<pre>import pandas as pd import numpy as np import matplotlib.pyplot as plt import seaborn as sns from sklearn.model_selection import train_test_split from sklearn.preprocessing import StandardScaler from sklearn.metrics import accuracy_score from sklearn.linear_model import LogisticRegression from sklearn.tree import DecisionTreeClassifier from sklearn.ensemble import RandomForestClassifier from sklearn.ensemble import RandomForestClassifier from sklearn.neighbors import KNeighborsClassifier</pre>
<pre>from sklearn.svm import SVC from sklearn.impute import SimpleImputer import joblib  In [30]: import re     df = pd.read_csv("cardio_train.csv", sep=None, engine="python")     df.columns = (df.columns.str.strip()</pre>
<pre>rename_map = {     "sex":"gender", "systolic":"ap_hi", "systolic_bp":"ap_hi", "aphi":"ap_hi",     "diastolic":"ap_lo", "diastolic_bp":"ap_lo", "aplo":"ap_lo",     "alcohol":"alco", "glucose":"gluc", "cardiovascular_disease":"cardio",     "height_cm":"height", "weight_kg":"weight" } rename_map = {k:v for k, v in rename_map.items() if k in df.columns and v not in df.columns} df = df.rename(columns=rename_map) print("Columns:", df.columns.tolist()) df.head()</pre>
Columns: ['id', 'age', 'gender', 'height', 'weight', 'ap_hi', 'ap_lo', 'cholesterol', 'gluc', 'smoke', 'alco', 'active', 'cardio']  Out[30]:  id age gender height weight ap_hi ap_lo cholesterol gluc smoke alco active cardio  0 0 18393
3 3 17623 2 169 82.0 150 100 1 1 0 0 1 1  4 4 17474 1 156 56.0 100 60 1 1 0 0 0 0  In [60]:  for c in ["age", "gender", "height", "weight", "ap_hi", "ap_lo",
<pre>if "age" in df.columns:     if df["age"].median() &gt; 150:         df["age_years"] = (df["age"] / 365.25).round(0)     else:         df["age_years"] = df["age"]  else:     df["age_years"] = (df["id"] % 60) + 20     df["age"] = df["age_years"]  if {"height", "weight"}.issubset(df.columns):</pre>
h_m = df["height"] / 100.0  df["BMI"] = df["weight"] / (h_m ** 2)  df.loc[(h_m == 0)   (h_m.isna()), "BMI"] = np.nan  else:  df["BMI"] = np.nan  if {"ap_hi", "ap_lo"}.issubset(df.columns):     swap_mask = df["ap_lo"] > df["ap_hi"]  df.loc[swap_mask, ["ap_lo"]] = df.loc[swap_mask, ["ap_lo", "ap_hi"]].values  df["ap_hi"] = df["ap_hi"].clip(60, 250)
<pre>df["ap_lo"] = df["ap_lo"].clip(30, 150)  if "height" in df.columns:     df["height"] = df["height"].clip(120, 230)  if "weight" in df.columns:     df["weight"] = df["weight"].clip(30, 200)  num_cols = df.select_dtypes(include=[np.number]).columns imp = SimpleImputer(strategy="median") df[num_cols] = imp.fit_transform(df[num_cols])</pre>
<pre>print ("After preprocessing shape:", df.shape)     df[["id", "age_years", "BMI", "ap_hi", "ap_lo"]].head()  After preprocessing shape: (70000, 15)  Out[60]: id age age_years BMI ap_hi ap_lo  0 0.0 18393.0 50.0 21.967120 110.0 80.0</pre>
1 1.0 20228.0 55.0 34.927679 140.0 90.0 2 2.0 18857.0 52.0 23.507805 130.0 70.0 3 3.0 17623.0 48.0 28.710479 150.0 100.0 4 4.0 17474.0 48.0 23.011177 100.0 60.0  In [32]: df.describe()
Cut   32    32
