CISC_5800_Final_Project_Sameera_Aluri

May 15, 2025

[123]:
```python
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt

# LOAD DATASET
df = pd.read_csv("METABRIC_RNA_Mutation.csv")
df.head()
```

```
/var/folders/1m/mr1tf7dx7_q8p8wrx2fq7dyr0000gn/T/ipykernel_40480/3965884430.py:6
: DtypeWarning: Columns (678,688,690,692) have mixed types. Specify dtype option
on import or set low_memory=False.
  df = pd.read_csv("METABRIC_RNA_Mutation.csv")
```

[123]:
```
   patient_id  age_at_diagnosis type_of_breast_surgery    cancer_type  \
0           0             75.65             MASTECTOMY  Breast Cancer
1           2             43.19      BREAST CONSERVING  Breast Cancer
2           5             48.87             MASTECTOMY  Breast Cancer
3           6             47.68             MASTECTOMY  Breast Cancer
4           8             76.97             MASTECTOMY  Breast Cancer

                       cancer_type_detailed cellularity  chemotherapy  \
0           Breast Invasive Ductal Carcinoma         NaN             0
1           Breast Invasive Ductal Carcinoma        High             0
2           Breast Invasive Ductal Carcinoma        High             1
3  Breast Mixed Ductal and Lobular Carcinoma    Moderate             1
4  Breast Mixed Ductal and Lobular Carcinoma        High             1

  pam50_+_claudin-low_subtype  cohort er_status_measured_by_ihc  … mtap_mut  \
0                 claudin-low     1.0                   Positve  …        0
1                        LumA     1.0                   Positve  …        0
2                        LumB     1.0                   Positve  …        0
3                        LumB     1.0                   Positve  …        0
4                        LumB     1.0                   Positve  …        0

  ppp2cb_mut smarcd1_mut nras_mut ndfip1_mut  hras_mut prps2_mut smarcb1_mut  \
0          0           0        0          0         0         0           0
1          0           0        0          0         0         0           0
2          0           0        0          0         0         0           0
```

```
3            0            0         0          0          0          0            0
4            0            0         0          0          0          0            0

  stmn2_mut  siah1_mut
0         0          0
1         0          0
2         0          0
3         0          0
4         0          0

[5 rows x 693 columns]
```

[124]:

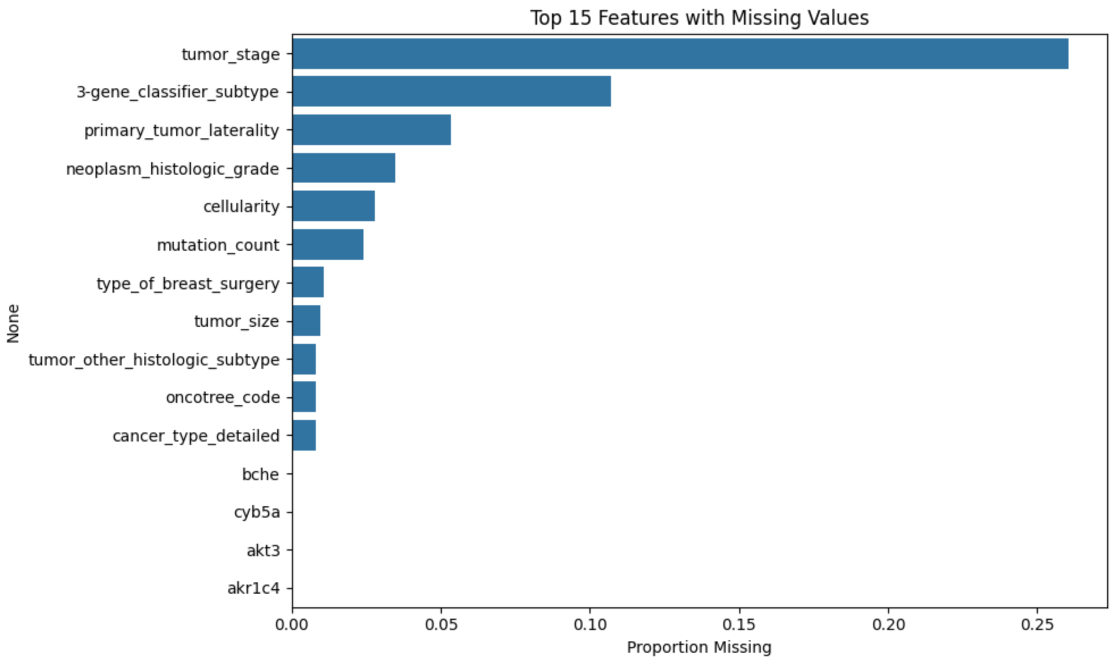
```python
# DATA CLEANING

# Fix typo: "Positve" to "Positive"
df['er_status_measured_by_ihc'] = df['er_status_measured_by_ihc'].
 ↪replace({'Positve': 'Positive'})

# Convert to binary (1 = Positive, 0 = Negative)
df['er_status_binary'] = df['er_status_measured_by_ihc'].map({'Positive': 1,␣
 ↪'Negative': 0})

# Drop rows with missing ER status
df = df.dropna(subset=['er_status_binary'])

# Drop leaky columns from the main df (before defining X)
leaky_columns = ['chemotherapy', 'hormone_therapy', 'death_from_cancer']
df = df.drop(columns=[col for col in leaky_columns if col in df.columns])

# Drop ID and original string target
if 'patient_id' in df.columns:
    df = df.drop(columns=['patient_id'])
df = df.drop(columns=['er_status_measured_by_ihc'])

# Define X and y
X = df.drop(columns=['er_status_binary'])
y = df['er_status_binary']

# Identify categorical features
categorical_features = X.select_dtypes(include=['object']).columns.tolist()

# Fix all categorical columns to be strings
X[categorical_features] = X[categorical_features].astype(str)

# % of missing values
missing_percent = X.isnull().mean().sort_values(ascending=False)
```

