HEALTHCARE – CARDIOVASCULAR DATASET

COURCE CODE

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
# read an excel file and convert
# into a dataframe object
data = pd.DataFrame(pd.read excel("cep.xlsx"))
data.isna().sum()
data.describe()
continuousFeatures = ['age', 'trestbps', 'chol', 'thalach', 'oldpeak']
def outlier treatment(data, drop=False):
    for eachFeature in continuousFeatures:
        featureData = data[eachFeature]
       Q1, Q3 = np.percentile(featureData, [25, 75])
       IQR = Q3 - Q1
       outlierCalc = 1.5 * IQR
        outliers = featureData[~((featureData >= Q1 - outlierCalc) & (featureData <=</pre>
Q3 + outlierCalc))].index.tolist()
       if not drop:
            print('For the feature {}, No of Outliers is {}'.format(eachFeature,
len(outliers)))
       if drop:
            data.drop(outliers, inplace=True)
            print('Outliers from {} feature removed'.format(eachFeature))
outlier treatment(data[continuousFeatures], drop=True)
```

b. Identify the data variables which are categorical

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color='white', weight='bold')
plt.tight layout()
plt.show()
fig, ax = plt.subplots(figsize=(8, 5))
sns.countplot(x='cp', hue='target', data=data, palette='Set2', ax=ax)
ax.set title("Distribution of chest pain w.r.to Target", fontsize=13, weight='bold')
ax.set xticklabels(name, rotation=0)
totals = []
for i in ax.patches:
   totals.append(i.get height())
total = sum(totals)
for i in ax.patches:
    ax.text(i.get_x() + i.get_width() / 2, i.get_height() - 15,
            f"{round((i.get height() / total) * 100, 2)}%", fontsize=14,
            color='white', weight='bold')
plt.tight layout()
plt.show()
fig, ax = plt.subplots(figsize=(8, 5))
sns.countplot(x='fbs', hue='target', data=data, palette='Set3', ax=ax)
ax.set title("Distribution of Fasting Blood Sugar w.r.to Target", fontsize=13,
weight='bold')
ax.set xticklabels(['True', 'False'], rotation=0)
totals = []
for i in ax.patches:
    totals.append(i.get height())
total = sum(totals)
for i in ax.patches:
    ax.text(i.get_x() + i.get_width() / 2, i.get_height() - 15,
            f"{round((i.get_height() / total) * 100, 2)}%", fontsize=14,
            color='white', weight='bold')
plt.tight layout()
plt.show()
# c. Study the occurrence of CVD across the Age category
fig, ax = plt.subplots(figsize=(10, 6))
sns.countplot(x='age', hue='target', data=data, palette='Set2', ax=ax)
ax.set title("Distribution of CVD across age categories", fontsize=13, weight='bold')
ax.set xlabel("Age", fontsize=12)
ax.set_ylabel("Count", fontsize=12)
ax.legend(title="CVD", labels=["No", "Yes"])
totals = []
for i in ax.patches:
totals.append(i.get height())
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total = sum(totals)
for i in ax.patches:
    ax.text(i.get x() + i.get width() / 2, i.get height() - 15,
            f"{round((i.get height() / total) * 100, 2)}%", fontsize=14,
            color='white', weight='bold')
plt.tight layout()
plt.show()
#d. Study the composition of all patients with respect to the Sex category
sex_counts = data['sex'].value_counts()
labels = ['Male', 'Female']
fig, ax = plt.subplots(figsize=(6, 6))
ax.pie(sex counts, labels=labels, autopct='%1.1f%%', startangle=90, colors=['skyblue',
'lightgreen'])
ax.set title("Composition of Patients by Sex", fontsize=14, weight='bold')
plt.show()
# e. Study if one can detect heart attacks based on anomalies in the resting blood
pressure (trestbps) of a patient
fig, ax = plt.subplots(figsize=(8, 6))
sns.boxplot(x='target', y='trestbps', data=data, ax=ax)
ax.set title("Resting Blood Pressure (trestbps) vs. Heart Attack", fontsize=14,
weight='bold')
ax.set_xlabel("Heart Attack", fontsize=12)
ax.set ylabel("Resting Blood Pressure (mm Hg)", fontsize=12)
ax.set xticklabels(["No", "Yes"])
plt.tight layout()
plt.show()
# f. Describe the relationship between cholesterol levels and a target variable
plt.figure(figsize=(8, 6))
sns.histplot(data=data, x='chol', hue='target', kde=True, palette='Set2')
plt.title("Distribution of Cholesterol Levels by Target", fontsize=14, weight='bold')
plt.xlabel("Cholesterol Levels", fontsize=12)
plt.ylabel("CVD", fontsize=12)
plt.legend(title="Target", labels=["No", "Yes"])
plt.tight_layout()
plt.show()
plt.figure(figsize=(8, 6))
sns.boxplot(x='target', y='chol', data=data, palette='Set2')
plt.title("Cholesterol Levels by Target Variable", fontsize=14, weight='bold')
plt.xlabel("CVD", fontsize=12)
plt.ylabel("Cholesterol Levels", fontsize=12)
plt.xticks(ticks=[0, 1], labels=["No", "Yes"])
plt.tight layout()
plt.show()
fig, ax = plt.subplots(figsize=(8, 5))
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sns.countplot(x='slope', hue='target', data=data, palette='Set1', ax=ax)
ax.set title("Slope Distribution w.r.to Target", fontsize=13, weight='bold')
ax.set xticklabels(['Upsloping','Flat','Downsloping'], rotation=0)
totals = []
for i in ax.patches:
   totals.append(i.get height())
total = sum(totals)
for i in ax.patches:
    ax.text(i.get_x() + i.get_width() / 2, i.get_height() - 15,
            f"{round((i.get height() / total) * 100, 2)}%", fontsize=14,
