1. Introduction

This project uses the `stroke-data.csv` dataset from Kaggle to build a machine learning model that predicts a patient's risk of stroke. Due to the rarity of stroke cases, we address class imbalance and focus on metrics like **Recall** and **ROC-AUC** to avoid missing high-risk patients.

Key steps:

- Data cleaning and feature selection
- Model testing and evaluation
- Emphasis on accuracy and clinical usefulness

The goal is a reliable, easy-to-use tool to help doctors detect stroke risk early.

In [1]:
```
!pip install imbalanced-learn
```

```
Requirement already satisfied: imbalanced-learn in /usr/lo
cal/lib/python3.11/dist-packages (0.13.0)
Requirement already satisfied: numpy<3,>=1.24.3 in /usr/lo
cal/lib/python3.11/dist-packages (from imbalanced-learn)
(1.26.4)
Requirement already satisfied: scipy<2,>=1.10.1 in /usr/lo
cal/lib/python3.11/dist-packages (from imbalanced-learn)
(1.15.2)
Collecting scikit-learn<2,>=1.3.2 (from imbalanced-learn)
  Downloading scikit_learn-1.6.1-cp311-cp311-manylinux_2_1
7_x86_64.manylinux2014_x86_64.whl.metadata (18 kB)
Requirement already satisfied: sklearn-compat<1,>=0.1 in /
usr/local/lib/python3.11/dist-packages (from imbalanced-le
arn) (0.1.3)
Requirement already satisfied: joblib<2,>=1.1.1 in /usr/lo
cal/lib/python3.11/dist-packages (from imbalanced-learn)
(1.4.2)
Requirement already satisfied: threadpoolctl<4,>=2.0.0 in
/usr/local/lib/python3.11/dist-packages (from imbalanced-l
earn) (3.6.0)
Requirement already satisfied: mkl_fft in /usr/local/lib/p
ython3.11/dist-packages (from numpy<3,>=1.24.3->imbalanced
-learn) (1.3.8)
Requirement already satisfied: mkl_random in /usr/local/li
b/python3.11/dist-packages (from numpy<3,>=1.24.3->imbalan
ced-learn) (1.2.4)
Requirement already satisfied: mkl_umath in /usr/local/li
b/python3.11/dist-packages (from numpy<3,>=1.24.3->imbalan
ced-learn) (0.1.1)
Requirement already satisfied: mkl in /usr/local/lib/pytho
n3.11/dist-packages (from numpy<3,>=1.24.3->imbalanced-lea
rn) (2025.1.0)
```

```
Requirement already satisfied: mkl in /usr/local/lib/pytho
n3.11/dist-packages (from numpy<3,>=1.24.3->imbalanced-lea
rn) (2025.1.0)
Requirement already satisfied: tbb4py in /usr/local/lib/py
thon3.11/dist-packages (from numpy<3,>=1.24.3->imbalanced-
learn) (2022.1.0)
Requirement already satisfied: mkl-service in /usr/local/l
ib/python3.11/dist-packages (from numpy<3,>=1.24.3->imbala
nced-learn) (2.4.1)
Requirement already satisfied: intel-openmp<2026,>=2024 in
/usr/local/lib/python3.11/dist-packages (from mkl->numpy<
3,>=1.24.3->imbalanced-learn) (2024.2.0)
Requirement already satisfied: tbb==2022.* in /usr/local/l
ib/python3.11/dist-packages (from mkl->numpy<3,>=1.24.3->i
mbalanced-learn) (2022.1.0)
Requirement already satisfied: tcmlib==1.* in /usr/local/l
ib/python3.11/dist-packages (from tbb==2022.*->mkl->numpy<
3,>=1.24.3->imbalanced-learn) (1.2.0)
Requirement already satisfied: intel-cmplr-lib-rt in /usr/
local/lib/python3.11/dist-packages (from mkl_umath->numpy<
3,>=1.24.3->imbalanced-learn) (2024.2.0)
Requirement already satisfied: intel-cmplr-lib-ur==2024.2.
0 in /usr/local/lib/python3.11/dist-packages (from intel-o
penmp<2026,>=2024->mkl->numpy<3,>=1.24.3->imbalanced-lear
n) (2024.2.0)
Downloading scikit_learn-1.6.1-cp311-cp311-manylinux_2_17_
x86_64.manylinux2014_x86_64.whl (13.5 MB)
   ━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━━ 13.5/1
3.5 MB 81.1 MB/s eta 0:00:00
Installing collected packages: scikit-learn
  Attempting uninstall: scikit-learn
    Found existing installation: scikit-learn 1.2.2
    Uninstalling scikit-learn-1.2.2:
      Successfully uninstalled scikit-learn-1.2.2
ERROR: pip's dependency resolver does not currently take i
nto account all the packages that are installed. This beha
viour is the source of the following dependency conflicts.
category-encoders 2.7.0 requires scikit-learn<1.6.0,>=1.0.
0, but you have scikit-learn 1.6.1 which is incompatible.
bigframes 1.36.0 requires rich<14,>=12.4.4, but you have r
ich 14.0.0 which is incompatible.
Successfully installed scikit-learn-1.6.1
```

2. Data Overview (EDA)

In this section, we load the dataset, inspect its structure, and provide an initial understanding of the available features.

In [2]:

```python
import pandas as pd

# Loading the dataset
data = pd.read_csv('/kaggle/input/stroke-prediction-dataset/h
ealthcare-dataset-stroke-data.csv')

# Displaying the first five rows
data.head()
```

```
/usr/local/lib/python3.11/dist-packages/pandas/io/formats/
format.py:1458: RuntimeWarning: invalid value encountered
in greater
  has_large_values = (abs_vals > 1e6).any()
/usr/local/lib/python3.11/dist-packages/pandas/io/formats/
format.py:1459: RuntimeWarning: invalid value encountered
in less
  has_small_values = ((abs_vals < 10 ** (-self.digits)) &
(abs_vals > 0)).any()
/usr/local/lib/python3.11/dist-packages/pandas/io/formats/
format.py:1459: RuntimeWarning: invalid value encountered
in greater
  has_small_values = ((abs_vals < 10 ** (-self.digits)) &
(abs_vals > 0)).any()
```

