austin_race_analysis

May 13, 2025

0.1 Unsupervised Learning to Predict Race from Merged Dataset

[1]:
```python
#imports
import os
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
```

0.2 Load Data and Inspect

[2]:
```python
full_data_df = pd.read_csv('final_merged.csv')
full_data_df

print("Shape of the data: ", full_data_df.shape)

full_data_df.info()
full_data_df.head()
```

```
Shape of the data:  (9222, 140)
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 9222 entries, 0 to 9221
Columns: 140 entries, Patient ID to Survival Months
dtypes: float64(77), int64(2), object(61)
memory usage: 9.9+ MB
```

```
/tmp/ipykernel_29693/3584519652.py:1: DtypeWarning: Columns (0,3,4,5,6,7,9,12,15
,16,17,18,22,24,26,28,29,30,40,65,66,67,68,69,70,71,72,73,74,75,76,82,83,89,90,9
1,92,93,96,97,98,99,100,101,102,103,104,105,106,107,108,109,115) have mixed
types. Specify dtype option on import or set low_memory=False.
  full_data_df = pd.read_csv('final_merged.csv')
```

[2]:
```
     Patient ID  Age  Surgery Cancer Type Cancer Type Detailed Cellularity  \
0  Breast_MRI_001   41      NaN         NaN                  NaN         NaN
1  Breast_MRI_001   41      NaN         NaN                  NaN         NaN
2  Breast_MRI_002   38      NaN         NaN                  NaN         NaN
3  Breast_MRI_003   62      NaN         NaN                  NaN         NaN
4  Breast_MRI_003   62      NaN         NaN                  NaN         NaN
```

```
  Chemotherapy Pam50 + Claudin-low subtype  Cohort ER status measured by IHC  \
0          NaN                         NaN     NaN                       NaN   
1          NaN                         NaN     NaN                       NaN   
2          NaN                         NaN     NaN                       NaN   
3          NaN                         NaN     NaN                       NaN   
4          NaN                         NaN     NaN                       NaN   

   …  Unnamed: 3  T Stage  6th Stage                                Grade  \
0  …         NaN       T2        IIB     Poorly differentiated; Grade III   
1  …         NaN       T2        IIB  Moderately differentiated; Grade II   
2  …         NaN      NaN        NaN                                  NaN   
3  …         NaN       T2        IIB     Poorly differentiated; Grade III   
4  …         NaN       T2        IIB  Moderately differentiated; Grade II   

    A Stage Estrogen Status Progesterone Status Regional Node Examined  \
0  Regional        Positive            Negative                    6.0   
1  Regional        Positive            Positive                    9.0   
2       NaN             NaN                 NaN                    NaN   
3  Regional        Positive            Positive                    6.0   
4  Regional        Positive            Positive                   19.0   

  Reginol Node Positive  Survival Months  
0                   1.0             66.0  
1                   1.0             72.0  
2                   NaN              NaN  
3                   1.0             52.0  
4                   1.0             55.0  

[5 rows x 140 columns]
```

0.3 Data Cleaning

[13]:
```python
#Dropping any duplicate rows
full_data_df.drop_duplicates(inplace=True)

# Drop features with a lot of missing values
missing__ratio = full_data_df.isnull().mean()
columns_to_drop = missing__ratio[missing__ratio > 0.8].index
full_data_df.drop(columns=columns_to_drop, inplace=True)
```

[15]:
```python
# Look at new shape of the data
print("Shape of the data after dropping columns with a lot of missing values:␣
 ↪", full_data_df.shape)
```

```
Shape of the data after dropping columns with a lot of missing values:  (6693,
111)
```

```
[16]: #inspecting the race column
full_data_df['Race'].value_counts(dropna=False)

#Drop rows with missing values in Race column

full_data_df = full_data_df.dropna(subset=['Race'])

#Drop rows where race is = 0
full_data_df = full_data_df[full_data_df['Race'] != 0]

full_data_df['Race'].value_counts()
```

```
[16]: Race
1.0    5856
2.0     470
4.0     321
5.0      18
3.0      14
6.0       9
8.0       4
7.0       1
Name: count, dtype: int64
```

