```
import numpy as np
import pandas as pd
```

```
df_train = pd.read_csv("/content/sample_data/train_dataset.csv")
df_test = pd.read_csv("/content/sample_data/test_dataset.csv")
```

```
df_train.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 38984 entries, 0 to 38983
Data columns (total 23 columns):
 #   Column               Non-Null Count  Dtype  
---  ------               --------------  -----  
 0   age                  38984 non-null  int64  
 1   height(cm)           38984 non-null  int64  
 2   weight(kg)           38984 non-null  int64  
 3   waist(cm)            38984 non-null  float64
 4   eyesight(left)       38984 non-null  float64
 5   eyesight(right)      38984 non-null  float64
 6   hearing(left)        38984 non-null  int64  
 7   hearing(right)       38984 non-null  int64  
 8   systolic             38984 non-null  int64  
 9   relaxation           38984 non-null  int64  
 10  fasting blood sugar  38984 non-null  int64  
 11  Cholesterol          38984 non-null  int64  
 12  triglyceride         38984 non-null  int64  
 13  HDL                  38984 non-null  int64  
 14  LDL                  38984 non-null  int64  
 15  hemoglobin           38984 non-null  float64
 16  Urine protein        38984 non-null  int64  
 17  serum creatinine     38984 non-null  float64
 18  AST                  38984 non-null  int64  
 19  ALT                  38984 non-null  int64  
 20  Gtp                  38984 non-null  int64  
 21  dental caries        38984 non-null  int64  
 22  smoking              38984 non-null  int64  
dtypes: float64(5), int64(18)
memory usage: 6.8 MB
```

```
df_train.describe()
```

	age	height(cm)	weight(kg)	waist(cm)	eyesight(left)	eyesight(right)	hearing(left)	hearing(right)
count	38984.000000	38984.000000	38984.000000	38984.000000	38984.000000	38984.000000	38984.000000	38984.000000
mean	44.127591	164.689488	65.938718	82.062115	1.014955	1.008768	1.025369	1.026190
std	12.063564	9.187507	12.896581	9.326798	0.498527	0.493813	0.157246	0.159703
min	20.000000	130.000000	30.000000	51.000000	0.100000	0.100000	1.000000	1.000000
25%	40.000000	160.000000	55.000000	76.000000	0.800000	0.800000	1.000000	1.000000
50%	40.000000	165.000000	65.000000	82.000000	1.000000	1.000000	1.000000	1.000000
75%	55.000000	170.000000	75.000000	88.000000	1.200000	1.200000	1.000000	1.000000
max	85.000000	190.000000	135.000000	129.000000	9.900000	9.900000	2.000000	2.000000

8 rows × 23 columns

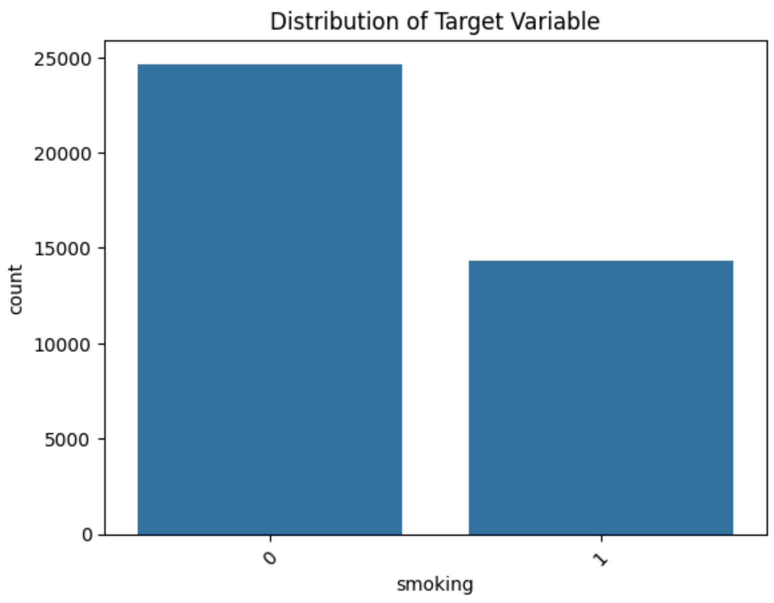
```
df_train.head()
```

	age	height(cm)	weight(kg)	waist(cm)	eyesight(left)	eyesight(right)	hearing(left)	hearing(right)	systolic	relaxati
0	35	170	85	97.0	0.9	0.9	1	1	118	
1	20	175	110	110.0	0.7	0.9	1	1	119	
2	45	155	65	86.0	0.9	0.9	1	1	110	
3	45	165	80	94.0	0.8	0.7	1	1	158	
4	20	165	60	81.0	1.5	0.1	1	1	109	

5 rows × 23 columns

Exploratory Data Analysis (EDA)

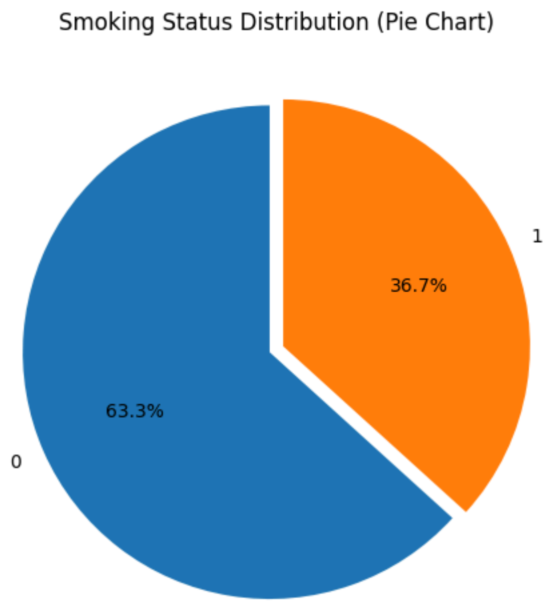
```
import seaborn as sns
import matplotlib.pyplot as plt

sns.countplot(x='smoking', data=df_train)
plt.title("Distribution of Target Variable")
plt.xticks(rotation=45)
plt.show()

df_train['smoking'].value_counts(normalize=True)
```



