A

Assesment Report

on

“Predict Heart Disease:”

submitted as partial fulfillment for the award of

BACHELOR OF TECHNOLOGY DEGREE

SESSION 2024-25

in

Computer Science & Engineering (AI & ML)

By

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Introduction:

Heart disease is one of the leading causes of death globally. The goal of this project is to use machine learning to predict whether a person has heart disease or not, based on medical attributes such as age, cholesterol levels, blood pressure, etc.
The dataset used for this task was provided in CSV format and included various health-related features along with a target column indicating presence (1) or absence (0) of heart disease.

🔍 Methodology:

1. Dataset Loading: The dataset was uploaded directly to Google Colab using files.upload() to avoid manual input.
2. Data Inspection: The first five rows were displayed to understand the data structure.
3. Missing Values: All columns were checked, and it was confirmed that there were no missing values.
4. Feature and Target Separation: Features (X) were separated from the target (y).
5. Scaling: Features were standardized using StandardScaler to ensure uniformity across different scales.
6. Train-Test Split: The dataset was split into 80% training and 20% testing sets.
7. Model Selection: A RandomForestClassifier was chosen for its robustness and efficiency in classification tasks.
8. Training: The model was trained using the training data.
9. Evaluation: Performance was assessed using accuracy, precision, recall, and a confusion matrix.

