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Promoting Healthier Lifestyle Behaviors: Smoking Prediction Analysis

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→ Promoting Healthier Lifestyle Behaviors: Smoking Prediction Analysis

Introduction

Problem Statement:

Given the approaching annual events, the Great American Smokeout, and Lung Cancer Awareness Month, the concern for public health related to tobacco use and lung cancer has once again come to the spotlight. In addition to raising public awareness, this project also aims to contribute by predicting individuals' smoking and drinking habits. This is conducted through the analysis of people's physiological and health-related data. Such identification plays a crucial role in public health and personalized healthcare, helping to encourage healthier lifestyle choices.

Data Sources:

The dataset was obtained from the Korea National Health Insurance Service and comprises 22 variables and 2 target variables. The dataset can be found, which was originally sourced here.

→ Data Dictionary:

This dataset consists of 910306 rows and 24 columns, encompassing mixture of types of variables: categorical variables (sex, hearing ability, smoking and drinking pattern), numerical variables (all other demographic details and health indicators).

Column	Description(US)
Sex	male, female
age	round up to 5 years
height	round up to 5 cm [cm]
weight	[kg]
sight_left	eyesight (left)
sight_right	eyesight (right)
hear_left	hearing left, 1(normal), 2(abnormal)
hear_right	hearing right, 1(normal), 2(abnormal)
SBP	Systolic blood pressure [mmHg]
DBP	Diastolic blood pressure [mmHg]
BLDS	BLDS or FSG (fasting blood glucose) [mg/dL]
tot_chole	total cholesterol [mg/dL]
HDL_chole	HDL cholesterol [mg/dL]
LDL_chole	LDL cholesterol [mg/dL]
triglyceride	triglyceride [mg/dL]
hemoglobin	hemoglobin [g/dL]
urine_protein	protein in urine, 1(-), 2(+/-), 3(+1), 4(+2), 5(+3), 6(+4)
serum_creatinine	serum(blood) creatinine [mg/dL]
SGOT_AST	SGOT (Glutamate-oxaloacetate transaminase) AST (Aspartate transaminase) [IU/L]
SGOT_ALT	ALT (Alanine transaminase) [IU/L]
gamma_GTP	y-glutamyl transpeptidase [IU/L]
SMK_stat_type_cd	Smoking state, 1(never), 2(used to smoke but quit), 3(still smoke)
DRK_YN	Drinker or Not

✓ In-Depth Exploration of Dataset Variables

Column	Description(US)	Data Type	Examples	Variable Type
sex	Gender	Categorical	Male, Female	Discrete
age	Age in years	Numeric	35, 30, 40,	Continuous
height	Height rounded up to 5 cm [cm]	Numeric	170, 180, 165,	Continuous
weight	Weight in kilograms [kg]	Numeric	75, 80, 60,	Continuous
waistline	Waistline in centimeters	Numeric	90.0, 89.0, 91.0,	Continuous
sight_left	Eyesight in left eye	Numeric	1.0, 0.9, 1.2,	Continuous
sight_right	Eyesight in right eye	Numeric	1.0, 1.2, 1.5,	Continuous
hear_left	Hearing in left ear (1: normal, 2: abnormal)	Categorical	1.0, 2.0	Discrete
hear_right	Hearing in right ear (1: normal, 2: abnormal)	Categorical	1.0, 2.0	Discrete
SBP	Systolic Blood Pressure [mmHg]	Numeric	120.0, 130.0,	Continuous
DBP	Diastolic Blood Pressure [mmHg]	Numeric	80.0, 82.0,	Continuous
BLDS	Fasting Blood Glucose [mg/dL]	Numeric	99.0, 106.0,	Continuous
tot_chole	Total Cholesterol [mg/dL]	Numeric	193.0, 228.0,	Continuous
HDL_chole	HDL Cholesterol [mg/dL]	Numeric	48.0, 55.0,	Continuous
LDL_chole	LDL Cholesterol [mg/dL]	Numeric	126.0, 148.0,	Continuous
triglyceride	Triglyceride [mg/dL]	Numeric	92.0, 121.0,	Continuous
hemoglobin	Hemoglobin [g/dL]	Numeric	17.1, 15.8,	Continuous
urine_protein	Urine Protein (1: -, 2: +/-, 3: +1, 4: +2, 5: +3, 6: +4)	Categorical	1.0, 3.0, 2.0,	Discrete
serum_creatinine	Serum Creatinine [mg/dL]	Numeric	1.0, 0.9,	Continuous
SGOT_AST	SGOT (AST) [IU/L]	Numeric	21.0, 20.0,	Continuous
SGOT_ALT	ALT [IU/L]	Numeric	35.0, 36.0,	Continuous
gamma_GTP	Gamma-GTP [IU/L]	Numeric	40.0, 27.0,	Continuous
SMK_stat_type_cd	Smoking State (1: never, 2: used to smoke, 3: still smoke)	Categorical	1.0, 3.0, 2.0	Discrete
DRK_YN	Drinker or Not (Y: Yes, N: No)	Categorical	Y, N	Discrete

Motivation

We care about this Analysis and prediction for the following reasons:

Addressing Public Health Challenges

This project is motivated by the urgent need to address critical public health challenges associated with tobacco and alcohol consumption. Smoking and excessive drinking contribute significantly to preventable health issues, including respiratory diseases, cardiovascular problems, and various cancers. By leveraging advanced data analysis techniques, we aim to contribute to the identification and understanding of patterns related to these behaviors.

Early Intervention and Personalized Healthcare

Predicting smoking and drinking habits through data analysis holds the potential for early intervention and personalized healthcare. Identifying individuals at risk allows healthcare providers to offer timely guidance, support, and tailored interventions to mitigate health risks associated with these behaviors. This proactive approach can significantly improve health outcomes and reduce the burden on healthcare systems.

Public Health Impact

The outcomes of this project have broader implications for public health initiatives and policies. Policymakers can utilize the insights gained to tailor targeted interventions aimed at reducing smoking and drinking habits at a population level. By aligning with broader public health goals, this project contributes to the creation of evidence-based strategies for promoting healthier lifestyles.

Leveraging Data for Better Health

In an era of data-driven decision-making, leveraging advanced analytics to address health challenges becomes crucial. This project exemplifies the power of data analysis in extracting meaningful insights from large datasets, offering a valuable tool for healthcare professionals, policymakers, and public health advocates.

Comprehensive Health Analysis

This project aligns with the overarching goal of promoting comprehensive health analysis. By exploring the relationships between demographic, physiological, and behavioral variables, we strive to contribute to a holistic understanding of individual health and well-being. Such an approach is essential for fostering a culture of proactive health management and prevention.

In summary, this project is motivated by the desire to make a meaningful impact on public health, leveraging data analytics to drive actionable insights, and contributing to the ongoing efforts to create a healthier and more informed society.

Our Stakeholders and Their Interest

Healthcare Providers:

. Why They Care:

- Early Intervention: Healthcare providers are deeply invested in identifying individuals at risk due to smoking or drinking habits to enable early intervention.
- Tailored Health Advice: Predictive analysis allows for the customization of health advice and interventions, improving patient outcomes.