	proportion
smoking	
0	0.632721
1	0.367279

dtype: float64

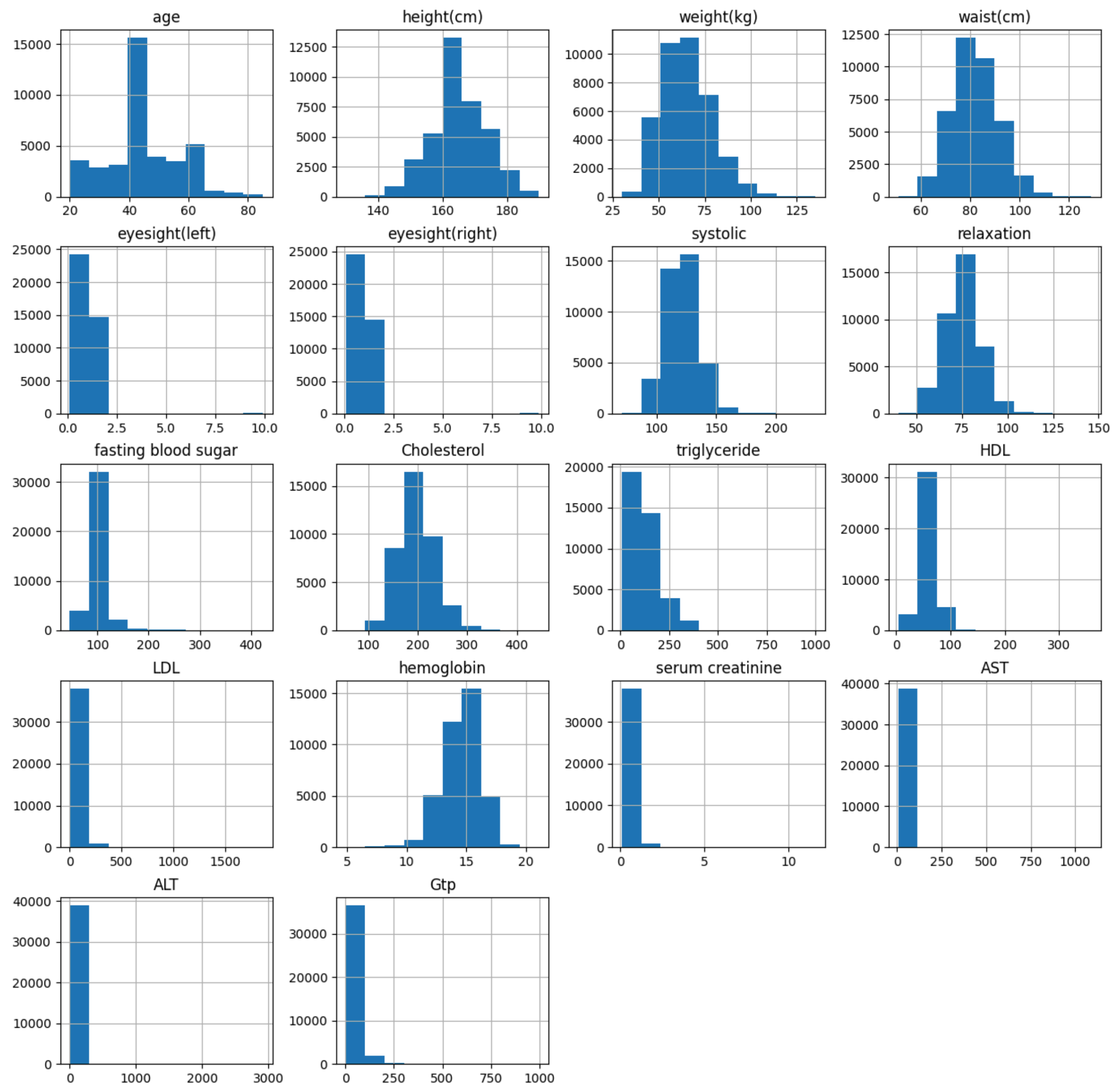
```
# Value counts
counts = df_train['smoking'].value_counts(normalize=True)

# Plot
plt.figure(figsize=(6,6))
plt.pie(
    counts,
    labels=counts.index,
    autopct='%1.1f%%',
    startangle=90,
    explode=[0.03]*len(counts),         # small separation for clarity
)
plt.title("Smoking Status Distribution (Pie Chart)")
plt.show()
```



Clear imbalance in data class a has 63.33% and class b has 37% ie appx 2:1 ratio hence we ll apply smote

Univariate Analysis

```
numerical_cols = ['age', 'height(cm)', 'weight(kg)', 'waist(cm)', 'eyesight(left)',
       'eyesight(right)', 'systolic',
       'relaxation', 'fasting blood sugar', 'Cholesterol', 'triglyceride',
       'HDL', 'LDL', 'hemoglobin', 'serum creatinine', 'AST',
       'ALT', 'Gtp']
df_train[numerical_cols].hist(figsize=(15, 15))
plt.show()
```

