gen-expression

September 15, 2023

Data Loading and Exploration:

Loading the dataset from CSV files into Pandas DataFrames. Printing the data types, first few rows, and summary statistics of the dataset. Visualizing the distribution of patients using a histogram. Outlier Detection and Handling:

Detecting and handling outliers in the 'patient' column using the Z-score method. Visualizing the effect of removing outliers using boxplots. Handling Missing Data:

Checking for missing data in the dataset and confirming that there are no missing values. Data Preprocessing:

Converting the 'cancer' column to string data type. Checking the data type of the 'cancer' column. Class Distribution:

Displaying the distribution of cancer types ('ALL' and 'AML'). Feature Engineering:

Encoding the 'cancer' column using one-hot encoding. Correlation Analysis:

Calculating and visualizing the correlation matrix among features. Statistical Test for Differential Expression:

Performing a t-test to evaluate the statistical significance of gene expression differences between cancer types ('ALL' and 'AML'). Machine Learning Model:

Splitting the data into training and testing sets. Scaling the features using StandardScaler. Building a Random Forest Classifier model. Evaluating the model's accuracy and creating a confusion matrix. Principal Component Analysis (PCA):

Applying PCA to reduce the dimensionality of the gene expression data. Visualizing the results of PCA in a scatterplot colored by cancer type. Gene Expression Profile Visualization:

Visualizing the expression profile of a selected gene (e.g., 'GENE_12345') across different cancer types using a line plot. Gene Enrichment Analysis Visualization:

Performing gene enrichment analysis and visualizing the results to identify biological processes associated with gene expression. ROC Curve and AUC:

Evaluating the model's performance using ROC curves and calculating the Area Under the Curve (AUC) score.

[ ]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
```

```
import seaborn as sns
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import LabelEncoder
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score, classification_report
import warnings
warnings.filterwarnings('ignore')
```

[ ]:
```
actual_data_path = "C:/Users/pnrde/OneDrive/Masaüstü/Data Science Projects/Gen␣
↪Expression Project/Kaggle/Gen Expression/actual.csv"
independent_data_path = "C:/Users/pnrde/OneDrive/Masaüstü/Data Science Projects/
↪Gen Expression Project/Kaggle/Gen Expression/data_set_ALL_AML_independent.
↪csv"
train_data_path = "C:/Users/pnrde/OneDrive/Masaüstü/Data Science Projects/Gen␣
↪Expression Project/Kaggle/Gen Expression/data_set_ALL_AML_train.csv"
```

[ ]:
```
actual_data = pd.read_csv(actual_data_path)
independent_data = pd.read_csv(independent_data_path)
train_data = pd.read_csv(train_data_path)
```

[ ]:
```
actual_data.tail(5)
```

[ ]:
```
    patient cancer
67       68    ALL
68       69    ALL
69       70    ALL
70       71    ALL
71       72    ALL
```

[ ]:
```
actual_data.dtypes
```

[ ]:
```
patient     int64
cancer     object
dtype: object
```

[ ]:
```
actual_data.head(5)
```

[ ]:
```
   patient cancer
0        1    ALL
1        2    ALL
2        3    ALL
3        4    ALL
4        5    ALL
```

[ ]:
```
actual_data.shape
```

[ ]:
```
(72, 2)
```

[ ]:
```
actual_data.nunique
```

[ ]:
```
<bound method DataFrame.nunique of     patient cancer
0         1    ALL
1         2    ALL
2         3    ALL
3         4    ALL
4         5    ALL
..      …    …
67       68    ALL
68       69    ALL
69       70    ALL
70       71    ALL
71       72    ALL

[72 rows x 2 columns]>
```

[ ]:
```
actual_data.describe()
```

[ ]:
```
         patient
count  72.00000
mean   36.50000
std    20.92845
min     1.00000
25%    18.75000
50%    36.50000
75%    54.25000
max    72.00000
```

[ ]:
```
actual_data.columns
```

[ ]:
```
Index(['patient', 'cancer'], dtype='object')
```

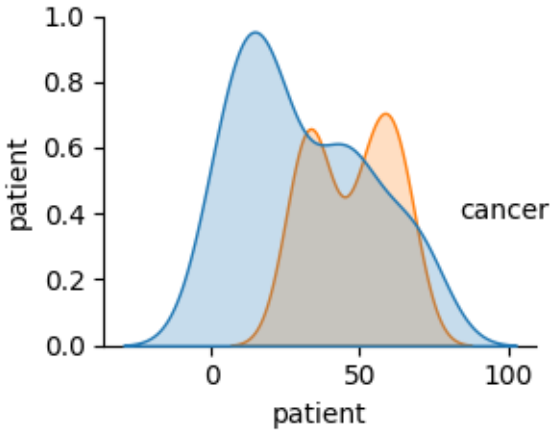
[ ]:
```
actual_data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 72 entries, 0 to 71
Data columns (total 2 columns):
 #   Column   Non-Null Count  Dtype
---  ------   --------------  -----
 0   patient  72 non-null     int64
 1   cancer   72 non-null     object
dtypes: int64(1), object(1)
memory usage: 1.3+ KB
```

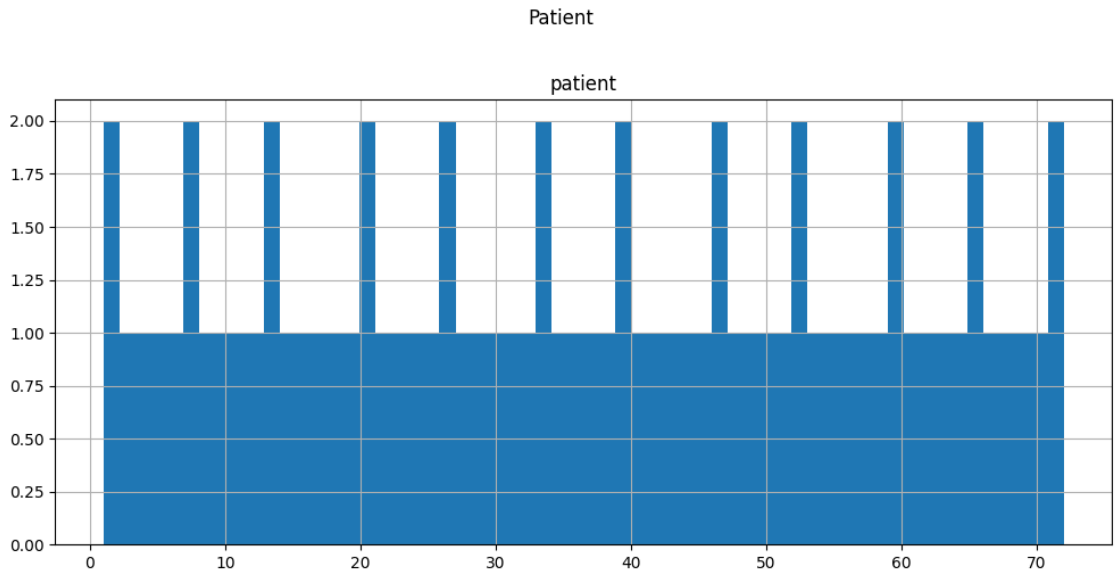
[ ]:
```
plt.figure(figsize=(20,20))

sns.pairplot(data=actual_data,hue='cancer')
```

```
plt.tight_layout()
```

```
<Figure size 2000x2000 with 0 Axes>
```



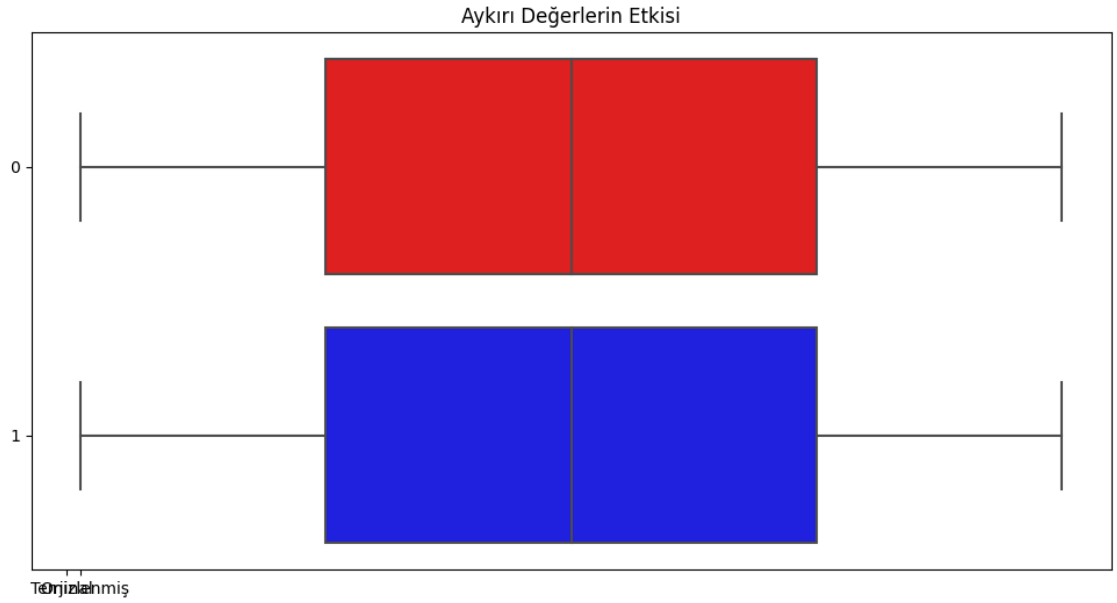
[ ]:
```
actual_data.hist(bins=60, figsize=(10,5))
plt.suptitle('Patient', x=0.5, y=1.02, ha='center', fontsize='large')
plt.tight_layout()
```



[ ]:
```
from scipy import stats
```