Policymakers and Public Health Organizations:

. Why They Care:

- Population-Level Impact: Policymakers and public health organizations can utilize insights to design interventions and initiatives aimed at reducing smoking and drinking habits at a population level.
- Evidence-Based Decision-Making: Data-driven strategies enable evidence-based decision-making, ensuring targeted efforts for maximum impact.

Individuals and the General Public:

. Why They Care:

- Personal Health Awareness: Individuals benefit from a better understanding of their own health risks associated with smoking and drinking, empowering them to make informed lifestyle choices.
- Community Well-being: The project contributes to broader community well-being by fostering awareness and promoting healthier lifestyle choices.

Mental Health Advocates:

. Why They Care:

Holistic Health Promotion: Mental health advocates recognize the interconnectedness of physical and mental well-being.
 Promoting healthier lifestyle choices aligns with the broader goal of comprehensive health analysis, including mental health.

Researchers and Academia:

• Why They Care:

- Advancing Knowledge: Researchers are motivated to contribute to the body of knowledge related to predictive analysis in public health.
- Academic Contribution: The project offers opportunities for academic contribution, furthering the understanding of patterns and correlations in health-related behaviors.

Insurance Providers:

. Why They Care:

- Risk Management: Insurance providers have a vested interest in understanding and managing health risks associated with smoking and drinking habits among their policyholders.
- o Premium Adjustment: Insights from the project can inform premium adjustments based on individual health behaviors.

In summary, a diverse set of stakeholders, including healthcare providers, policymakers, individuals, mental health advocates, researchers, and insurance providers, care about this problem due to its potential impact on health outcomes, community well-being, and the advancement of knowledge in the field of public health.

Data Load and Preprocessing

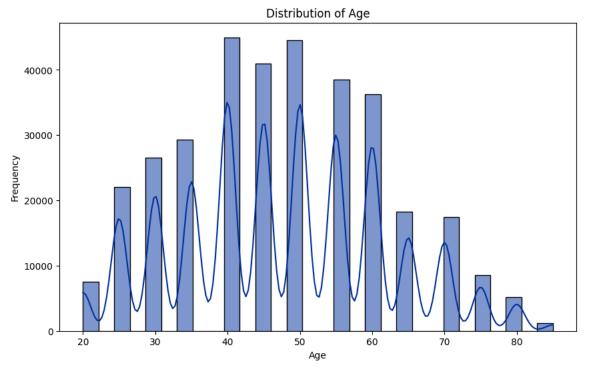
```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns

! pip install kaggle
! mkdir ~/.kaggle
! cp kaggle.json ~/.kaggle/
! chmod 600 ~/.kaggle/kaggle.json

Requirement already satisfied: kaggle in /usr/local/lib/python3.10/dist-packages (1.5.16)
Requirement already satisfied: six>=1.10 in /usr/local/lib/python3.10/dist-packages (from kaggle) (1.16.0)
```

```
Requirement already satisfied: certifi in /usr/local/lib/python3.10/dist-packages (from kaggle) (2023.11.17)
     Requirement already satisfied: python-dateutil in /usr/local/lib/python3.10/dist-packages (from kaggle) (2.8.2)
     Requirement already satisfied: requests in /usr/local/lib/python3.10/dist-packages (from kaggle) (2.31.0)
     Requirement already satisfied: tqdm in /usr/local/lib/python3.10/dist-packages (from kaggle) (4.66.1)
     Requirement already satisfied: python-slugify in /usr/local/lib/python3.10/dist-packages (from kaggle) (8.0.1)
     Requirement already satisfied: urllib3 in /usr/local/lib/python3.10/dist-packages (from kaggle) (2.0.7)
     Requirement already satisfied: bleach in /usr/local/lib/python3.10/dist-packages (from kaggle) (6.1.0)
     Requirement already satisfied: webencodings in /usr/local/lib/python3.10/dist-packages (from bleach->kaggle) (0.5.1)
     Requirement already satisfied: text-unidecode>=1.3 in /usr/local/lib/python3.10/dist-packages (from python-slugify->kaggle) Requirement already satisfied: charset-normalizer<4,>=2 in /usr/local/lib/python3.10/dist-packages (from requests->kaggle) (
     Requirement already satisfied: idna<4,>=2.5 in /usr/local/lib/python3.10/dist-packages (from requests->kaggle) (3.6)
     cp: cannot stat 'kaggle.json': No such file or directory
     chmod: cannot access '/root/.kaggle/kaggle.json': No such file or directory
! kaggle datasets download sooyoungher/smoking-drinking-dataset
! unzip smoking-drinking-dataset.zip
→ Traceback (most recent call last):
       File "/usr/local/bin/kaggle", line 5, in <module>
         from kaggle.cli import main
       File "/usr/local/lib/python3.10/dist-packages/kaggle/__init__.py", line 23, in <module>
         ani.authenticate()
       File "/usr/local/lib/python3.10/dist-packages/kaggle/api/kaggle_api_extended.py", line 403, in authenticate
         raise IOError('Could not find {}. Make sure it\'s located in'
     OSError: Could not find kaggle.json. Make sure it's located in /root/.kaggle. Or use the environment method.
     unzip: cannot find or open smoking-drinking-dataset.zip, smoking-drinking-dataset.zip.zip or smoking-drinking-dataset.zip.Z
from google.colab import drive
drive.mount('/content/gdrive', force_remount=True )
→ Mounted at /content/gdrive
df = pd.read_csv('//content/smoking_driking_dataset_Ver01.csv')
data_folder = '/content/drive/MyDrive/Colab Notebooks/BA810/Data/'
# Assuming your DataFrame is named df
df['SMK_stat_type_cd'] = df['SMK_stat_type_cd'].replace({1: 0, 2: 1, 3: 1})
df['DRK_YN'] = df['DRK_YN'].replace({'Y':1,'N':0})
df['sex'] = df['sex'].replace({'Male':1, 'Female':0})
  EDA
Importing necessary libraries
import matplotlib.pyplot as plt
import seaborn as sns
import seaborn as sns
Age Distribution
plt.figure(figsize=(10, 6))
sns.histplot(df['age'], bins=30, kde=True, color='#0033A0')
plt.title('Distribution of Age')
plt.xlabel('Age')
plt.ylabel('Frequency')
plt.show()
```





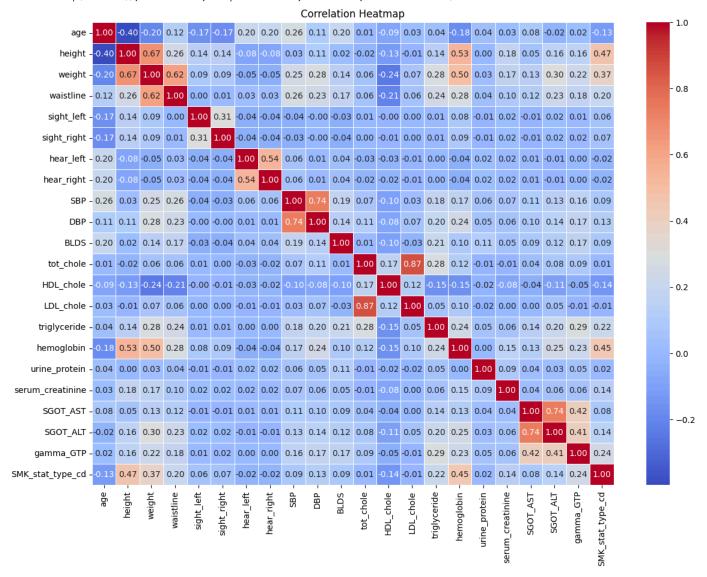
The age distribution histoplot provides a comprehensive overview of the dataset's age demographics.