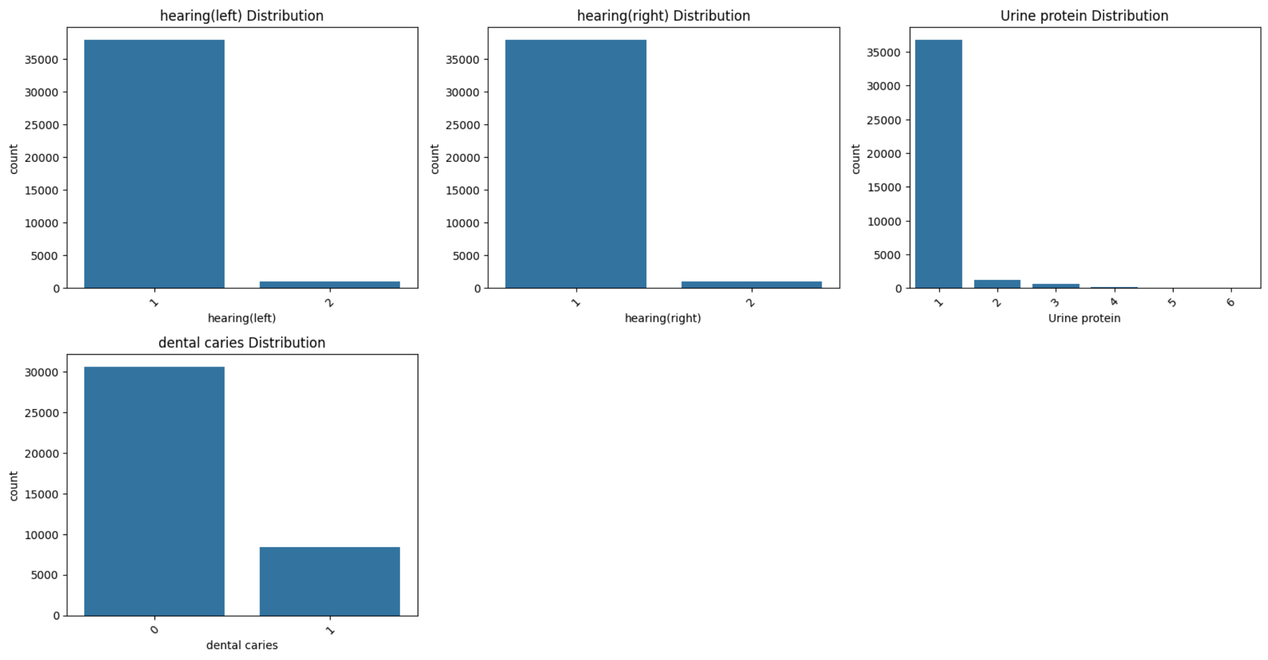


Most features (height, weight, BP, hemoglobin, waist) are well-behaved and roughly normal.

Some features (eyesight, cholesterol, triglycerides, LDL/HDL, creatinine, liver enzymes) are highly right-skewed with outliers.

A few features (age, fasting blood sugar) show irregular or clustered patterns, suggesting cohort effects or categorical-like behavior.

```
categorical_cols = ['hearing(left)', 'hearing(right)', 'Urine protein', 'dental caries']
plt.figure(figsize=(16, 12))
for i, col in enumerate(categorical_cols, 1):
    plt.subplot(3, 3, i)
    sns.countplot(x=col, data=df_train)
    plt.title(f"{col} Distribution")
    plt.xticks(rotation=45)
    plt.tight_layout()
plt.show()
```



Most features show normal or mildly skewed distributions (e.g., height, weight, blood pressure). Several health indicators are highly right-skewed with strong outliers (lipids, liver enzymes, eyesight, creatinine). A few features show irregular patterns like bimodality or heavy clustering (age, fasting blood sugar).

```
print(df_train.duplicated().sum())
```

```
5517
```

```
df_train = df_train.drop_duplicates()
```

```
print(df_train.duplicated().sum())
```

```
0
```

```
df_train.isna().sum()
```

```
                        0
               age      0
        height(cm)      0
        weight(kg)      0
         waist(cm)      0
     eyesight(left)     0
    eyesight(right)     0
      hearing(left)     0
     hearing(right)     0
          systolic      0
        relaxation      0
fasting blood sugar     0
       Cholesterol      0
      triglyceride      0
               HDL      0
               LDL      0
        hemoglobin      0
     Urine protein      0
  serum creatinine      0
               AST      0
               ALT      0
               Gtp      0
     dental caries      0
           smoking      0

dtype: int64
```

```
df_train.isna().sum().sum()
```