```
z_scores = np.abs(stats.zscore(actual_data['patient']))
threshold = 3
actual_data_no_outliers = actual_data[(z_scores < threshold)]
```

[ ]:
```
plt.figure(figsize=(12, 6))
sns.boxplot(data=[actual_data['patient'], actual_data_no_outliers['patient']],␣
↪orient='h', palette=['red', 'blue'])
plt.title("Aykırı Değerlerin Etkisi")
plt.xticks([0, 1], ['Orjinal', 'Temizlenmiş'])
plt.show()
```



[ ]:
```
actual_data = actual_data.isnull().sum()
print("Eksik Veriler:")
print(actual_data)
```

```
Eksik Veriler:
patient    0
cancer     0
dtype: int64
```

[ ]:
```
actual_data['cancer'] = actual_data['cancer'].astype(str)
```

[ ]:
```
print(actual_data['cancer'].dtype)
```

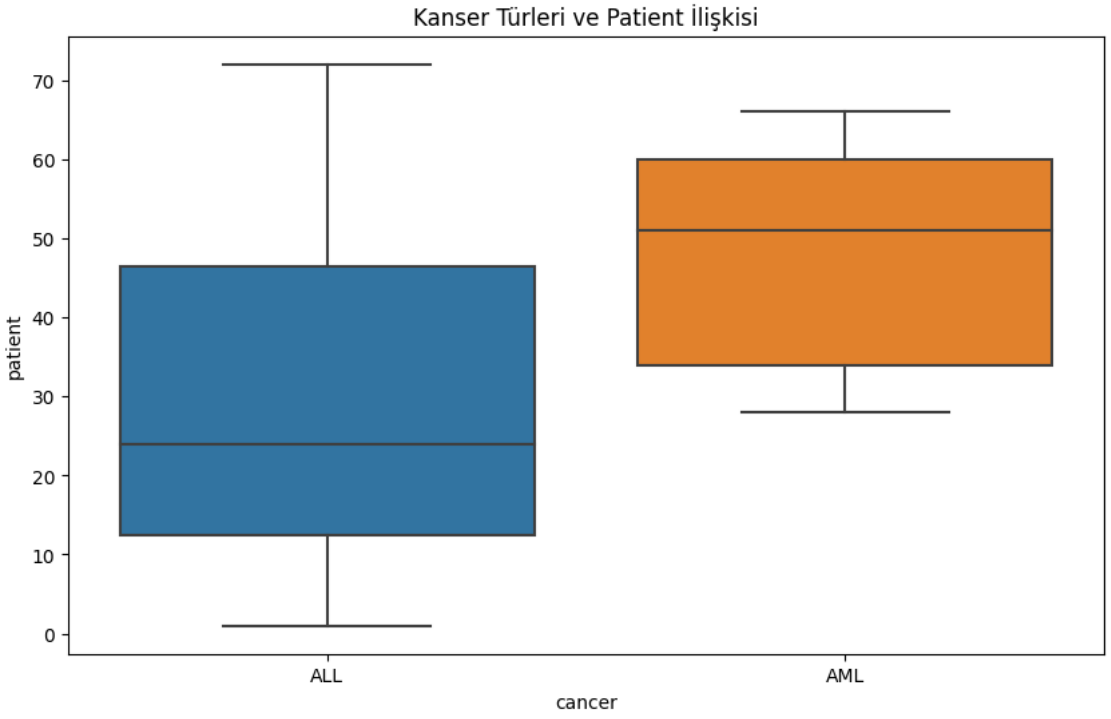
```
<U1
```

[ ]:
```
actual_data = pd.read_csv(actual_data_path, dtype={'cancer': str})
```

[ ]:
```
cancer_counts = actual_data['cancer'].value_counts()
print("Kanser Türleri Dağılımı:")
print(cancer_counts)
```

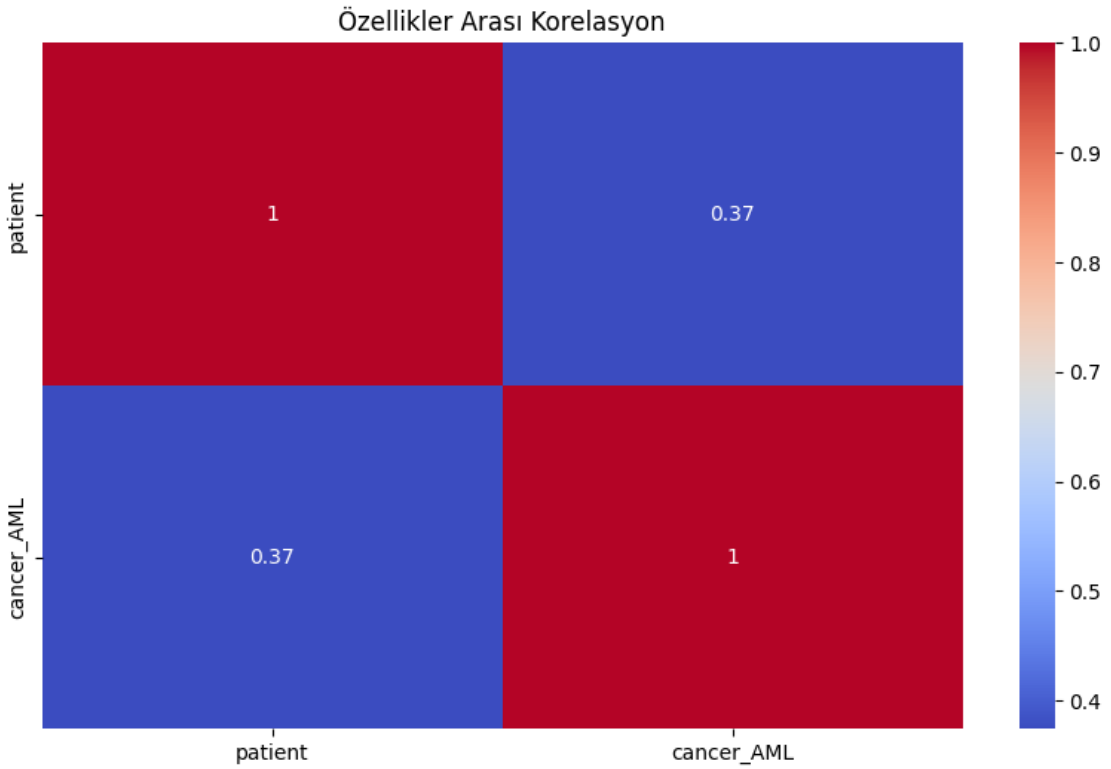
```
Kanser Türleri Dağılımı:
cancer
ALL    47
AML    25
Name: count, dtype: int64
```

[ ]:
```
plt.figure(figsize=(10, 6))
sns.boxplot(data=actual_data, x='cancer', y='patient')
plt.title("Kanser Türleri ve Patient İlişkisi")
plt.show()
```



[ ]:
```
actual_data = pd.get_dummies(actual_data, columns=['cancer'], drop_first=True)
```

[ ]:
```
correlation_matrix = actual_data.corr()
plt.figure(figsize=(10, 6))
sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm')
plt.title("Özellikler Arası Korelasyon")
plt.show()
```



[ ]:
```
cancer1_data = actual_data[actual_data['cancer_AML'] == 0]
cancer2_data = actual_data[actual_data['cancer_AML'] == 1]
```

[ ]:
```
aml_stats = cancer1_data.describe()
all_stats = cancer2_data.describe()
```

[ ]:
```
gene_expression1 = cancer1_data['cancer_AML']
gene_expression2 = cancer2_data['cancer_AML']
```

[ ]:
```
t_statistic, p_value = stats.ttest_ind(gene_expression1, gene_expression2)
```

[ ]:
```
if p_value < 0.05:
    print("İki kanser türü arasındaki gen ifadesi farkı istatistiksel olarak␣
 ↪anlamlıdır.")
else:
    print("İki kanser türü arasındaki gen ifadesi farkı istatistiksel olarak␣
 ↪anlamlı değildir.")
```

```
İki kanser türü arasındaki gen ifadesi farkı istatistiksel olarak anlamlıdır.
```

[ ]:
```
X = actual_data.drop(columns=['cancer_AML'])
y = actual_data['cancer_AML']
```

[ ]:
```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,␣
↪random_state=42)
```

[ ]:
```
from sklearn.discriminant_analysis import StandardScaler

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

[ ]:
```
rf_model = RandomForestClassifier(random_state=42)
```

[ ]:
```
rf_model.fit(X_train, y_train)
```

[ ]:
```
RandomForestClassifier(random_state=42)
```

[ ]:
```
# Modelin tahminlerini yapın
y_pred = rf_model.predict(X_test)

# Doğruluk ve sınıflandırma raporu hesaplayın
accuracy = accuracy_score(y_test, y_pred)
report = classification_report(y_test, y_pred)

print(f"Accuracy: {accuracy}")
print(report)
```

```
Accuracy: 0.9333333333333333
              precision    recall  f1-score   support

       False       1.00      0.90      0.95        10
        True       0.83      1.00      0.91         5

    accuracy                           0.93        15
   macro avg       0.92      0.95      0.93        15
weighted avg       0.94      0.93      0.93        15
```

[ ]:
```
from sklearn.metrics import confusion_matrix


conf_matrix = confusion_matrix(y_test, y_pred)
print("Confusion Matrix:\n", conf_matrix)
```