Out[2]:

id	gender	age	hypertension	heart_disease	ever_married	work_type	Resic
9046	Male	67.0	0	1	Yes	Private	Urbar
51676	Female	61.0	0	0	Yes	Self-employed	Rural
31112	Male	80.0	0	1	Yes	Private	Rural
60182	Female	49.0	0	0	Yes	Private	Urbar
1665	Female	79.0	1	0	Yes	Self-employed	Rural

Dataset Description

The dataset contains 5110 patient records and 12 columns, including information about demographics, medical history, and stroke occurrence. Each column is described below:

Column Name	Description
id	Unique identifier for each patient
gender	Gender of the patient (Male, Female, Other)
age	Age of the patient (numeric)
hypertension	0 = No hypertension, 1 = Has hypertension
heart_disease	0 = No heart disease, 1 = Has heart disease
ever_married	Yes or No
work_type	Type of work: children, Govt_job, Never_worked, Private, Self-employed
Residence_type	Urban or Rural
avg_glucose_level	Average glucose level in blood (numeric)
bmi	Body Mass Index (numeric)
smoking_status	formerly smoked, never smoked, smokes, or Unknown
stroke	0 = No stroke, 1 = Stroke occurred

Initial Data Summary

In [3]:
```
# Checking for missing values
data.isnull().sum()
```

Out[3]:
```
id                     0
gender                 0
age                    0
hypertension           0
heart_disease          0
ever_married           0
work_type              0
Residence_type         0
avg_glucose_level      0
bmi                  201
smoking_status         0
stroke                 0
dtype: int64
```

In [4]:
```
# Checking the distribution of the target variable
data['stroke'].value_counts(normalize=True)
```

Out[4]:
```
stroke
0    0.951272
1    0.048728
Name: proportion, dtype: float64
```

Findings,

1. Some missing values exist, especially in the **BMI column**.
2. The **"smoking_status"** column includes an **"Unknown" category**, which will need special handling.
3. The dataset is highly **imbalanced**, with only about **5%** of patients having had a stroke.

3. Data Cleaning

In this section, we address missing values and prepare the dataset for further analysis.

Handling Missing Values

In [5]:
```
# Imputing median by age group
data['bmi'] = data['bmi'].fillna(data.groupby('age')['bmi'].transform('median'))

# Removing rows where smoking_status is "Unknown"
data = data[data['smoking_status'] != 'Unknown']

data.shape
```

Out[5]:
```
(3566, 12)
```

In [6]:
```
# Checking again for missing values
data.isnull().sum()
```

Out[6]:
```
id                   0
gender               0
age                  0
hypertension         0
heart_disease        0
ever_married         0
work_type            0
Residence_type       0
```

In [7]:

```python
# Checking the stroke distribution again
data['stroke'].value_counts(normalize=True)
```

Out[7]:

```
stroke
0    0.943354
1    0.056646
Name: proportion, dtype: float64
```

Findings:

The class imbalance remains; strokes still account for a small minority of cases (~5%), which we will address later during model training.

4. Feature Selection

In this section, we select the most relevant features for stroke prediction based on medical research and domain knowledge.

Choosing Relevant Features

Following guidance from the medical team and supported by **(Stroke risk factors and prevention, n.d.)**, the following features are known to have a significant impact on stroke risk:

Feature	Reason for Selection
age	Stroke risk increases significantly with age.
hypertension	High blood pressure is a leading risk factor for stroke.
heart_disease	Existing heart conditions are linked to higher stroke risk.
avg_glucose_level	Elevated glucose levels can indicate diabetes, increasing stroke risk.
bmi	Obesity is a major stroke risk factor.
smoking_status	Smoking significantly raises the risk of stroke.
gender	Some studies show gender-based differences in stroke incidence.

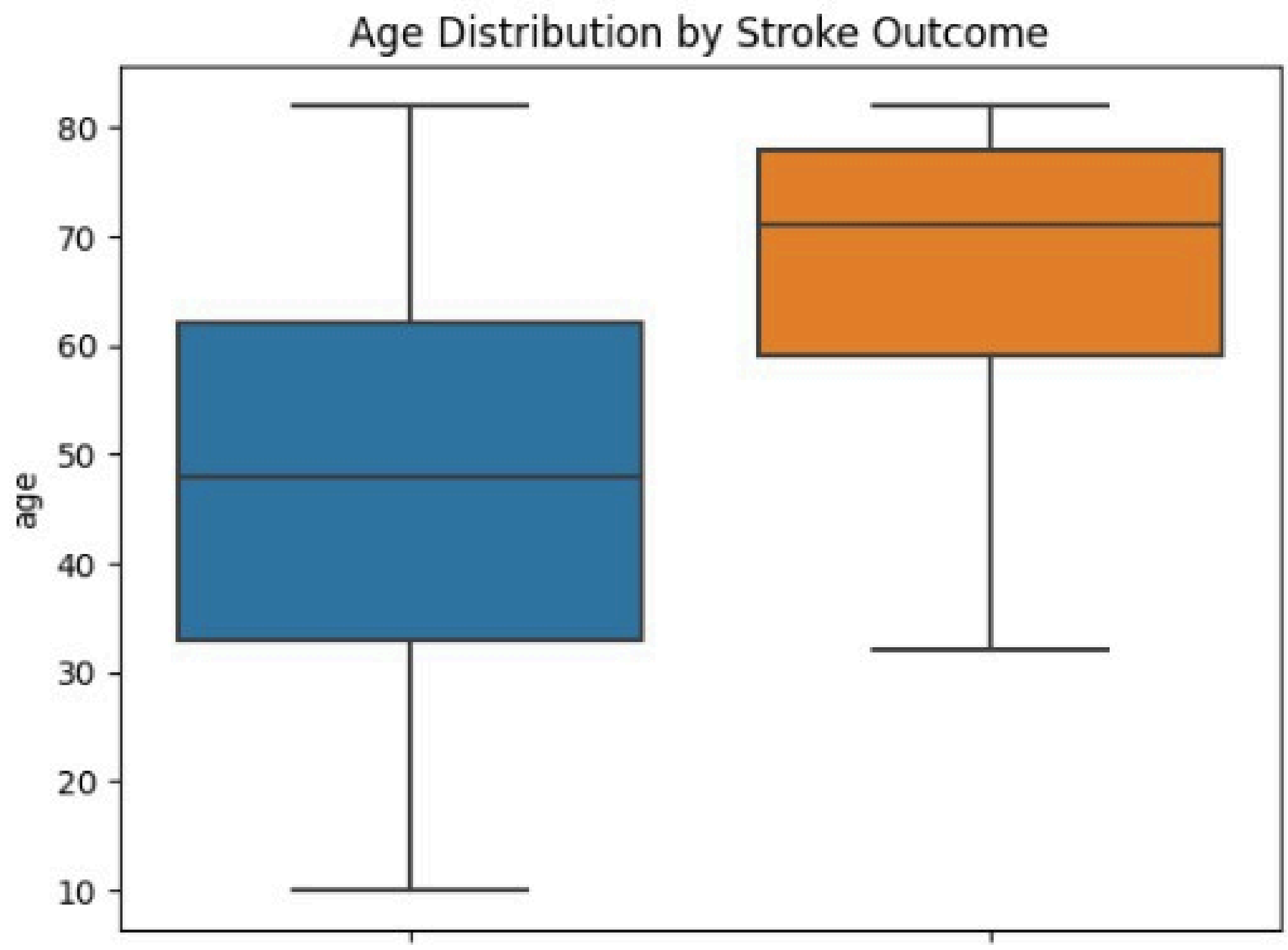
In [8]:
```
selected_features = ['gender', 'age', 'hypertension', 'heart_
disease',
                     'avg_glucose_level',
                      'bmi', 'smoking_status', 'stroke']

# Creating a new DataFrame with only the selected features
data_selected = data[selected_features]

# Displaying the first few rows
data_selected.head()
```