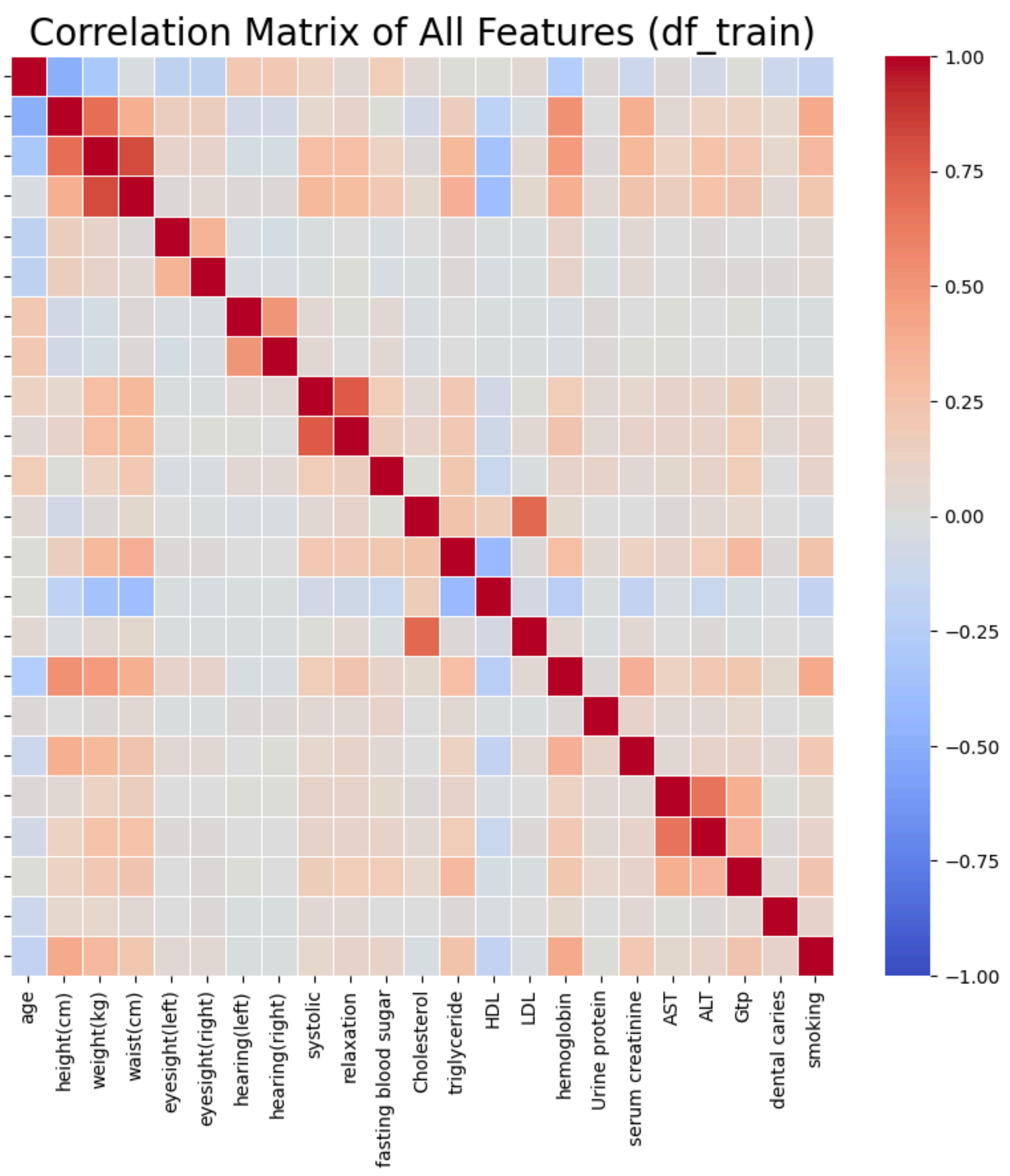
```
np.int64(0)
```

Removed all duplicates and there are no missing values

```
df_train.isna().sum()[df_train.isna().sum() > 0]
```

```
   0

dtype: int64
```

```
import seaborn as sns
import matplotlib.pyplot as plt

# 1. Calculate the correlation matrix

corr_matrix = df_train.corr()

# 2. Set up the figure size
plt.figure(figsize=(10, 9))

# 3. Create the heatmap
# annot=False is used here to prevent clutter since there are many features.
# 'vmax' and 'vmin' set the color bar range from -1 to 1.
sns.heatmap(corr_matrix, annot=False, cmap='coolwarm', vmin=-1, vmax=1, linewidths=.5)

plt.title('Correlation Matrix of All Features (df_train)', fontsize=20)
plt.show()
```