0.4 EDA

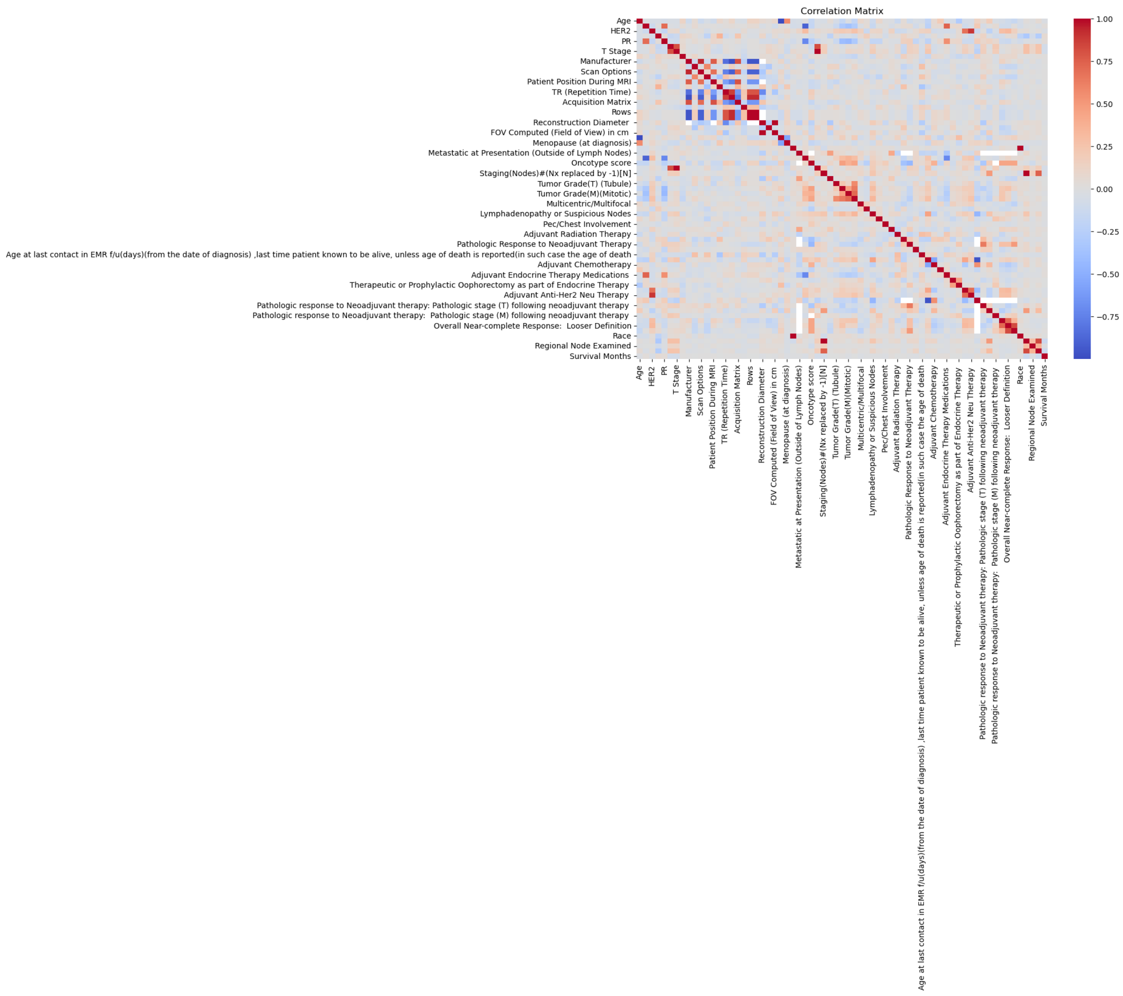
```
[17]: full_data_df.describe()
```

```
[17]:               Age           ER         HER2  Histologic type           PR  \
count  6693.000000  4944.000000  4944.000000      6693.000000  4944.000000
mean     53.247124     0.803600     0.189523         0.596145     0.702063
std       8.718803     0.397314     0.391963         0.623003     0.457398
min      21.000000     0.000000     0.000000         0.000000     0.000000
25%      47.000000     1.000000     0.000000         0.000000     0.000000
50%      53.000000     1.000000     0.000000         1.000000     1.000000
75%      60.000000     1.000000     0.000000         1.000000     1.000000
max      89.000000     1.000000     1.000000         9.000000     1.000000

        Tumor Size      T Stage  Days to MRI (From the Date of Diagnosis)  \
count  6056.000000  6687.000000                               4944.000000
mean     28.519815     1.708689                                 12.528519
std      19.264544     0.714212                                 17.320590
min       1.000000     1.000000                               -123.000000
25%      16.000000     1.000000                                  7.000000
50%      23.000000     2.000000                                 12.000000
75%      35.000000     2.000000                                 19.250000
max     140.000000     4.000000                                381.000000
```

```
       Manufacturer  Manufacturer Model Name  …  \
count   4944.000000              4944.000000  …
mean       0.582120                 2.893811  …
std        0.908594                 1.904946  …
min        0.000000                 0.000000  …
25%        0.000000                 1.000000  …
50%        0.000000                 3.000000  …
75%        2.000000                 4.000000  …
max        2.000000                 7.000000  …

       Pathologic response to Neoadjuvant therapy:  Pathologic stage (N)
following neoadjuvant therapy  \
count                                                  1722.000000
mean                                                      0.660859
std                                                       0.837785
min                                                      -1.000000
25%                                                       0.000000
50%                                                       1.000000
75%                                                       1.000000
max                                                       3.000000

       Pathologic response to Neoadjuvant therapy:  Pathologic stage (M)
following neoadjuvant therapy   \
count                                                  1673.000000
mean                                                     -0.982666
std                                                       0.180538
min                                                      -1.000000
25%                                                      -1.000000
50%                                                      -1.000000
75%                                                      -1.000000
max                                                       1.000000

       Overall Near-complete Response:  Stricter Definition  \
count                                                  1929.000000
mean                                                      0.444272
std                                                       0.770387
min                                                       0.000000
25%                                                       0.000000
50%                                                       0.000000
75%                                                       1.000000
max                                                       3.000000

       Overall Near-complete Response:  Looser Definition  \
count                                                  1929.000000
mean                                                      0.670295
std                                                       0.890914
min                                                       0.000000
```

```
25%                                                 0.000000
50%                                                 0.000000
75%                                                 1.000000
max                                                 3.000000

       Near-complete Response (Graded Measure)         Race      N Stage  \
count                               1929.00000  6693.000000  6671.000000
mean                                   2.39606     1.240849     1.204317
std                                    4.75256     0.750747     0.685523
min                                    0.00000     1.000000     0.000000
25%                                    0.00000     1.000000     1.000000
50%                                    0.00000     1.000000     1.000000
75%                                    1.00000     1.000000     1.000000
max                                   19.00000     8.000000     3.000000

       Regional Node Examined  Reginol Node Positive  Survival Months
count             6056.000000            6056.000000      6056.000000
mean                13.934610               3.410337        72.084544
std                  8.070807               4.475298        22.470205
min                  1.000000               1.000000         1.000000
25%                  8.000000               1.000000        57.000000
50%                 13.000000               2.000000        74.000000
75%                 18.000000               3.000000        90.000000
max                 61.000000              46.000000       107.000000

[8 rows x 67 columns]
```