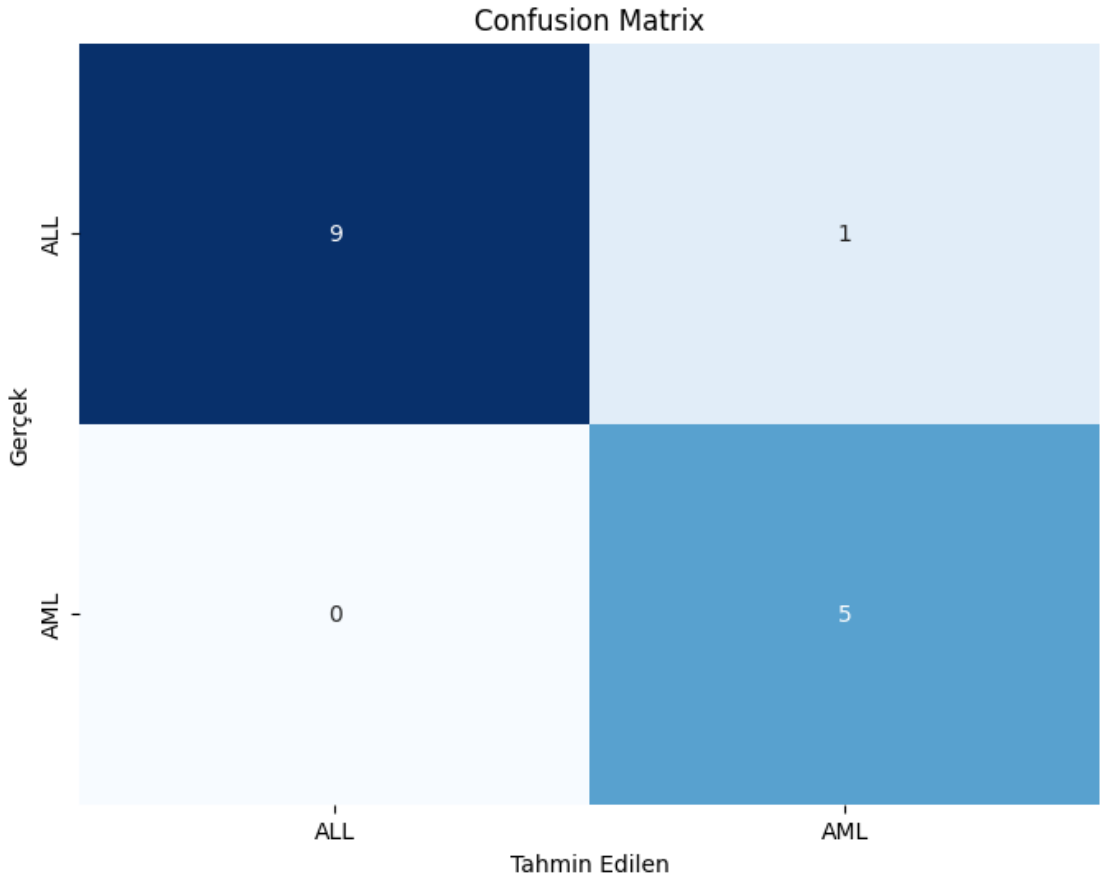
```
Confusion Matrix:
 [[9 1]
 [0 5]]
```

[ ]:
```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,␣
↪random_state=42)
```

[ ]:
```
y_pred = rf_model.predict(X_test)
```

[ ]:
```
cm = confusion_matrix(y_test, y_pred)
```

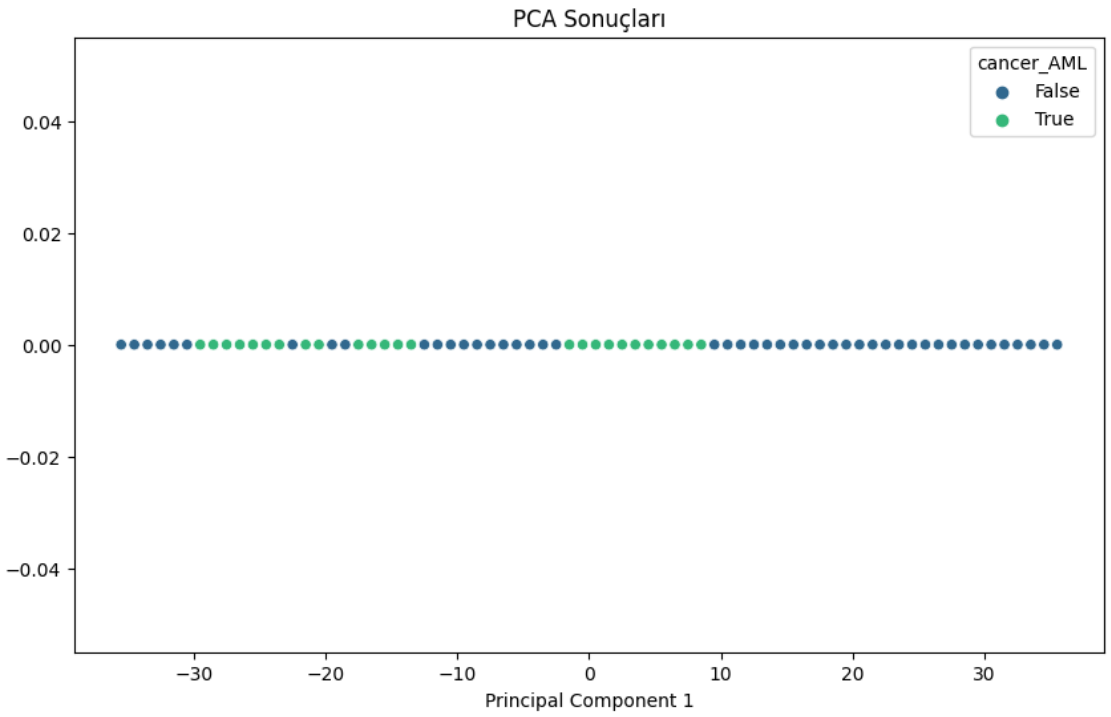
[ ]:
```
plt.figure(figsize=(8, 6))
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues', cbar=False,
            xticklabels=['ALL', 'AML'], yticklabels=['ALL', 'AML'])
plt.xlabel('Tahmin Edilen')
plt.ylabel('Gerçek')
plt.title("Confusion Matrix")
plt.show()
```



[ ]:
```
from sklearn.decomposition import PCA

X = actual_data.drop(columns=['cancer_AML'])
y = actual_data['cancer_AML']
```

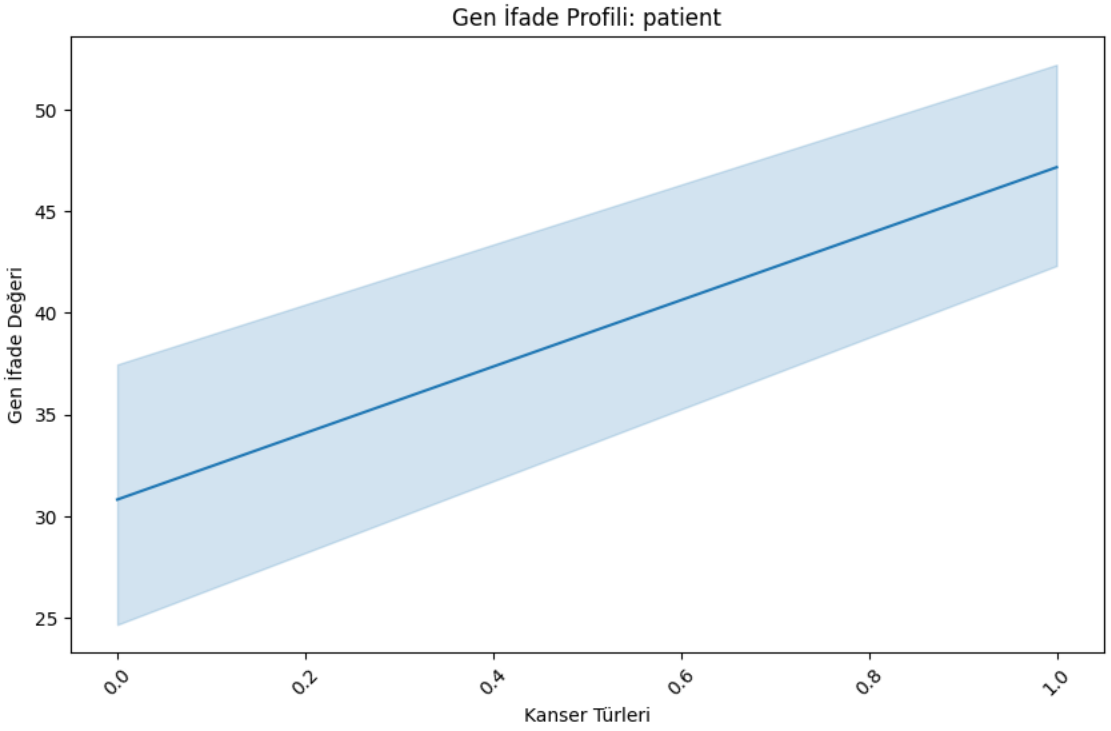
[ ]:
```
pca = PCA(n_components=min(X.shape[0], X.shape[1]))
X_pca = pca.fit_transform(X)
```