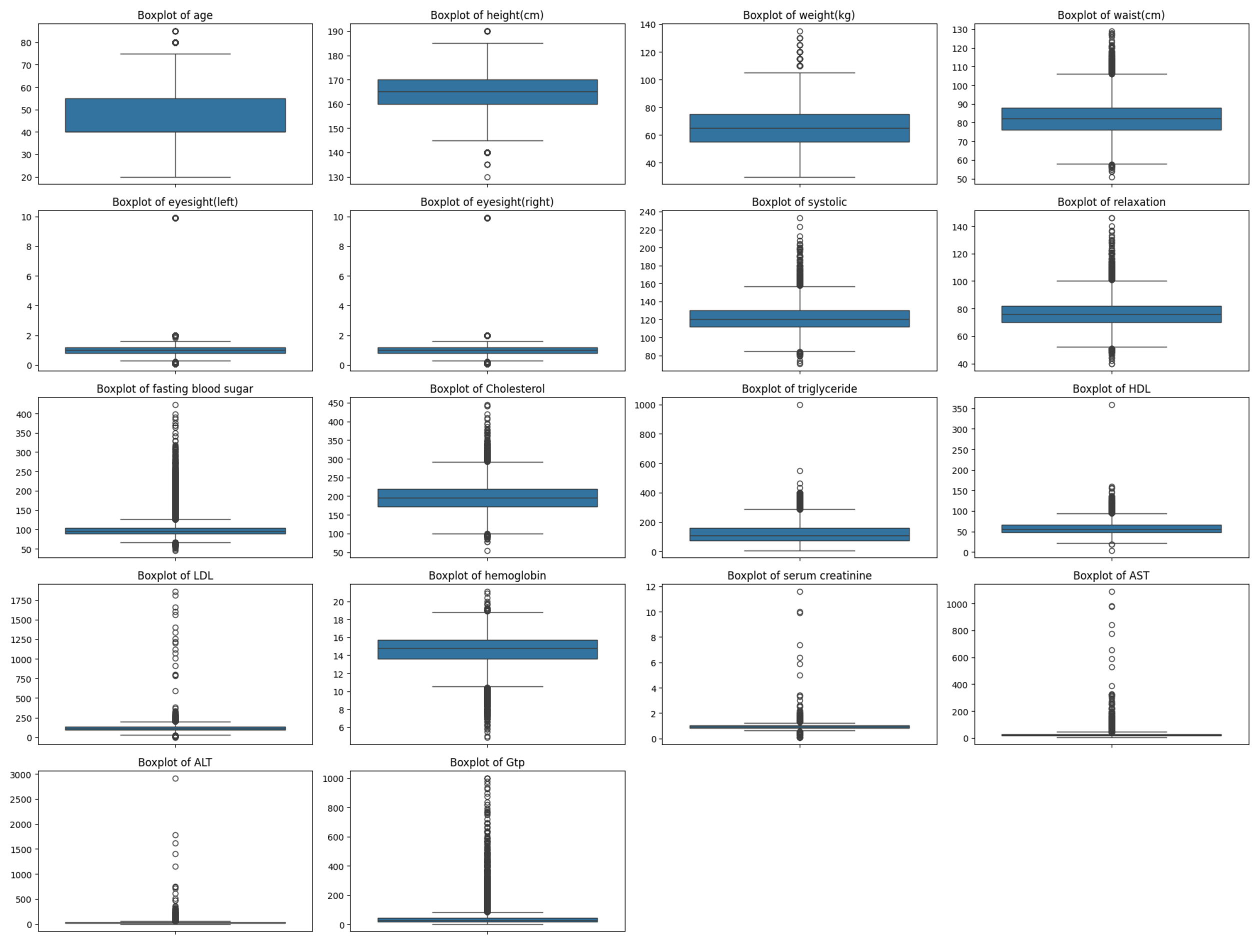


Outlier Detection

```
print("--- Outlier Detection using IQR ---")
for col in numerical_cols:
    q1 = df_train[col].quantile(0.25)
    q3 = df_train[col].quantile(0.75)
    IQR = q3 - q1
    lower_bound = q1 - 1.5 * IQR
    upper_bound = q3 + 1.5 * IQR

    outliers = df_train[(df_train[col] < lower_bound) | (df_train[col] > upper_bound)]
    print(f"Column '{col}': {len(outliers)} outliers detected.")
```

```
--- Outlier Detection using IQR ---
Column 'age': 184 outliers detected.
Column 'height(cm)': 155 outliers detected.
Column 'weight(kg)': 127 outliers detected.
Column 'waist(cm)': 329 outliers detected.
Column 'eyesight(left)': 810 outliers detected.
Column 'eyesight(right)': 823 outliers detected.
Column 'systolic': 414 outliers detected.
Column 'relaxation': 427 outliers detected.
Column 'fasting blood sugar': 1987 outliers detected.
Column 'Cholesterol': 373 outliers detected.
Column 'triglyceride': 1412 outliers detected.
Column 'HDL': 595 outliers detected.
Column 'LDL': 403 outliers detected.
Column 'hemoglobin': 476 outliers detected.
Column 'serum creatinine': 1905 outliers detected.
Column 'AST': 1800 outliers detected.
Column 'ALT': 2255 outliers detected.
Column 'Gtp': 2901 outliers detected.
```

```
plt.figure(figsize=(20, 15))
for i, col in enumerate(numerical_cols, 1):
    plt.subplot(5, 4, i) # Adjust subplot grid as needed
    sns.boxplot(y=df_train[col])
    plt.title(f'Boxplot of {col}')
    plt.ylabel('')
plt.tight_layout()
plt.show()
```



Feature TransformationThe most critical remaining issue, based on your EDA, is the severe skewness and the resulting high number of outliers in many features (e.g., Gtp, ALT, triglyceride).To stabilize the variance, reduce the outlier impact, and normalize the distributions, we must apply Log Transformation to these features. Log Transformation CodeWe can apply a log transformation (ln(x+1)) to the most problematic, right-skewed columns in both your training and test sets simultaneously:

```
import numpy as np

# List of highly skewed features identified from the histograms and outlier report
skewed_features = [
    'Gtp',
    'ALT',
    'triglyceride',
    'serum creatinine',
    'fasting blood sugar',
    'eyesight(left)',
    'eyesight(right)',
    'AST'
]

# Apply log(x+1) transformation to handle potential zeros and reduce skewness
for col in skewed_features:
    df_train[col] = np.log1p(df_train[col])
    df_test[col] = np.log1p(df_test[col])

print("Successfully applied log transformation to the most skewed features in both df_train and df_test.")
```

```
Successfully applied log transformation to the most skewed features in both df_train and df_test.
```

```
# List of redundant columns to drop
cols_to_drop = [
    'Cholesterol',
    'hearing(right)', # Keeping hearing(left)
]

# Drop the columns from both the training and test DataFrames
df_train = df_train.drop(columns=cols_to_drop, errors='ignore')
df_test = df_test.drop(columns=cols_to_drop, errors='ignore')

print(f"Successfully dropped redundant columns: {cols_to_drop}")
print(f"df_train now has {df_train.shape[1]} columns.")
```

```
Successfully dropped redundant columns: ['Cholesterol', 'hearing(right)']
df_train now has 21 columns.
```

Feature Engineering

```
# Create BMI for both df_train and df_test

# BMI = weight(kg) / (height(cm) / 100)^2
df_train['BMI'] = df_train['weight(kg)'] / (df_train['height(cm)'] / 100)**2
df_test['BMI'] = df_test['weight(kg)'] / (df_test['height(cm)'] / 100)**2

print("Successfully calculated and added the 'BMI' feature to both DataFrames.")
print(df_train[['weight(kg)', 'height(cm)', 'BMI']].head())
```

```
Successfully calculated and added the 'BMI' feature to both DataFrames.
   weight(kg)  height(cm)        BMI
0          85         170  29.411765
1         110         175  35.918367
2          65         155  27.055151
3          80         165  29.384757
4          60         165  22.038567
```

Scaling

```
from sklearn.preprocessing import StandardScaler

# 1. Identify Numerical Columns
# Redefine numerical_cols based on the current state of df_train
# Exclude 'smoking' (target) and any other columns that should not be scaled,
# e.g., 'hearing(left)', 'Urine protein', 'dental caries' if treated as categorical/ordinal.
# 'Cholesterol' was dropped, and 'BMI' was added.

# Get all columns in df_train
all_cols = set(df_train.columns)

# Columns to explicitly exclude from numerical scaling (target, and already processed categoricals)
exclude_cols = {'smoking', 'hearing(left)', 'Urine protein', 'dental caries'}

# Create the updated numerical_cols list
current_numerical_cols = list(all_cols - exclude_cols)

# Ensure the order is consistent if necessary, or let scaler handle it.
# For a more controlled list, you could explicitly define it:
# current_numerical_cols = [
#     'age', 'height(cm)', 'weight(kg)', 'waist(cm)', 'eyesight(left)',
#     'eyesight(right)', 'systolic', 'relaxation', 'fasting blood sugar',
#     'triglyceride', 'HDL', 'LDL', 'hemoglobin', 'serum creatinine', 'AST',
#     'ALT', 'Gtp', 'BMI'
# ]

# 2. Initialize the StandardScaler
scaler = StandardScaler()
```

```
# 3. Fit the scaler ONLY on the training data and transform it
df_train[current_numerical_cols] = scaler.fit_transform(df_train[current_numerical_cols])

# 4. Transform the test data using the scaler FIT on the training data
df_test[current_numerical_cols] = scaler.transform(df_test[current_numerical_cols])
print("Successfully applied Standardization (StandardScaler) to all numerical features.")
print("\nSample of scaled numerical data in df_train:")
print(df_train[current_numerical_cols].head())
```

```
Successfully applied Standardization (StandardScaler) to all numerical features.

Sample of scaled numerical data in df_train:
   systolic  fasting blood sugar       ALT        AST       HDL  triglyceride  \
0 -0.255927            -0.046681  2.966505   2.604903  0.872903      0.616696
1 -0.182778            -0.635557  0.179281  -0.665598  0.941406      0.285122
2 -0.841115            -1.211328  7.609758  10.894500 -0.017642      0.165285
3  2.670014             5.678147  0.836851   0.781974 -0.771180      2.242197
4 -0.914264             0.137646  0.382801   0.201903 -0.702677      1.115258

        Gtp  eyesight(right)  eyesight(left)  weight(kg)       BMI       age  \
0  2.053934        -0.200017       -0.212203    1.480822  1.497471 -0.758305
1  0.039631        -0.200017       -0.813007    3.422153  3.359380 -2.000892
2  3.185464        -0.200017       -0.212203   -0.072242  0.823109  0.070087
3  0.293780        -0.800096       -0.504256    1.092556  1.489742  0.070087
4 -0.910424        -3.148705        1.270215   -0.460509 -0.612421 -2.000892

   serum creatinine  waist(cm)  height(cm)  hemoglobin  relaxation       LDL
0          0.612410   1.602349    0.578044    3.312576    0.204964  0.621382
1          1.078237   2.998638    1.121774    0.816401    0.308356 -0.027389
2         -1.518069   0.420874   -1.053148   -0.591698    0.411748 -0.073730
3          0.122684   1.280128    0.034313    1.456446    1.238885 -0.560309
4          1.522390  -0.116161    0.034313    0.176356   -1.242524 -0.537138
```