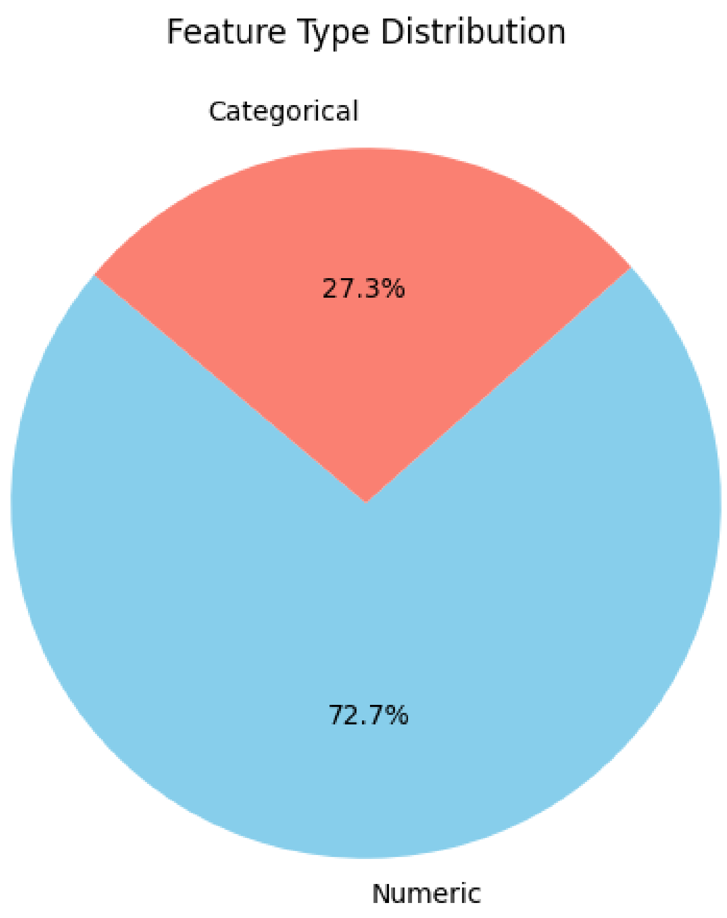
```
# Top 15 most missing columns
missing_percent.head(15)
```

[124]:
```
tumor_stage                    0.260406
neoplasm_histologic_grade      0.034685
mutation_count                 0.024013
tumor_size                     0.009605
cdk8                           0.000000
ackr3                          0.000000
akr1c1                         0.000000
akr1c2                         0.000000
akr1c3                         0.000000
akr1c4                         0.000000
akt3                           0.000000
ar                             0.000000
bche                           0.000000
age_at_diagnosis               0.000000
cyb5a                          0.000000
dtype: float64
```

[159]:
```
import seaborn as sns
import matplotlib.pyplot as plt

# Bar plot of top 15 missing value columns
missing_percent = X.isnull().mean().sort_values(ascending=False)[:15]
plt.figure(figsize=(10, 6))
sns.barplot(x=missing_percent.values, y=missing_percent.index)
plt.title("Top 15 Features with Missing Values")
plt.xlabel("Proportion Missing")
plt.tight_layout()

types = ['Numeric', 'Categorical']
counts = [len(numeric_features), len(categorical_features)]
plt.figure(figsize=(6, 6))
plt.pie(counts, labels=types, autopct='%1.1f%%', startangle=140,␣
  ↪colors=["skyblue", "salmon"])
plt.title("Feature Type Distribution")
```

