Sam_failed_life_models

May 13, 2025

0.1 Unsupervised Learning to Predict Race from Merged Dataset

```
[ ]:
```

```
[23]: #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

```
[24]: 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, 135)
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 9222 entries, 0 to 9221
Columns: 135 entries, Patient ID to Survival Months
dtypes: float64(74), int64(2), object(59)
memory usage: 9.5+ MB
```

```
C:\Users\smcca\AppData\Local\Temp\ipykernel_48032\3584519652.py:1: DtypeWarning:
Columns (5,7,12,15,16,17,18,30,65,82,83,91,92,94,95,96,97,98,99,100,101,102,103,
104,105,106,107) have mixed types. Specify dtype option on import or set
low_memory=False.
  full_data_df = pd.read_csv('final_merged.csv')
```

```
[24]:   Patient ID  Age  Surgery    Cancer Type          Cancer Type Detailed  \
0    MB-0110   45      1.0  Breast Cancer    Invasive Breast Carcinoma
1    MB-0156   60      1.0  Breast Cancer    Invasive Breast Carcinoma
2    MB-0159   51      1.0  Breast Cancer    Invasive Breast Carcinoma
```

```
3    MB-0230   41      1.0   Breast Cancer  Breast Invasive Ductal Carcinoma
4    MB-0281   52      1.0  Breast Sarcoma             Breast Angiosarcoma

  Cellularity  Chemotherapy Pam50 + Claudin-low subtype  Cohort  \
0         Low           0.0                 claudin-low     1.0
1         Low           0.0                 claudin-low     1.0
2         Low           0.0                       Basal     1.0
3         NaN           0.0                        Her2     1.0
4         NaN           0.0                 claudin-low     1.0

  ER status measured by IHC  …  Marital Status  T Stage  6th Stage  Grade  \
0                       NaN  …             NaN      NaN        NaN    NaN
1                       NaN  …             NaN      NaN        NaN    NaN
2                       NaN  …             NaN      NaN        NaN    NaN
3                       NaN  …             NaN      NaN        NaN    NaN
4                       NaN  …             NaN      NaN        NaN    NaN

   A Stage Estrogen Status Progesterone Status Regional Node Examined  \
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

  Reginol Node Positive  Survival Months
0                   NaN              NaN
1                   NaN              NaN
2                   NaN              NaN
3                   NaN              NaN
4                   NaN              NaN

[5 rows x 135 columns]
```

[3]:
```
'Radio Therapy' in full_data_df.columns
```

[3]:
```
True
```

[4]:
```
'Clinical Response, Evaluated Through Imaging ' in full_data_df.columns
```

[4]:
```
True
```

[5]:
```
full_data_df['Radio Therapy'].value_counts()
```

[5]:
```
Radio Therapy
0.0    5702
1.0    1233
Name: count, dtype: int64
```

```
[6]: full_data_df['Chemotherapy'].value_counts()
```

```
[6]: Chemotherapy
     0.0    4613
     1.0    2252
     Name: count, dtype: int64
```

```
[7]: full_data_df['T Stage'].value_counts()
```

```
[7]: T Stage
     2.0    4053
     1.0    3484
     3.0     802
     4.0     132
     0.0      24
     Name: count, dtype: int64
```

```
[8]: full_data_df['Survival Months'].value_counts()
```

```
[8]: Survival Months
     69.0     119
     63.0     116
     66.0     115
     102.0    114
     50.0     109
             …
     7.0        5
     26.0       5
     11.0       4
     2.0        4
     1.0        1
     Name: count, Length: 107, dtype: int64
```

```
[9]: full_data_df['N Stage'].value_counts()
```

```
[9]: N Stage
     1.0    4779
     2.0     874
     0.0     529
     3.0     507
     Name: count, dtype: int64
```

```
[25]: from sklearn.model_selection import train_test_split
      from sklearn.linear_model import LinearRegression
      from sklearn.metrics import mean_squared_error, r2_score
      import matplotlib.pyplot as plt
      import seaborn as sns
```

```python
import numpy as np

# Define target
target_col = 'Survival Months'

# Select numeric features
num_features = full_data_df.select_dtypes(include=[np.number])
num_features = num_features.drop(columns=[target_col])
```

[26]:
```python
# Define the threshold (60% of the total number of rows)
threshold = 0.2 * len(full_data_df)

# Drop columns where the number of NaN values is greater than the threshold
full_data_df_cleaned = full_data_df.dropna(thresh=threshold, axis=1)
```

[27]:
```python
num_features
```

[27]:
```
      Age  Surgery  Chemotherapy  Cohort   ER  Neoplasm Histologic Grade  \
0      45      1.0           0.0     1.0  0.0                        NaN
1      60      1.0           0.0     1.0  0.0                        1.0
2      51      1.0           0.0     1.0  0.0                        NaN
3      41      1.0           0.0     1.0  0.0                        NaN
4      52      1.0           0.0     1.0  0.0                        NaN
…     …        …             …       …    …                          …
9217   43      0.0           NaN     1.0  0.0                        3.0
9218   59      0.0           NaN     1.0  0.0                        2.0
9219   64      0.0           NaN     1.0  0.0                        2.0
9220   72      0.0           NaN     9.0  0.0                        3.0
9221   49      NaN           NaN     NaN  1.0                        NaN

      HER2  Histologic type  Lymph nodes examined positive  Mutation Count  \
0      0.0                0                            NaN             NaN
1      0.0                0                            NaN             NaN
2      0.0                0                            NaN             NaN
3      0.0                0                            0.0             2.0
4      0.0                0                            NaN             NaN
…      …                  …                              …               …
9217   0.0                0                            2.0             5.0
9218   0.0                0                            2.0             4.0
9219   0.0                0                            1.0             3.0
9220   0.0                0                            0.0             NaN
9221   0.0                0                            NaN             NaN

      …  \
0     …
1     …
2     …
```

```
3     …
4     …
…   …
9217  …
9218  …
9219  …
9220  …
9221  …

      Pathologic response to Neoadjuvant therapy: Pathologic stage (T) following
neoadjuvant therapy   \
0                                                   NaN
1                                                   NaN
2                                                   NaN
3                                                   NaN
4                                                   NaN
…                                                 …
9217                                                NaN
9218                                                NaN
9219                                                NaN
9220                                                NaN
9221                                                NaN

      Pathologic response to Neoadjuvant therapy:  Pathologic stage (N)
following neoadjuvant therapy  \
0                                                   NaN
1                                                   NaN
2                                                   NaN
3                                                   NaN
4                                                   NaN
…                                                 …
9217                                                NaN
9218                                                NaN
9219                                                NaN
9220                                                NaN
9221                                                NaN

      Pathologic response to Neoadjuvant therapy:  Pathologic stage (M)
following neoadjuvant therapy   \
0                                                   NaN
1                                                   NaN
2                                                   NaN
3                                                   NaN
4                                                   NaN
…                                                 …
9217                                                NaN
9218                                                NaN
```

```
9219                                              NaN
9220                                              NaN
9221                                              NaN

      Overall Near-complete Response:  Stricter Definition  \
0                                                 NaN
1                                                 NaN
2                                                 NaN
3                                                 NaN
4                                                 NaN
…                                               …
9217                                              NaN
9218                                              NaN
9219                                              NaN
9220                                              NaN
9221                                              NaN