One Hot Encoding

```
import pandas as pd

# List the nominal categorical columns that need OHE
nominal_cols = ['hearing(left)', 'dental caries']

# Apply One-Hot Encoding to df_train and df_test
df_train = pd.get_dummies(df_train, columns=nominal_cols, drop_first=True)
df_test = pd.get_dummies(df_test, columns=nominal_cols, drop_first=True)

print("1. Successfully applied One-Hot Encoding.")
```

```
1. Successfully applied One-Hot Encoding.
```

```
df_train.head()
```

	age	height(cm)	weight(kg)	waist(cm)	eyesight(left)	eyesight(right)	systolic	relaxation	fasting blood sugar	triglycerid
0	-0.758305	0.578044	1.480822	1.602349	-0.212203	-0.200017	-0.255927	0.204964	-0.046681	0.61669
1	-2.000892	1.121774	3.422153	2.998638	-0.813007	-0.200017	-0.182778	0.308356	-0.635557	0.28512
2	0.070087	-1.053148	-0.072242	0.420874	-0.212203	-0.200017	-0.841115	0.411748	-1.211328	0.16528
3	0.070087	0.034313	1.092556	1.280128	-0.504256	-0.800096	2.670014	1.238885	5.678147	2.24219
4	-2.000892	0.034313	-0.460509	-0.116161	1.270215	-3.148705	-0.914264	-1.242524	0.137646	1.11525

5 rows × 22 columns

SMOTE

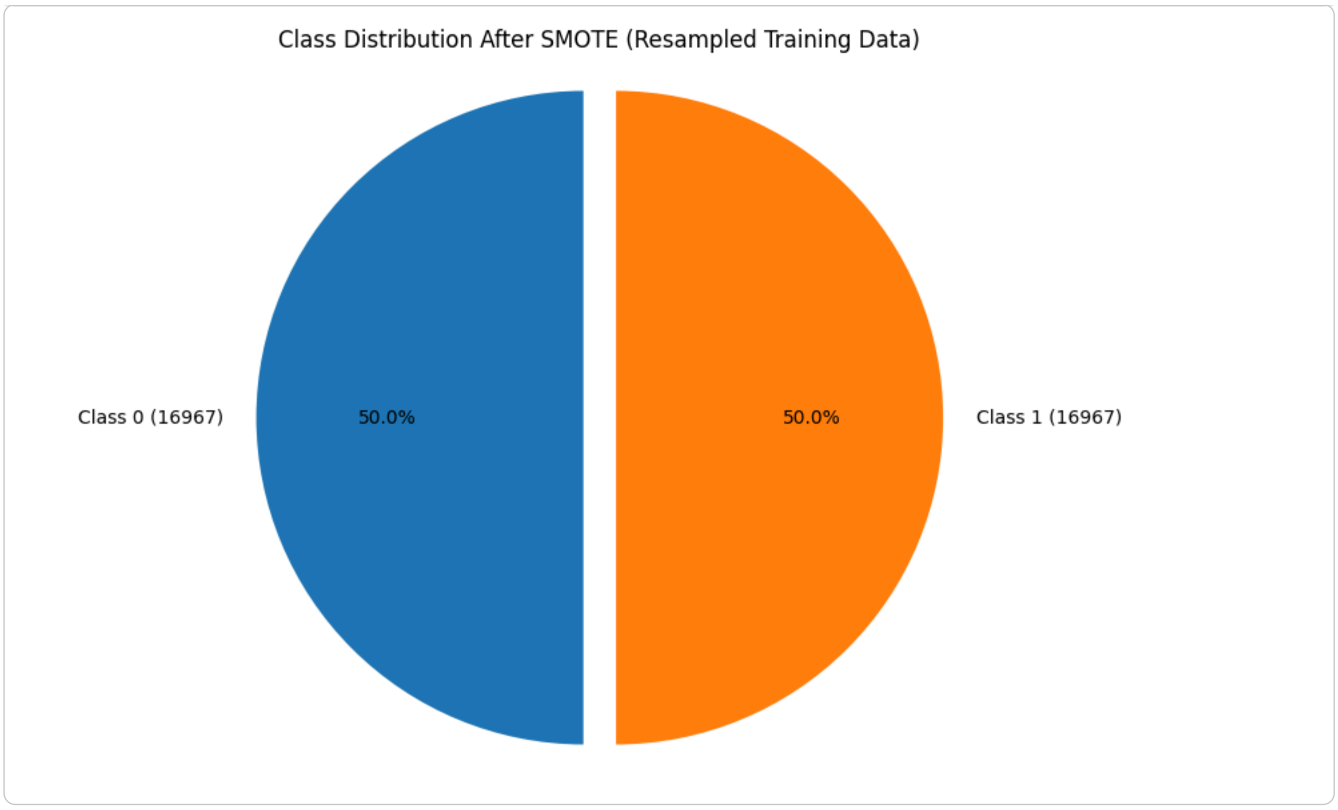
```
!pip install imblearn
from sklearn.model_selection import train_test_split
from imblearn.over_sampling import SMOTE
from collections import Counter

# --- A. Split the Data ---
# 1. Separate Features and Target from the fully preprocessed df_train
X_full = df_train.drop('smoking', axis=1)
y_full = df_train['smoking']

# 2. Split into Training (80%) and Validation (20%) sets
# stratify=y_full ensures the class ratio is maintained in both splits
X_train, X_val, y_train, y_val = train_test_split(
    X_full,
    y_full,
    test_size=0.2,
    random_state=42,
    stratify=y_full
)
```

```
Collecting imblearn
  Downloading imblearn-0.0-py2.py3-none-any.whl.metadata (355 bytes)
Requirement already satisfied: imbalanced-learn in /usr/local/lib/python3.12/dist-packages (from imblearn) (0.14.0)
Requirement already satisfied: numpy<3,>=1.25.2 in /usr/local/lib/python3.12/dist-packages (from imbalanced-learn->imblearn)
Requirement already satisfied: scipy<2,>=1.11.4 in /usr/local/lib/python3.12/dist-packages (from imbalanced-learn->imblearn)
Requirement already satisfied: scikit-learn<2,>=1.4.2 in /usr/local/lib/python3.12/dist-packages (from imbalanced-learn->imb
Requirement already satisfied: joblib<2,>=1.2.0 in /usr/local/lib/python3.12/dist-packages (from imbalanced-learn->imblearn)
Requirement already satisfied: threadpoolctl<4,>=2.0.0 in /usr/local/lib/python3.12/dist-packages (from imbalanced-learn->im
Downloading imblearn-0.0-py2.py3-none-any.whl (1.9 kB)
Installing collected packages: imblearn
Successfully installed imblearn-0.0
```

```
# --- B. Apply SMOTE ---
print("\nOriginal Training Split class balance: %s" % Counter(y_train))

# Initialize SMOTE
sm = SMOTE(random_state=42)

# Apply SMOTE ONLY to the new 80% training set
X_resampled, y_resampled = sm.fit_resample(X_train, y_train)

# Check the new, balanced class distribution
print("2. SMOTE successfully applied to the training set.")
print("Resampled Training Set class balance: %s" % Counter(y_resampled))
print(f"Validation Set size (untouched for evaluation): {X_val.shape[0]} rows.")
```

```

Original Training Split class balance: Counter({0: 16967, 1: 9806})
2. SMOTE successfully applied to the training set.
Resampled Training Set class balance: Counter({0: 16967, 1: 16967})
Validation Set size (untouched for evaluation): 6694 rows.
```

```
import matplotlib.pyplot as plt
from collections import Counter

# Get class counts after SMOTE
class_counts = Counter(y_resampled)
labels = [f"Class {cls} ({count})" for cls, count in class_counts.items()]
sizes = list(class_counts.values())

# Plotting the pie chart
plt.figure(figsize=(7, 7))
plt.pie(sizes, labels=labels, autopct='%1.1f%%', startangle=90, explode=[0.05]*len(sizes))
plt.title('Class Distribution After SMOTE (Resampled Training Data)')
plt.axis('equal') # Equal aspect ratio ensures that pie is drawn as a circle.
plt.show()
```