Out[8]:

	gender	age	hypertension	heart_disease	avg_glucose_level	bmi	smoking_
0	Male	67.0	0	1	228.69	36.60	formerly smoked
1	Female	61.0	0	0	202.21	29.45	never smo
2	Male	80.0	0	1	105.92	32.50	never smo
3	Female	49.0	0	0	171.23	34.40	smokes
4	Female	79.0	1	0	174.12	24.00	never smo

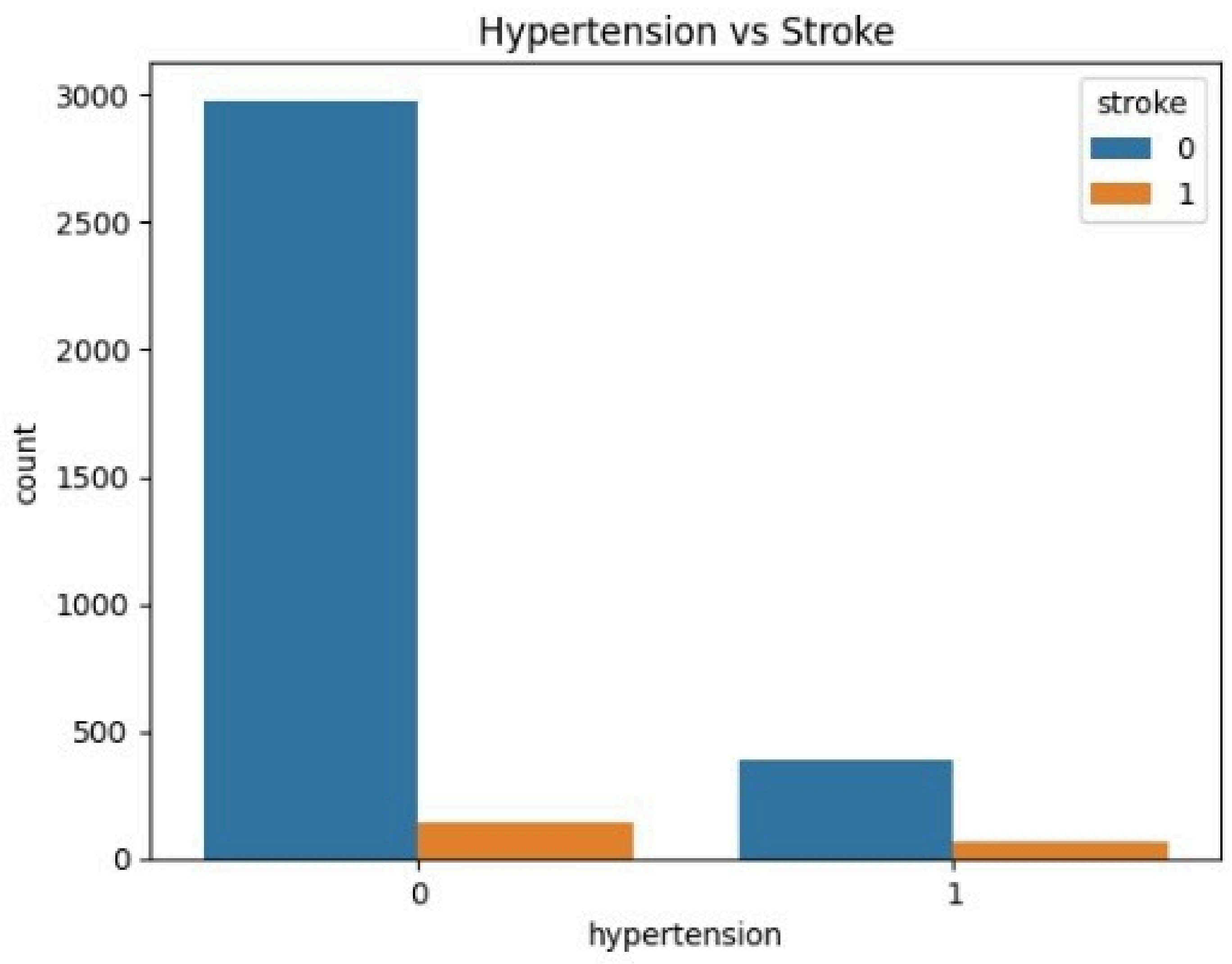
Visual Support for Feature Selection (EDA)

In [9]:
```
import seaborn as sns
import matplotlib.pyplot as plt

sns.boxplot(x='stroke', y='age', data=data_selected)
plt.title('Age Distribution by Stroke Outcome')
plt.show()
```



The boxplot shows that **age** strongly separates stroke vs. non-stroke patients: stroke cases have a **median age over 60**, while non-stroke patients are **younger and more varied**. This confirms age as a **key risk factor** and supports its use in our model.