      Overall Near-complete Response:  Looser Definition  \
0                                                 NaN
1                                                 NaN
2                                                 NaN
3                                                 NaN
4                                                 NaN
…                                               …
9217                                              NaN
9218                                              NaN
9219                                              NaN
9220                                              NaN
9221                                              NaN

      Near-complete Response (Graded Measure)  Race  N Stage  \
0                                         NaN   NaN      NaN
1                                         NaN   NaN      NaN
2                                         NaN   NaN      NaN
3                                         NaN   NaN      NaN
4                                         NaN   NaN      NaN
…                                       …   …       …
9217                                      NaN   NaN      NaN
9218                                      NaN   NaN      NaN
9219                                      NaN   NaN      NaN
9220                                      NaN   NaN      NaN
9221                                      NaN   1.0      NaN

      Regional Node Examined  Reginol Node Positive
0                        NaN                    NaN
1                        NaN                    NaN
2                        NaN                    NaN
```

```
3                        NaN                     NaN
4                        NaN                     NaN
…                      …                     …
9217                     NaN                     NaN
9218                     NaN                     NaN
9219                     NaN                     NaN
9220                     NaN                     NaN
9221                     NaN                     NaN

[9222 rows x 75 columns]
```

[ ]:

```

```

[28]:

```
len(num_features.columns)
```

[28]:

```
75
```

[29]:

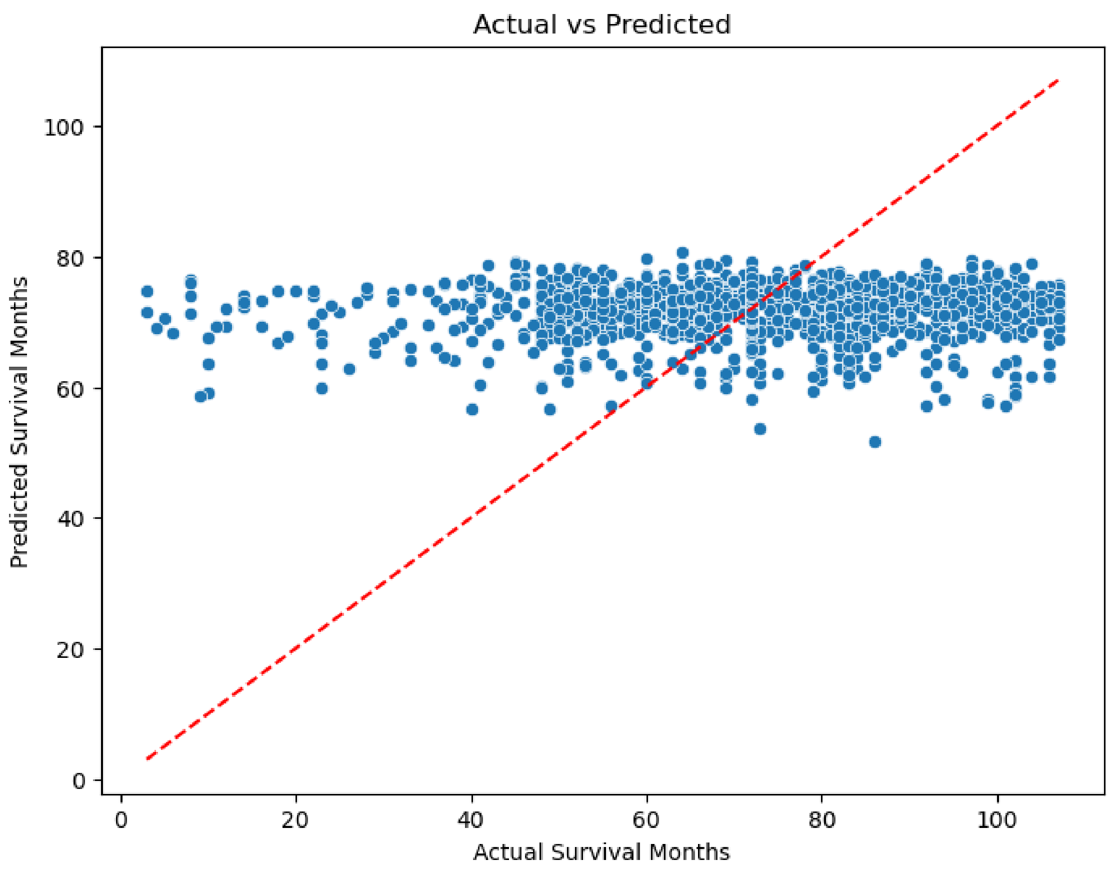
```
# Ensure num_features only contains numeric columns

from sklearn.impute import SimpleImputer
# Initialize the imputer to fill NaNs with the mean
imputer = SimpleImputer(strategy='mean')

# Ensure that num_features only contains numeric columns
num_features = full_data_df.select_dtypes(include=[np.number])

# Check the shape of num_features to make sure it has the expected number of␣
 ↪columns
print("Shape of num_features:", num_features.shape)

# List of columns in num_features
print("Columns in num_features:", num_features.columns)
print("Shape of num_features:", num_features.shape)


# Apply the imputer to your DataFrame
full_data_df_imputed = pd.DataFrame(imputer.
 ↪fit_transform(num_features),columns=num_features.columns)

# Check the result
print(full_data_df_imputed.isna().sum())  # Should show 0 NaN values
```

```
Shape of num_features: (9222, 76)
Columns in num_features: Index(['Age', 'Surgery', 'Chemotherapy', 'Cohort',
'ER',
       'Neoplasm Histologic Grade', 'HER2', 'Histologic type',
       'Lymph nodes examined positive', 'Mutation Count',
       'Nottingham prognostic index', 'Overall Survival (Months)', 'PR',
       'Radio Therapy', 'Relapse Free Status (Months)', 'Tumor Size',
       'T Stage', 'Days to MRI (From the Date of Diagnosis)', 'Manufacturer',
       'Manufacturer Model Name', 'Scan Options', 'Field Strength (Tesla)',
       'Patient Position During MRI', 'Contrast Agent',
       'Contrast Bolus Volume (mL)', 'TR (Repetition Time)', 'TE (Echo Time)',
       'Acquisition Matrix', 'Slice Thickness ', 'Rows', 'Columns',
       'Reconstruction Diameter ', 'Flip Angle ',
       'FOV Computed (Field of View) in cm ', 'Date of Birth (Days)',
       'Menopause (at diagnosis)', 'Race and Ethnicity',
       'Metastatic at Presentation (Outside of Lymph Nodes)', 'Mol Subtype',
       'Oncotype score', 'Staging(Tumor Size)# [T]',
       'Staging(Nodes)#(Nx replaced by -1)[N]',
       'Staging(Metastasis)#(Mx -replaced by -1)[M]',
       'Tumor Grade(T) (Tubule)', 'Tumor Grade(N)(Nuclear)',
       'Tumor Grade(M)(Mitotic)', 'Nottingham grade',
       'Multicentric/Multifocal', 'Contralateral Breast Involvement',
       'Lymphadenopathy or Suspicious Nodes', 'Skin/Nipple Invovlement',
       'Pec/Chest Involvement', 'Adjuvant Radiation Therapy',
       'Clinical Response, Evaluated Through Imaging ',
       'Pathologic Response to Neoadjuvant Therapy', 'Recurrence event(s)',
       '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',
       'Adjuvant Chemotherapy', 'Neoadjuvant Endocrine Therapy Medications ',
       'Adjuvant Endocrine Therapy Medications ', 'Known Ovarian Status ',
       'Therapeutic or Prophylactic Oophorectomy as part of Endocrine Therapy ',
       'Neoadjuvant Anti-Her2 Neu Therapy', 'Adjuvant Anti-Her2 Neu Therapy ',
       'Received Neoadjuvant Therapy or Not',
       'Pathologic response to Neoadjuvant therapy: Pathologic stage (T)
following neoadjuvant therapy ',
       'Pathologic response to Neoadjuvant therapy:  Pathologic stage (N)
following neoadjuvant therapy',
       'Pathologic response to Neoadjuvant therapy:  Pathologic stage (M)
following neoadjuvant therapy ',
       'Overall Near-complete Response:  Stricter Definition',
       'Overall Near-complete Response:  Looser Definition',
       'Near-complete Response (Graded Measure)', 'Race', 'N Stage',
       'Regional Node Examined', 'Reginol Node Positive', 'Survival Months'],
      dtype='object')
Shape of num_features: (9222, 76)
Age                        0
Surgery                    0
Chemotherapy               0
Cohort                     0
ER                         0
                          ..
Race                       0
```

