output

# Compile the CNN model
cnn_model.compile(optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])

[10]

--- /usr/local/lib/python3.10/dist-packages/keras/src/layers/convolutional/base_conv.py:187: UserWarning: Do not pass an 'input_shape'/'input_dim' argument to a layer
super().__init__(activity_regularizer=activity_regularizer, **kwargs)

# Train the CNN model

```

```

File Edit Selection View Go Run ... Search
AHM_Epi_Applb X
C:\Users> Ana > Downloads > AHM_Epi_Applb > AI for disease prognosis
+ Code + Markdown | Run All | Clear All Outputs | Outline ... Python 3.11.9

# Train the CNN model
history = cnn_model.fit(
    train_generator,
    epochs=10, # You can adjust the number of epochs
    validation_data=validation_generator
)

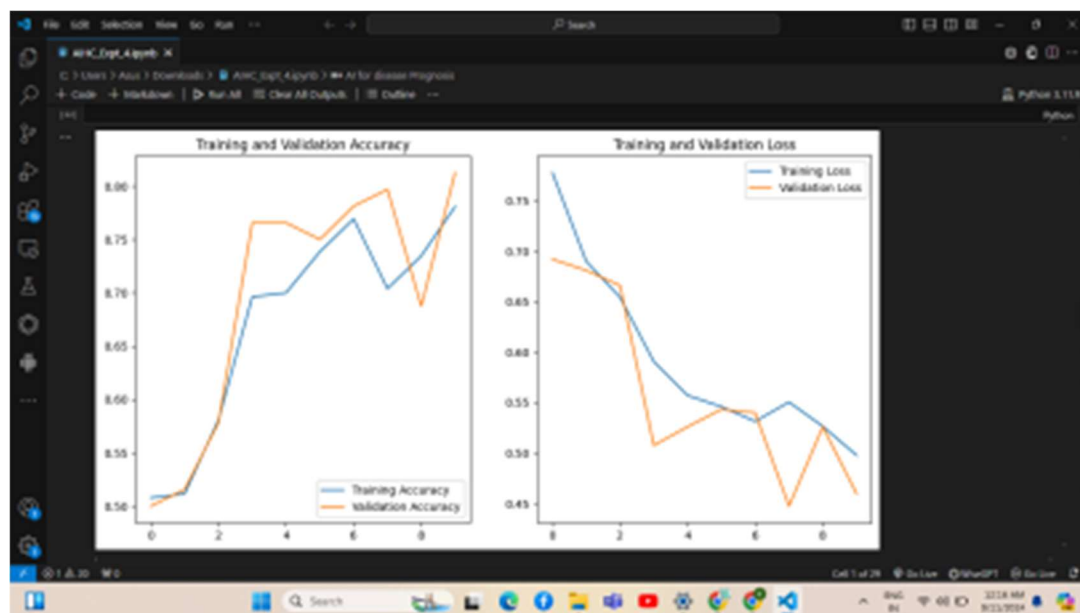
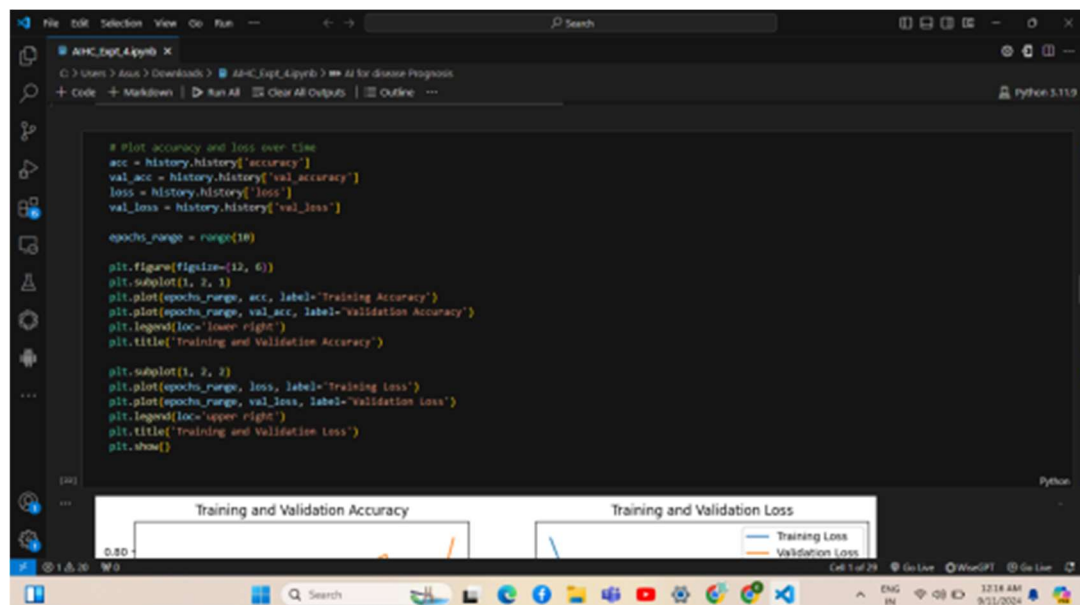
[10]