Model Training

1.Logistic Regression

```
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import confusion_matrix, classification_report, roc_auc_score
```

```
log_reg = LogisticRegression(random_state=42, max_iter=500)
```

```
log_reg.fit(X_resampled, y_resampled)
```

```
▾            LogisticRegression
LogisticRegression(max_iter=500, random_state=42)
```

```
y_val_pred = log_reg.predict(X_val)
```

```
y_val_proba = log_reg.predict_proba(X_val)[:, 1]
print("Logistic Regression model trained and predictions made on the Validation Set.")
```

```
Logistic Regression model trained and predictions made on the Validation Set.
```

```
# Print the Confusion Matrix
print("\n--- Confusion Matrix on Validation Data ---")
print(confusion_matrix(y_val, y_val_pred))

# Print the Classification Report (Precision, Recall, F1-Score)
print("\n--- Classification Report (Validation Data) ---")
print(classification_report(y_val, y_val_pred))

# Print the ROC AUC Score
roc_auc = roc_auc_score(y_val, y_val_proba)
print(f"\nROC AUC Score: {roc_auc:.4f}")
```

```

--- Confusion Matrix on Validation Data ---
[[2955 1287]
 [ 547 1905]]

--- Classification Report (Validation Data) ---
              precision    recall  f1-score   support

           0       0.84      0.70      0.76      4242
           1       0.60      0.78      0.68      2452

    accuracy                           0.73      6694
   macro avg       0.72      0.74      0.72      6694
weighted avg       0.75      0.73      0.73      6694


ROC AUC Score: 0.8122
```

```
from sklearn.metrics import accuracy_score

accuracy = accuracy_score(y_val, y_val_pred)
print("\nValidation Accuracy:", accuracy)
```

```

Validation Accuracy: 0.7260233044517478
```

2.Support Vector Machine

```
from sklearn.svm import SVC
from sklearn.metrics import confusion_matrix, classification_report, roc_auc_score

# 1. Initialize the SVM Classifier
# kernel='rbf' (Radial Basis Function) is the non-linear kernel
# probability=True allows us to use predict_proba for the ROC AUC score
svm_model = SVC(
    kernel='rbf',
    probability=True,
    random_state=42
)

# 2. Train the model using the BALANCED data
# This step may take a significant amount of time
svm_model.fit(X_resampled, y_resampled)

# 3. Predict on the UNTOUCHED Validation Set
y_val_pred_svm = svm_model.predict(X_val)

# 4. Predict probabilities (for ROC AUC score)
y_val_proba_svm = svm_model.predict_proba(X_val)[:, 1]

print("SVM model with RBF kernel trained and predictions made on the Validation Set.")
```

```
SVM model with RBF kernel trained and predictions made on the Validation Set.
```

```
# Print the Confusion Matrix
print("\n--- SVM (RBF Kernel) Confusion Matrix (Validation) ---")
print(confusion_matrix(y_val, y_val_pred_svm))

# Print the Classification Report (Precision, Recall, F1-Score)
print("\n--- SVM (RBF Kernel) Classification Report (Validation) ---")
print(classification_report(y_val, y_val_pred_svm))

# Print the ROC AUC Score
roc_auc_svm = roc_auc_score(y_val, y_val_proba_svm)
print(f"\nROC AUC Score (SVM RBF): {roc_auc_svm:.4f}")
```

```

--- SVM (RBF Kernel) Confusion Matrix (Validation) ---
[[2823 1419]
 [ 384 2068]]

--- SVM (RBF Kernel) Classification Report (Validation) ---
              precision    recall  f1-score   support

           0       0.88      0.67      0.76      4242
           1       0.59      0.84      0.70      2452

    accuracy                           0.73      6694
   macro avg       0.74      0.75      0.73      6694
weighted avg       0.78      0.73      0.74      6694


ROC AUC Score (SVM RBF): 0.8227
```

```
accuracy = accuracy_score(y_val, y_val_pred_svm)
print("\nValidation Accuracy:", accuracy)
```

```

Validation Accuracy: 0.7306543172990738
```

```
pip install tensorflow
```

```
Requirement already satisfied: tensorflow in /usr/local/lib/python3.12/dist-packages (2.19.0)
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Requirement already satisfied: charset_normalizer<4,>=2 in /usr/local/lib/python3.12/dist-packages (from requests<3,>=2.21.0
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Requirement already satisfied: mdurl~=0.1 in /usr/local/lib/python3.12/dist-packages (from markdown-it-py>=2.2.0->rich->kera
```