Most individuals in the dataset fall within the age range of 35 to 60 years, indicating a higher prevalence of data in this age group. There's a notable concentration of individuals in the 40 to 50 years age range, suggesting a substantial representation in this demographic. Also, individuals in their 20s and 70s and above have lower representation, indicating a potential gap in data for these age groups.

Insights for Intervention: For health interventions or studies, focusing on individuals in the 40 to 50 years range might be crucial due to their significant representation.

Correlation Matrix

```
plt.figure(figsize=(14, 10))
sns.heatmap(df.corr(), annot=True, cmap='coolwarm', fmt='.2f', linewidths=0.5)
plt.title('Correlation Heatmap')
plt.show()
```



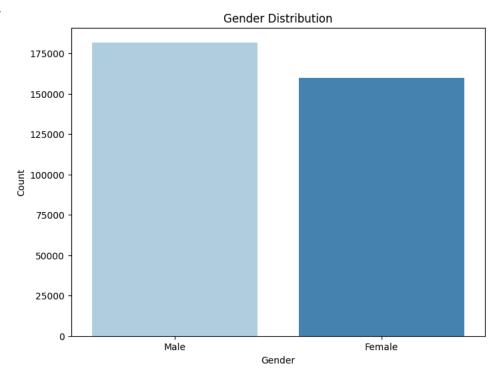
The correlation matrix provides insightful connections among various health indicators, uncovering meaningful associations in the dataset. Notably, positive correlations between Systolic Blood Pressure (SBP) and Diastolic Blood Pressure (DBP) align with physiological expectations. The inter-correlation among Total, HDL, and LDL Cholesterol highlights the importance of comprehensive cholesterol monitoring. Exploring relationships between blood pressure and waistline measurements suggests the influence of central obesity on blood pressure. Moreover, correlations between hemoglobin and serum creatinine indicate potential connections between blood oxygen levels and kidney function. Liver enzyme relationships, as reflected in SGOT (AST), SGOT (ALT), and Gamma-GTP, provide insights into potential patterns in liver health. Age-related trends and correlations with behavioral variables like Smoking State (SMK_stat_type_cd) and Drinking Patterns (DRK_YN) offer valuable information for targeted health strategies. Gender disparities in correlations with physiological measures shed light on potential gender-related health variations. While leveraging these correlations for targeted health interventions, it's essential to exercise caution against spurious correlations and ensure that observed associations are meaningful and not driven by outliers or data artifacts. Overall, the correlation matrix serves as a valuable guide for understanding health connections and shaping future health interventions and research efforts.

Gender Distribution

```
plt.figure(figsize=(8, 6))
sns.countplot(x='sex', data=df, palette='Blues')
```

```
plt.title('Gender Distribution')
plt.xlabel('Gender')
plt.ylabel('Count')
plt.show()
```

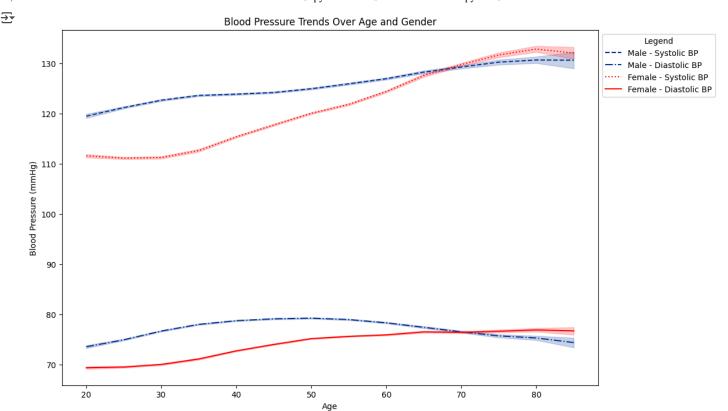




The gender distribution plot illustrates the prevalence of males and females in the dataset. The count plot indicates that the dataset contains a relatively balanced representation of both males and females. This balanced distribution is essential for ensuring that analyses and models built on this data are not biased towards one gender. Additionally, it allows for meaningful comparisons and generalizations across genders in various analyses. The visualization provides a quick overview of the gender composition, laying the foundation for more detailed gender-specific analyses.

Blood Pressure Trend Over Age and Gender

```
red_palette = sns.color_palette(['#FF0000', '#FF0000'])
plt.figure(figsize=(12, 8))
sns.lineplot(x='age', y='SBP', data=df[df['sex'] == 'Male'], label='Male - Systolic BP', color='#043399', linestyle='--')
sns.lineplot(x='age', y='DBP', data=df[df['sex'] == 'Male'], label='Male - Diastolic BP', color='#043399', linestyle='--')
sns.lineplot(x='age', y='SBP', data=df[df['sex'] == 'Female'], label='Female - Systolic BP', color='#FF0000', linestyle=':')
sns.lineplot(x='age', y='DBP', data=df[df['sex'] == 'Female'], label='Female - Diastolic BP', color='#FF0000', linestyle='-')
plt.xlabel('Age')
plt.xlabel('Blood Pressure (mmHg)')
plt.title('Blood Pressure Trends Over Age and Gender')
plt.legend(title='Legend', loc='upper left', bbox_to_anchor=(1, 1))
plt.show()
```



The line graph illustrates blood pressure trends in males and females across different age groups.

Male Trends: Systolic BP - Demonstrates a consistent increase with age.

Diastolic BP - Shows a gradual rise over the age range, followed by a decline after the age of 50.

Female Trends: *Systolic BP* - Exhibits more fluctuations. Initially lower than male systolic BP, it gradually increases over time. Interestingly, it surpasses male systolic BP around the age of 70 and remains higher through the age of 80 and beyond.

Diastolic BP - Displays fluctuations with an overall upward trend as age increases.

Age Range: The trends are observed across different age groups, providing insights into how blood pressure changes as individuals age.

Clinical Considerations: The visualization might be useful for healthcare professionals to identify age-related patterns in blood pressure for males and females.

Further statistical analysis could be performed to validate any observed trends and identify potential risk factors.