In [10]:
```
sns.countplot(x='hypertension', hue='stroke', data=data_selec
ted)
plt.title('Hypertension vs Stroke')
plt.show()
```



The countplot shows that **hypertensive patients have a higher stroke rate**: even though there are fewer of them overall, a larger share of hypertensive individuals experienced strokes compared to those without hypertension. This confirms hypertension as a **key modifiable risk factor** and supports its inclusion in our model.

5. Feature Engineering

We engineered features to boost model performance and reflect clinical practice by converting continuous variables into meaningful categories, simplifying complex features, and creating new interaction variables.

5.1 Categorizing Age

Medical literature suggests age-related stroke risk increases sharply in later life, as learnt from **(Park *et al.*, 2013)**. To better capture this pattern, we grouped patients into clinically relevant age bands, using the age ranges reported in the research by **(Yao *et al.*, 2012)**.

In [11]:

```
data_selected = data_selected.copy()

def categorize_age(age):
    if age < 50:
        return 'young_adult'
    elif 50 <= age <= 80:
        return 'middle_aged'
    else:
        return 'very_old'

data_selected['age_group'] = data_selected['age'].apply(categ
orize_age)
```

5.2 Categorizing BMI & Glucose

We learned from **Centers for Disease Control and Prevention, 2024** that BMI and glucose are continuous variables with medically defined thresholds that indicate risk groups. Therefore, we transformed these variables into standard categories.

In [12]:

```
def categorize_bmi(bmi):
    if bmi < 18.5:
        return 'bmi_0_underweight'
    elif 18.5 <= bmi < 25:
        return 'bmi_1_healthy'
    elif 25 <= bmi < 30:
        return 'bmi_2_overweight'
    elif 30 <= bmi < 35:
        return 'bmi_3_obesity_class_1'
    elif 35 <= bmi < 40:
        return 'bmi_4_obesity_class_2'
    else:
        return 'bmi_5_obesity_class_3'

data_selected['bmi_category'] = data_selected['bmi'].apply(ca
tegorize_bmi)
```

In [13]:
```
import numpy as np

def glucose_category(glucose):
    if glucose < 70:
        return 'glucose_0_<70'
    elif 70 <= glucose <= 84:
        return 'glucose_1_70_84'
    elif 85 <= glucose <= 99:
        return 'glucose_2_85_99'
    elif 100 <= glucose <= 109:
        return 'glucose_3_100_109'
    elif 110 <= glucose <= 125:
        return 'glucose_4_110_125'
    elif 126 <= glucose <= 139:
        return 'glucose_5_126_139'
    else:
        return 'glucose_6_140_plus'

# Applying glucose category
data_selected['glucose_category'] = data_selected['avg_glucos
e_level'].apply(glucose_category)
# Dropping the original column once
data_selected.drop('avg_glucose_level', axis=1, inplace=True)
```

5.3 Binary Smoking Status

To reduce complexity and highlight overall exposure, this is the ordinal encode of smoking status

In [14]:
```
smoking_mapping = {
    'never smoked': 0,
    'formerly smoked': 1,
    'smokes': 2
}
data_selected['smoking_status_encoded'] = data_selected['smok
ing_status'].map(smoking_mapping)
```

5.4 Creating Risk Indicators & Interactions

We created new features that combines hypertension with heart disease and age status into seperate risk indicators and encoded glucose and BMI categories numerically, created interaction features (glucose × age, glucose × BMI), and added binary flags (`is_elderly` , `is_obese` , `high_glucose`) to highlight key stroke risk patterns.

In [15]:

```python
data_selected['health_risk'] = data_selected['hypertension'] + data_selected['heart_disease']
# 0 = no risk, 1 = moderate risk, 2 = high risk
```

In [16]:

```python
data_selected['lifestyle_risk'] = data_selected['smoking_status_encoded'] + data_selected['health_risk']
```

In [17]:

```python
data_selected['total_risk'] = data_selected['health_risk'] + data_selected['lifestyle_risk']
```

In [18]:

```python
glucose_mapping = {
    'glucose_0_<70': 0,
    'glucose_1_70_84': 1,
    'glucose_2_85_99': 2,
    'glucose_3_100_109': 3,
    'glucose_4_110_125': 4,
    'glucose_5_126_139': 5,
    'glucose_6_140_plus': 6
}

data_selected['glucose_category_encoded'] = data_selected['glucose_category'].map(glucose_mapping)
```

In [19]:

```python
bmi_mapping = {
    'bmi_0_underweight': 0,
    'bmi_1_healthy': 1,
    'bmi_2_overweight': 2,
    'bmi_3_obesity_class_1': 3,
    'bmi_4_obesity_class_2': 4,
    'bmi_5_obesity_class_3': 5
}

data_selected['bmi_category_encoded'] = data_selected['bmi_category'].map(bmi_mapping)
```

In [20]:

```python
data_selected['age_glucose_interaction'] = data_selected['glucose_category_encoded'] * data_selected['age']
data_selected['bmi_glucose_interaction'] = data_selected['glucose_category_encoded'] * data_selected['bmi_category_encoded']
```

In [21]:
```
data_selected['is_elderly'] = (data_selected['age'] > 80).ast
ype(int)
data_selected['is_obese'] = data_selected['bmi_category'].st
r.contains('obesity').astype(int)
data_selected['high_glucose'] = data_selected['glucose_catego
ry'].str.contains('140').astype(int)
```

5.5 Encoding Categorical Variables

To prepare the dataset for machine learning, all categorical features were encoded using one-hot encoding:

In [22]:
```
# Encoding selected categorical variables
categorical_features = [
    'gender',
    'age_group',
    'glucose_category',
    'bmi_category',
    'smoking_status'
]

data_encoded = pd.get_dummies(data_selected, columns=categori
cal_features, drop_first=True)

data_encoded.head()
```

Out[22]:

	age	hypertension	heart_disease	bmi	stroke	smoking_status_encoded	hea
0	67.0	0	1	36.60	1	1	1
1	61.0	0	0	29.45	1	0	0
2	80.0	0	1	32.50	1	0	1
3	49.0	0	0	34.40	1	2	0
4	79.0	1	0	24.00	1	0	1