            color='white', weight='bold')
plt.tight layout()
plt.show()
fig, ax = plt.subplots(figsize=(8, 5))
sns.countplot(x='thal', hue='target', data=data, palette='Set1', ax=ax)
ax.set title(" Effect of Thalassemia on CVD", fontsize=13, weight='bold')
ax.set xticklabels(['reversable defect','normal','fixed defect'], rotation=0)
totals = []
for i in ax.patches:
   totals.append(i.get height())
total = sum(totals)
for i in ax.patches:
   ax.text(i.get x() + i.get width() / 2, i.get height() - 15,
            f"{round((i.get height() / total) * 100, 2)}%", fontsize=14,
            color='white', weight='bold')
plt.tight layout()
plt.show()
sns.set(style="ticks")
sns.pairplot(data, hue="target", palette="Set2")
plt.suptitle("Pair Plot of All Features", fontsize=14, fontweight='bold')
plt.show()
from sklearn.preprocessing import OneHotEncoder
data[categorical features] = data[categorical features].astype(str)
categorical_data = data[categorical_features]
numerical_data = data.drop(categorical_features, axis=1)
encoder = OneHotEncoder(sparse output=False, drop='first')
categorical encoded = encoder.fit transform(categorical data)
categorical encoded df = pd.DataFrame(categorical encoded,
columns=encoder.get feature names out(categorical features))
encoded data = pd.concat([numerical data, categorical encoded df], axis=1)
#Seperate data as features and label
features = encoded data.iloc[:,:-1].values
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label = encoded data.iloc[:,-1].values
from sklearn.preprocessing import StandardScaler
X std=StandardScaler().fit transform(encoded data)
#Create train test split
from sklearn.model selection import train test split
X train, X test, y train, y test =
train test split(features, label, test size=0.2, random state=4)
#Apply LogisticRegression
from sklearn.linear model import LogisticRegression
model = LogisticRegression()
model.fit(X train,y train)
print(model.score(X train, y train))
print(model.score(X test, y test))
from sklearn.metrics import f1 score, precision score, recall score
predictTrain = model.predict(X train)
predictTest = model.predict(X test)
print("F1 Score of Training Set : ",f1 score(y train,predictTrain,average=None))
print("F1 Score of Testing Set : ",f1 score(y test,predictTest,average=None))
print("F1 Score of Training Set :
",precision score(y train,predictTrain,average=None))
print("F1 Score of Testing Set : ",precision score(y test,predictTest,average=None))
print("F1 Score of Training Set : ",recall score(y train,predictTrain,average=None))
print("F1 Score of Testing Set : ",recall score(y test,predictTest,average=None))
from sklearn.metrics import classification report
print(classification_report(y_train,predictTrain))
from sklearn.ensemble import RandomForestClassifier
from sklearn.model selection import train test split, cross val score
from sklearn.metrics import accuracy score
# random forest algorithm
modelrf = RandomForestClassifier(n estimators=100, random state=42)
modelrf.set params(min samples leaf=15)
modelrf.set params(max depth=6)
cv scores = cross val score(modelrf, X train, y train, cv=10)
modelrf.fit(X train, y train)
from sklearn.metrics import accuracy score
y pred = modelrf.predict(X test)
accuracy = accuracy score(y test, y pred)
print("Accuracy:", accuracy)
# Accuracy, Precision, f1 score for RFC
from sklearn.metrics import classification report
from sklearn.metrics import confusion matrix
print(accuracy score(y test, y pred ))
print(classification_report(y_test,y_pred))
print("Cross-validation scores:", cv scores)
# Create Confusion Matrix
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from sklearn.metrics import confusion matrix
confusion matrix(y test,y pred)
# Evaluate random forest model
rf_accuracy = accuracy_score(y_test, rf predictions)
rf precision = precision score(y test, rf predictions)
rf recall = recall score(y test, rf predictions)
rf auc = roc auc score(y test, rf predictions)
modellr= LogisticRegression()
modellr.fit(X_train, y_train)
print (modellr.score (X train, y train))
print (modellr.score(X_test,y_test))
#Evaluate model
from sklearn.metrics import f1 score, precision score, recall score
predictTrain = modellr.predict(X train)
predictTest = modellr.predict(X test)
print("F1 Score of Training Set : ",f1_score(y_train,predictTrain,average=None))
print("F1 Score of Testing Set : ",f1 score(y test,predictTest,average=None))
print("F1 Score of Training Set :
",precision score(y train,predictTrain,average=None))
print("F1 Score of Testing Set : ",precision score(y test,predictTest,average=None))
print("F1 Score of Training Set : ",recall_score(y_train,predictTrain,average=None))
print("F1 Score of Testing Set : ",recall_score(y_test,predictTest,average=None))
import statsmodels.api as sm
X = encoded data[['age', 'thalach', 'restecg Abnormal', 'thal reversable defect']]
y = encoded data['target Possible CVD']
X = sm.add_constant(X)
logistic model = sm.Logit(y, X)
result = logistic model.fit()
summary = result.summary()
p_values = result.pvalues
print(summary)
print(p values)
```