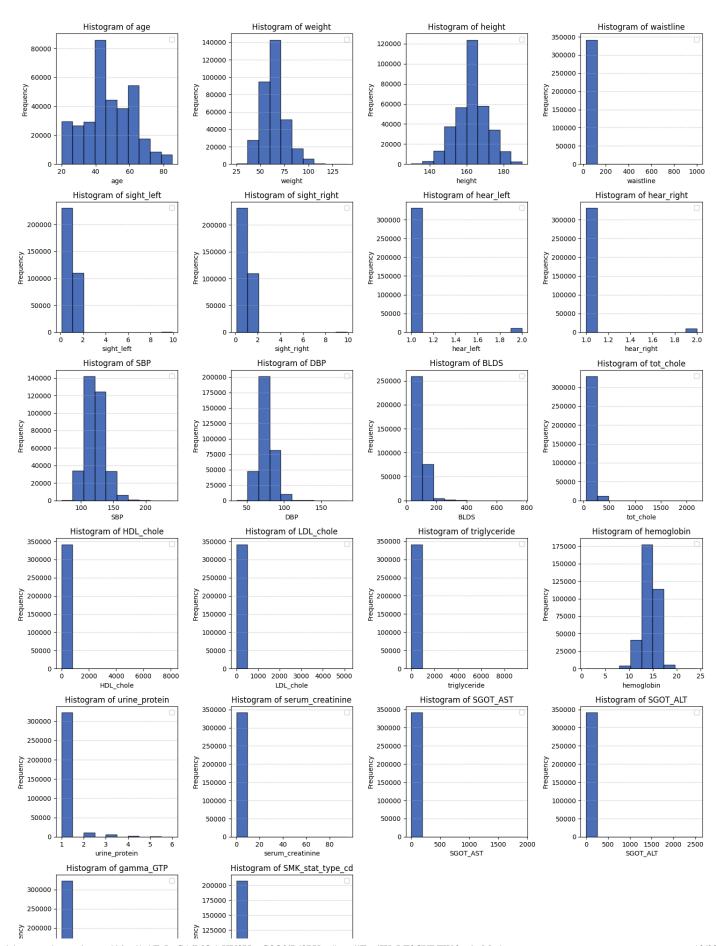
Distribution of Numeric Columns in the dataset

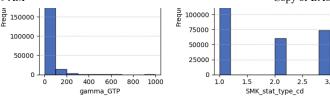
```
axes[i].set_title(f'Histogram of {col}', fontsize=12)
axes[i].set_xlabel(col, fontsize=10)
axes[i].set_ylabel('Frequency', fontsize=10)
axes[i].grid(axis='y', linestyle='--', alpha=0.6)
axes[i].legend([])

# Removing the empty subplots
for i in range(num_cols, len(axes)):
    fig.delaxes(axes[i])

plt.tight_layout(rect=[0, 0.03, 1, 0.95]) # For adjusting the layout
plt.show()
```

Distribution of Numeric Columns in Dataset

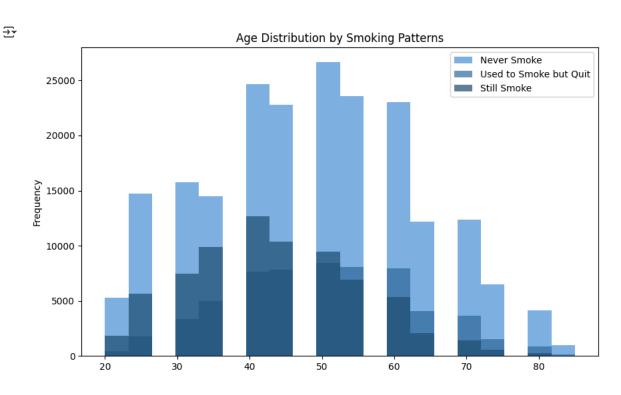




This visualization offers valuable insights into the underlying patterns and variability present in key variables. Each histogram serves as a visual summary, allowing for a quick assessment of the data's central tendencies, ranges, and potential outliers. Overall, the graph provides a concise and informative overview of the dataset's numerical features through a structured and visually appealing arrangement of histograms.

```
# Creating subsets of the DataFrame based on smoking patterns
smk_1 = df[df['SMK_stat_type_cd'] == 1]
smk_2 = df[df['SMK_stat_type_cd'] == 2]
smk_3 = df[df['SMK_stat_type_cd'] == 3]

plt.figure(figsize=(10, 6))
plt.hist(smk_1['age'], bins=20, alpha=0.7, label='Never Smoke', color='#4B92DB')
plt.hist(smk_2['age'], bins=20, alpha=0.7, label='Used to Smoke but Quit', color='#346D9E')
plt.hist(smk_3['age'], bins=20, alpha=0.7, label='Still Smoke', color='#1E4B6E')
plt.ylabel('Frequency')
plt.title('Age Distribution by Smoking Patterns')
plt.legend()
plt.show()
```



We can observe age distribution by smoking patterns from the histogram reveal insightful numerical trends. Notably, the analysis indicates a obvious pattern in smoking behaviors across age groups. Around the age of 25, there is a noticeable uptick in the number of individuals who smoke, with the trend peaking at approximately age 45. Subsequently, there is a gradual decline in the number of smokers as age increases.

This enhances our understanding of the relationship between age and smoking patterns, emphasizing a significant age-related variation in smoking behaviors over the analyzed dataset.

Pipeline Creation

```
from sklearn.ensemble import RandomForestClassifier
from sklearn.pipeline import Pipeline, make_pipeline
from sklearn.impute import SimpleImputer
from sklearn.preprocessing import StandardScaler, OneHotEncoder
from sklearn.compose import ColumnTransformer, make_column_selector
from sklearn import set_config
set_config(display='diagram') # shows the pipeline graphically when printed
# Categorical and Numerical Columns
cat_columns = ['sex', 'hear_left', 'hear_right', 'urine_protein']
num_columns = [
    'age', 'height', 'weight', 'waistline', 'sight_left', 'sight_right',
    'SBP', 'DBP', 'BLDS', 'tot_chole', 'HDL_chole', 'LDL_chole',
    'triglyceride', 'hemoglobin', 'serum_creatinine', 'SGOT_AST',
    'SGOT_ALT', 'gamma_GTP'
num_pipeline = Pipeline([
        ('imputer', SimpleImputer(strategy='median')),
        ('scaler', StandardScaler())
    1)
cat_pipeline = Pipeline([
        ('imputer', SimpleImputer(strategy='most_frequent')),
        ('cat_encoder', OneHotEncoder(drop='first'))
    ])
prep_pipeline = ColumnTransformer([
    ('num', num_pipeline, num_columns),
    ('cat', cat_pipeline, cat_columns)
])
prep_pipeline
₹
               ColumnTransformer
              num
                         ▶ SimpleImputer
       ▶ SimpleImputer
       ▶ StandardScaler
                         ▶ OneHotEncoder
```

✓ Train Test Split

```
from sklearn.model_selection import train_test_split

# Assuming 'SMK_stat_type_cd' and 'DRK_YN' are the columns to drop
X = df.drop(['SMK_stat_type_cd', 'DRK_YN'], axis=1)

# Assuming 'DRK_YN' is the column representing your classes
X_train, X_test, y_train, y_test = train_test_split(
    X,  # Features without 'SMK_stat_type_cd' and 'DRK_YN'
    df['DRK_YN'],  # Target variable
    train_size=12000,  # Number of samples for training
    test_size=3000,  # Number of samples for testing
    stratify=df['SMK_stat_type_cd'],  # Maintain class distribution
    random_state=42  # Set a random state for reproducibility
)

X_train.shape, X_test.shape, y_train.shape, y_test.shape # check sizes

→ ((12000, 22), (3000, 22), (12000,), (3000,))
```