[ ]:
```
pca_df = pd.DataFrame({'Principal Component 1': X_pca[:, 0]})
pca_df['cancer_AML'] = y

# PCA sonuçlarını görselleştirin
plt.figure(figsize=(10, 6))
sns.scatterplot(data=pca_df, x='Principal Component 1', y=np.zeros_like(X_pca[:
 ↪, 0]), hue='cancer_AML', palette='viridis')
plt.title("PCA Sonuçları")
plt.xlabel("Principal Component 1")
plt.show()
```

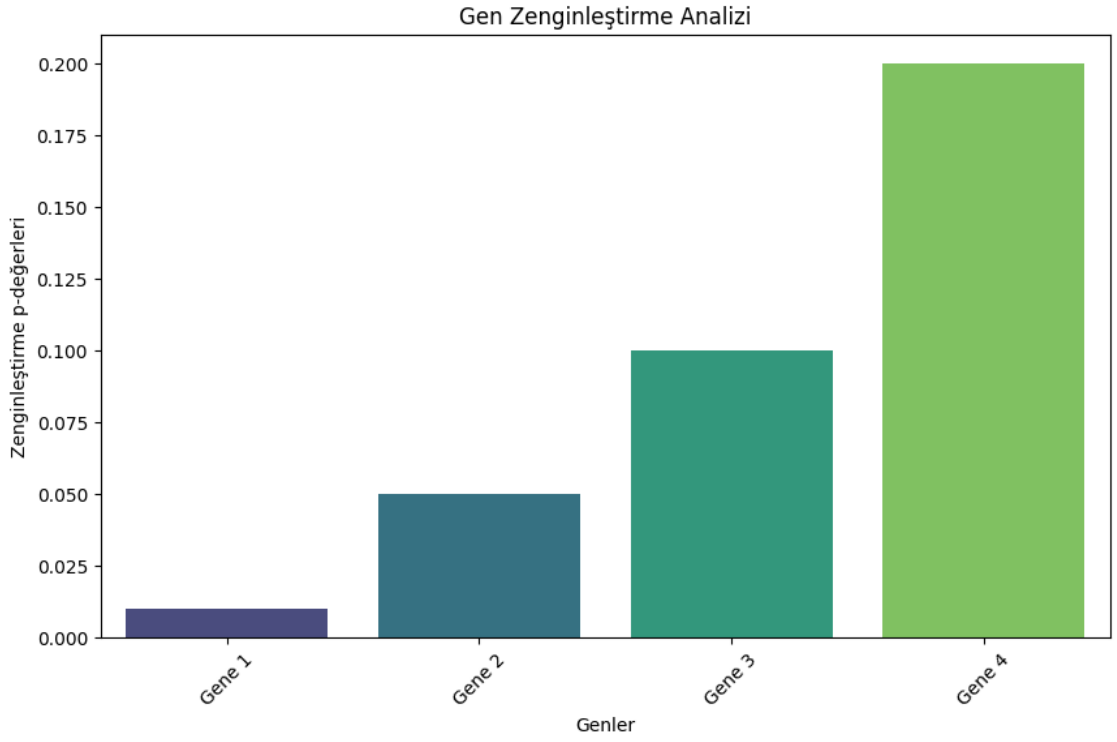


[ ]:
```
# Veri kümenizde bulunan bir gen adını seçin (örneğin, ilk sıradaki gen adı)
selected_gene = X.columns[0]

# Seçilen genin ifade profilini çıkarın
gene_expression = X[selected_gene]

# Gen ifade profilini kanser türlerine göre gösteren çizgi grafiği oluşturun
plt.figure(figsize=(10, 6))
sns.lineplot(data=pd.DataFrame({'Gene Expression': gene_expression, 'Cancer␣
 ↪Type': y}), x='Cancer Type', y='Gene Expression')
plt.title(f'Gen İfade Profili: {selected_gene}')
plt.xlabel('Kanser Türleri')
```

```
plt.ylabel('Gen İfade Değeri')
plt.xticks(rotation=45)
plt.show()
```



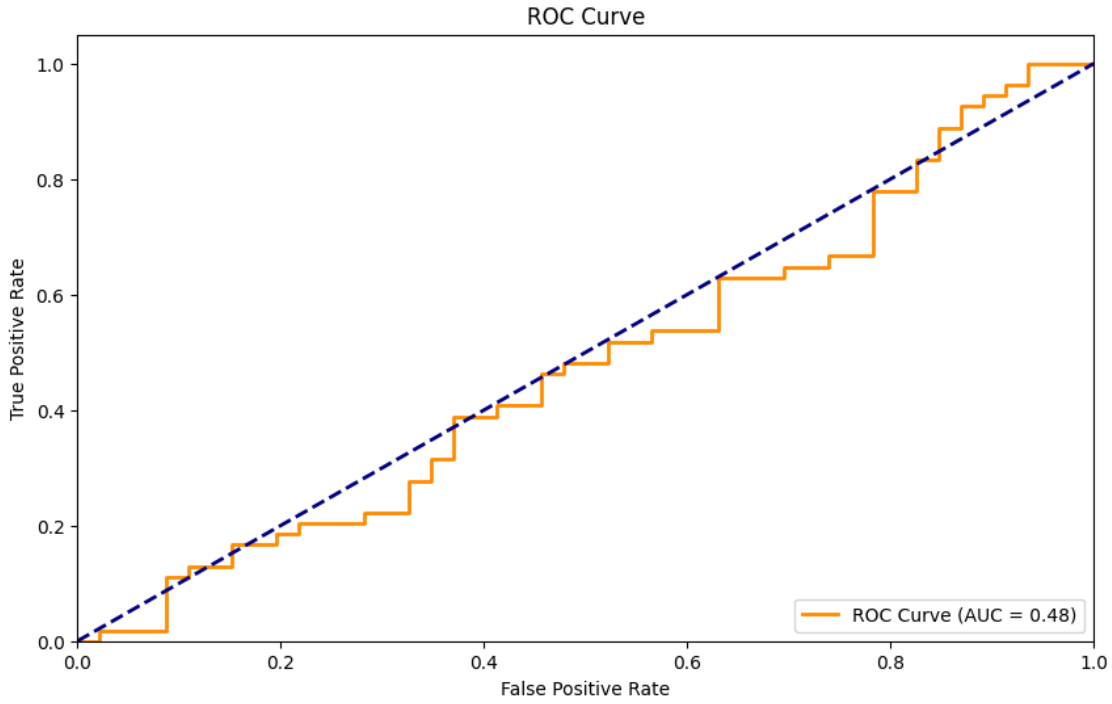
[ ]:
```
# Örnek olarak bazı genlerin zenginleştirilme p-değerleri
enrichment_p_values = [0.01, 0.05, 0.1, 0.2]

# Zenginleştirme p-değerlerini gösteren çubuk grafiği çizin
plt.figure(figsize=(10, 6))
sns.barplot(x=['Gene 1', 'Gene 2', 'Gene 3', 'Gene 4'], y=enrichment_p_values,␣
↪palette='viridis')
plt.title('Gen Zenginleştirme Analizi')
plt.xlabel('Genler')
plt.ylabel('Zenginleştirme p-değerleri')
plt.xticks(rotation=45)
plt.show()
```



[ ]:
```
from sklearn.metrics import roc_curve, auc

y_true = np.random.randint(2, size=100)
y_scores = np.random.rand(100)
```

[ ]:
```
fpr, tpr, _ = roc_curve(y_true, y_scores)
roc_auc = auc(fpr, tpr)
```

[ ]:
```
plt.figure(figsize=(10, 6))
plt.plot(fpr, tpr, color='darkorange', lw=2, label=f'ROC Curve (AUC = {roc_auc:.
↪2f})')
plt.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('ROC Curve')
plt.legend(loc='lower right')
plt.show()
```



[ ]:
```
independent_data.tail(5)
```

[ ]:
```
                                          Gene Description Gene Accession Number  \
7124  PTGER3 Prostaglandin E receptor 3 (subtype EP3…              X83863_at
7125  HMG2 High-mobility group (nonhistone chromosom…              Z17240_at
7126      RB1 Retinoblastoma 1 (including osteosarcoma)             L49218_f_at
7127  GB DEF = Glycophorin Sta (type A) exons 3 and …             M71243_f_at
7128                          GB DEF = mRNA (clone 1A7)             Z78285_f_at

        39 call   40 call.1    42 call.2   47 call.3  …   65 call.29    66  \
7124  1074    A   67      A   893      P  722      A  …  707       A   423
7125   475    A  263      A   297      A  170      A  …  354       A    41
7126    48    A  -33      A     6      A    0      A  …  -22       A     0
7127   168    A  -33      A  1971      P  510      P  …  260       A  1777
7128   -70    A  -21      A   -42      A  -73      A  …    5       A   -49

     call.30   63 call.31   64 call.32   62 call.33
7124       A  809       A  466       A  551       A
7125       A  445       A  349       A  194       A
7126       A   -2       A    0       A   20       A
7127       P  210       A  284       A  379       A
7128       A   16       A  -73       A  -60       A

[5 rows x 70 columns]
```

[ ]:
```
independent_data.dtypes
```

[ ]:
```
Gene Description         object
Gene Accession Number    object
39                        int64
call                     object
40                        int64
                          …
call.31                  object
64                        int64
call.32                  object
62                        int64
call.33                  object
Length: 70, dtype: object
```