```
N Stage                   0
Regional Node Examined    0
Reginol Node Positive     0
Survival Months           0
Length: 76, dtype: int64
```

[31]:
```
target_col = 'Survival Months'

# Define features and target from the imputed DataFrame
X = full_data_df_imputed  # Features from imputed data
y = full_data_df_imputed[target_col]  # Target from imputed data

# Drop the target column from X (features)
X = X.drop(columns=[target_col])

# Drop NaNs from features and align target
X = X.dropna()
y = y.loc[X.index]

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

# Fit linear regression model
model = LinearRegression()
model.fit(X_train, y_train)

# Predict
y_pred = model.predict(X_test)

# Evaluate
print("Mean Squared Error:", mean_squared_error(y_test, y_pred))
print("R^2 Score:", r2_score(y_test, y_pred))

# Optional: plot predicted vs actual
plt.figure(figsize=(8, 6))
sns.scatterplot(x=y_test, y=y_pred)
plt.xlabel("Actual Survival Months")
plt.ylabel("Predicted Survival Months")
plt.title("Actual vs Predicted")
plt.plot([y_test.min(), y_test.max()], [y_test.min(), y_test.max()],␣
 ↪color='red', linestyle='--')
plt.show()
```

```
Mean Squared Error: 307.16179089356694
R^2 Score: -0.018432886493055856
```



[20]:
```python
import pandas as pd
from sklearn.linear_model import LinearRegression
from sklearn.model_selection import train_test_split
from sklearn.metrics import mean_squared_error, r2_score

model = LinearRegression()
model.fit(X_train, y_train)

# Prediction
y_pred = model.predict(X_test)

# Evaluation
print("Mean Squared Error:", mean_squared_error(y_test, y_pred))
print("R^2 Score:", r2_score(y_test, y_pred))
print("Intercept:", model.intercept_)
print("Coefficient:", model.coef_[0])
```

```
---------------------------------------------------------------------------
ValueError                                Traceback (most recent call last)
~\AppData\Local\Temp\ipykernel_19180\1385663674.py in ?()
```

```
      3 from sklearn.model_selection import train_test_split
      4 from sklearn.metrics import mean_squared_error, r2_score
      5 
      6 model = LinearRegression()
----> 7 model.fit(X_train, y_train)
      8 
      9 # Prediction
     10 y_pred = model.predict(X_test)

c:\Users\smcca\anaconda3\Lib\site-packages\sklearn\base.py in ?(estimator, *args, **kwargs)
   1469                 skip_parameter_validation=(
   1470                     prefer_skip_nested_validation or global_skip_validation
   1471                 )
   1472             ):
-> 1473                 return fit_method(estimator, *args, **kwargs)

c:\Users\smcca\anaconda3\Lib\site-packages\sklearn\linear_model\_base.py in ?(self, X, y, sample_weight)
    605         n_jobs_ = self.n_jobs
    606 
    607         accept_sparse = False if self.positive else ["csr", "csc", "coo
    608 
--> 609         X, y = self._validate_data(
    610             X,
    611             y,
    612             accept_sparse=accept_sparse,

c:\Users\smcca\anaconda3\Lib\site-packages\sklearn\base.py in ?(self, X, y, reset, validate_separately, cast_to_ndarray, **check_params)
    646                 if "estimator" not in check_y_params:
    647                     check_y_params = {**default_check_params, **check_y_params}
    648                 y = check_array(y, input_name="y", **check_y_params)
    649             else:
--> 650                 X, y = check_X_y(X, y, **check_params)
    651             out = X, y
    652 
    653         if not no_val_X and check_params.get("ensure_2d", True):

c:\Users\smcca\anaconda3\Lib\site-packages\sklearn\utils\validation.py in ?(X, y, accept_sparse, accept_large_sparse, dtype, order, copy, force_writeable, force_all_finite, ensure_2d, allow_nd, multi_output, ensure_min_samples, ensure_min_features, y_numeric, estimator)
   1297         raise ValueError(
   1298             f"{estimator_name} requires y to be passed, but the target is None"
   1299         )
   1300 
-> 1301     X = check_array(
   1302         X,
   1303         accept_sparse=accept_sparse,
   1304         accept_large_sparse=accept_large_sparse,

c:\Users\smcca\anaconda3\Lib\site-packages\sklearn\utils\validation.py in ?
 ↪(array, accept_sparse, accept_large_sparse, dtype, order, copy,␣
 ↪force_writeable, force_all_finite, ensure_2d, allow_nd, ensure_min_samples,␣
 ↪ensure_min_features, estimator, input_name)
   1009                     )
   1010                 array = xp.astype(array, dtype, copy=False)
   1011             else:
   1012                 array = _asarray_with_order(array, order=order,␣
 ↪dtype=dtype, xp=xp)
-> 1013         except ComplexWarning as complex_warning:
   1014             raise ValueError(
   1015                 "Complex data not supported\n{}\n".format(array)
   1016             ) from complex_warning

c:\Users\smcca\anaconda3\Lib\site-packages\sklearn\utils\_array_api.py in ?
 ↪(array, dtype, order, copy, xp, device)
    747         # Use NumPy API to support order
    748         if copy is True:
    749             array = numpy.array(array, order=order, dtype=dtype)
    750         else:
--> 751             array = numpy.asarray(array, order=order, dtype=dtype)
    752 
    753         # At this point array is a NumPy ndarray. We convert it to an␣
 ↪array
    754         # container that is consistent with the input's namespace.

c:\Users\smcca\anaconda3\Lib\site-packages\pandas\core\generic.py in ?(self,␣
 ↪dtype, copy)
   2149     def __array__(
   2150         self, dtype: npt.DTypeLike | None = None, copy: bool_t | None =
 ↪None
   2151     ) -> np.ndarray:
   2152         values = self._values
-> 2153         arr = np.asarray(values, dtype=dtype)
   2154         if (
   2155             astype_is_view(values.dtype, arr.dtype)
   2156             and using_copy_on_write()