Feature Selection

SelectKBest

```
from sklearn.feature_selection import SelectKBest, f_classif
from sklearn.model_selection import GridSearchCV
from sklearn.pipeline import Pipeline
from sklearn.linear_model import LogisticRegression
# Define the feature selection pipeline
feature_selection_pipeline = Pipeline([
    ('prep', prep_pipeline),
    ('select', SelectKBest(score_func=f_classif)),
    ('model', LogisticRegression(random_state=42))
])
# Define the parameter grid for GridSearchCV
param_grid = {
    'select__k': range(1, X_train.shape[1] + 1)
# Perform GridSearchCV
grid_search = GridSearchCV(feature_selection_pipeline, param_grid, cv=5, scoring='balanced_accuracy')
grid_search.fit(X_train, y_train)
# Display results
cv_res = pd.DataFrame(grid_search.cv_results_).sort_values(by='mean_test_score', ascending=False)
display(cv_res.filter(regex='(^param_|mean_test_score)', axis=1))
# Get the best model
best_model = grid_search.best_estimator_
selected_features = best_model["prep"].get_feature_names_out()[best_model["select"].get_support()]
print(f'The selected features are {selected_features}')
```

 \rightarrow

19 21 20 18 17 16 15 14 12 13 11 5 6 10 7	param_selectk 20 22 21 19 18 17	mean_test_score 0.720025 0.719850 0.719787 0.719750 0.718937
21 20 18 17 16 15 14 12 13 11 5 6	22 21 19 18 17	0.719850 0.719787 0.719750
20 18 17 16 15 14 12 13 11 5 6	21 19 18 17	0.719787 0.719750
18 17 16 15 14 12 13 11 5 6	19 18 17	0.719750
17 16 15 14 12 13 11 5 6	18 17	
16 15 14 12 13 11 5 6	17	0.718937
15 14 12 13 11 5 6		
14 12 13 11 5 6	16	0.717712
12 13 11 5 6	10	0.713987
13 11 5 6 10	15	0.711236
11 5 6 10	13	0.711223
5 6 10	14	0.711173
6 10	12	0.710323
10	6	0.706974
	7	0.706948
7	11	0.706873
	8	0.706861
8	9	0.706811
9	10	0.706811
4	5	0.702393
3	4	0.702355
2	3	0.685393
1	2	0.684106
0	1	0.667109
'nu 'nu 'nu	<pre>msight_right' mLDL_chole' 'n mserum_creatin</pre>	s are ['numage' 'numSBP' 'num umtriglyceride' ine' 'numSGOT_Ahear_left_2.0'

SelectFromModel

```
from sklearn.feature_selection import SelectFromModel, SelectKBest, f_classif
from sklearn.linear_model import Lasso
from sklearn.model_selection import GridSearchCV
from sklearn.pipeline import Pipeline
from sklearn.linear_model import LogisticRegression
# Define the feature selection pipeline with SelectFromModel using Lasso
lasso_select_model = Lasso()
select_from_model_pipeline = Pipeline([
    ('transformer', prep_pipeline),
    ('select', SelectFromModel(estimator=lasso_select_model)),
    ('model', LogisticRegression(random_state=42))
])
# Define the parameter grid for GridSearchCV
param_grid = {
    'select__estimator__alpha': [0.01, 0.1, 1.0, 10, 100],
    'select__threshold': ['mean', 'median']
}
# Perform GridSearchCV
grid_search = GridSearchCV(select_from_model_pipeline, param_grid, cv=5, scoring='balanced_accuracy')
grid_search.fit(X_train, y_train)
# Display results
cv_res = pd.DataFrame(grid_search.cv_results_).sort_values(by='mean_test_score', ascending=False)
display(cv_res.filter(regex='(^param_|mean_test_score)', axis=1))
# Get the best model
```

₹

```
best_model = grid_search.best_estimator_
selected_features = best_model["transformer"].get_feature_names_out()[best_model["select"].get_support()]
num_selected_features = len(selected_features)
print(f'The selected features are {selected_features}')
print(f'Number of selected features: {num_selected_features}')
```

	param_selectestimatoralpha	${\tt param_select_threshold}$	mean_test_score
1	0.01	median	0.719812
3	0.1	median	0.719812
4	1.0	mean	0.719812
5	1.0	median	0.719812
6	10	mean	0.719812
7	10	median	0.719812
8	100	mean	0.719812
9	100	median	0.719812
0	0.01	mean	0.715138
2	0.1	mean	0.683526

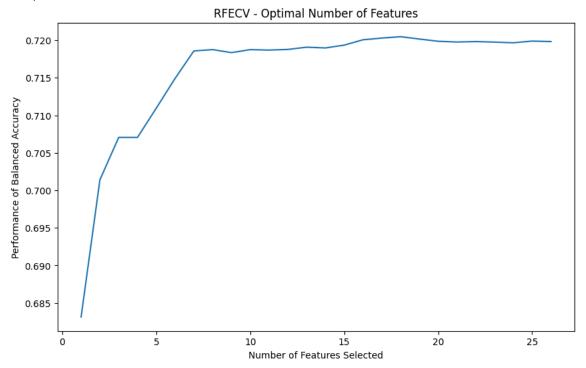
```
The selected features are ['num_age' 'num_height' 'num_weight' 'num_waistline' 'num_sight_left' 'num_sight_right' 'num_SBP' 'num_BLDS' 'num_tot_chole' 'num_tot_chole' 'num_LDL_chole' 'num_triglyceride' 'num_hemoglobin' 'num_serum_creatinine' 'num_SGOT_AST' 'num_SGOT_ALT' 'num_gamma_GTP' 'cat_sex_1.0' 'cat_hear_left_2.0' 'cat_hear_right_2.0' 'cat_urine_protein_2.0' 'cat_urine_protein_3.0' 'cat_urine_protein_4.0' 'cat_urine_protein_5.0' 'cat_urine_protein_6.0']

Number of selected features: 26
```

Recursive Feature Elimination RFECV

```
from sklearn.feature_selection import RFECV
from sklearn.linear_model import LogisticRegression
from sklearn.pipeline import Pipeline
# Define the RFECV feature selection with Logistic Regression as estimator
rfecv = RFECV(LogisticRegression(random_state=42), scoring='balanced_accuracy')
# Define the full feature selection pipeline with RFECV
rfecv_pipeline = Pipeline([
    ('transformer', prep_pipeline),
    ('select', rfecv),
    ('model', LogisticRegression(random_state=42))
])
# Fit the pipeline to the training data
rfecv_pipeline.fit(X_train, y_train)
# Display the results
print('Optimal number of features:', rfecv.n_features_)
print('The selected features are:\n', rfecv_pipeline['transformer'].get_feature_names_out()[rfecv.support_])
#Plotting the features vs performance
plt.figure(figsize=(10, 6))
plt.title("RFECV - Optimal Number of Features")
plt.xlabel("Number of Features Selected")
plt.ylabel("Performance of Balanced Accuracy")
mean_test_score = rfecv.cv_results_['mean_test_score']
plt.plot(range(1, len(mean_test_score ) + 1), mean_test_score)
```

```
Optimal number of features: 18
The selected features are:
    ['num_age' 'num_height' 'num_weight' 'num_DBP' 'num_HDL_chole'
    'num_LDL_chole' 'num_triglyceride' 'num_hemoglobin'
    'num_serum_creatinine' 'num_SGOT_AST' 'num_SGOT_ALT' 'num_gamma_GTP'
    'cat_sex_1.0' 'cat_hear_left_2.0' 'cat_hear_right_2.0'
    'cat_urine_protein_2.0' 'cat_urine_protein_3.0'
    'cat_urine_protein_5.0']
[<matplotlib.lines.Line2D at 0x7bb68f7153c0>]
```