5 rows × 33 columns

6. Data Preprocessing

n [23]:

```
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler

# Defining features and target
X = data_encoded.drop(columns=['stroke'])
y = data_encoded['stroke']

# Train-test split (80-20)
X_train, X_test, y_train, y_test = train_test_split(X, y, tes
t_size=0.2, random_state=42, stratify=y)

# Feature scaling
scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)
```

7. Handling Class Imbalance

In this section, as discussed by **He *et al.*, 2009**, imbalanced datasets require techniques like resampling to avoid bias toward the majority class. So, we address the issue of class imbalance, and since stroke cases are rare in the dataset, the model may become biased toward predicting the majority class (no stroke). To overcome this, we use **SMOTE (Synthetic Minority Oversampling Technique)** to balance the training data by generating synthetic examples of the minority class.

n [24]:

```
from imblearn.over_sampling import SMOTE

# Applying SMOTE only on the training set
smote = SMOTE(random_state=42)
X_train_balanced, y_train_balanced = smote.fit_resample(X_tra
in_scaled, y_train)
```

n [25]:

```
from collections import Counter
print("Before SMOTE:", Counter(y_train))
print("After SMOTE:", Counter(y_train_balanced))
```

```
Before SMOTE: Counter({0: 2690, 1: 162})
After SMOTE: Counter({0: 2690, 1: 2690})
```

8. Model Training

Now that the data is balanced and preprocessed, we can train machine learning models. We will start with **Logistic Regression**, a widely used linear classification algorithm.

We selected multiple models because research shows that **ensemble methods**, such as **Random Forest** ,**Gradient Boosting**, have demonstrated robust performance in imbalanced classification tasks **(Dong et al., 2020)**.

We used **SelectKBest with ANOVA F-statistics** to select the top 10 most predictive features from the training data. This helps reduce dimensionality and improve model focus.

In [26]:

```
from sklearn.feature_selection import SelectKBest, f_classif

# Selecting top k features based on ANOVA F-statistics
selector = SelectKBest(score_func=f_classif, k=10)
X_train_selected = selector.fit_transform(X_train_balanced, y
_train_balanced)
X_test_selected = selector.transform(X_test_scaled)

# Checking which features were selected
mask = selector.get_support()
selected_features = X.columns[mask]
print("Selected features:", selected_features.tolist())
```

```
Selected features: ['age', 'hypertension', 'heart_diseas
e', 'health_risk', 'lifestyle_risk', 'total_risk', 'age_gl
ucose_interaction', 'high_glucose', 'age_group_young_adul
t', 'glucose_category_glucose_6_140_plus']
```

```
# Logistic Regression
model_lr = LogisticRegression(class_weight='balanced', random
_state=42)
model_lr.fit(X_train_selected, y_train_balanced)

# Random Forest
model_rf = RandomForestClassifier(class_weight='balanced', ra
ndom_state=42)
model_rf.fit(X_train_selected, y_train_balanced)

# Gradient Boosting
model_gb = GradientBoostingClassifier(random_state=42)
model_gb.fit(X_train_selected, y_train_balanced)

# Decision Tree
model_dt = DecisionTreeClassifier(class_weight='balanced', ma
x_depth=4, random_state=42)
model_dt.fit(X_train_selected, y_train_balanced)
```

Out[27]:

```
DecisionTreeClassifier

DecisionTreeClassifier(class_weight='balanced', max_depth=4,
random_state=42)
```

9. Model Evaluation

In [28]:

```
from sklearn.metrics import (
    accuracy_score, precision_score, recall_score,
    f1_score, roc_auc_score, confusion_matrix, classification
_report
)

def evaluate_model(model, name):
    y_pred = model.predict(X_test_selected)
    y_proba = model.predict_proba(X_test_selected)[:, 1]

    acc = accuracy_score(y_test, y_pred)
    prec = precision_score(y_test, y_pred)
    rec = recall_score(y_test, y_pred)
    f1 = f1_score(y_test, y_pred)
    roc = roc_auc_score(y_test, y_proba)

    tn, fp, fn, tp = confusion_matrix(y_test, y_pred).ravel()

    print(f"\n=== Classification Report for {name} ===")
    print(classification_report(y_test, y_pred, digits=3))
```

```python
    print(f"\n=== Classification Report for {name} ===")
    print(classification_report(y_test, y_pred, digits=3))

    model_results.append({
        'Model': name,
        'Accuracy': acc,
        'Precision': prec,
        'Recall': rec,
        'F1-Score': f1,
        'ROC AUC': roc,
        'True Positives': tp,
        'False Negatives': fn
    })

model_results = []
evaluate_model(model_lr, "Logistic Regression")
evaluate_model(model_rf, "Random Forest")
evaluate_model(model_gb, "Gradient Boosting")
evaluate_model(model_dt, "Decision Tree")
```

```
=== Classification Report for Logistic Regression ===
              precision    recall  f1-score   support

           0      0.980     0.737     0.842       674
           1      0.145     0.750     0.243        40

    accuracy                          0.738       714
   macro avg      0.563     0.744     0.542       714
weighted avg      0.933     0.738     0.808       714


=== Classification Report for Random Forest ===
              precision    recall  f1-score   support

           0      0.949     0.939     0.944       674
           1      0.128     0.150     0.138        40

    accuracy                          0.895       714
   macro avg      0.538     0.545     0.541       714
weighted avg      0.903     0.895     0.899       714


=== Classification Report for Gradient Boosting ===
              precision    recall  f1-score   support

           0      0.952     0.890     0.920       674
           1      0.119     0.250     0.161        40
    accuracy                        0.710       714
   macro avg       0.545     0.682     0.512       714
weighted avg       0.924     0.710     0.788       714
```

In [29]:

```
# Summarize results
results_df = pd.DataFrame(model_results)

performance_metrics = results_df[['Model', 'Accuracy', 'Preci
sion', 'Recall', 'F1-Score', 'ROC AUC']]
error_analysis = results_df[['Model', 'True Positives', 'Fals
e Negatives']]

print("\n=== Model Performance Metrics ===\n")
print(performance_metrics.round(3).to_string(index=False))

print("\n=== Error Analysis by Model ===\n")
print(error_analysis.to_string(index=False))
```