[18]:
```python
#Coorelation heatmap for numerical features

numeric_features = full_data_df.select_dtypes(include=[np.number])
plt.figure(figsize=(12, 8))
sns.heatmap(numeric_features.corr(), annot=False, fmt=".2f", cmap='coolwarm')
plt.title('Correlation Matrix')
plt.show()
```



0.5 Guassian and PCA

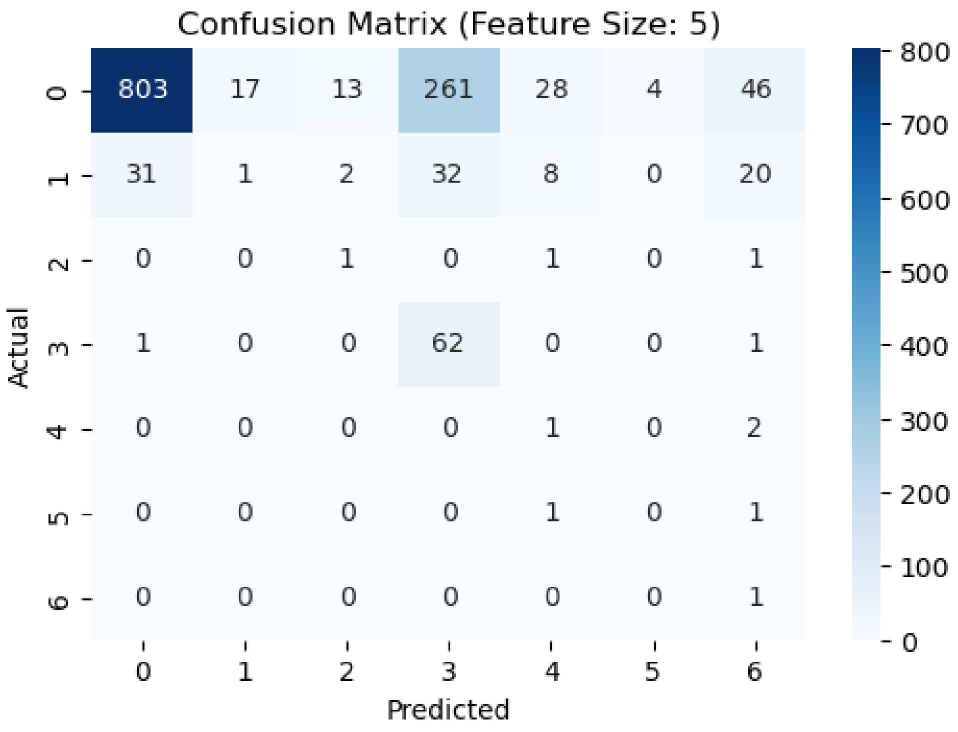
```
[46]: from sklearn.preprocessing import StandardScaler

# Assuming 'full_data_df' is your merged breast cancer dataset
# Define race label and drop it from feature set
target_col = 'Race'

# 1. Drop columns with too much missing data (>80% missing already dropped␣
↪earlier)
# 2. Keep only numeric columns (Naive Bayes needs numeric features)
numeric_cols = full_data_df.select_dtypes(include=[np.number]).columns.
↪drop(target_col)
features = numeric_cols

# Strategy 1: Drop rows with any missing values
```

```
df_dropped = full_data_df[features.union([target_col])].dropna()

# Strategy 2: Fill numeric NaNs with column means
df_filled = full_data_df[features.union([target_col])].copy()
df_filled[features] = df_filled[features].fillna(df_filled[features].mean())

# Scale features
scaler = StandardScaler()
df_dropped[features] = scaler.fit_transform(df_dropped[features])
df_filled[features] = scaler.fit_transform(df_filled[features])

print("Dropped dataset shape:", df_dropped.shape)
print("Filled dataset shape:", df_filled.shape)
```