25% 2506.750000 17664.000000 1.000000 159.000000 65.000000 120.000000 80.000000 1.000000 1.000000 0.000000 1.000000 0.000000 1.000000 0.000000 1.000000 23.875115  50% 50001.500000 19703.000000 1.000000 1.000000 120.000000 120.000000 1.000000 1.000000 1.000000 0.000000 1.000000 0.000000 1.000000 54.000000 26.374068  75% 74889.250000 21327.000000 2.000000 170.000000 82.000000 140.000000 90.000000 2.000000 1.000000 1.000000 1.000000 1.000000 1.000000 1.000000 58.000000 30.222222  max 99999.000000 23713.000000 2.000000 230.000000 250.000000 150.000000 3.000000 1.000000 1.000000 1.000000 1.000000 1.000000 298.666667  In [33]: plt.figure(figsize=(6,4))
sns.countplot (x="cardio", data=df) plt.title("Cardiovascular Disease Distribution") plt.show()  Cardiovascular Disease Distribution  35000 - 30000 -
25000 - 20000 - 15000 - 10000 -
In [34]: plt.figure(figsize=(6,4)) plt.hist(df["age_years"], bins=30, edgecolor="black") plt.hist(df["age_years"])
plt.xlabel("Age (years)") plt.ylabel("Count") plt.title("Age Distribution") plt.show()  Age Distribution  7000 - 6000 -
5000 - ti 4000 - 3000 - 2000 -
1000 -
plt.xlabel("BMI") plt.ylabel("Count") plt.show()  BMI Distribution  50000
30000 -
In [8]: plt.figure(figsize=(6,4)) sns.countplot(x="gender", data=df) sns.countplot(x="gender", data=df)
sns.countplot(x="gender", data=df) plt.title("Gender Distribution") plt.show()  Gender Distribution  40000 -
30000 - 20000 - 10000 -
In [36]: plt.figure(figsize=(6,4)) sns.countplot(x="cholesterol", data=df) plt.title("Cholesterol Levels") plt.show()
Cholesterol Levels  50000 - 40000 -
20000 - 10000 -
1.0 2.0 3.0  cholesterol  In [10]: plt.figure(figsize=(6,4)) sns.countplot(x="gluc", data=df) plt.title("Glucose Levels") plt.show()  Glucose Levels
60000 - 50000 - 40000 - 150 30000 -
20000 - 10000 - 1.0 2.0 3.0
<pre>gluc  In [37]: plt.figure(figsize=(6,4))     sns.countplot(x="smoke", data=df)     plt.title("Smoking Habit")     plt.show()  Smoking Habit</pre> Smoking Habit
60000 - 50000 - 40000 - 19 30000 -
20000 - 10000 - 0.0 smoke
In [12]: plt.figure(figsize=(6,4)) sns.countplot(x="alco", data=df) plt.title("Alcohol Consumption") plt.show()  Alcohol Consumption  60000 -
50000 - 40000 - 20000 - 20000 -
In [38]: plt.figure(figsize=(6,4)) sns.countplot(x="active", data=df) plt.title("Active Lifestyle")
Active Lifestyle  50000 - 40000 -
20000 - 10000 -
O.0 active  In [39]: plt.figure(figsize=(12,5)) plt.subplot(1,2,1) plt.hist(df["ap_hi"], bins=30, edgecolor="black") plt.title("Systolic BP Distribution") plt.subplot(1,2,2)
plt.hist(df["ap_lo"], bins=30, edgecolor="black") plt.title("Diastolic BP Distribution") plt.show()  Systolic BP Distribution  Diastolic BP Distribution  25000 - 300000 - 300
2000 - 15000 - 10000 -
5000 - 5000 - 5000 - 5000 - 75 100 125 150 175 200 225 250 40 60 80 100 120 140
In [40]: plt.figure(figsize=(6,4)) sns.boxplot(x="cardio", y="BMI", data=df) plt.title("BMI vs Cardiovascular Disease") plt.show()  BMI vs Cardiovascular Disease  300 -
200 -
In [41]: corr = df.corr() plt.figure(figsize=(10,8)) sns.heatmap(corr, cmap="coolwarm", annot=False)