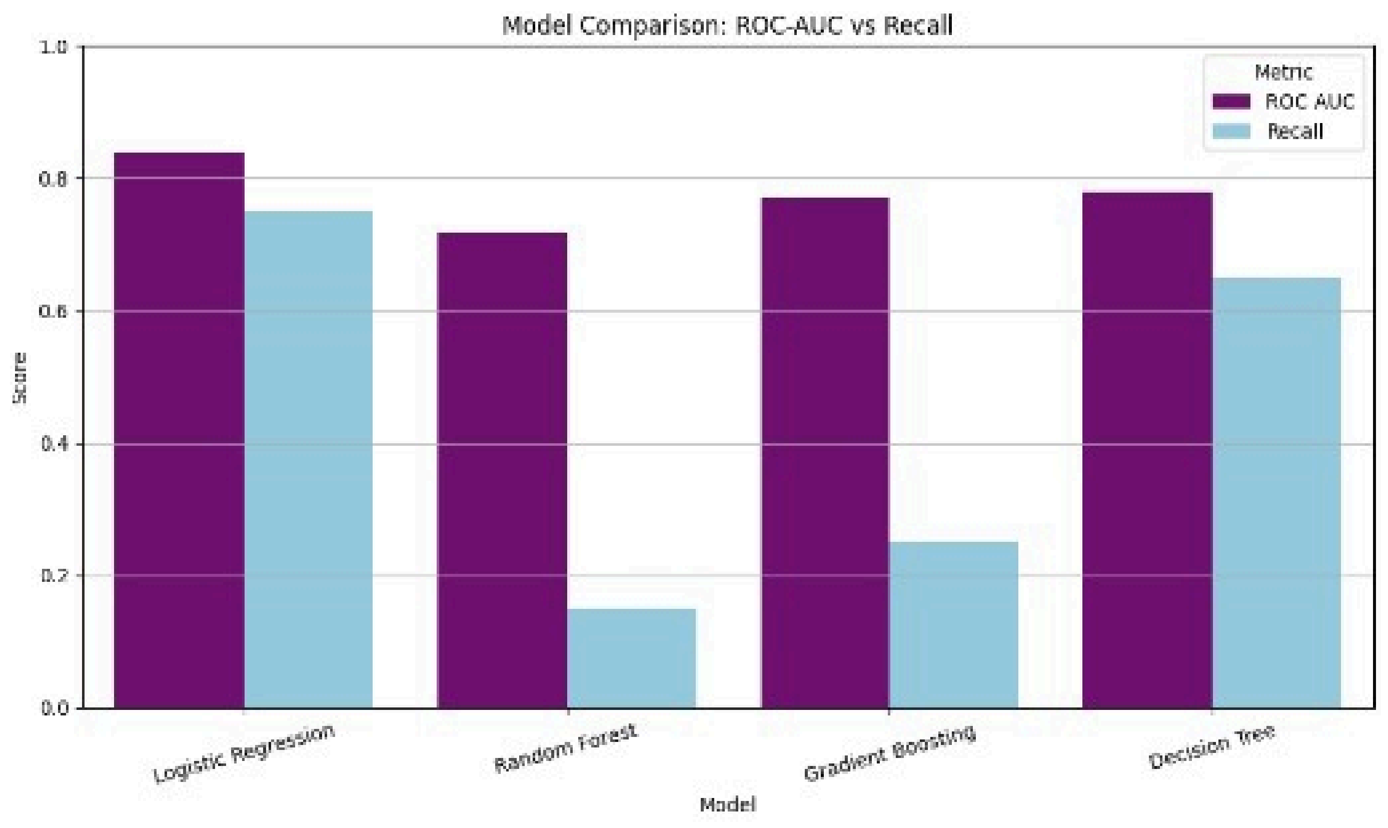
```
=== Model Performance Metrics ===

              Model  Accuracy  Precision  Recall  F1-Score
ROC AUC
Logistic Regression     0.738      0.145    0.75     0.243
0.839
      Random Forest     0.895      0.128    0.15     0.138
0.718
  Gradient Boosting     0.854      0.119    0.25     0.161
0.771
      Decision Tree     0.710      0.119    0.65     0.201
0.780

=== Error Analysis by Model ===

              Model  True Positives  False Negatives
Logistic Regression              30               10
      Random Forest               6               34
  Gradient Boosting              10               30
      Decision Tree              26               14
```

10. Results Discussion

In this section, we compare and interpret the performance of the trained models, using **Recall and ROC-AUC**.

n [30]:

```
import seaborn as sns
# Reshaping the DataFrame
melted = results_df.melt(id_vars='Model', value_vars=['ROC AU
C', 'Recall'],
                         var_name='Metric', value_name='Scor
e')

plt.figure(figsize=(10, 6))
sns.barplot(data=melted, x='Model', y='Score', hue='Metric',
palette=['purple', 'skyblue'])
plt.title('Model Comparison: ROC-AUC vs Recall')
plt.ylim(0, 1)
plt.xticks(rotation=15)
plt.grid(axis='y')
plt.tight_layout()
plt.show()
```