Sequential Feature Selection

Forward Selection

```
from mlxtend.feature_selection import SequentialFeatureSelector
from sklearn.linear_model import LogisticRegression
from sklearn.pipeline import Pipeline
# Define the SFS feature selection with Logistic Regression as estimator
sfs = SequentialFeatureSelector(LogisticRegression(random_state=42),
                                  k_features="best",
                                  scoring='balanced_accuracy',
                                  forward=True)
# Define the full feature selection pipeline with SFS
sfs_pipeline = Pipeline([
    ('transformer', prep_pipeline),
    ('select', sfs),
    ('model', LogisticRegression(random_state=42))
])
# Fit the pipeline to the training data
sfs_pipeline.fit(X_train, y_train)
# Display the results
sfs_result = pd.DataFrame.from_dict(sfs.get_metric_dict()).T
display(sfs_result.sort_values(by='avg_score', ascending=False))
```

→▼	

3	feature_idx	cv_scores	avg_score	feature_names	ci_bound	std_dev	std_err
1	5 (0, 1, 2, 8, 9, 10, 11, 13, 15, 16, 17, 18, 22	[0.7214996327108858, 0.7181236478611379, 0.725	0.72115	(0, 1, 2, 8, 9, 10, 11, 13, 15, 16, 17, 18, 22	0.003241	0.002521	0.001261
1	3 (0, 1, 2, 8, 9, 10, 11, 13, 15, 16, 17, 18, 22)	[0.7214371561396, 0.7181236478611379, 0.725313	0.721138	(0, 1, 2, 8, 9, 10, 11, 13, 15, 16, 17, 18, 22)	0.003216	0.002502	0.001251
1	4 (0, 1, 2, 8, 9, 10, 11, 13, 15, 16, 17, 18, 22	[0.7214996327108858, 0.7181236478611379, 0.725	0.721138	(0, 1, 2, 8, 9, 10, 11, 13, 15, 16, 17, 18, 22	0.003254	0.002532	0.001266
1	6 (0, 1, 2, 3, 8, 9, 10, 11, 13, 15, 16, 17, 18,	[0.7214371561396, 0.7179986478435598, 0.725626	0.721125	(0, 1, 2, 3, 8, 9, 10, 11, 13, 15, 16, 17, 18,	0.003409	0.002652	0.001326
1	7 (0, 1, 2, 3, 8, 9, 10, 11, 13, 15, 16, 17, 18,	[0.7211245389081382, 0.7177485540583903, 0.725	0.721113	(0, 1, 2, 3, 8, 9, 10, 11, 13, 15, 16, 17, 18,	0.003612	0.00281	0.001405
2	2 (0, 1, 2, 3, 6, 8, 9, 10, 11, 12, 13, 14, 15,	[0.7209363591941755, 0.717998741593573, 0.7272	0.7211	(0, 1, 2, 3, 6, 8, 9, 10, 11, 12, 13, 14, 15,	0.004205	0.003272	0.001636
1	2 (0, 1, 2, 9, 10, 11, 13, 15, 16, 17, 18, 22)	[0.7211243045331053, 0.7180611712898521, 0.725	0.721088	(0, 1, 2, 9, 10, 11, 13, 15, 16, 17, 18, 22)	0.003358	0.002613	0.001306
1	1 (0, 1, 2, 10, 11, 13, 15, 16, 17, 18, 22)	[0.7226875313154341, 0.7185620151102834, 0.724	0.721063	(0, 1, 2, 10, 11, 13, 15, 16, 17, 18, 22)	0.002813	0.002189	0.001094
2	3 (0, 1, 2, 3, 4, 6, 8, 9, 10, 11, 12, 13, 14, 1	[0.720686499784039, 0.7174988352732737, 0.7274	0.721062	(0, 1, 2, 3, 4, 6, 8, 9, 10, 11, 12, 13, 14, 1	0.004373	0.003402	0.001701
1	8 (0, 1, 2, 3, 8, 9, 10, 11, 13, 15, 16, 17, 18,	[0.7205621560165532, 0.7178736009509752, 0.725	0.721025	(0, 1, 2, 3, 8, 9, 10, 11, 13, 15, 16, 17, 18,	0.003602	0.002802	0.001401
2	1 (0, 1, 2, 3, 6, 8, 9, 10, 11, 13, 14, 15, 16,	[0.7206239294627401, 0.718436593217646, 0.7264	0.720987	(0, 1, 2, 3, 6, 8, 9, 10, 11, 13, 14, 15, 16,	0.003792	0.00295	0.001475
2	4 (0, 1, 2, 3, 4, 5, 6, 8, 9, 10, 11, 12, 13, 14	[0.7207491638553511, 0.717311452434423, 0.7273	0.720987	(0, 1, 2, 3, 4, 5, 6, 8, 9, 10, 11, 12, 13, 14	0.004399	0.003422	0.001711
1	9 (0, 1, 2, 3, 8, 9, 10, 11, 13, 15, 16, 17, 18,	[0.7202497731601243, 0.717686030612098, 0.7255	0.720913	(0, 1, 2, 3, 8, 9, 10, 11, 13, 15, 16, 17, 18,	0.003556	0.002766	0.001383
2	0 (0, 1, 2, 3, 6, 8, 9, 10, 11, 13, 15, 16, 17,	[0.7206235075876808, 0.7177487884334234, 0.726	0.720912	(0, 1, 2, 3, 6, 8, 9, 10, 11, 13, 15, 16, 17,	0.004134	0.003216	0.001608
2	5 (0, 1, 2, 3, 4, 5, 6, 8, 9, 10, 11, 12, 13, 14	[0.720686499784039, 0.7171866399168713, 0.7270	0.720887	(0, 1, 2, 3, 4, 5, 6, 8, 9, 10, 11, 12, 13, 14	0.004247	0.003304	0.001652
1	0 (0, 1, 2, 10, 11, 13, 15, 16, 17, 18)	[0.7223751015839988, 0.7186244448065625, 0.723	0.720838	(0, 1, 2, 10, 11, 13, 15, 16, 17, 18)	0.002753	0.002142	0.001071
9	(0, 1, 10, 11, 13, 15, 16, 17, 18)	[0.7211256639082965, 0.7176878118623486, 0.724	0.720514	(0, 1, 10, 11, 13, 15, 16, 17, 18)	0.003249	0.002528	0.001264
2	6 (0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13,	[0.7185614526102042, 0.7185619682352768, 0.725	0.719825	(0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13,	0.003449	0.002683	0.001342
8	3 (0, 10, 11, 13, 15, 16, 17, 18)	[0.71981290591119, 0.7195633746260995, 0.72237	0.719677	(0, 10, 11, 13, 15, 16, 17, 18)	0.002645	0.002058	0.001029
7	7 (0, 10, 13, 15, 16, 17, 18)	[0.7191875776982531, 0.7196250074472667, 0.722	0.719326	(0, 10, 13, 15, 16, 17, 18)	0.002861	0.002226	0.001113
(6 (0, 10, 15, 16, 17, 18)	[0.7185629057354086, 0.718687999503, 0.7208147	0.718676	(0, 10, 15, 16, 17, 18)	0.002496	0.001942	0.000971
į	(0, 10, 16, 17, 18)	[0.7188128120205517, 0.7175630930948099, 0.720	0.718089	(0, 10, 16, 17, 18)	0.002213	0.001722	0.000861
4	(0, 10, 17, 18)	[0.7156871553310062, 0.7119374829287085, 0.717	0.714351	(0, 10, 17, 18)	0.002826	0.002199	0.001099
;	(0, 10, 18)	[0.7061951696211957, 0.7086339590266505, 0.708	0.707472	(0, 10, 18)	0.001876	0.00146	0.00073
2	(0, 18)	[0.6996890749562762, 0.7047518334807266, 0.702	0.70139	(0, 18)	0.003176	0.002471	0.001236
-	I (18,)	[0.6821972287464853, 0.6842002759031638, 0.682	0.683124	(18,)	0.000838	0.000652	0.000326