3.Neural Networks

```
import tensorflow as tf
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Dense
from sklearn.metrics import confusion_matrix, classification_report, roc_auc_score

# Get the number of features (columns) from your data
input_dim = X_resampled.shape[1]

# 1. Initialize the Sequential model
model = Sequential()

# 2. Add the first Hidden Layer
# 64 neurons, using ReLU (Rectified Linear Unit) activation
model.add(Dense(64, activation='relu', input_shape=(input_dim,)))

# 3. Add a second Hidden Layer
model.add(Dense(32, activation='relu'))

# 4. Add the Output Layer
# 1 neuron with sigmoid activation for binary classification (output is probability)
model.add(Dense(1, activation='sigmoid'))

# 5. Compile the model
# optimizer='adam' is a good general-purpose choice
# loss='binary_crossentropy' is the standard loss function for binary classification
model.compile(optimizer='adam',
              loss='binary_crossentropy',
              metrics=['accuracy'])

print("Neural Network model architecture defined and compiled.")
```

```
/usr/local/lib/python3.12/dist-packages/keras/src/layers/core/dense.py:93: UserWarning: Do not pass an `input_shape`/`input_
  super().__init__(activity_regularizer=activity_regularizer, **kwargs)
Neural Network model architecture defined and compiled.
```

```
# Train the model
# epochs=20 is a starting point, batch_size=32 is a standard size
history = model.fit(
    X_resampled,
    y_resampled,
    epochs=20,
    batch_size=32,
    validation_split=0.1, # Use 10% of the resampled data for internal validation
    verbose=0 # Suppress output during training
)

print("\nNeural Network trained over 20 epochs.")
```

```
Neural Network trained over 20 epochs.
```

```
# Make predictions on the UNTOUCHED Validation Set
# y_val_proba_nn will contain the probabilities of being Class 1 (Smoker)
y_val_proba_nn = model.predict(X_val).flatten()

# Convert probabilities to binary predictions (0 or 1) using the default threshold of 0.5
y_val_pred_nn = (y_val_proba_nn > 0.5).astype(int)

# --- Evaluation Metrics ---
print("\n--- Neural Network Classification Report (Validation) ---")
print(classification_report(y_val, y_val_pred_nn))

# Print the ROC AUC Score
roc_auc_nn = roc_auc_score(y_val, y_val_proba_nn)
print(f"\nROC AUC Score (Neural Network): {roc_auc_nn:.4f}")
```

```
210/210 ━━━━━━━━━━━━━━━━━━━━ 0s 1ms/step

--- Neural Network Classification Report (Validation) ---
              precision    recall  f1-score   support

           0       0.83      0.74      0.78      4242
           1       0.62      0.74      0.67      2452

    accuracy                           0.74      6694
   macro avg       0.72      0.74      0.73      6694
weighted avg       0.75      0.74      0.74      6694


ROC AUC Score (Neural Network): 0.8172
```

```
accuracy = accuracy_score(y_val, y_val_pred_nn)
print("\nValidation Accuracy:", accuracy)
```

```
Validation Accuracy: 0.7358828801912161
```

Adding Dropout and Early Stopping are standard and highly effective methods to improve a Neural Network's performance and prevent overfitting.

Here is the revised code for your Neural Network, incorporating these two techniques:

Revised Neural Network Architecture We'll add a Dropout layer after the first hidden layer to introduce regularization.

```
import tensorflow as tf
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Dense, Dropout
from sklearn.metrics import confusion_matrix, classification_report, roc_auc_score

input_dim = X_resampled.shape[1]

model = Sequential()
model.add(Dense(64, activation='relu', input_shape=(input_dim,)))

# Dropout Layer (drops 30% of neurons during each training step)
model.add(Dropout(0.3))

# Second Hidden Layer
model.add(Dense(32, activation='relu'))

# Output Layer
model.add(Dense(1, activation='sigmoid'))

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

print("Revised Neural Network architecture with Dropout defined and compiled.")
```

```
Revised Neural Network architecture with Dropout defined and compiled.
/usr/local/lib/python3.12/dist-packages/keras/src/layers/core/dense.py:93: UserWarning: Do not pass an `input_shape`/`input_
  super().__init__(activity_regularizer=activity_regularizer, **kwargs)
```

```
from tensorflow.keras.callbacks import EarlyStopping

# 1. Define Early Stopping
# Monitor the validation loss ('val_loss')
# patience=5 means training will stop if val_loss doesn't improve for 5 consecutive epochs
early_stopping = EarlyStopping(
    monitor='val_loss',
    patience=5,
    restore_best_weights=True
)

# 2. Train the model (Now monitoring 'val_loss' and using EarlyStopping)
# Increased epochs to 50, but Early Stopping will likely terminate it sooner.
history = model.fit(
    X_resampled,
    y_resampled,
    epochs=50,
    batch_size=32,
    validation_split=0.1,
    callbacks=[early_stopping], #  NEW: Add the callback
    verbose=0
```