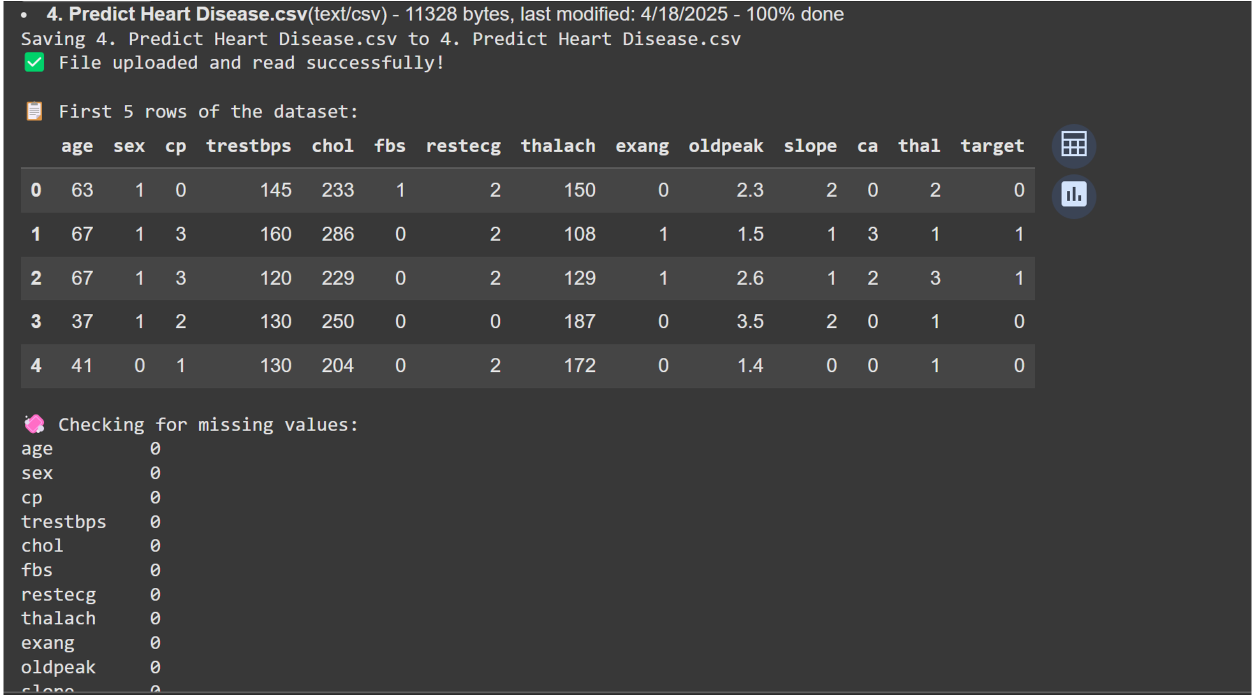
Code:

```
# 🗁 Step 1: Upload CSV directly (No manual input)

from google.colab import files
import pandas as pd
uploaded = files.upload()
```

```
# □ Step 2: Read uploaded CSV

import io
filename = list(uploaded.keys())[0]
df = pd.read_csv(io.BytesIO(uploaded[filename]))
print("✅ File uploaded and read successfully!")


# 📊 Step 3: Show first 5 rows in neat format

from IPython.display import display
print("\n📋 First 5 rows of the dataset:")
display(df.head())


# □ Step 4: Check missing values

print("\n□ Checking for missing values:")
print(df.isnull().sum())


# □ Step 5: Prepare features and labels

if 'target' not in df.columns:
    print("❌ 'target' column not found.")
else:
    X = df.drop('target', axis=1)
    y = df['target']


    # 🔧 Step 6: Feature scaling
    from sklearn.preprocessing import StandardScaler
    scaler = StandardScaler()
    X_scaled = scaler.fit_transform(X)

    # 🔀 Step 7: Train-test split
    from sklearn.model_selection import train_test_split
    X_train, X_test, y_train, y_test = train_test_split(X_scaled, y, test_size=0.2, random_state=42)
```

```
# 🌲 Step 8: Train model
from sklearn.ensemble import RandomForestClassifier
model = RandomForestClassifier(n_estimators=150, max_depth=7, random_state=42)
model.fit(X_train, y_train)

# 📈 Step 9: Evaluation

from sklearn.metrics import accuracy_score, precision_score, recall_score, confusion_matrix
y_pred = model.predict(X_test)

acc = accuracy_score(y_test, y_pred)
prec = precision_score(y_test, y_pred)
rec = recall_score(y_test, y_pred)

print("\n✅ Evaluation Metrics:")
print(f"✔ Accuracy: {acc*100:.2f}%")
print(f"✔ Precision: {prec:.2f}")
print(f"✔ Recall: {rec:.2f}")

# 🔥 Step 10: Confusion matrix heatmap

import seaborn as sns
import matplotlib.pyplot as plt

cm = confusion_matrix(y_test, y_pred)
plt.figure(figsize=(6,4))
sns.heatmap(cm, annot=True, fmt="d", cmap="coolwarm",
            xticklabels=["No Disease", "Disease"],
            yticklabels=["No Disease", "Disease"])
plt.title("❤ Heart Disease Prediction - Confusion Matrix")
plt.xlabel("Predicted")
plt.ylabel("Actual")
plt.show()
```

📸 Output / Result:

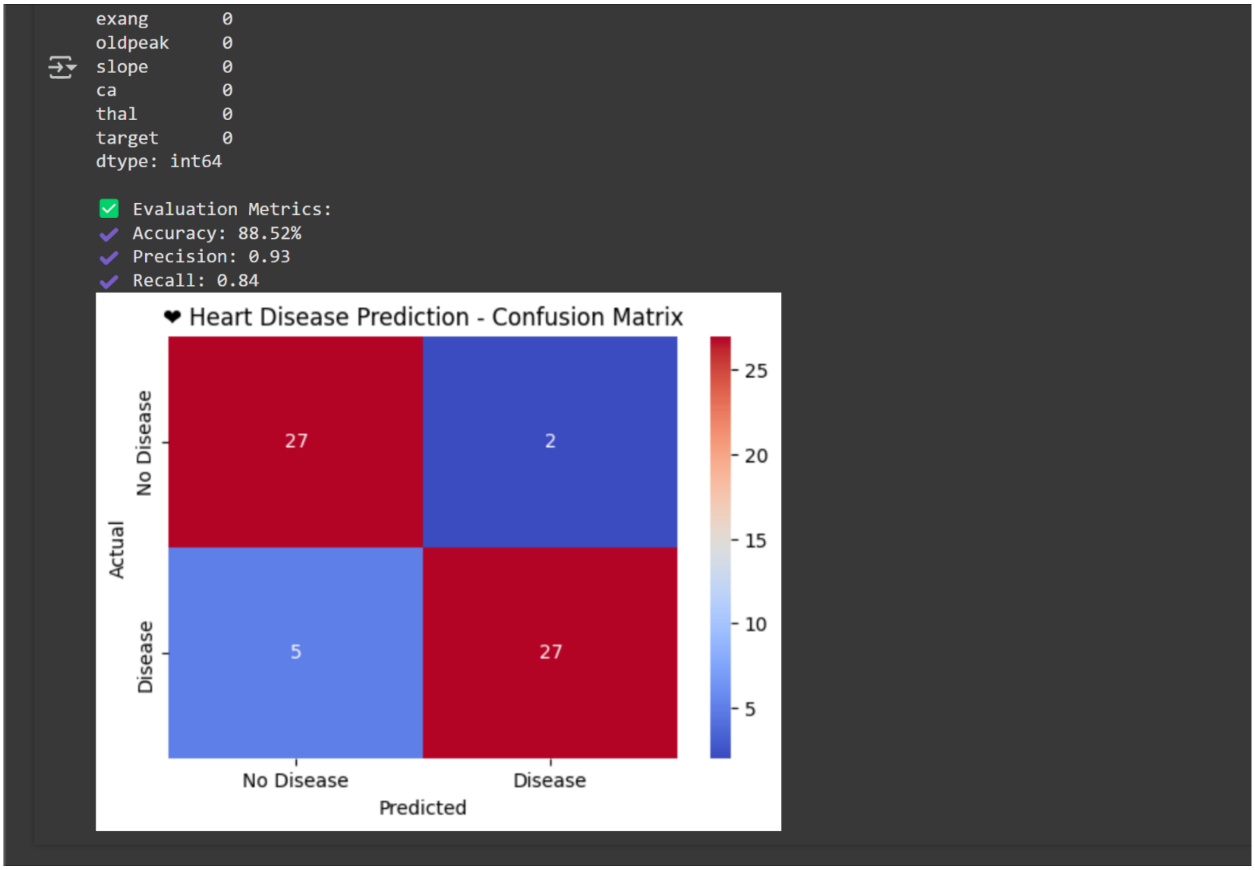


- **4. Predict Heart Disease.csv**(text/csv) - 11328 bytes, last modified: 4/18/2025 - 100% done

```
Saving 4. Predict Heart Disease.csv to 4. Predict Heart Disease.csv
✅ File uploaded and read successfully!

📋 First 5 rows of the dataset:
```

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	63	1	0	145	233	1	2	150	0	2.3	2	0	2	0
1	67	1	3	160	286	0	2	108	1	1.5	1	3	1	1
2	67	1	3	120	229	0	2	129	1	2.6	1	2	3	1
3	37	1	2	130	250	0	0	187	0	3.5	2	0	1	0
4	41	0	1	130	204	0	2	172	0	1.4	0	0	1	0

```
🧼 Checking for missing values:
age         0
sex         0
cp          0
trestbps    0
chol        0
fbs         0
restecg     0
thalach     0
exang       0
oldpeak     0
slope       0
```



```
exang       0
oldpeak     0
slope       0
ca          0
thal        0
target      0
dtype: int64

✅ Evaluation Metrics:
✔️ Accuracy: 88.52%
✔️ Precision: 0.93
✔️ Recall: 0.84
```

References / Credits:

- Dataset taken from the “Cleveland Heart Disease Dataset”
- Coding done on **Google Colab**.
- Libraries used: **pandas**, **matplotlib**, **seaborn**, **scikit-learn**.