ValueError: could not convert string to float: 'Positive'
```

0.3 Data Cleaning

[15]:
```
#Dropping any duplicate rows
full_data_df.drop_duplicates(inplace=True)

print('Radio Therapy' in full_data_df.columns)

# Drop features with a lot of missing values
missing__ratio = full_data_df.isnull().mean()
columns_to_drop = missing__ratio[missing__ratio > 0.9].index
full_data_df.drop(columns=columns_to_drop, inplace=True)


print('Radio Therapy' in full_data_df.columns)
```

```
True
True
```

[16]:
```
# 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:  (9221,
135)
```

[ ]:
```

```

[17]:
```
#inspecting the race column
full_data_df['Overall Near-complete Response:  Stricter Definition'].
  ↪value_counts(dropna=False)

#Drop rows with missing values in Race column

full_data_df = full_data_df.dropna(subset=['Overall Near-complete Response: ␣
  ↪Stricter Definition'])

#Drop rows where race is = 0
full_data_df = full_data_df[full_data_df['Overall Near-complete Response: ␣
  ↪Stricter Definition'] != 0]

full_data_df['Overall Near-complete Response:  Stricter Definition'].
  ↪value_counts()

full_data_df.drop('Clinical Response, Evaluated Through Imaging ',axis=1)

full_data_df.drop('Pathologic Response to Neoadjuvant Therapy',axis=1)
full_data_df.drop('Pathologic Response to Neoadjuvant Therapy',axis=1)

full_data_df.drop('Overall Near-complete Response:  Looser Definition',axis=1)

full_data_df.drop('Near-complete Response (Graded Measure)',axis=1)



full_data_df['Radio Therapy']
```

```
[17]: 2739    0.0
      3731    0.0
      3737    0.0
      3738    0.0
      3739    0.0
             …
      5627    0.0
      6816    1.0
      6817    1.0
      6818    1.0
      6934    1.0
      Name: Radio Therapy, Length: 572, dtype: float64
```

```
[ ]: 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

     # Define target
     target_col = 'Overall Near-complete Response:  Stricter Definition'



     # Define features and target
     X = full_data_df[['Radio Therapy','Chemotherapy', 'Tumor Size','Age','T␣
      ↪Stage','Survival Months']]
     y = full_data_df[target_col]

     # Drop NaNs from features and align target
     X = X.dropna()
     y = y.loc[X.index]

     # 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)]

# Re-align X and y again just to be sure
X = X.loc[y.index]

# 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
)

# Ready to test different subset sizes
```

[19]:
```
X_train
```

[19]:
```
      Radio Therapy  Chemotherapy  Tumor Size  Age  T Stage  Survival Months
4055            0.0           1.0        17.0   49      1.0             50.0
3739            0.0           1.0        10.0   60      1.0             51.0
4249            0.0           1.0        16.0   40      1.0             66.0
4199            0.0           1.0        10.0   47      1.0             85.0
5573            0.0           1.0        69.0   54      3.0             74.0
…               …             …           …  …    …              …
4216            0.0           1.0        16.0   47      1.0             76.0
4298            0.0           1.0        20.0   59      1.0             99.0
4449            0.0           1.0        40.0   51      2.0             67.0
4749            0.0           1.0        34.0   59      2.0             81.0
4761            0.0           1.0        22.0   53      2.0             61.0

[402 rows x 6 columns]
```

[27]:
```
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

# Define target
target_col = 'Overall Near-complete Response:  Stricter Definition'

# Define features and target
X = full_data_df[['Radio Therapy','Chemotherapy', 'Tumor Size','Age','T␣
↪Stage','Survival Months']]
y = full_data_df[target_col]

# Drop NaNs from features and align target
X = X.dropna()
y = y.loc[X.index]
```

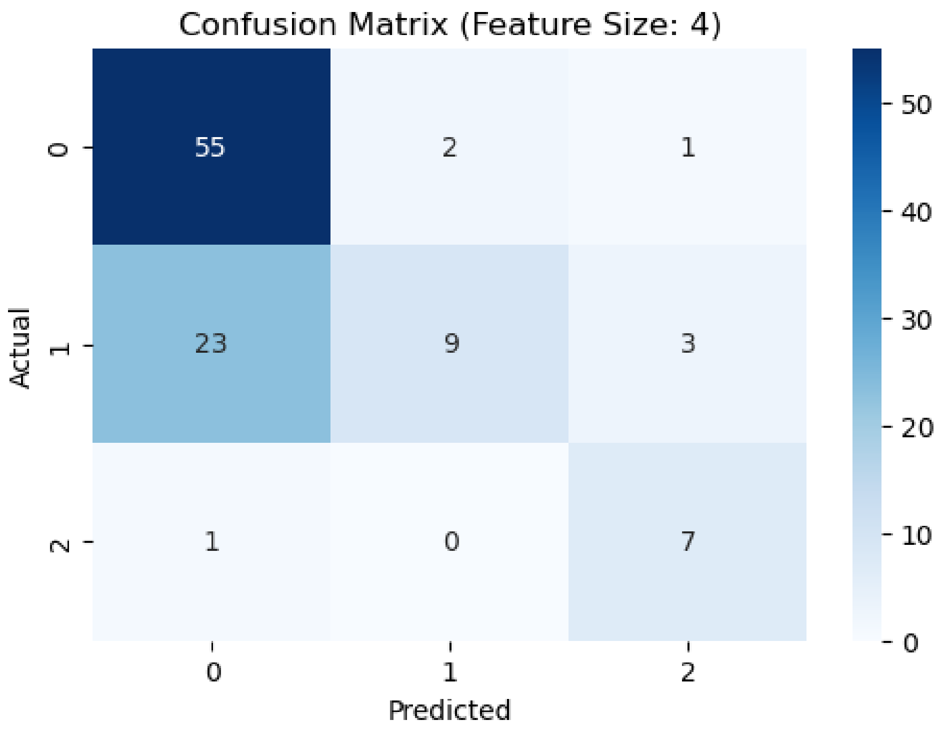
```
# Drop classes with fewer than 2 samples
class_counts = y.value_counts()
valid_classes = class_counts[class_counts >= 2].index
X = X[y.isin(valid_classes)]
y = y[y.isin(valid_classes)]

# Re-align X and y again just to be sure
X = X.loc[y.index]

# 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
)

# Ready to test different subset sizes
```

[10]:
```
results = {}
```

[26]:
```
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

selected_features = ['Radio Therapy','Chemotherapy','Age','T Stage']

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)

size = 4

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: 4
Selected Features: ['Radio Therapy', 'Chemotherapy', 'Age', 'T Stage']
Accuracy: 0.7030
```



[ ]:

```

```

0.4 EDA

[12]:
```
full_data_df.describe()
```

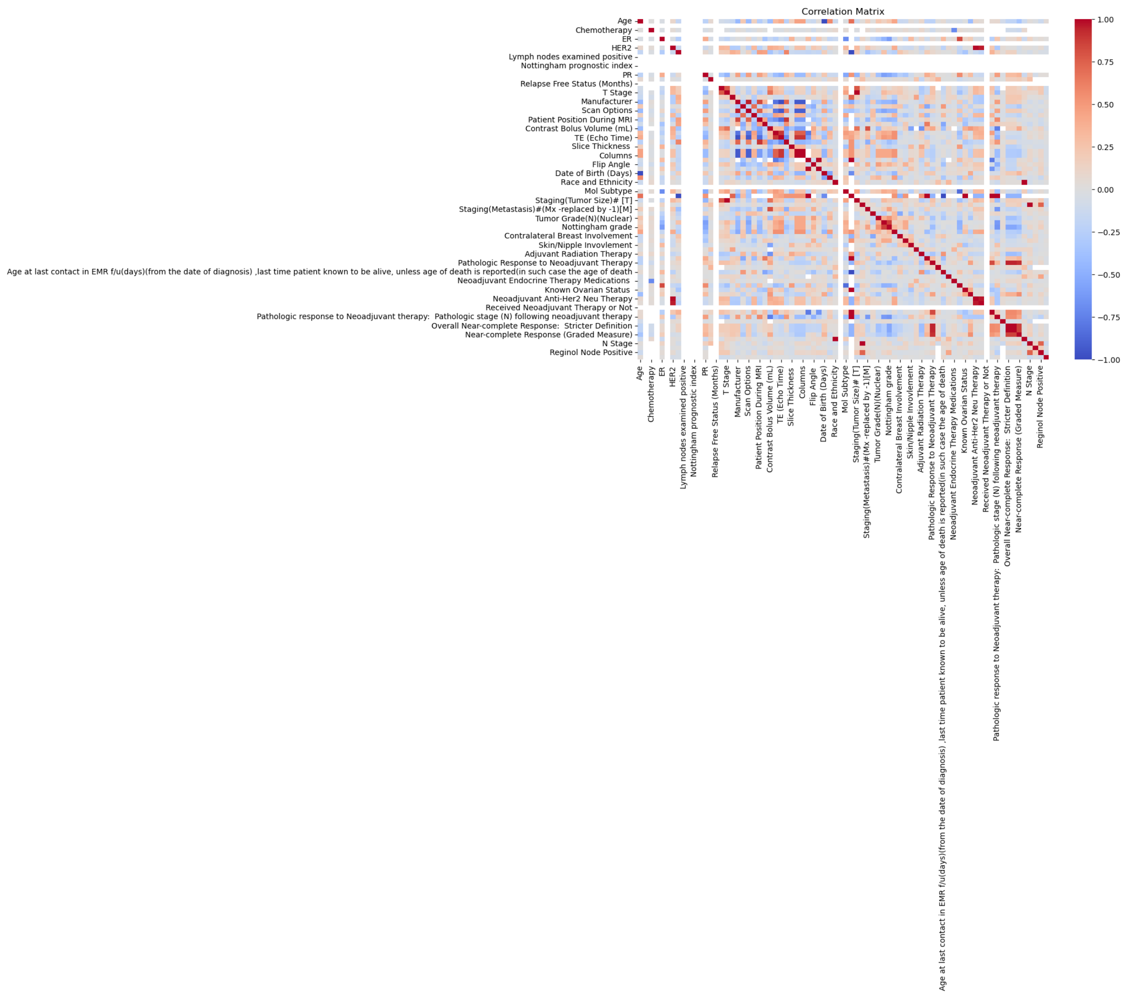
[12]:
```
              Age  Surgery  Chemotherapy  Cohort          ER  \
count  572.000000     27.0    572.000000     0.0  572.000000
mean    50.846154      0.0      0.998252     NaN    0.603147
std      7.900039      0.0      0.041812     NaN    0.489673
min     21.000000      0.0      0.000000     NaN    0.000000
25%     47.000000      0.0      1.000000     NaN    0.000000
```

```
50%     53.000000      0.0      1.000000     NaN    1.000000
75%     58.000000      0.0      1.000000     NaN    1.000000
max     73.000000      0.0      1.000000     NaN    1.000000

       Neoplasm Histologic Grade        HER2  Histologic type  \
count                        0.0  572.000000       572.000000
mean                         NaN    0.477273         0.669580
std                          NaN    0.499920         0.496133
min                          NaN    0.000000         0.000000
25%                          NaN    0.000000         0.000000
50%                          NaN    0.000000         1.000000
75%                          NaN    1.000000         1.000000
max                          NaN    1.000000         2.000000

       Lymph nodes examined positive  Mutation Count  …  \
count                            0.0             0.0  …
mean                             NaN             NaN  …
std                              NaN             NaN  …
min                              NaN             NaN  …
25%                              NaN             NaN  …
50%                              NaN             NaN  …
75%                              NaN             NaN  …
max                              NaN             NaN  …

       Pathologic response to Neoadjuvant therapy:  Pathologic stage (N)
following neoadjuvant therapy  \
count                                         378.000000
mean                                            0.142857
std                                             0.515761
min                                            -1.000000
25%                                             0.000000
50%                                             0.000000
75%                                             0.000000
max                                             1.000000

       Pathologic response to Neoadjuvant therapy:  Pathologic stage (M)
following neoadjuvant therapy   \
count                                         376.000000
mean                                           -0.997340
std                                             0.051571
min                                            -1.000000
25%                                            -1.000000
50%                                            -1.000000
75%                                            -1.000000
max                                             0.000000

       Overall Near-complete Response:  Stricter Definition  \
count                                          572.000000
mean                                             1.503497
std                                              0.649657
min                                              1.000000
25%                                              1.000000
50%                                              1.000000
75%                                              2.000000
max                                              3.000000

       Overall Near-complete Response:  Looser Definition  \
count                                          572.000000
mean                                             1.503497
std                                              0.649657
min                                              1.000000
25%                                              1.000000
50%                                              1.000000
75%                                              2.000000
max                                              3.000000

       Near-complete Response (Graded Measure)        Race     N Stage  \
count                               572.000000  572.000000  568.000000
mean                                  3.524476    1.152098    1.010563
std                                   5.058789    0.631579    0.432247
min                                   1.000000    0.000000    0.000000
25%                                   1.000000    1.000000    1.000000
50%                                   1.000000    1.000000    1.000000
75%                                   4.000000    1.000000    1.000000
max                                  19.000000    7.000000    3.000000

       Regional Node Examined  Reginol Node Positive  Survival Months
count              503.000000             503.000000       503.000000
mean                12.789264               2.075547        71.854871
std                  8.106815               2.453199        22.094888
min                  1.000000               1.000000         4.000000
25%                  7.000000               1.000000        58.000000
50%                 12.000000               1.000000        73.000000
75%                 18.000000               2.000000        89.000000
max                 49.000000              26.000000       107.000000

[8 rows x 76 columns]
```

[ ]:

```
[13]: #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

```
[14]: from sklearn.preprocessing import StandardScaler
import pandas as pd
import numpy as np

# Define target
target_col = 'Overall Near-complete Response:  Stricter Definition'

# Drop columns with too many NaNs (>80%)
full_data_df = full_data_df.loc[:, full_data_df.isnull().mean() < 0.8]
```