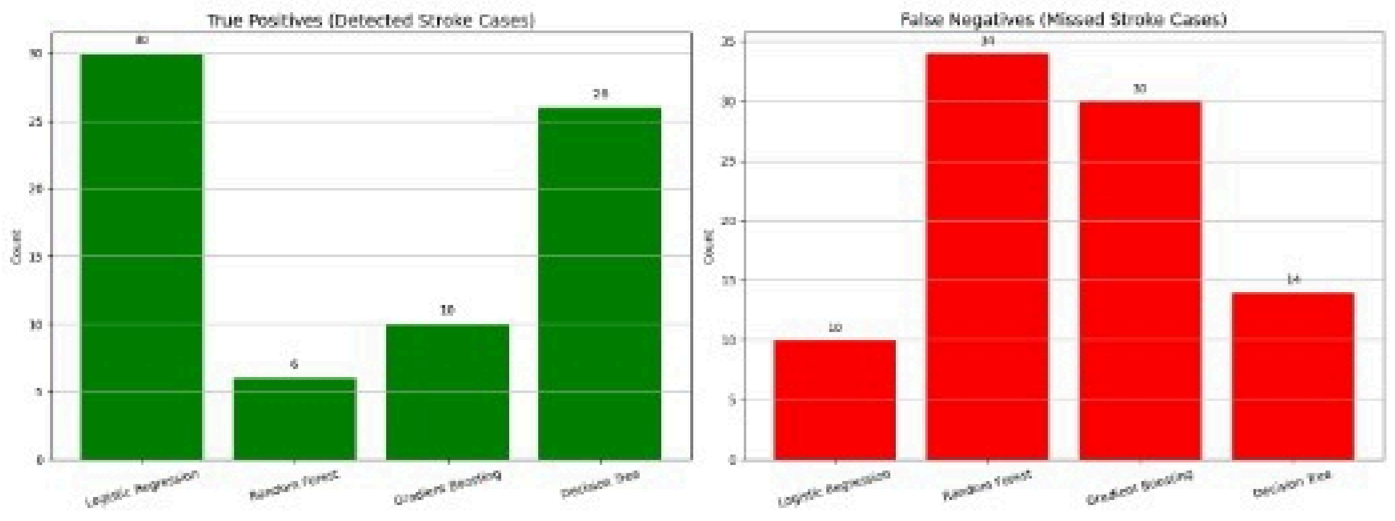
Model Performance Summary

Metric	Logistic Regression	Random Forest	Gradient Boosting	Decision Tree
Recall	**0.750 (high)**	0.150	0.250	0.650
Precision	0.145	0.128	0.119	0.119
Accuracy	0.738	**0.895**	0.854	0.710
ROC-AUC	**0.839 (highest)**	0.718	0.771	0.780

Model Trade-offs and Clinical Relevance

Logistic Regression achieved the highest **ROC-AUC (0.839)** and strong **recall (0.75)**, making it effective at identifying stroke cases. Although its **precision (0.145)** is low, this is acceptable in clinical contexts where missing a true case is more harmful than a false alarm.

In [31]:
```python
models = results_df['Model']
tp_values = results_df['True Positives']
fn_values = results_df['False Negatives']

fig, axes = plt.subplots(1, 2, figsize=(16, 6))

# True Positives Plot
axes[0].bar(models, tp_values, color='green')
axes[0].set_title('True Positives (Detected Stroke Cases)', f
ontsize=14)
axes[0].set_ylabel('Count')
axes[0].tick_params(axis='x', rotation=15)
axes[0].grid(axis='y')

# Annotating TP values
for i, val in enumerate(tp_values):
    axes[0].text(i, val + 0.5, str(val), ha='center', va='bot
tom', fontsize=10)

# False Negatives Plot
axes[1].bar(models, fn_values, color='red')
axes[1].set_title('False Negatives (Missed Stroke Cases)', fo
ntsize=14)
axes[1].set_ylabel('Count')
axes[1].tick_params(axis='x', rotation=15)
axes[1].grid(axis='y')

# Annotating FN values
for i, val in enumerate(fn_values):
    axes[1].text(i, val + 0.5, str(val), ha='center', va='bot
tom', fontsize=10)

plt.tight_layout()
plt.show()
```



We evaluated four machine learning models based on their ability to correctly detect

We evaluated four machine learning models based on their ability to correctly detect stroke cases. The focus was on:

- **True Positives**: Correctly identified stroke cases
- **False Negatives**: Missed stroke cases

These metrics are critical in medical diagnostics, where failing to detect a stroke can have serious consequences. We got,

Model	True Positives	False Negatives
Logistic Regression	**30**	**10**
Random Forest	6	34
Gradient Boosting	10	30
Decision Tree	26	14

Best Model: Logistic Regression

- Detected the **most stroke cases (30)**
- Missed only **10**, yielding strong recall
- Suitable for **high-sensitivity medical screening**

Weakest Model: Random Forest

- Detected just **6 stroke cases**
- Missed **34 cases**, the **highest false negative count**
- Not reliable for clinical decision support

Hyperparameter Tuning in the best model

In [32]:

```
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import GridSearchCV
from sklearn.metrics import (
    accuracy_score, precision_score, recall_score,
    f1_score, roc_auc_score, confusion_matrix, ConfusionMatri
xDisplay
)
import pandas as pd
import matplotlib.pyplot as plt

# Grid search for Logistic Regression
param_grid = {
    'C': [0.01, 0.1, 1, 10, 100],
    'penalty': ['l2'],
    'solver': ['liblinear']
}

grid_search = GridSearchCV(
```