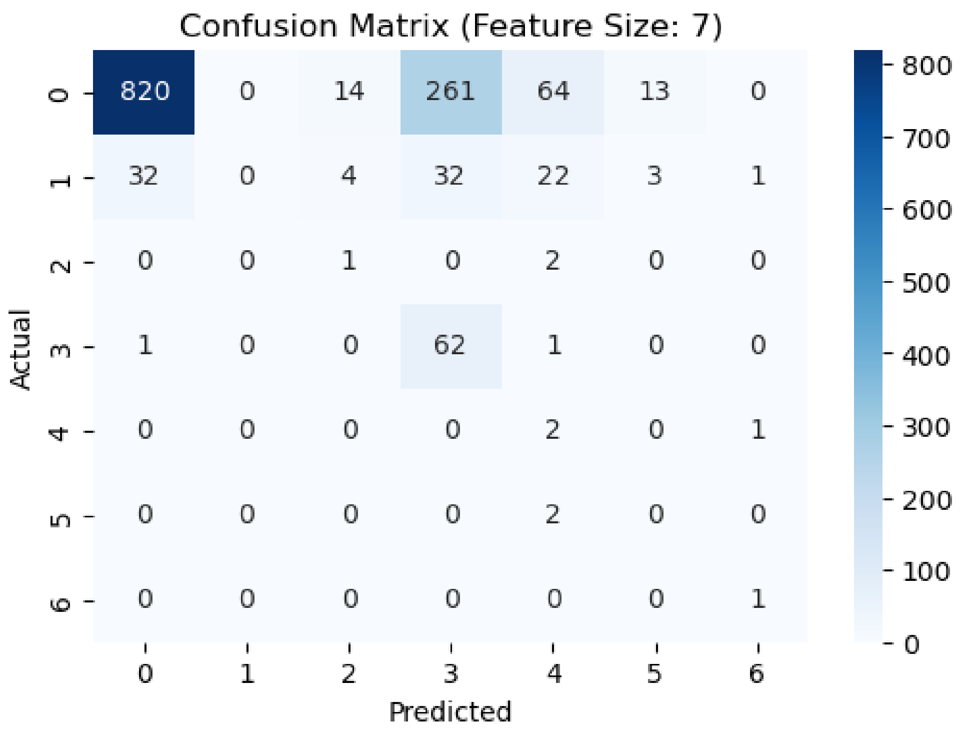
```
Dropped dataset shape: (118, 67)
Filled dataset shape: (6693, 67)
```

[48]:
```
from sklearn.model_selection import train_test_split
from sklearn.naive_bayes import GaussianNB
from sklearn.metrics import accuracy_score, confusion_matrix
import matplotlib.pyplot as plt
import seaborn as sns
import random


# Define features and target
X = df_filled[features]
y = df_filled[target_col]

# Drop classes with fewer than 2 samples
class_counts = y.value_counts()
valid_classes = class_counts[class_counts >= 2].index

X = X[y.isin(valid_classes)]
y = y[y.isin(valid_classes)]

# Train-test split
X_train, X_test, y_train, y_test = train_test_split(X, y, stratify=y,␣
 ↪test_size=0.2, random_state=42)

# Test different subset sizes
feature_sizes = [5, 7, 10]
results = {}

for size in feature_sizes:
    selected_features = random.sample(list(X.columns), size)
    model = GaussianNB()
    model.fit(X_train[selected_features], y_train)
    y_pred = model.predict(X_test[selected_features])

    acc = accuracy_score(y_test, y_pred)
    conf_matrix = confusion_matrix(y_test, y_pred)

    results[size] = {
        "features": selected_features,
        "accuracy": acc,
        "conf_matrix": conf_matrix
    }

    print(f"\nFeature Subset Size: {size}")
    print("Selected Features:", selected_features)
    print(f"Accuracy: {acc:.4f}")

    plt.figure(figsize=(6, 4))
    sns.heatmap(conf_matrix, annot=True, fmt='d', cmap='Blues')
    plt.title(f"Confusion Matrix (Feature Size: {size})")
    plt.xlabel("Predicted")
    plt.ylabel("Actual")
    plt.show()
```