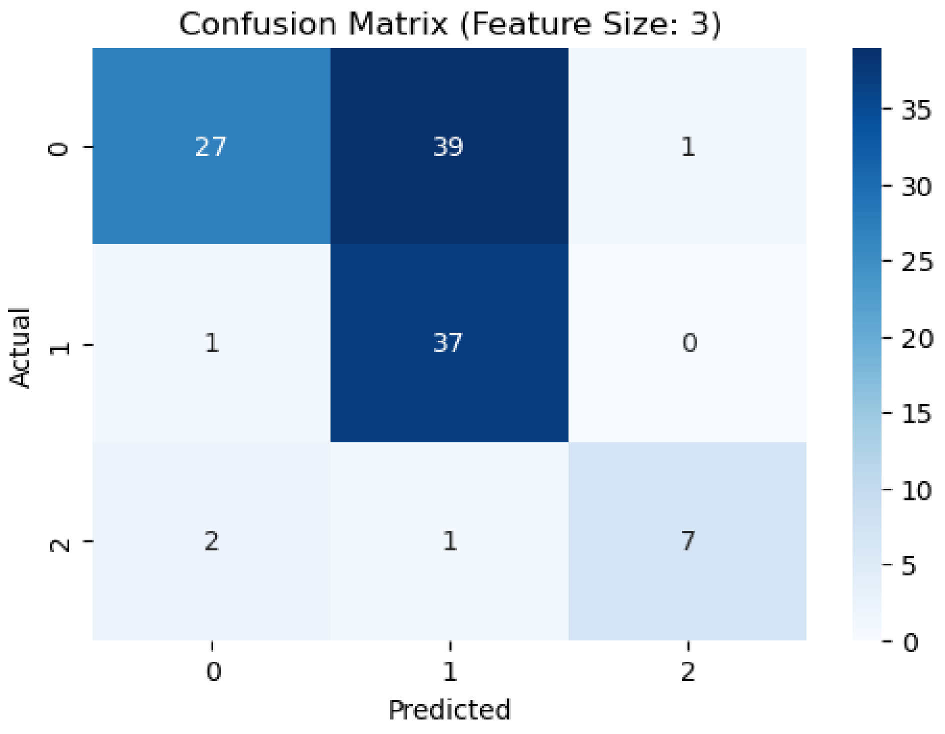
```
# Keep only numeric columns and exclude the target
numeric_cols = full_data_df.select_dtypes(include=[np.number]).columns
features = numeric_cols.drop(target_col, errors='ignore')  # in case target_col␣
↪isn't numeric

# Strategy 1: Drop rows with any NaNs
df_dropped = full_data_df[features.union([target_col])].dropna()

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

# Scale features only if rows exist
scaler = StandardScaler()

if not df_dropped.empty:
    df_dropped[features] = scaler.fit_transform(df_dropped[features])
else:
    print("No rows left in df_dropped after dropna().")

if not df_filled.empty:
    df_filled[features] = scaler.fit_transform(df_filled[features])
else:
    print("No rows left in df_filled after fillna().")

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

```
No rows left in df_dropped after dropna().
 Dropped dataset shape: (0, 67)
 Filled dataset shape: (572, 67)
```

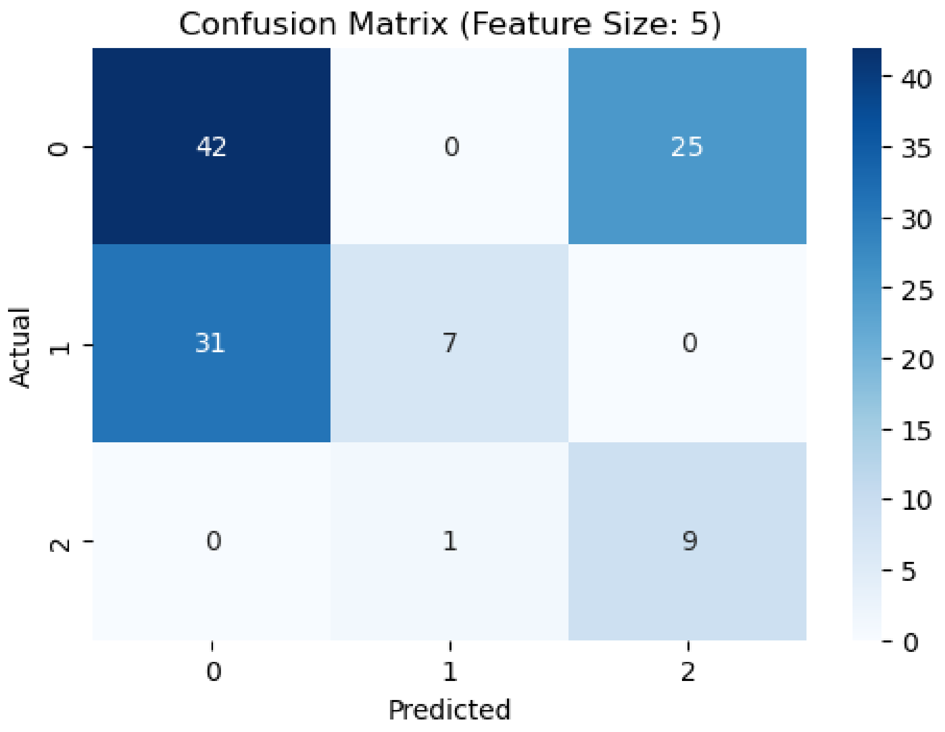
[15]:
```
from sklearn.model_selection import train_test_split
from sklearn.naive_bayes import GaussianNB
from sklearn.metrics import accuracy_score, confusion_matrix
import matplotlib.pyplot as plt
import seaborn as sns
import random