[ ]:
```
independent_data.head()
```

[ ]:
```
                     Gene Description Gene Accession Number   39 call   40  \
0  AFFX-BioB-5_at (endogenous control)        AFFX-BioB-5_at -342    A  -87
1  AFFX-BioB-M_at (endogenous control)        AFFX-BioB-M_at -200    A -248
2  AFFX-BioB-3_at (endogenous control)        AFFX-BioB-3_at   41    A  262
3  AFFX-BioC-5_at (endogenous control)        AFFX-BioC-5_at  328    A  295
4  AFFX-BioC-3_at (endogenous control)        AFFX-BioC-3_at -224    A -226

  call.1   42 call.2   47 call.3  …   65 call.29   66 call.30   63 call.31  \
0      A   22      A -243      A  …  -62       A  -58       A -161       A
1      A -153      A -218      A  … -198       A -217       A -215       A
2      A   17      A -163      A  …   -5       A   63       A  -46       A
3      A  276      A  182      A  …  141       A   95       A  146       A
4      A -211      A -289      A  … -256       A -191       A -172       A

    64 call.32   62 call.33
0  -48       A -176       A
1 -531       A -284       A
2 -124       A  -81       A
3  431       A    9       A
4 -496       A -294       A

[5 rows x 70 columns]
```

[ ]:
```
independent_data.shape
```

[ ]:
```
(7129, 70)
```

[ ]:
```
independent_data.nunique
```

[ ]:
```
<bound method DataFrame.nunique of                                                    Gene
Description Gene Accession Number  \
0                    AFFX-BioB-5_at (endogenous control)        AFFX-BioB-5_at
1                    AFFX-BioB-M_at (endogenous control)        AFFX-BioB-M_at
2                    AFFX-BioB-3_at (endogenous control)        AFFX-BioB-3_at
3                    AFFX-BioC-5_at (endogenous control)        AFFX-BioC-5_at
4                    AFFX-BioC-3_at (endogenous control)        AFFX-BioC-3_at
…                                                      …                   …
7124  PTGER3 Prostaglandin E receptor 3 (subtype EP3…              X83863_at
7125  HMG2 High-mobility group (nonhistone chromosom…              Z17240_at
7126      RB1 Retinoblastoma 1 (including osteosarcoma)             L49218_f_at
7127  GB DEF = Glycophorin Sta (type A) exons 3 and …             M71243_f_at
7128                           GB DEF = mRNA (clone 1A7)             Z78285_f_at

        39 call   40 call.1    42 call.2   47 call.3  …   65 call.29    66  \
0     -342    A  -87      A    22      A -243      A  …  -62       A   -58
1     -200    A -248      A  -153      A -218      A  … -198       A  -217
2       41    A  262      A    17      A -163      A  …   -5       A    63
3      328    A  295      A   276      A  182      A  …  141       A    95
4     -224    A -226      A  -211      A -289      A  … -256       A  -191
…     …  …  …    …   …    …  …    …  …  …     …   …
7124  1074    A   67      A   893      P  722      A  …  707       A   423
7125   475    A  263      A   297      A  170      A  …  354       A    41
7126    48    A  -33      A     6      A    0      A  …  -22       A     0
7127   168    A  -33      A  1971      P  510      P  …  260       A  1777
7128   -70    A  -21      A   -42      A  -73      A  …    5       A   -49

     call.30   63 call.31   64 call.32   62 call.33
0          A -161       A  -48       A -176       A
1          A -215       A -531       A -284       A
2          A  -46       A -124       A  -81       A
3          A  146       A  431       A    9       A
4          A -172       A -496       A -294       A
…      …  …     …  …     …  …     …
7124       A  809       A  466       A  551       A
7125       A  445       A  349       A  194       A
7126       A   -2       A    0       A   20       A
7127       P  210       A  284       A  379       A
7128       A   16       A  -73       A  -60       A

[7129 rows x 70 columns]>
```

[ ]:
```
independent_data.describe()
```

[ ]:
```
                39            40            42            47            48  \
count   7129.000000   7129.000000   7129.000000   7129.000000   7129.000000
mean     582.194978    527.819329    603.813719    576.027213    751.464862
```

```
std     2473.986881   2304.800191   2377.775459   2436.848381   2437.815002
min   -21984.000000 -21296.000000 -10481.000000  -7861.000000 -16945.000000
25%     -33.000000    -36.000000    -17.000000     -8.000000     -6.000000
50%     125.000000    124.000000    116.000000    126.000000    158.000000
75%     439.000000    424.000000    420.000000    374.000000    577.000000
max    45815.000000  29136.000000  37529.000000  43221.000000  25231.000000

                49            41            43            44            45  \
count   7129.000000   7129.000000   7129.000000   7129.000000   7129.000000
mean     601.516763    565.152476    563.614252    531.401599    530.194137
std     2432.454360   2352.036107   2521.409254   2335.848476   2368.906095
min   -26775.000000  -7764.000000 -13905.000000  -9619.000000  -5353.000000
25%     -65.000000     -7.000000    -21.000000    -45.000000    -59.000000
50%     139.000000     93.000000    110.000000     74.000000     78.000000
75%     552.000000    342.000000    372.000000    321.000000    327.000000
max    29500.000000  31076.000000  49432.000000  35402.000000  34741.000000

       …            54            57            58            60  \
count  …   7129.00000   7129.000000   7129.000000   7129.000000
mean   …    668.70122    497.195820    561.964371    561.004629
std    …   2505.06701   2436.468032   2688.424072   2615.321812
min    … -11978.00000 -11067.000000 -16131.000000  -9338.000000
25%    …    -10.00000    -27.000000    -49.000000    -19.000000
50%    …    151.00000     82.000000    129.000000     98.000000
75%    …    469.00000    296.000000    435.000000    321.000000
max    …  35742.00000  38690.000000  59647.000000  40792.000000

                61            65            66            63            64  \
count   7129.000000   7129.000000   7129.000000   7129.000000   7129.000000
mean     581.006593    556.054145    530.495020    727.593351    686.850610
std     2467.740997   2360.238246   2463.108827   2488.340963   2703.734409
min   -16268.000000 -14244.000000  -7626.000000 -20782.000000 -26258.000000
25%     -36.000000    -31.000000    -15.000000    -21.000000    -51.000000
50%     117.000000     99.000000     73.000000    162.000000    195.000000
75%     422.000000    366.000000    280.000000    578.000000    683.000000
max    37374.000000  27447.000000  53204.000000  31585.000000  71369.000000

               62
count   7129.00000
mean     671.16496
std     2659.95898
min   -11973.00000
25%     -20.00000
50%     136.00000
75%     474.00000
max    48374.00000
```

```
[8 rows x 34 columns]
```

[ ]:
```
independent_data.columns
```

[ ]:
```
Index(['Gene Description', 'Gene Accession Number', '39', 'call', '40',
       'call.1', '42', 'call.2', '47', 'call.3', '48', 'call.4', '49',
       'call.5', '41', 'call.6', '43', 'call.7', '44', 'call.8', '45',
       'call.9', '46', 'call.10', '70', 'call.11', '71', 'call.12', '72',
       'call.13', '68', 'call.14', '69', 'call.15', '67', 'call.16', '55',
       'call.17', '56', 'call.18', '59', 'call.19', '52', 'call.20', '53',
       'call.21', '51', 'call.22', '50', 'call.23', '54', 'call.24', '57',
       'call.25', '58', 'call.26', '60', 'call.27', '61', 'call.28', '65',
       'call.29', '66', 'call.30', '63', 'call.31', '64', 'call.32', '62',
       'call.33'],
      dtype='object')
```

[ ]:
```
independent_data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 7129 entries, 0 to 7128
Data columns (total 70 columns):
 #   Column                 Non-Null Count  Dtype
---  ------                 --------------  -----
 0   Gene Description       7129 non-null   object
 1   Gene Accession Number  7129 non-null   object
 2   39                     7129 non-null   int64
 3   call                   7129 non-null   object
 4   40                     7129 non-null   int64
 5   call.1                 7129 non-null   object
 6   42                     7129 non-null   int64
 7   call.2                 7129 non-null   object
 8   47                     7129 non-null   int64
 9   call.3                 7129 non-null   object
 10  48                     7129 non-null   int64
 11  call.4                 7129 non-null   object
 12  49                     7129 non-null   int64
 13  call.5                 7129 non-null   object
 14  41                     7129 non-null   int64
 15  call.6                 7129 non-null   object
 16  43                     7129 non-null   int64
 17  call.7                 7129 non-null   object
 18  44                     7129 non-null   int64
 19  call.8                 7129 non-null   object
 20  45                     7129 non-null   int64
 21  call.9                 7129 non-null   object
 22  46                     7129 non-null   int64
 23  call.10                7129 non-null   object
 24  70                     7129 non-null   int64
```

```
 25  call.11               7129 non-null   object
 26  71                    7129 non-null   int64
 27  call.12               7129 non-null   object
 28  72                    7129 non-null   int64
 29  call.13               7129 non-null   object
 30  68                    7129 non-null   int64
 31  call.14               7129 non-null   object
 32  69                    7129 non-null   int64
 33  call.15               7129 non-null   object
 34  67                    7129 non-null   int64
 35  call.16               7129 non-null   object
 36  55                    7129 non-null   int64
 37  call.17               7129 non-null   object
 38  56                    7129 non-null   int64
 39  call.18               7129 non-null   object
 40  59                    7129 non-null   int64
 41  call.19               7129 non-null   object
 42  52                    7129 non-null   int64
 43  call.20               7129 non-null   object
 44  53                    7129 non-null   int64
 45  call.21               7129 non-null   object
 46  51                    7129 non-null   int64
 47  call.22               7129 non-null   object
 48  50                    7129 non-null   int64
 49  call.23               7129 non-null   object
 50  54                    7129 non-null   int64
 51  call.24               7129 non-null   object
 52  57                    7129 non-null   int64
 53  call.25               7129 non-null   object
 54  58                    7129 non-null   int64
 55  call.26               7129 non-null   object
 56  60                    7129 non-null   int64
 57  call.27               7129 non-null   object
 58  61                    7129 non-null   int64
 59  call.28               7129 non-null   object
 60  65                    7129 non-null   int64
 61  call.29               7129 non-null   object
 62  66                    7129 non-null   int64
 63  call.30               7129 non-null   object
 64  63                    7129 non-null   int64
 65  call.31               7129 non-null   object
 66  64                    7129 non-null   int64
 67  call.32               7129 non-null   object
 68  62                    7129 non-null   int64
 69  call.33               7129 non-null   object
dtypes: int64(34), object(36)
memory usage: 3.8+ MB
```