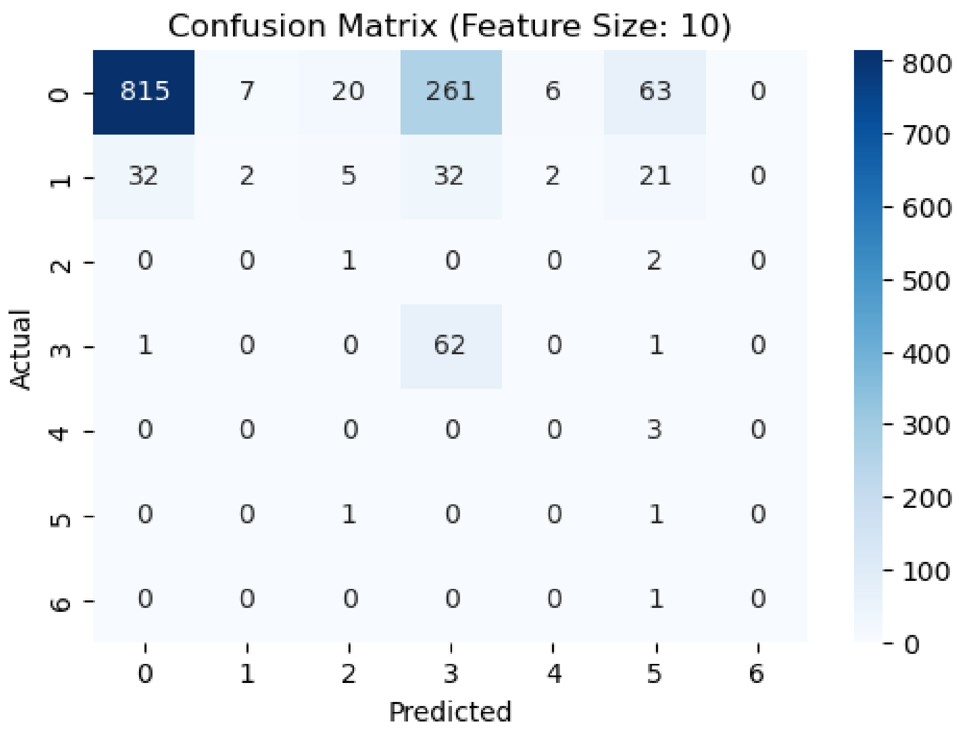
```
Feature Subset Size: 5
Selected Features: ['Tumor Size', 'Recurrence event(s)', 'Pathologic Response to
Neoadjuvant Therapy', 'Oncotype score', 'Staging(Metastasis)#(Mx -replaced by
-1)[M]']
Accuracy: 0.6490
```



```
Feature Subset Size: 7
Selected Features: ['Manufacturer Model Name', 'Age', 'Overall Near-complete
Response:  Looser Definition', 'Adjuvant Chemotherapy', 'Reginol Node Positive',
'Mol Subtype', 'N Stage']
Accuracy: 0.6617
```