# 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
```

```python
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 = [3,5, 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()
```

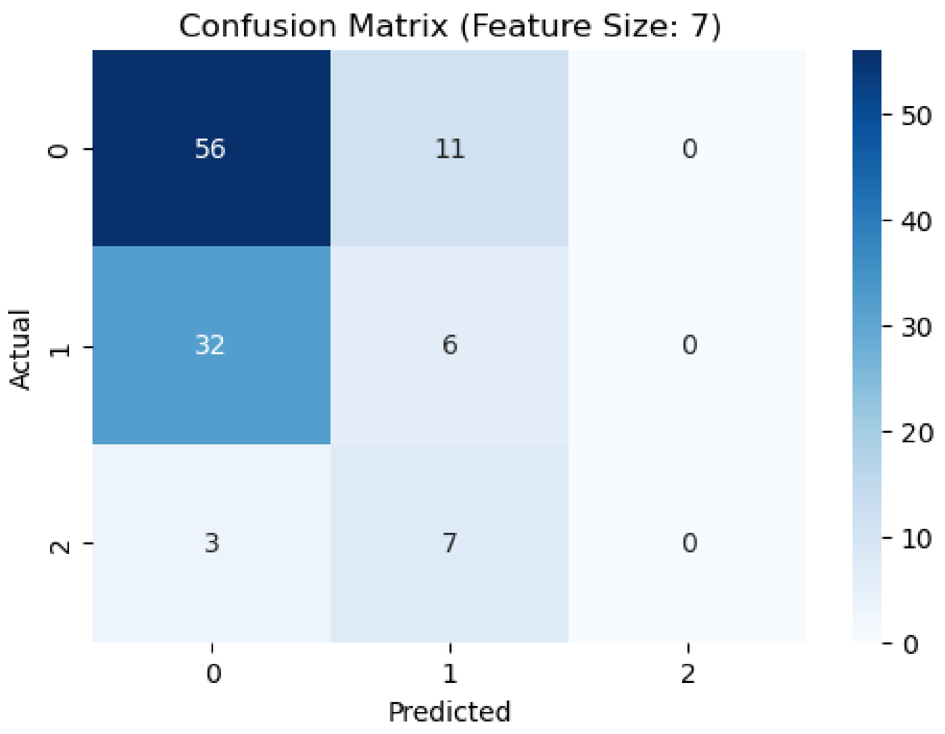
```
Feature Subset Size: 3
Selected Features: ['Reginol Node Positive', 'Contrast Bolus Volume (mL)',
'Known Ovarian Status ']
Accuracy: 0.6174
```



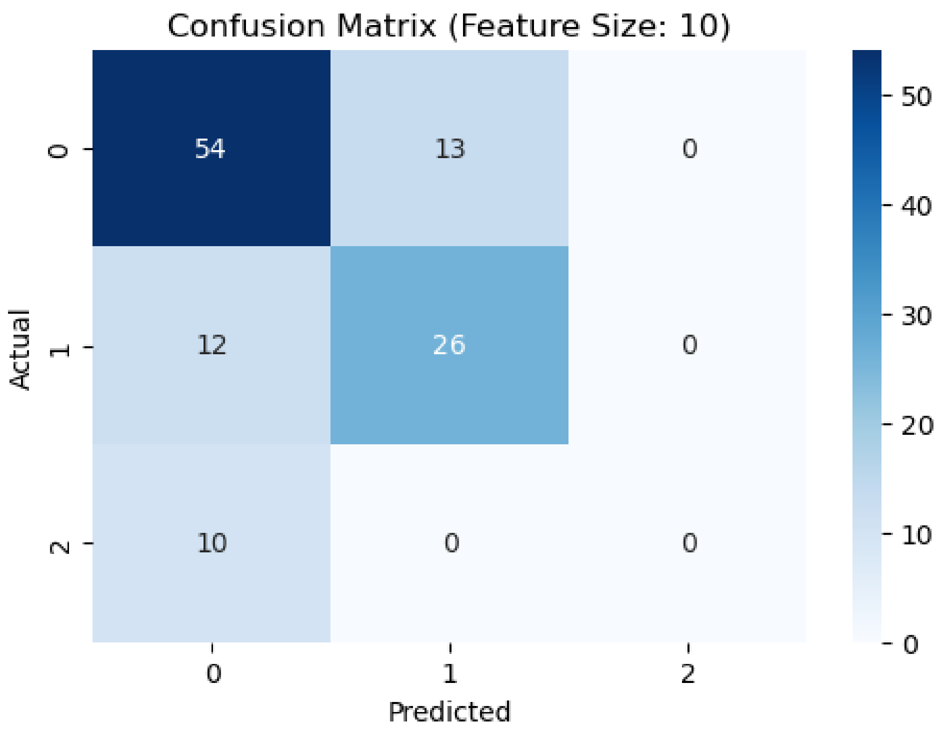
```
Feature Subset Size: 5
Selected Features: ['Recurrence event(s)', 'Adjuvant Radiation Therapy',
'Pathologic response to Neoadjuvant therapy: Pathologic stage (T) following
neoadjuvant therapy ', 'Mol Subtype', 'Race']
Accuracy: 0.5043
```



```
Feature Subset Size: 7
Selected Features: ['Pec/Chest Involvement', 'Skin/Nipple Invovlement',
'Columns', 'Chemotherapy', 'Race', 'Slice Thickness ', 'Manufacturer']
Accuracy: 0.5391
```