[ ]:
```
independent_data = pd.get_dummies(independent_data, drop_first=True)
```

[ ]:
```
scaler = StandardScaler()
```

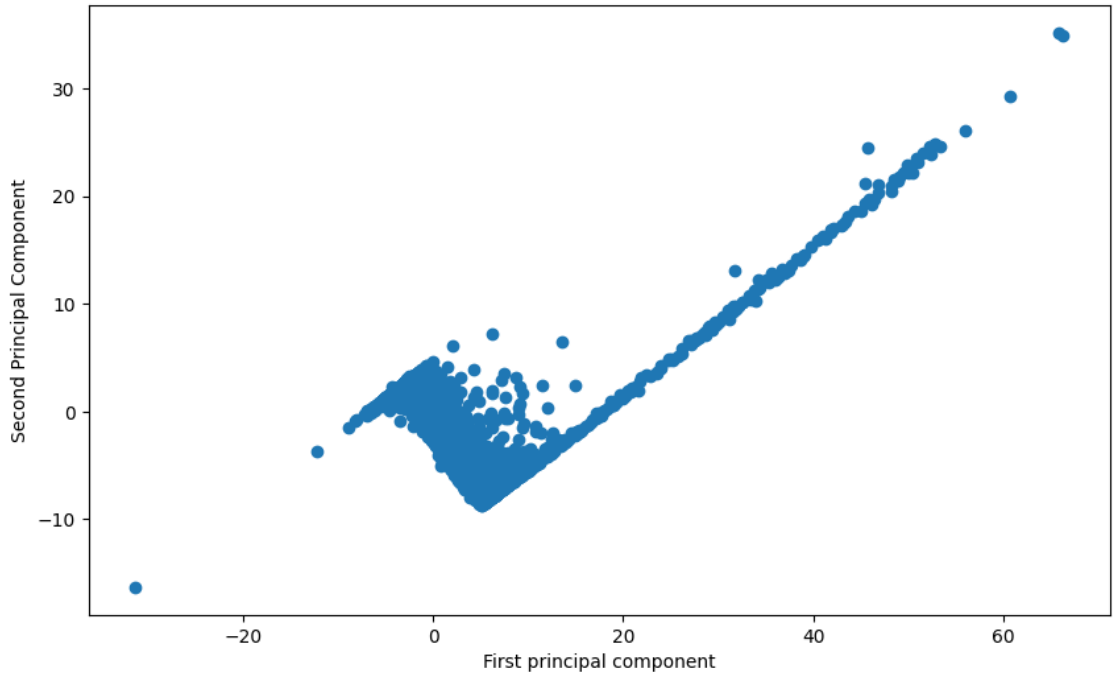
[ ]:
```
scaled_X = scaler.fit_transform(independent_data)
```

[ ]:
```
model = PCA(n_components=2)
```

[ ]:
```
principal_components = model.fit_transform(scaled_X)
```

[ ]:
```
plt.figure(figsize=(10,6))
plt.scatter(principal_components[:,0],principal_components[:,1])
plt.xlabel('First principal component')
plt.ylabel('Second Principal Component')
```

[ ]:
```
Text(0, 0.5, 'Second Principal Component')
```



[ ]:
```
model.n_components
```

[ ]:
```
2
```

[ ]:
```
model.components_
```

[ ]:
```
array([[ 0.13688445,  0.14109099,  0.1424812 , …,  0.09117882,
        -0.0002416 ,  0.09294923],
```

```
        [ 0.09156884,  0.0936133 ,  0.08244399, …, -0.11962566,
         -0.01065652, -0.13415528]])
```

[ ]:
```
df_comp = pd.DataFrame(model.
  ↪components_,index=['PC1','PC2'],columns=independent_data.columns)
```

[ ]:
```
df_comp
```

[ ]:
```
            39        40        42        47        48        49        41  \
PC1  0.136884  0.141091  0.142481  0.138498  0.145582  0.142220  0.143650
PC2  0.091569  0.093613  0.082444  0.096211  0.057470  0.085938  0.092268

            43        44        45  …  call.29_M  call.29_P  call.30_M  \
PC1  0.135674  0.141402  0.142309  …   0.003151   0.097565   0.001438
PC2  0.094433  0.091888  0.088797  …  -0.019487  -0.119714  -0.013674

     call.30_P  call.31_M  call.31_P  call.32_M  call.32_P  call.33_M  \
PC1   0.090663  -0.000022   0.091999    0.00148   0.091179  -0.000242
PC2  -0.128214  -0.010227  -0.147748   -0.01414  -0.119626  -0.010657

     call.33_P
PC1   0.092949
PC2  -0.134155

[2 rows x 13856 columns]
```

[ ]:
```
model.explained_variance_ratio_
```

[ ]:
```
array([0.0028036 , 0.00103782])
```

[ ]:
```
np.sum(model.explained_variance_ratio_)
```

[ ]:
```
0.0038414208895349643
```

[ ]:
```
pca_30 = PCA(n_components=30)
pca_30.fit(scaled_X)
```

[ ]:
```
PCA(n_components=30)
```

[ ]:
```
pca_30.explained_variance_ratio_
```

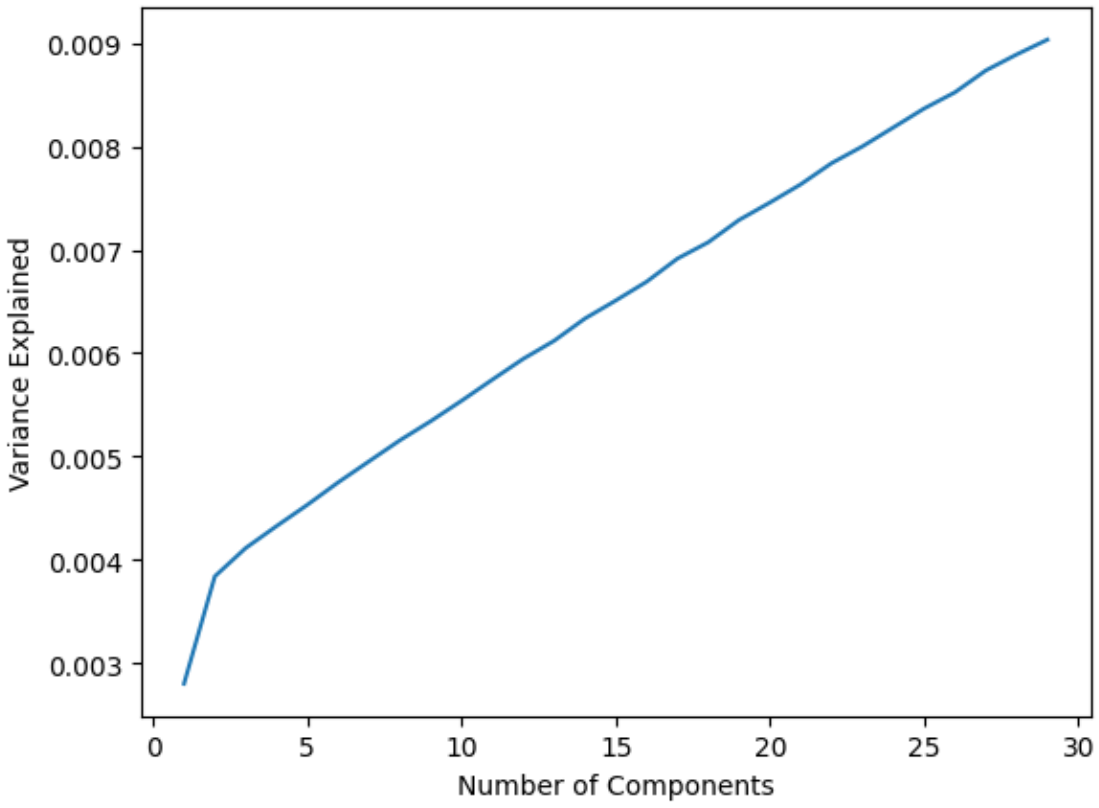
[ ]:
```
array([0.0028036 , 0.00103782, 0.00028015, 0.00022357, 0.00021572,
       0.00021391, 0.00021273, 0.00021107, 0.00020922, 0.00020455,
       0.00020267, 0.00020178, 0.00019668, 0.00019578, 0.00019444,
       0.00019222, 0.00019183, 0.00019088, 0.00018902, 0.00018584,
       0.00018397, 0.00018114, 0.00017841, 0.00017613, 0.00017331,
       0.00017087, 0.00016771, 0.0001647 , 0.00016092, 0.00016047])
```

[ ]:
```
np.sum(pca_30.explained_variance_ratio_)
```

[ ]:
```
0.0092711045883294
```

[ ]:
```
explained_variance = []

for n in range(1,30):
    pca = PCA(n_components=n)
    pca.fit(scaled_X)

    explained_variance.append(np.sum(pca.explained_variance_ratio_))
```

[ ]:
```
plt.plot(range(1,30),explained_variance)
plt.xlabel("Number of Components")
plt.ylabel("Variance Explained");
```