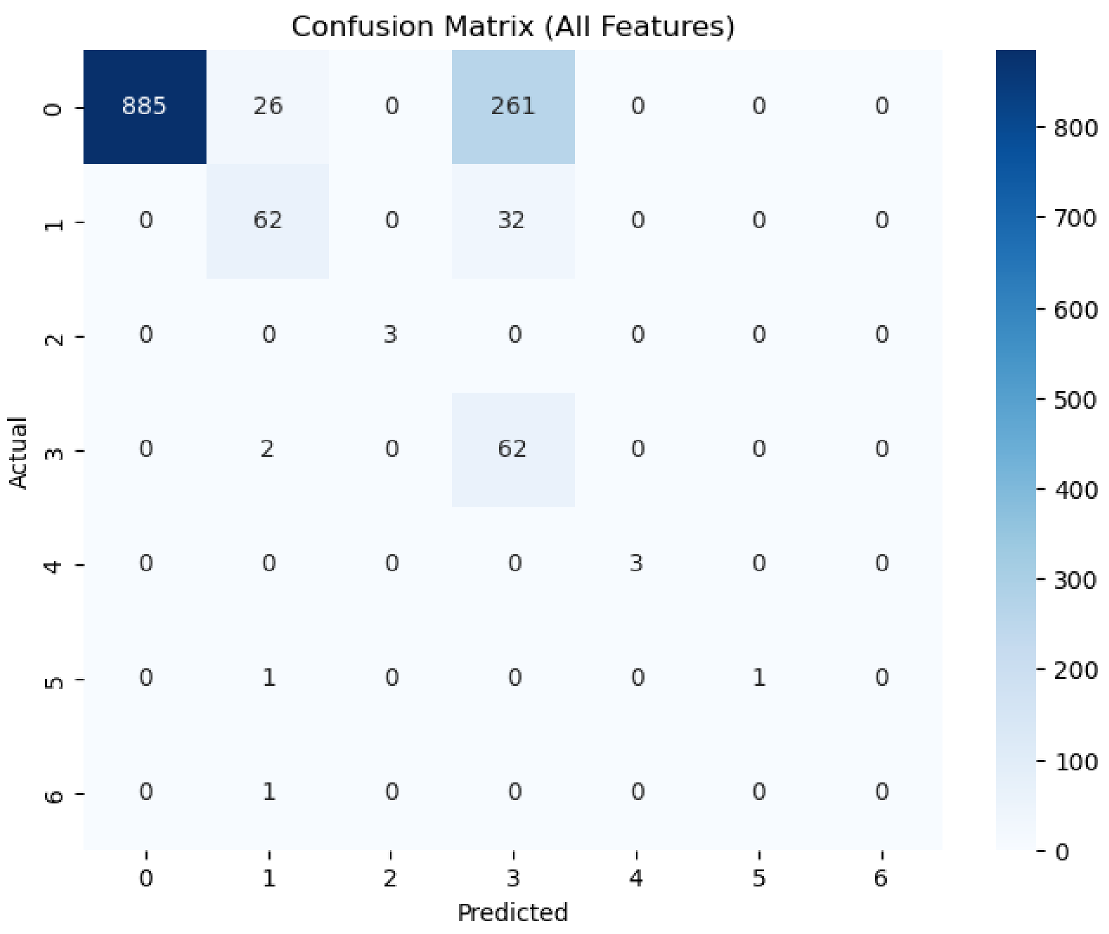
```
Feature Subset Size: 10
Selected Features: ['Age at last contact in EMR f/u(days)(from the date of
diagnosis) ,last time patient known to be alive, unless age of death is
reported(in such case the age of death', 'Overall Near-complete Response:
Stricter Definition', 'Neoadjuvant Radiation Therapy', 'Reconstruction Diameter
', 'Skin/Nipple Invovlement', 'PR', 'Reginol Node Positive', 'Known Ovarian
Status ', 'FOV Computed (Field of View) in cm ', 'Flip Angle ']
Accuracy: 0.6580
```