In [32]:
```
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import GridSearchCV
from sklearn.metrics import (
    accuracy_score, precision_score, recall_score,
    f1_score, roc_auc_score, confusion_matrix, ConfusionMatri
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# Grid search for Logistic Regression
param_grid = {
    'C': [0.01, 0.1, 1, 10, 100],
    'penalty': ['l2'],
    'solver': ['liblinear']
}

grid_search = GridSearchCV(
    LogisticRegression(class_weight='balanced', max_iter=100
0),
    param_grid, cv=5, scoring='recall', n_jobs=-1
)
grid_search.fit(X_train_selected, y_train_balanced)
best_lr_model = grid_search.best_estimator_

# Evaluation
y_pred = best_lr_model.predict(X_test_selected)
y_proba = best_lr_model.predict_proba(X_test_selected)[:, 1]

metrics = {
    'Model': 'Logistic Regression',
    'Accuracy': accuracy_score(y_test, y_pred),
    'Precision': precision_score(y_test, y_pred),
    'Recall': recall_score(y_test, y_pred),
    'F1-Score': f1_score(y_test, y_pred),
    'ROC AUC': roc_auc_score(y_test, y_proba),
    'True Positives': confusion_matrix(y_test, y_pred)[1, 1],
    'False Negatives': confusion_matrix(y_test, y_pred)[1, 0]
}

results_df = pd.DataFrame([metrics])

# Display results
print("=== Model Performance Metrics ===\n")
print(results_df[['Model', 'Accuracy', 'Precision', 'Recall',
'F1-Score', 'ROC AUC']].round(3).to_string(index=False))
```
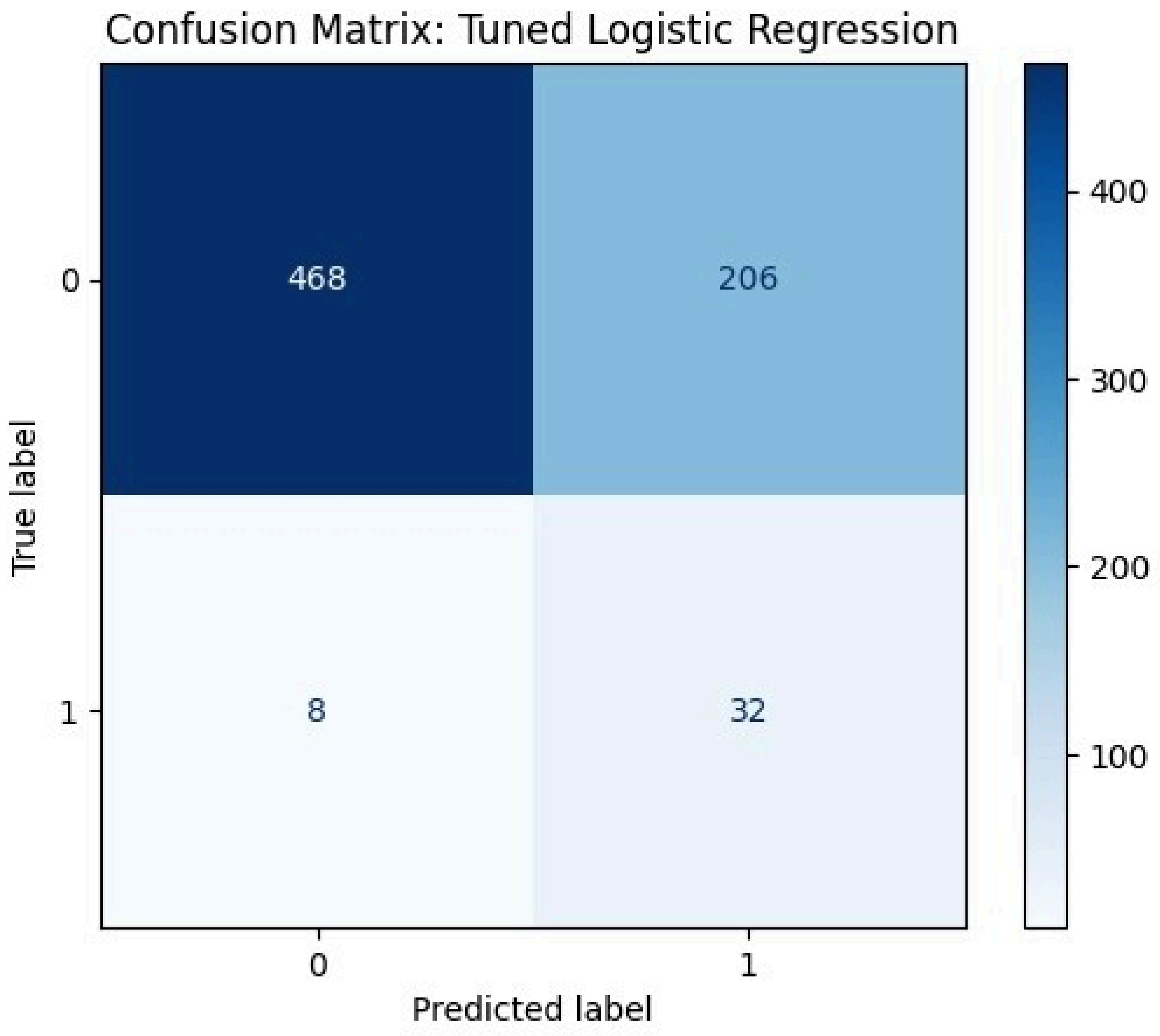

```
=== Model Performance Metrics ===

              Model  Accuracy  Precision  Recall  F1-Score
```

```
=== Model Performance Metrics ===

              Model  Accuracy  Precision  Recall  F1-Score
ROC AUC
Logistic Regression       0.7      0.134     0.8      0.23
0.841
```

In [33]:

```python
# Plotting confusion matrix
ConfusionMatrixDisplay.from_predictions(y_test, y_pred, cmap
='Blues')
plt.title("Confusion Matrix: Tuned Logistic Regression")
plt.show()
```



After tuning hyperparameters, Logistic Regression showed improved performance in stroke detection:

Model Performance Summary

- **Recall:** 0.80 (high) – correctly identified 32 stroke cases
- **Precision:** 0.134 – low, but acceptable in clinical settings prioritizing safety
- **ROC AUC:** 0.841 – indicates strong overall discrimination ability
- **Accuracy:** 0.70 – moderate overall correctness

The model achieved **high recall 0.80**, with only **8 missed stroke cases**, making it reliable for medical screening where identifying all possible stroke patients is critical. While precision remains low, this is an acceptable trade-off in safety-first applications.

11. Conclusion

Summary: Stroke Prediction Using Machine Learning

To sum up, we developed a machine learning solution to predict the probability of stroke using patient health records.

Key Insights

- **Visual error analysis** (true positives vs. false negatives) helped assess clinical impact of missed stroke cases.
- **Removed weak features** such as `work_type` (low relevance) and `gender=Other` (insufficient data).
- Prioritized **clinical safety** in model selection — **recall was more important than overall accuracy**.

Performance Highlights

- The tuned **Logistic Regression** model achieved:
  - **Recall:** 0.80 – correctly identified 32 stroke cases
  - **Precision:** 0.134 – expected trade-off due to prioritizing recall
  - **Accuracy:** 0.70
  - **ROC-AUC:** 0.841 – strong discrimination between stroke and non-stroke cases
- Only **8 stroke cases were missed**, showing strong sensitivity
- Performance reflects realistic and clinically meaningful results on an imbalanced dataset

Opportunities for Improvement

- Integrate **richer clinical data** (e.g., lab results, patient history, time-series records)
- Apply **threshold tuning** to better balance sensitivity and specificity (He *et al.*, 2009)
- Explore **advanced ensemble methods** or **AutoML** for optimized and interpretable performance

This solution supports early intervention and risk monitoring, providing valuable decision support in real-world clinical settings.