Backward Selection

 $from \ {\tt mlxtend.feature_selection} \ import \ {\tt SequentialFeatureSelector}$

from sklearn.linear_model import LogisticRegression

from sklearn.pipeline import Pipeline

```
# Define the SBS feature selection with Logistic Regression as estimator
sbs = SequentialFeatureSelector(LogisticRegression(random_state=42),
                                 k_features="best",
                                 scoring='balanced_accuracy',
                                 forward=False)
# Define the full feature selection pipeline with SBS
sbs_pipeline = Pipeline([
    ('transformer', prep_pipeline),
    ('select', sbs),
    ('model', LogisticRegression(random_state=42))
])
# Fit the pipeline to the training data
sbs_pipeline.fit(X_train, y_train)
# Display the results
sbs_result = pd.DataFrame.from_dict(sbs.get_metric_dict()).T
display(sbs_result.sort_values(by='avg_score', ascending=False))
```

24/23,4	:59 AM	Copy of BA8	Copy of BA810-Sricharan-Notebook.ipyno - Colab			
₹	feature_idx	cv_scores	avg_score	feature_names	ci_l	
	17 (0, 1, 2, 6, 8, 9, 10, 12, 13, 14,	[0.7211865467293581,	0.721212	(0, 1, 2, 6, 8, 9, 10, 12, 13, 14,	0.0	

3	feature_idx	cv_scores	avg_score	feature_names	ci_bound	std_dev	std_err
17	(0, 1, 2, 6, 8, 9, 10, 12, 13, 14, 15, 16, 17,	[0.7211865467293581, 0.7180613587898785, 0.726	0.721212	(0, 1, 2, 6, 8, 9, 10, 12, 13, 14, 15, 16, 17,	0.003867	0.003009	0.001504
18	(0, 1, 2, 3, 6, 8, 9, 10, 12, 13, 14, 15, 16,	[0.721374023318222, 0.7176863118621376, 0.7268	0.7212	(0, 1, 2, 3, 6, 8, 9, 10, 12, 13, 14, 15, 16,	0.003982	0.003098	0.001549
20	(0, 1, 2, 3, 4, 6, 8, 9, 10, 12, 13, 14, 15, 1	[0.7210614060867602, 0.7178113587547224, 0.726	0.7212	(0, 1, 2, 3, 4, 6, 8, 9, 10, 12, 13, 14, 15, 1	0.003995	0.003108	0.001554
19	(0, 1, 2, 3, 6, 8, 9, 10, 12, 13, 14, 15, 16,	[0.7213114998719297, 0.7176238352908518, 0.726	0.721187	(0, 1, 2, 3, 6, 8, 9, 10, 12, 13, 14, 15, 16,	0.003981	0.003097	0.001549
21	(0, 1, 2, 3, 4, 6, 8, 9, 10, 12, 13, 14, 15, 1	[0.7208113591765974, 0.7176863587371443, 0.726	0.721137	(0, 1, 2, 3, 4, 6, 8, 9, 10, 12, 13, 14, 15, 1	0.004053	0.003153	0.001577
16	(0, 1, 2, 6, 8, 9, 10, 12, 13, 14, 15, 16, 17,	[0.7211865467293581, 0.7179988822185928, 0.726	0.721125	(0, 1, 2, 6, 8, 9, 10, 12, 13, 14, 15, 16, 17,	0.003841	0.002988	0.001494
22	(0, 1, 2, 3, 4, 6, 8, 9, 10, 12, 13, 14, 15, 1	[0.7206864529090324, 0.7178115931297553, 0.726	0.721112	(0, 1, 2, 3, 4, 6, 8, 9, 10, 12, 13, 14, 15, 1	0.003952	0.003075	0.001538
15	(0, 1, 2, 6, 8, 9, 10, 12, 13, 14, 15, 16, 17,	[0.7211238357830394, 0.7178113587547224, 0.726	0.721112	(0, 1, 2, 6, 8, 9, 10, 12, 13, 14, 15, 16, 17,	0.00368	0.002863	0.001432
14	(0, 1, 2, 6, 9, 10, 12, 13, 14, 15, 16, 17, 18	[0.7206860310339731, 0.71774883530843, 0.72693	0.721087	(0, 1, 2, 6, 9, 10, 12, 13, 14, 15, 16, 17, 18	0.004015	0.003124	0.001562
23	(0, 1, 2, 3, 4, 5, 6, 8, 9, 10, 12, 13, 14, 15	[0.7206866404090588, 0.7173742102557483, 0.726	0.721075	(0, 1, 2, 3, 4, 5, 6, 8, 9, 10, 12, 13, 14, 15	0.004098	0.003189	0.001594
24	(0, 1, 2, 3, 4, 5, 6, 8, 9, 10, 12, 13, 14, 15	[0.7207491169803446, 0.7173741633807418, 0.727	0.721037	(0, 1, 2, 3, 4, 5, 6, 8, 9, 10, 12, 13, 14, 15	0.004196	0.003264	0.001632
13	(0, 1, 2, 6, 9, 10, 13, 14, 15, 16, 17, 18, 22)	[0.7209358904441097, 0.7191872964482136, 0.724	0.720937	(0, 1, 2, 6, 9, 10, 13, 14, 15, 16, 17, 18, 22)	0.002664	0.002072	0.001036
12	(0, 1, 2, 6, 9, 10, 13, 15, 16, 17, 18, 22)	[0.7214357030143957, 0.7190615464305299, 0.723	0.720912	(0, 1, 2, 6, 9, 10, 13, 15, 16, 17, 18, 22)	0.002863	0.002228	0.001114
25	(0, 1, 2, 3, 4, 5, 6, 8, 9, 10, 11, 12, 13, 14	[0.720686499784039, 0.7171866399168713, 0.7270	0.720887	(0, 1, 2, 3, 4, 5, 6, 8, 9, 10, 11, 12, 13, 14	0.004247	0.003304	0.001652
11	(0, 1, 2, 6, 9, 10, 13, 15, 16, 17, 18)	[0.7209982732653821, 0.7191239292518026, 0.723	0.720737	(0, 1, 2, 6, 9, 10, 13, 15, 16, 17, 18)	0.002733	0.002126	0.001063
10	(0, 2, 6, 9, 10, 13, 15, 16, 17, 18)	[0.7194987886795172, 0.7189362651629123, 0.723	0.72035	(0, 2, 6, 9, 10, 13, 15, 16, 17, 18)	0.003013	0.002344	0.001172
9	(0, 2, 6, 9, 10, 15, 16, 17, 18)	[0.7202486012849596, 0.7174992102733264, 0.723	0.719962	(0, 2, 6, 9, 10, 15, 16, 17, 18)	0.002951	0.002296	0.001148
26	(0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13,	[0.7185614526102042, 0.7185619682352768, 0.725	0.719825	(0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13,	0.003449	0.002683	0.001342
8	(0, 2, 9, 10, 15, 16, 17, 18)	[0.7208744451229688, 0.7171869680419174, 0.722	0.719438	(0, 2, 9, 10, 15, 16, 17, 18)	0.003242	0.002522	0.001261
7	(0, 2, 10, 15, 16, 17, 18)	[0.7201866403387462, 0.7175614993445858, 0.721	0.719225	(0, 2, 10, 15, 16, 17, 18)	0.002613	0.002033	0.001016
6	(0, 10, 15, 16, 17, 18)	[0.7185629057354086, 0.718687999503, 0.7208147	0.718676	(0, 10, 15, 16, 17, 18)	0.002496	0.001942	0.000971
5	(0, 10, 16, 17, 18)	[0.7188128120205517, 0.7175630930948099, 0.720	0.718089	(0, 10, 16, 17, 18)	0.002213	0.001722	0.000861
4	(0, 10, 17, 18)	[0.7156871553310062, 0.7119374829287085, 0.717	0.714351	(0, 10, 17, 18)	0.002826	0.002199	0.001099
3	(0, 10, 18)	[0.7061951696211957, 0.7086339590266505, 0.708	0.707472	(0, 10, 18)	0.001876	0.00146	0.00073
2	(0, 18)	[0.6996890749562762, 0.7047518334807266, 0.702	0.70139	(0, 18)	0.003176	0.002471	0.001236
1	(18,)	[0.6821972287464853, 0.6842002759031638, 0.682	0.683124	(18,)	0.000838	0.000652	0.000326