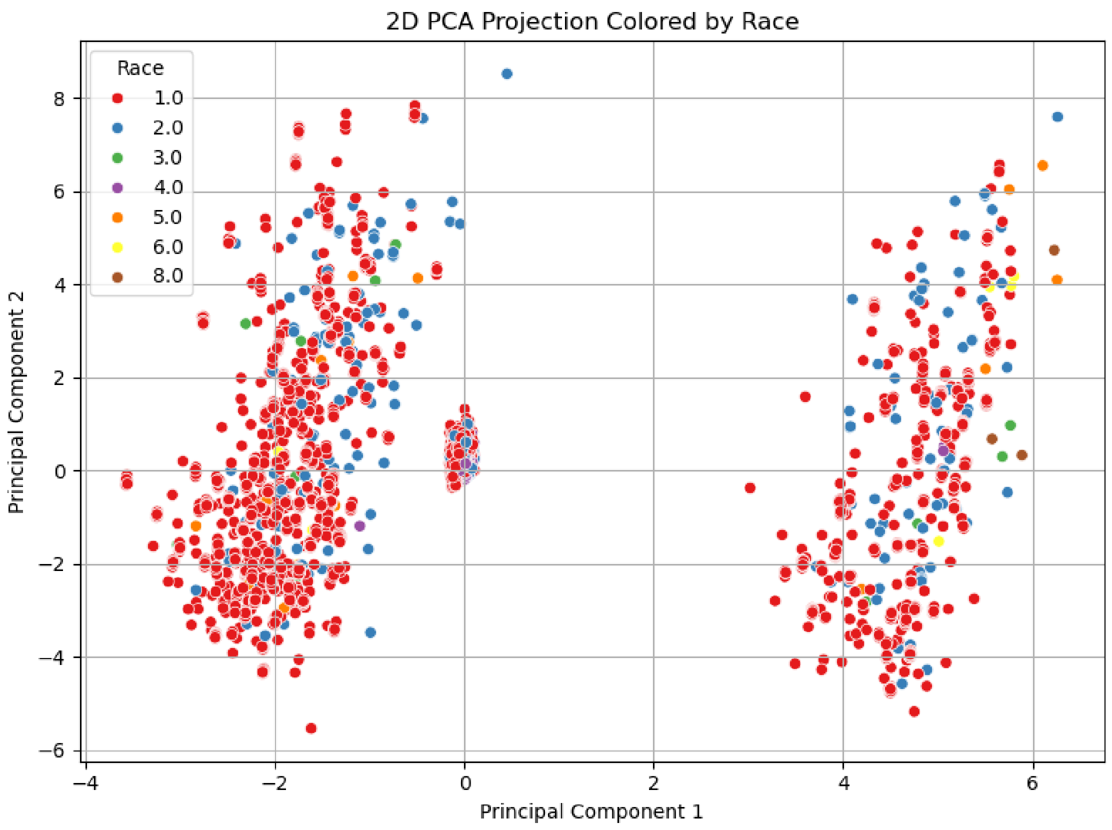
[49]:
```
# Baseline model
from sklearn.naive_bayes import GaussianNB
from sklearn.metrics import accuracy_score, classification_report,␣
 ↪confusion_matrix
import seaborn as sns
import matplotlib.pyplot as plt

# Train full-feature Naive Bayes model
model_full = GaussianNB()
model_full.fit(X_train, y_train)

# Predict on test set
y_pred_full = model_full.predict(X_test)

# Evaluate
accuracy_full = accuracy_score(y_test, y_pred_full)
print(f"Naive Bayes Accuracy (All Features): {accuracy_full:.4f}")

# Classification report
print("Classification Report:\n", classification_report(y_test, y_pred_full))

# Confusion Matrix
conf_matrix_full = confusion_matrix(y_test, y_pred_full)
```

```
plt.figure(figsize=(8, 6))
sns.heatmap(conf_matrix_full, annot=True, fmt="d", cmap="Blues")
plt.title("Confusion Matrix (All Features)")
plt.xlabel("Predicted")
plt.ylabel("Actual")
plt.show()
```

```
Naive Bayes Accuracy (All Features): 0.7588
Classification Report:
              precision    recall  f1-score   support

         1.0       1.00      0.76      0.86      1172
         2.0       0.67      0.66      0.67        94
         3.0       1.00      1.00      1.00         3
         4.0       0.17      0.97      0.30        64
         5.0       1.00      1.00      1.00         3
         6.0       1.00      0.50      0.67         2
         8.0       0.00      0.00      0.00         1

    accuracy                           0.76      1339
   macro avg       0.69      0.70      0.64      1339
weighted avg       0.94      0.76      0.82      1339


/home/austi/miniconda3/envs/msse/lib/python3.11/site-
packages/sklearn/metrics/_classification.py:1565: UndefinedMetricWarning:
Precision is ill-defined and being set to 0.0 in labels with no predicted
samples. Use `zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
/home/austi/miniconda3/envs/msse/lib/python3.11/site-
packages/sklearn/metrics/_classification.py:1565: UndefinedMetricWarning:
Precision is ill-defined and being set to 0.0 in labels with no predicted
samples. Use `zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
/home/austi/miniconda3/envs/msse/lib/python3.11/site-
packages/sklearn/metrics/_classification.py:1565: UndefinedMetricWarning:
Precision is ill-defined and being set to 0.0 in labels with no predicted
samples. Use `zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
```



[50]:
```
from sklearn.decomposition import PCA

# Reduce to 2D for visualization
pca_vis = PCA(n_components=2)
X_train_pca_2d = pca_vis.fit_transform(X_train)

# Plot PCA components colored by Race
plt.figure(figsize=(8, 6))
sns.scatterplot(x=X_train_pca_2d[:, 0], y=X_train_pca_2d[:, 1], hue=y_train,␣
  ↪palette="Set1")
plt.xlabel("Principal Component 1")
plt.ylabel("Principal Component 2")
plt.title("2D PCA Projection Colored by Race")
plt.legend(title="Race")
plt.grid(True)
plt.tight_layout()
plt.show()
```