```
Feature Subset Size: 10
Selected Features: ['Survival Months', 'Neoadjuvant Anti-Her2 Neu Therapy',
'Pathologic response to Neoadjuvant therapy:  Pathologic stage (N) following
neoadjuvant therapy', 'Reconstruction Diameter ', 'Staging(Tumor Size)# [T]',
'Scan Options', 'Tumor Grade(T) (Tubule)', 'Adjuvant Endocrine Therapy
Medications ', 'Days to MRI (From the Date of Diagnosis)', 'Chemotherapy']
Accuracy: 0.6957
```



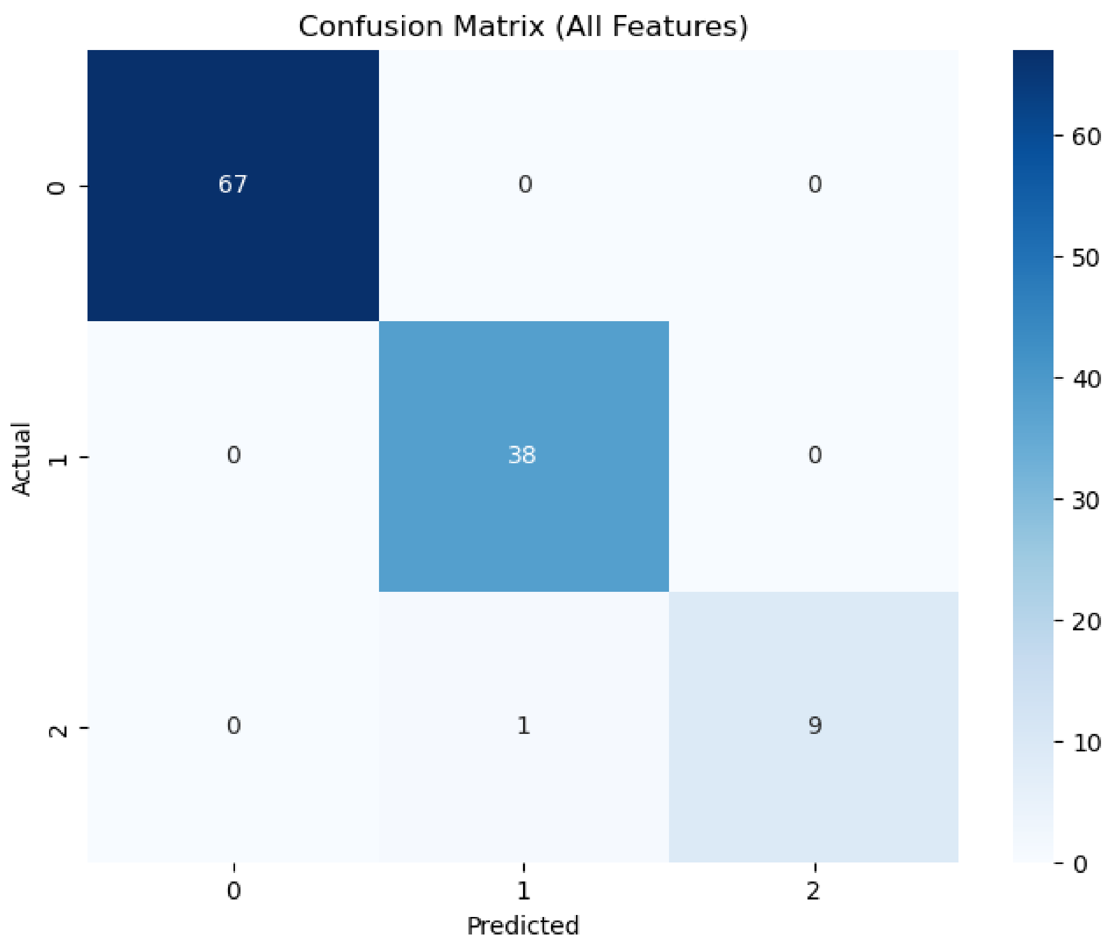
[ ]:

[ ]:

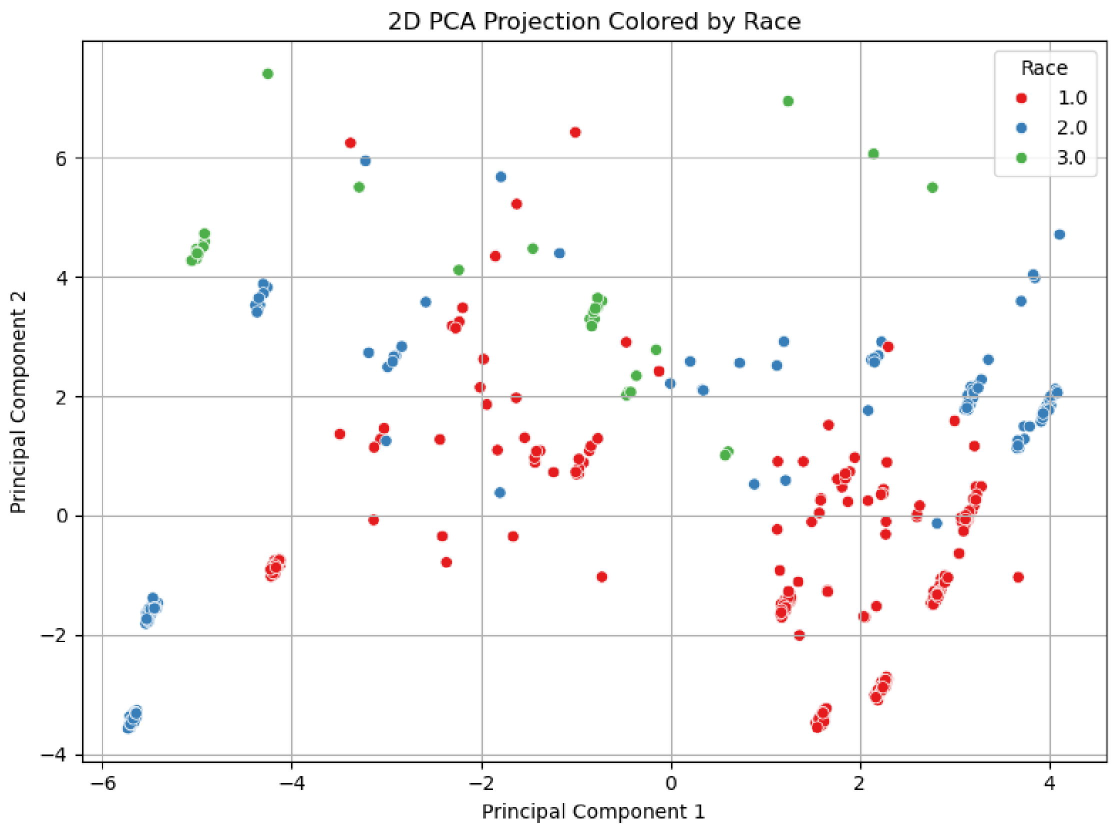
[16]:
```
# Baseline model
from sklearn.naive_bayes import GaussianNB
from sklearn.metrics import accuracy_score, classification_report,␣
 ↪confusion_matrix
import seaborn as sns
import matplotlib.pyplot as plt

# 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
```

```python
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): 0.9913
Classification Report:
               precision    recall  f1-score   support

         1.0       1.00      1.00      1.00        67
         2.0       0.97      1.00      0.99        38
         3.0       1.00      0.90      0.95        10

    accuracy                           0.99       115
   macro avg       0.99      0.97      0.98       115
weighted avg       0.99      0.99      0.99       115
```



[17]:
```python
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()
```

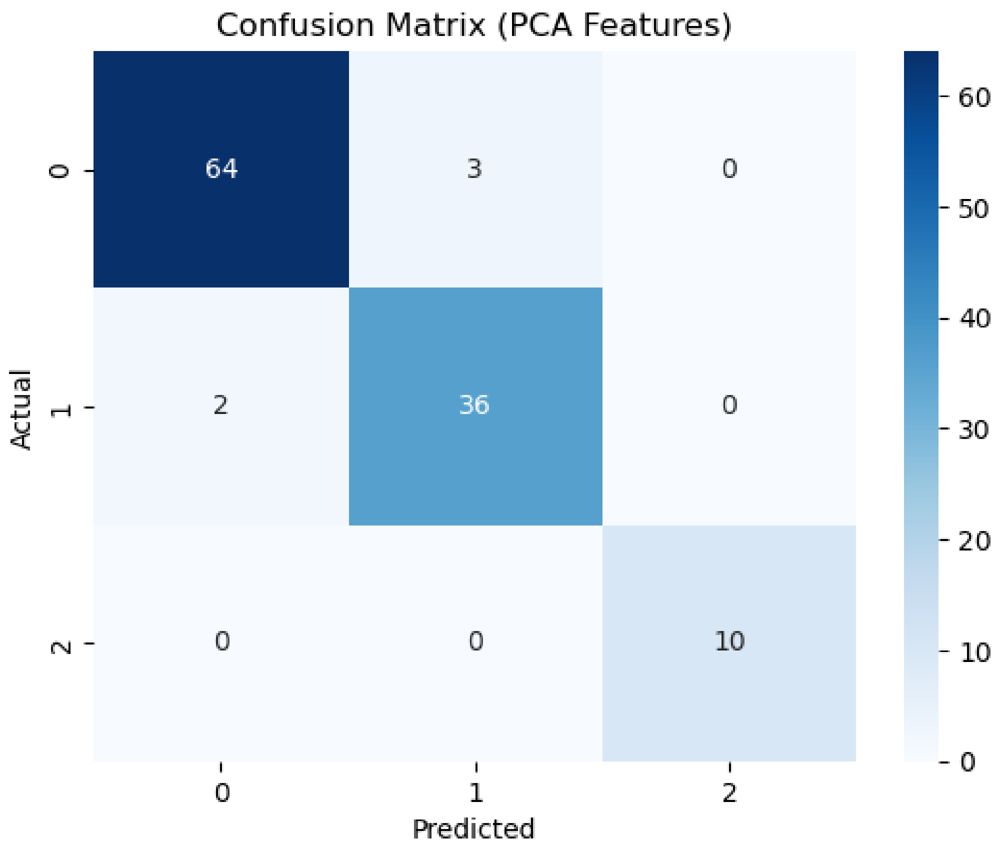


0.6 Evaluation

[18]:
```python
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: 23
Naive Bayes Accuracy (PCA Features): 0.9565
```



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

         1.0       0.97      0.96      0.96        67
         2.0       0.92      0.95      0.94        38
         3.0       1.00      1.00      1.00        10

    accuracy                           0.96       115
   macro avg       0.96      0.97      0.97       115
weighted avg       0.96      0.96      0.96       115
```