plt.title("Correlation Matrix") plt.show()  Correlation Matrix  id - age
Page
cholesterol -
active - cardio - age_years - BMI - BM + E E E O O O U S O S O S O S O S O S O S O S O
In [42]: X = df.drop(columns=["cardio","id"]) y = df["cardio"] scaler = StandardScaler()
<pre>X_scaled = scaler.fit_transform(X)  X_train, X_test, y_train, y_test = train_test_split(</pre>
Logistic Regression Accuracy: 0.7216428571428571  In [46]: dt = DecisionTreeClassifier(random_state=42)       dt.fit(X_train, y_train)       acc_dt = accuracy_score(y_test, dt.predict(X_test))       print("Decision Tree Accuracy:", acc_dt)        Decision Tree Accuracy: 0.6305714285714286  In [20]: rf = RandomForestClassifier(random_state=42)       rf.fit(X_train, y_train)
<pre>KNN Accuracy: 0.6965  In [45]: from sklearn.svm import SVC     from sklearn.preprocessing import StandardScaler     from sklearn.metrics import accuracy_score      scaler = StandardScaler()     X_train_scaled = scaler.fit_transform(X_train)     X_test_scaled = scaler.transform(X_test)  svm = SVC(kernel="linear", cache_size=1000)</pre>
<pre>svm.fit(X_train_scaled, y_train)  y_pred_svm = svm.predict(X_test_scaled)  acc_svm = accuracy_score(y_test, y_pred_svm)     print("SVM Accuracy:", round(acc_svm*100, 2), "%")  SVM Accuracy: 72.39 %  In [54]: X2 = df.drop(["id", "cardio"], axis=1)</pre>
<pre>y2 = df["cardio"]  X2_train, X2_test, y2_train, y2_test = train_test_split(X2, y2, test_size=0.2, random_state=42, stratify=y2)  scaler2 = StandardScaler()  X2_train = scaler2.fit_transform(X2_train)  X2_test = scaler2.transform(X2_test)  best_model.fit(X2_train, y2_train)</pre>
<pre>print("Best model retrained on 12 features (without 'id').")  Best model retrained on 12 features (without 'id').  In []: X2 = df.drop(["id", "cardio"], axis=1).values     y2 = df["cardio"].values      X2_train, X2_test, y2_train, y2_test = train_test_split(</pre>
<pre>scaler2 = StandardScaler() X2_train = scaler2.fit_transform(X2_train) X2_test = scaler2.transform(X2_test)  accuracies = {     "Logistic Regression": acc_lr,     "Decision Tree": acc_dt,     "Random Forest": acc_rf,     "KNN": acc_knn,     "SVM": acc_svm</pre>
<pre>"SVM": acc_svm }  best_model_name = max(accuracies, key=accuracies.get) print("\n Best Model is:", best_model_name, "with accuracy:", accuracies(best_model_name))  if best_model_name == "Logistic Regression":     best_model = log_reg elif best_model_name == "Decision Tree":     best_model = dt elif best_model_name == "Random Forest":</pre>
<pre>best_model = rf elif best_model_name == "KNN":     best_model = knn else:     best_model = svm  best_model.fit(X2_train, y2_train)  joblib.dump(best_model, "best_heart_model.joblib")</pre>
<pre>new_patient = np.array([[45, 1, 165, 70, 130, 85, 1, 1, 0, 0, 1, 25.7]]) new_patient_scaled = scaler2.transform(new_patient) prediction = best_model.predict(new_patient_scaled)  if prediction[0] == 1:     print("Prediction: Patient is at risk of Cardiovascular Disease") else:</pre>

print("Prediction: Patient is Healthy")

In [29]: **%matplotlib** inline