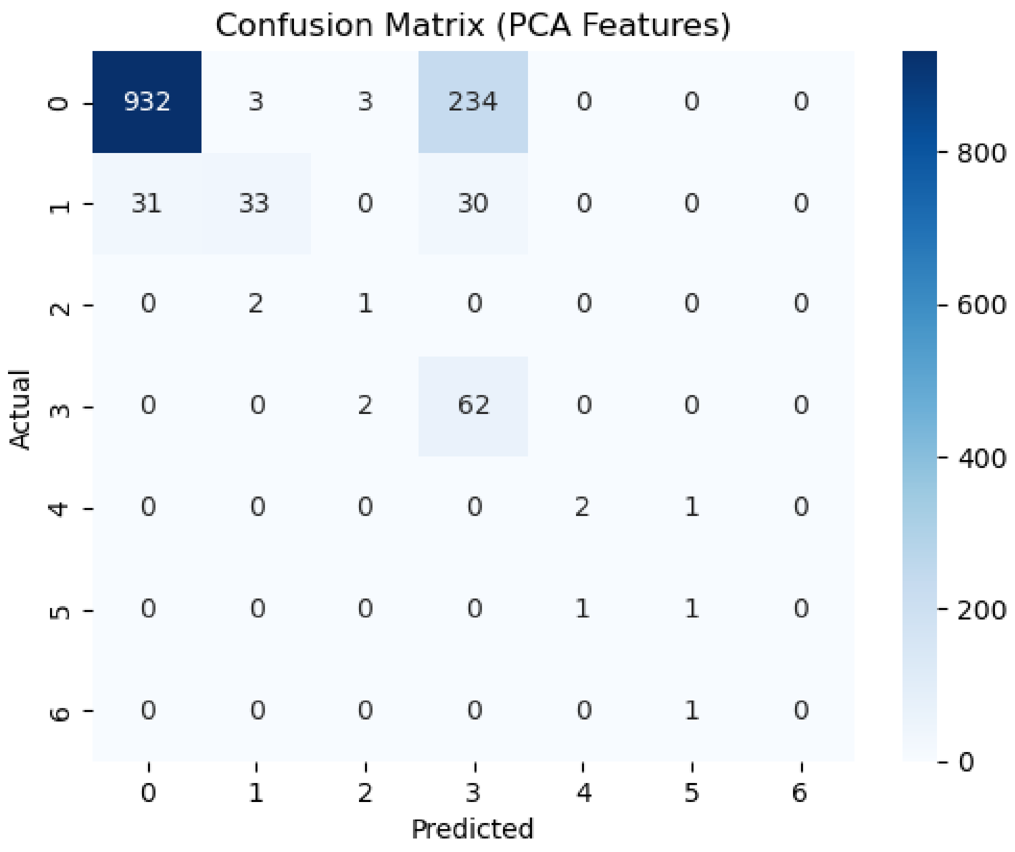


0.6 Evaluation

[51]:
```
from sklearn.decomposition import PCA
from sklearn.naive_bayes import GaussianNB
from sklearn.metrics import accuracy_score, confusion_matrix,␣
↪classification_report

# Fit PCA to retain 90% variance
pca_final = PCA(n_components=0.90)
X_train_pca = pca_final.fit_transform(X_train)
X_test_pca = pca_final.transform(X_test)

print(f"Number of PCA components selected: {pca_final.n_components_}")

# Train and predict
model_pca = GaussianNB()
model_pca.fit(X_train_pca, y_train)
y_pred_pca = model_pca.predict(X_test_pca)

# Evaluate
```

```python
acc_pca = accuracy_score(y_test, y_pred_pca)
print(f"Naive Bayes Accuracy (PCA Features): {acc_pca:.4f}")

conf_matrix_pca = confusion_matrix(y_test, y_pred_pca)
sns.heatmap(conf_matrix_pca, annot=True, fmt='d', cmap='Blues')
plt.title("Confusion Matrix (PCA Features)")
plt.xlabel("Predicted")
plt.ylabel("Actual")
plt.show()

print("Classification Report:\n", classification_report(y_test, y_pred_pca))
```

```
Number of PCA components selected: 36
Naive Bayes Accuracy (PCA Features): 0.7700
```



	0	1	2	3	4	5	6
0	932	3	3	234	0	0	0
1	31	33	0	30	0	0	0
2	0	2	1	0	0	0	0
3	0	0	2	62	0	0	0
4	0	0	0	0	2	1	0
5	0	0	0	0	1	1	0
6	0	0	0	0	0	1	0

```
Classification Report:
               precision    recall  f1-score   support

         1.0       0.97      0.80      0.87      1172
         2.0       0.87      0.35      0.50        94
         3.0       0.17      0.33      0.22         3
         4.0       0.19      0.97      0.32        64
         5.0       0.67      0.67      0.67         3
         6.0       0.33      0.50      0.40         2
         8.0       0.00      0.00      0.00         1

    accuracy                           0.77      1339
   macro avg       0.46      0.52      0.43      1339
weighted avg       0.92      0.77      0.82      1339

/home/austi/miniconda3/envs/msse/lib/python3.11/site-
packages/sklearn/metrics/_classification.py:1565: UndefinedMetricWarning:
Precision is ill-defined and being set to 0.0 in labels with no predicted
samples. Use `zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
/home/austi/miniconda3/envs/msse/lib/python3.11/site-
packages/sklearn/metrics/_classification.py:1565: UndefinedMetricWarning:
Precision is ill-defined and being set to 0.0 in labels with no predicted
samples. Use `zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
/home/austi/miniconda3/envs/msse/lib/python3.11/site-
packages/sklearn/metrics/_classification.py:1565: UndefinedMetricWarning:
Precision is ill-defined and being set to 0.0 in labels with no predicted
samples. Use `zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
```