--- Epoch 1/10
/usr/local/lib/python3.10/dist-packages/keras/src/trainers/data_adapters/py_dataset_adapter.py:321: UserWarning: Your 'PyDataset' class should call 'super().__init__'
unif._warn_if_super_not_called()
6/9 100% 1s/step - accuracy: 0.5364 - loss: 0.8447 - val_accuracy: 0.5800 - val_loss: 0.6028
Epoch 2/10
6/9 100% 1s/step - accuracy: 0.4324 - loss: 0.6954 - val_accuracy: 0.5554 - val_loss: 0.6034
Epoch 3/10
6/9 100% 1s/step - accuracy: 0.5825 - loss: 0.6781 - val_accuracy: 0.5701 - val_loss: 0.6068
Epoch 4/10
6/9 100% 2s/step - accuracy: 0.6557 - loss: 0.6186 - val_accuracy: 0.7056 - val_loss: 0.5078
Epoch 5/10
6/9 100% 1s/step - accuracy: 0.6637 - loss: 0.5523 - val_accuracy: 0.7056 - val_loss: 0.5268
Epoch 6/10
6/9 100% 1s/step - accuracy: 0.7187 - loss: 0.5437 - val_accuracy: 0.7500 - val_loss: 0.5433
Epoch 7/10
6/9 100% 1s/step - accuracy: 0.7627 - loss: 0.5269 - val_accuracy: 0.7813 - val_loss: 0.5368
Epoch 8/10
6/9 100% 1s/step - accuracy: 0.8035 - loss: 0.5024 - val_accuracy: 0.7808 - val_loss: 0.4874
Epoch 9/10
6/9 100% 1s/step - accuracy: 0.7135 - loss: 0.5486 - val_accuracy: 0.6875 - val_loss: 0.5259
Epoch 10/10
6/9 100% 1s/step - accuracy: 0.7135 - loss: 0.5486 - val_accuracy: 0.6875 - val_loss: 0.5259

Cell 1 of 29 Go Live AI/ML Go Live
12:13 AM 8/11/2024

```

HAIMLSBL701 AI&ML in Healthcare La



```
File Edit Selection View Go Run ... Search
AHC_Epi_Apyrb X
C:\Users> Anaconda> Downloads> AHC_Epi_Apyrb> AI for disease Prognosis
+ Code + Markdown | Run All | Clear All Outputs | Outline ... Python 3.11.8

from sklearn.preprocessing import LabelEncoder

# Step 2: Identify non-numeric columns and encode them
# Select only numeric columns and convert categorical columns into numeric values
for column in data.columns:
    if data[column].dtype == 'object': # If the column is categorical
        print(f"Converting {column} column")
        le = LabelEncoder() # Initialize LabelEncoder
        data[column] = le.fit_transform(data[column].astype(str)) # Convert to numerical values

# Step 3: Separate features and target
x = data.iloc[:, :-1].values # Features
y = data.iloc[:, -1].values # Target (e.g., heart attack risk)

# Step 4: Normalize the features
scaler = MinMaxScaler()
```

Converting Patient ID column
Converting Sex column
Converting Blood Pressure column
Converting Diet column
Converting Country column
Converting Continent column
Converting Hemisphere column

Speakers (Realtek®) Audio: 100%
Cell 1 of 29 | Go Live | WwiseDPT | Go Live

12:29 AM 9/11/2024

```
File Edit Selection View Go Run ... Search
AHC_Epi_Apyrb X
C:\Users> Anaconda> Downloads> AHC_Epi_Apyrb> AI for disease Prognosis
+ Code + Markdown | Run All | Clear All Outputs | Outline ... Python 3.11.8