[ ]:
```
train_data.tail(5)
```

[ ]:
```
                                  Gene Description Gene Accession Number  \
7124  PTGER3 Prostaglandin E receptor 3 (subtype EP3…              X83863_at
7125  HMG2 High-mobility group (nonhistone chromosom…              Z17240_at
```

```
7126      RB1 Retinoblastoma 1 (including osteosarcoma)          L49218_f_at
7127  GB DEF = Glycophorin Sta (type A) exons 3 and …          M71243_f_at
7128                          GB DEF = mRNA (clone 1A7)          Z78285_f_at

        1 call    2 call.1     3 call.2    4 call.3  …    29 call.33   30  \
7124  793    A  782      A  1138      A  627      A  …   279       A  737
7125  329    A  295      A   777      P  170      A  …    51       A  227
7126   36    A   11      A    41      A -50      A  …     6       A   -9
7127  191    A   76      A   228      A  126      A  …  2484       P  371
7128  -37    A  -14      A   -41      A -91      A  …    -2       A -31

     call.34   31 call.35    32 call.36    33 call.37
7124       A  588       A  1170       A  2315       A
7125       A  361       A   284       A   250       A
7126       A  -26       A    39       A   -12       A
7127       A  133       A   298       A   790       P
7128       A  -32       A    -3       A   -10       A

[5 rows x 78 columns]
```

[ ]:
```
train_data.dtypes
```

[ ]:
```
Gene Description         object
Gene Accession Number    object
1                         int64
call                     object
2                         int64
                          …
call.35                  object
32                        int64
call.36                  object
33                        int64
call.37                  object
Length: 78, dtype: object
```

[ ]:
```
train_data.head()
```

[ ]:
```
                     Gene Description Gene Accession Number    1 call    2  \
0  AFFX-BioB-5_at (endogenous control)        AFFX-BioB-5_at -214    A -139
1  AFFX-BioB-M_at (endogenous control)        AFFX-BioB-M_at -153    A  -73
2  AFFX-BioB-3_at (endogenous control)        AFFX-BioB-3_at  -58    A   -1
3  AFFX-BioC-5_at (endogenous control)        AFFX-BioC-5_at   88    A  283
4  AFFX-BioC-3_at (endogenous control)        AFFX-BioC-3_at -295    A -264

  call.1    3 call.2    4 call.3  …   29 call.33   30 call.34   31 call.35  \
0      A  -76      A -135      A  …   15       A -318       A  -32       A
1      A  -49      A -114      A  … -114       A -192       A  -49       A
```

```
2      A -307      A  265      A  …    2       A  -95       A   49       A
3      A  309      A   12      A  …  193       A  312       A  230       P
4      A -376      A -419      A  …  -51       A -139       A -367       A

    32 call.36   33 call.37
0 -124       A -135       A
1  -79       A -186       A
2  -37       A  -70       A
3  330       A  337       A
4 -188       A -407       A

[5 rows x 78 columns]
```

[ ]:
```
train_data.shape
```

[ ]:
```
(7129, 78)
```

[ ]:
```
train_data.nunique
```

[ ]:
```
<bound method DataFrame.nunique of                                                  Gene
Description Gene Accession Number  \
0                    AFFX-BioB-5_at (endogenous control)        AFFX-BioB-5_at
1                    AFFX-BioB-M_at (endogenous control)        AFFX-BioB-M_at
2                    AFFX-BioB-3_at (endogenous control)        AFFX-BioB-3_at
3                    AFFX-BioC-5_at (endogenous control)        AFFX-BioC-5_at
4                    AFFX-BioC-3_at (endogenous control)        AFFX-BioC-3_at
…                                                      …                  …
7124  PTGER3 Prostaglandin E receptor 3 (subtype EP3…             X83863_at
7125  HMG2 High-mobility group (nonhistone chromosom…             Z17240_at
7126      RB1 Retinoblastoma 1 (including osteosarcoma)            L49218_f_at
7127  GB DEF = Glycophorin Sta (type A) exons 3 and …           M71243_f_at
7128                           GB DEF = mRNA (clone 1A7)           Z78285_f_at

        1 call    2 call.1     3 call.2    4 call.3  …    29 call.33   30  \
0    -214    A -139      A   -76      A -135      A  …    15       A -318
1    -153    A  -73      A   -49      A -114      A  …  -114       A -192
2     -58    A   -1      A  -307      A  265      A  …     2       A  -95
3      88    A  283      A   309      A   12      A  …   193       A  312
4    -295    A -264      A  -376      A -419      A  …   -51       A -139
…    …  …   …    …    …  …    …  …    …  …    …      …  …
7124  793    A  782      A  1138      A  627      A  …   279       A  737
7125  329    A  295      A   777      P  170      A  …    51       A  227
7126   36    A   11      A    41      A  -50      A  …     6       A   -9
7127  191    A   76      A   228      A  126      A  …  2484       P  371
7128  -37    A  -14      A   -41      A  -91      A  …    -2       A  -31

     call.34   31 call.35    32 call.36    33 call.37
```

```
0          A  -32       A  -124       A  -135       A
1          A  -49       A   -79       A  -186       A
2          A   49       A   -37       A   -70       A
3          A  230       P   330       A   337       A
4          A -367       A  -188       A  -407       A
…      …   …     …   …     …   …     …
7124       A  588       A  1170       A  2315       A
7125       A  361       A   284       A   250       A
7126       A  -26       A    39       A   -12       A
7127       A  133       A   298       A   790       P
7128       A  -32       A    -3       A   -10       A

[7129 rows x 78 columns]>
```

[ ]:
```
train_data.describe()
```

[ ]:
```
                 1             2             3             4             5  \
count   7129.000000   7129.000000   7129.000000   7129.000000   7129.000000
mean     641.367092    690.246318    698.307897    600.985271    679.532894
std     2264.294361   2468.814372   2485.656277   2340.047428   2375.895416
min   -19826.000000 -17930.000000 -27182.000000 -23396.000000 -10339.000000
25%      -21.000000    -14.000000    -31.000000    -33.000000      8.000000
50%      159.000000    130.000000    177.000000    139.000000    146.000000
75%      535.000000    488.000000    610.000000    497.000000    471.000000
max    31086.000000  29288.000000  28056.000000  31449.000000  29543.000000

                 6             7             8             9            10  \
count   7129.000000   7129.000000   7129.000000   7129.000000   7129.000000
mean     564.797728    584.437649    571.359097    789.713705    599.483097
std     2494.604090   2412.812263   2378.780450   2580.157021   2421.156219
min   -21658.000000 -24024.000000 -27570.000000 -25171.000000 -12500.000000
25%      -26.000000    -33.000000    -58.000000    -14.000000    -15.000000
50%      106.000000    134.000000    140.000000    166.000000    103.000000
75%      401.000000    497.000000    527.000000    609.000000    386.000000
max    38467.000000  41911.000000  40065.000000  23602.000000  28033.000000

       …            35            36            37            38  \
count  …   7129.000000   7129.000000   7129.000000   7129.000000
mean   …    514.496704    775.143498    689.248141    626.885959
std    …   2440.722824   2676.664777   2543.537830   2473.180838
min    … -16281.000000 -27398.000000 -23673.000000 -23645.000000
25%    …    -43.000000    -27.000000    -23.000000    -22.000000
50%    …    108.000000    144.000000    134.000000    133.000000
75%    …    396.000000    569.000000    505.000000    490.000000
max    …  61228.000000  37164.000000  32204.000000  29169.000000

                28            29            30            31            32  \
```

```
count   7129.000000   7129.000000   7129.000000   7129.000000   7129.000000
mean     673.279422    556.463179    718.934493    598.648899    676.920887
std     2413.149603   2376.681824   2533.678058   2405.268550   2436.964933
min   -20376.000000  -9501.000000 -17580.000000 -25491.000000 -28400.000000
25%      -16.000000    -13.000000    -25.000000    -32.000000    -22.000000
50%      150.000000     82.000000    128.000000    107.000000    155.000000
75%      517.000000    309.000000    488.000000    443.000000    549.000000
max    29833.000000  30354.000000  25055.000000  28350.000000  25093.000000

                33
count   7129.000000
mean     723.563473
std     2507.382019
min   -27811.000000
25%      -38.000000
50%      170.000000
75%      649.000000
max    32946.000000

[8 rows x 38 columns]
```

[ ]:
```
train_data.columns
```

[ ]:
```
Index(['Gene Description', 'Gene Accession Number', '1', 'call', '2', 'call.1',
       '3', 'call.2', '4', 'call.3', '5', 'call.4', '6', 'call.5', '7',
       'call.6', '8', 'call.7', '9', 'call.8', '10', 'call.9', '11', 'call.10',
       '12', 'call.11', '13', 'call.12', '14', 'call.13', '15', 'call.14',
       '16', 'call.15', '17', 'call.16', '18', 'call.17', '19', 'call.18',
       '20', 'call.19', '21', 'call.20', '22', 'call.21', '23', 'call.22',
       '24', 'call.23', '25', 'call.24', '26', 'call.25', '27', 'call.26',
       '34', 'call.27', '35', 'call.28', '36', 'call.29', '37', 'call.30',
       '38', 'call.31', '28', 'call.32', '29', 'call.33', '30', 'call.34',
       '31', 'call.35', '32', 'call.36', '33', 'call.37'],
      dtype='object')
```