from mlxtend.feature_selection import SequentialFeatureSelector from sklearn.linear_model import LogisticRegression from sklearn.pipeline import Pipeline import pandas as pd

[#] Assume X_train is your training data

```
# Define the SBS feature selection with Logistic Regression as estimator
sbs = SequentialFeatureSelector(LogisticRegression(random_state=42),
                                 k_features="best",
                                 scoring='balanced_accuracy',
                                 forward=False)
# Define the full feature selection pipeline with SBS
sbs_pipeline = Pipeline([
    ('select', sbs),
    ('model', LogisticRegression(random_state=42))
])
# Fit the pipeline to the training data
sbs_pipeline.fit(X_train, y_train)
# Get the selected feature indices
selected_feature_indices = sbs_pipeline.named_steps['select'].k_feature_idx_
# Get the column names of the selected features
selected_feature_names = X_train.columns[selected_feature_indices]
# Display the selected feature names
print("Selected Features:")
print(selected_feature_names)
```

```
🚁 /usr/local/lib/python3.10/dist-packages/sklearn/linear_model/_logistic.py:458: ConvergenceWarning: lbfgs failed to converge
    STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.
    Increase the number of iterations (max_iter) or scale the data as shown in:
       https://scikit-learn.org/stable/modules/preprocessing.html
    Please also refer to the documentation for alternative solver options:
       https://scikit-learn.org/stable/modules/linear model.html#logistic-regression
      n_iter_i = _check_optimize_result(
    /usr/local/lib/python3.10/dist-packages/sklearn/linear_model/_logistic.py:458: ConvergenceWarning: lbfgs failed to converge
    STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.
    Increase the number of iterations (max_iter) or scale the data as shown in:
       https://scikit-learn.org/stable/modules/preprocessing.html
    Please also refer to the documentation for alternative solver options:
       https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
      n_iter_i = _check_optimize_result(
    /usr/local/lib/python3.10/dist-packages/sklearn/linear_model/_logistic.py:458: ConvergenceWarning: lbfgs failed to converge
    STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.
    Increase the number of iterations (max_iter) or scale the data as shown in:
       https://scikit-learn.org/stable/modules/preprocessing.html
    Please also refer to the documentation for alternative solver options:
        https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
      n_iter_i = _check_optimize_result(
    /usr/local/lib/python3.10/dist-packages/sklearn/linear_model/_logistic.py:458: ConvergenceWarning: lbfgs failed to converge
    STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.
    Increase the number of iterations (max_iter) or scale the data as shown in:
       https://scikit-learn.org/stable/modules/preprocessing.html
    Please also refer to the documentation for alternative solver options:
       https://scikit-learn.org/stable/modules/linear model.html#logistic-regression
      n_iter_i = _check_optimize_result(
    /usr/local/lib/python3.10/dist-packages/sklearn/linear_model/_logistic.py:458: ConvergenceWarning: lbfgs failed to converge
    STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.
    Increase the number of iterations (max_iter) or scale the data as shown in:
       https://scikit-learn.org/stable/modules/preprocessing.html
    Please also refer to the documentation for alternative solver options:
       https://scikit-learn.org/stable/modules/linear model.html#logistic-regression
      n_iter_i = _check_optimize_result(
    /usr/local/lib/python3.10/dist-packages/sklearn/linear_model/_logistic.py:458: ConvergenceWarning: lbfgs failed to converge
    STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.
    Increase the number of iterations (max_iter) or scale the data as shown in:
       https://scikit-learn.org/stable/modules/preprocessing.html
    Please also refer to the documentation for alternative solver options:
       https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
      n_iter_i = _check_optimize_result(
    /usr/local/lib/python3.10/dist-packages/sklearn/linear_model/_logistic.py:458: ConvergenceWarning: lbfgs failed to converge
    STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.
    Increase the number of iterations (max_iter) or scale the data as shown in:
       https://scikit-learn.org/stable/modules/preprocessing.html
    Please also refer to the documentation for alternative solver options:
       https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
      n_iter_i = _check_optimize_result(
    /usr/local/lib/python3.10/dist-packages/sklearn/linear_model/_logistic.py:458: ConvergenceWarning: lbfgs failed to converge
    STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.
    Increase the number of iterations (max_iter) or scale the data as shown in:
       https://scikit-learn.org/stable/modules/preprocessing.html
    Please also refer to the documentation for alternative solver options:
       https://scikit-learn.org/stable/modules/linear model.html#logistic-regression
      n_iter_i = _check_optimize_result(
    /usr/local/lib/python3.10/dist-packages/sklearn/linear_model/_logistic.py:458: ConvergenceWarning: lbfgs failed to converge
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