# Step 4: Normalize the features
scaler = MinMaxScaler()
X_scaled = scaler.fit_transform(X)

# Reshape the data for RNN
timesteps = 5 # You can adjust this based on your data
X_rnn = []
y_rnn = []

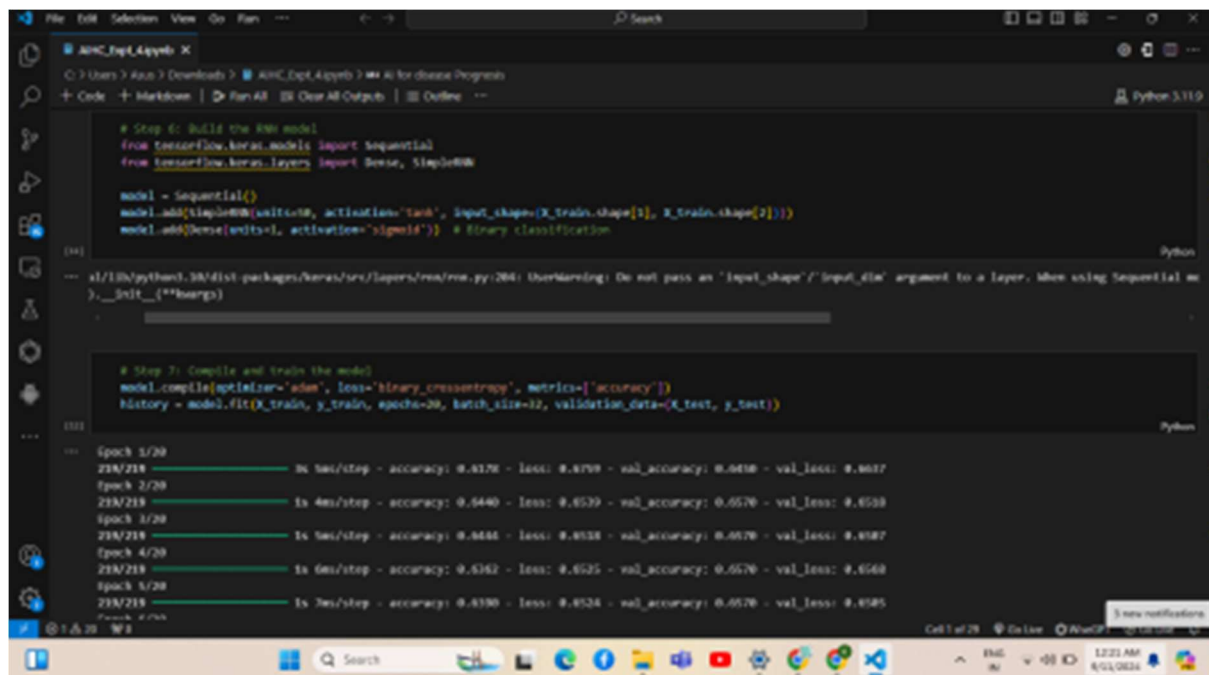
# Create sequences (for RNN input)
for i in range(timesteps, len(X_scaled)):
    X_rnn.append(X_scaled[i-timesteps:i, :]) # Create sequences of 'timesteps' length
    y_rnn.append(y[i])

X_rnn = np.array(X_rnn)
y_rnn = np.array(y_rnn)

# Step 5: Split the data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X_rnn, y_rnn, test_size=0.2, random_state=42)
```

Cell 1 of 29 | Go Live | WwiseDPT | Go Live

12:30 AM 9/11/2024



```
# Step 6: Build the RNN model
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Dense, SimpleRNN

model = Sequential()
model.add(SimpleRNN(units=10, activation='tanh', input_shape=(X_train.shape[1], X_train.shape[2])))
model.add(Dense(units=1, activation='sigmoid')) # binary classification

# Step 7: Compile and train the model
model.compile(optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])
history = model.fit(X_train, y_train, epochs=20, batch_size=32, validation_data=(X_test, y_test))

Epoch 1/20: 21s/step - accuracy: 0.8178 - loss: 0.8709 - val_accuracy: 0.6618 - val_loss: 0.9817
Epoch 2/20: 1s/step - accuracy: 0.8440 - loss: 0.8539 - val_accuracy: 0.6570 - val_loss: 0.9558
Epoch 3/20: 1s/step - accuracy: 0.8446 - loss: 0.8538 - val_accuracy: 0.6570 - val_loss: 0.9587
Epoch 4/20: 1s/step - accuracy: 0.8362 - loss: 0.8525 - val_accuracy: 0.6570 - val_loss: 0.9568
Epoch 5/20: 1s/step - accuracy: 0.8380 - loss: 0.8524 - val_accuracy: 0.6570 - val_loss: 0.9585
```

Google Collaboratory Link: -

<https://colab.research.google.com/drive/1ulgCXcFxMf4hXX7PIZphH61qYi2gRtWH?usp=sharing>

Conclusion: -

Comment on how useful it is to use AI for prognosis of a disease

Using AI for disease prognosis is highly beneficial due to its ability to improve diagnostic accuracy, offer early detection, and support personalized treatment plans. The application of AI models like CNNs and RNNs helps streamline healthcare, making it more data-driven, cost-effective, and proactive. While challenges like data privacy and model explainability exist, the advantages of AI in medical prognosis outweigh these issues, promising better patient outcomes and more efficient healthcare systems.