[ ]:
```
train_data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 7129 entries, 0 to 7128
Data columns (total 78 columns):
 #   Column                 Non-Null Count  Dtype
---  ------                 --------------  -----
 0   Gene Description       7129 non-null   object
 1   Gene Accession Number  7129 non-null   object
 2   1                      7129 non-null   int64
 3   call                   7129 non-null   object
 4   2                      7129 non-null   int64
 5   call.1                 7129 non-null   object
```

```
6   3                  7129 non-null   int64
7   call.2             7129 non-null   object
8   4                  7129 non-null   int64
9   call.3             7129 non-null   object
10  5                  7129 non-null   int64
11  call.4             7129 non-null   object
12  6                  7129 non-null   int64
13  call.5             7129 non-null   object
14  7                  7129 non-null   int64
15  call.6             7129 non-null   object
16  8                  7129 non-null   int64
17  call.7             7129 non-null   object
18  9                  7129 non-null   int64
19  call.8             7129 non-null   object
20  10                 7129 non-null   int64
21  call.9             7129 non-null   object
22  11                 7129 non-null   int64
23  call.10            7129 non-null   object
24  12                 7129 non-null   int64
25  call.11            7129 non-null   object
26  13                 7129 non-null   int64
27  call.12            7129 non-null   object
28  14                 7129 non-null   int64
29  call.13            7129 non-null   object
30  15                 7129 non-null   int64
31  call.14            7129 non-null   object
32  16                 7129 non-null   int64
33  call.15            7129 non-null   object
34  17                 7129 non-null   int64
35  call.16            7129 non-null   object
36  18                 7129 non-null   int64
37  call.17            7129 non-null   object
38  19                 7129 non-null   int64
39  call.18            7129 non-null   object
40  20                 7129 non-null   int64
41  call.19            7129 non-null   object
42  21                 7129 non-null   int64
43  call.20            7129 non-null   object
44  22                 7129 non-null   int64
45  call.21            7129 non-null   object
46  23                 7129 non-null   int64
47  call.22            7129 non-null   object
48  24                 7129 non-null   int64
49  call.23            7129 non-null   object
50  25                 7129 non-null   int64
51  call.24            7129 non-null   object
52  26                 7129 non-null   int64
53  call.25            7129 non-null   object
```

```
 54  27                      7129 non-null   int64
 55  call.26                 7129 non-null   object
 56  34                      7129 non-null   int64
 57  call.27                 7129 non-null   object
 58  35                      7129 non-null   int64
 59  call.28                 7129 non-null   object
 60  36                      7129 non-null   int64
 61  call.29                 7129 non-null   object
 62  37                      7129 non-null   int64
 63  call.30                 7129 non-null   object
 64  38                      7129 non-null   int64
 65  call.31                 7129 non-null   object
 66  28                      7129 non-null   int64
 67  call.32                 7129 non-null   object
 68  29                      7129 non-null   int64
 69  call.33                 7129 non-null   object
 70  30                      7129 non-null   int64
 71  call.34                 7129 non-null   object
 72  31                      7129 non-null   int64
 73  call.35                 7129 non-null   object
 74  32                      7129 non-null   int64
 75  call.36                 7129 non-null   object
 76  33                      7129 non-null   int64
 77  call.37                 7129 non-null   object
dtypes: int64(38), object(40)
memory usage: 4.2+ MB
```

[ ]:
```
train_data = pd.get_dummies(train_data, drop_first=True)
```

[ ]:
```
scaler = StandardScaler()
```

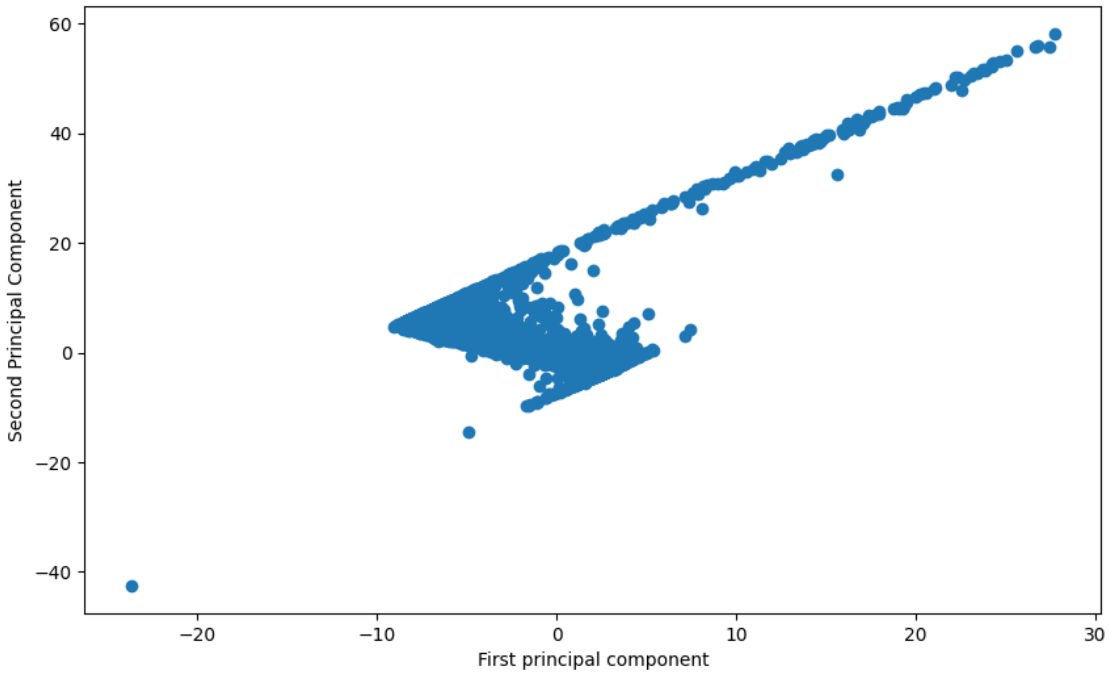
[ ]:
```
scaled_Y = scaler.fit_transform(train_data)
```

[ ]:
```
model = PCA(n_components=2)
```

[ ]:
```
principal_components1 = model.fit_transform(scaled_Y)
```

[ ]:
```
plt.figure(figsize=(10,6))
plt.scatter(principal_components1[:,1],principal_components1[:,0])
plt.xlabel('First principal component')
plt.ylabel('Second Principal Component')
```

[ ]:
```
Text(0, 0.5, 'Second Principal Component')
```



[ ]:
```
model.n_components
```

[ ]: 2

[ ]:
```
model.components_
```

[ ]:
```
array([[ 0.13563518,  0.13561635,  0.1330917 , …,  0.08910061,
         0.00126767,  0.0874186 ],
       [ 0.08241284,  0.07893647,  0.07636058, …, -0.13011445,
        -0.0146688 , -0.11616845]])
```

[ ]:
```
df_comp1 = pd.DataFrame(model.
 ↪components_,index=['PC1','PC2'],columns=train_data.columns)
```

[ ]:
```
df_comp1
```

[ ]:
```
            1         2         3         4         5         6         7  \
PC1  0.135635  0.135616  0.133092  0.135982  0.136671  0.125829  0.129148
PC2  0.082413  0.078936  0.076361  0.089316  0.082128  0.091322  0.088349

            8         9        10  …  call.33_M  call.33_P  call.34_M  \
PC1  0.131517  0.134360  0.131408  …   0.000664   0.088992  -0.000840
PC2  0.087407  0.063705  0.089684  …  -0.008998  -0.119514  -0.005677

     call.34_P  call.35_M  call.35_P  call.36_M  call.36_P  call.37_M  \
```

```
PC1   0.084958   0.000900   0.091381  -0.000117   0.089101   0.001268
PC2  -0.127983  -0.013864  -0.122095  -0.011345  -0.130114  -0.014669

     call.37_P
PC1   0.087419
PC2  -0.116168

[2 rows x 13868 columns]
```

[ ]:
```
model.explained_variance_ratio_
```

[ ]:
```
array([0.00320606, 0.00118327])
```

[ ]:
```
np.sum(model.explained_variance_ratio_)
```

[ ]:
```
0.004389333025737921
```

[ ]:
```
pca_50 = PCA(n_components=50)
pca_50.fit(scaled_Y)
```

[ ]:
```
PCA(n_components=50)
```

[ ]:
```
pca_50.explained_variance_ratio_
```

[ ]:
```
array([0.00320606, 0.00118327, 0.00031838, 0.00023296, 0.00022148,
       0.00021955, 0.00021665, 0.00021535, 0.00021301, 0.00021145,
       0.00020935, 0.00020915, 0.00020865, 0.00020396, 0.00020237,
       0.00020072, 0.00019829, 0.00019806, 0.00019691, 0.00019506,
       0.00019354, 0.00019105, 0.00018979, 0.00018897, 0.00018324,
       0.00018272, 0.00018239, 0.00018038, 0.00017757, 0.00017517,
       0.00017319, 0.00017305, 0.00016965, 0.00016873, 0.00016536,
       0.00016391, 0.00016356, 0.00015871, 0.0001539 , 0.0001534 ,
       0.00015311, 0.0001522 , 0.00014928, 0.00014805, 0.00014784,
       0.00014678, 0.00014653, 0.00014612, 0.00014589, 0.0001457 ])
```

[ ]:
```
np.sum(pca_50.explained_variance_ratio_)
```

[ ]:
```
0.013230480646624238
```

[ ]:
```
explained_variance = []

for n in range(1,30):
    pca = PCA(n_components=n)
    pca.fit(scaled_Y)

    explained_variance.append(np.sum(pca.explained_variance_ratio_))
```

[ ]:
```
y_true = np.random.randint(2, size=100)
y_scores = np.random.rand(100)
```