[159]:
```
Text(0.5, 1.0, 'Feature Type Distribution')
```


Top 15 Features with Missing Values
tumor_stage
3-gene_classifier_subtype
primary_tumor_laterality
neoplasm_histologic_grade
cellularity
mutation_count
type_of_breast_surgery
tumor_size
tumor_other_histologic_subtype
oncotree_code
cancer_type_detailed
bche
cyb5a
akt3
akr1c4
None
0.00
0.05
0.10
0.15
0.20
0.25
Proportion Missing



[126]:
```
# DATA PREPROCESSING

from sklearn.pipeline import Pipeline
from sklearn.compose import ColumnTransformer
from sklearn.impute import SimpleImputer
from sklearn.preprocessing import StandardScaler, OneHotEncoder

# Define numeric and categorical feature lists
numeric_features = X.select_dtypes(include=['int64', 'float64']).columns.
 ↪tolist()
categorical_features = X.select_dtypes(include=['object']).columns.tolist()


from sklearn.feature_selection import SelectKBest, f_classif

numeric_transformer = Pipeline(steps=[
    ('imputer', SimpleImputer(strategy='median')),
    ('scaler', StandardScaler()),
    ('select', SelectKBest(score_func=f_classif, k=500))  # Choose top 500␣
  ↪features
])



# Categorical pipeline - impute most frequent, then one-hot encode
categorical_transformer = Pipeline(steps=[
    ('imputer', SimpleImputer(strategy='most_frequent')),
    ('encoder', OneHotEncoder(handle_unknown='ignore', sparse_output=False))
])

# Combine both into a full preprocessor
preprocessor = ColumnTransformer(transformers=[
    ('num', numeric_transformer, numeric_features),
    ('cat', categorical_transformer, categorical_features)
])

# Run and preprocesser and confirm results
X_transformed = preprocessor.fit_transform(X, y)
print("Original shape:", X.shape)
print("Transformed shape:", X_transformed.shape)
print("Any NaNs in transformed data?", np.isnan(X_transformed).any())
```

```
Original shape: (1874, 688)
Transformed shape: (1874, 8375)
Any NaNs in transformed data? False
```

[127]:
```
# MODEL IMPLEMENTATION

from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import classification_report, roc_auc_score
from sklearn.model_selection import cross_val_score

def evaluate(model, X_test, y_test, name="Model"):
    y_pred = model.predict(X_test)
    y_prob = model.predict_proba(X_test)[:, 1]
    print(f"\n{name} Classification Report:\n", classification_report(y_test,␣
  ↪y_pred))
    print(f"{name} AUC: {roc_auc_score(y_test, y_prob):.4f}")



# Split the data 80/20, stratified to maintain class balance
X_train, X_test, y_train, y_test = train_test_split(
    X, y,
    test_size=0.2,
    stratify=y,
    random_state=42
)

# Full pipeline with preprocessor and logistic regression
logreg_model = Pipeline(steps=[
    ('preprocessing', preprocessor),
    ('classifier', LogisticRegression(class_weight='balanced', max_iter=1000))
])
# 5-fold cross-validation on the logistic regression model
cv_scores = cross_val_score(logreg_model, X, y, cv=5, scoring='roc_auc')

print("Logistic Regression CV AUC Scores:", cv_scores)
print("Mean CV AUC:", cv_scores.mean())

from sklearn.model_selection import GridSearchCV

# Define hyperparameter grid
param_grid = {
    'classifier__C': [0.01, 0.1, 1, 10, 100],
    'classifier__penalty': ['l2']  # l1 not supported by default solver
}

# Wrap with GridSearchCV
grid = GridSearchCV(logreg_model, param_grid, cv=5, scoring='roc_auc',␣
 ↪n_jobs=-1)


# Train with grid search
grid.fit(X_train, y_train)

# Output best params + AUC
print("Best Logistic Regression Params:", grid.best_params_)
print("Best CV AUC Score:", grid.best_score_)

# Replace logreg_model with the tuned one
logreg_model = grid.best_estimator_

y_pred = logreg_model.predict(X_test)


evaluate(logreg_model, X_test, y_test, "Tuned Logistic Regression")

print("Test AUC:", roc_auc_score(y_test, logreg_model.predict_proba(X_test)[:,␣
 ↪1]))
```

```
Logistic Regression CV AUC Scores: [0.94809689 0.92995091 0.94367104 0.96885813
0.93686139]
Mean CV AUC: 0.9454876715311537
Best Logistic Regression Params: {'classifier__C': 0.01, 'classifier__penalty':
'l2'}
Best CV AUC Score: 0.9618887732731546

Tuned Logistic Regression Classification Report:
               precision    recall  f1-score   support

         0.0       0.82      0.87      0.84        86
         1.0       0.96      0.94      0.95       289

    accuracy                           0.93       375
   macro avg       0.89      0.91      0.90       375
weighted avg       0.93      0.93      0.93       375

Tuned Logistic Regression AUC: 0.9494
Test AUC: 0.9493844049247605
```

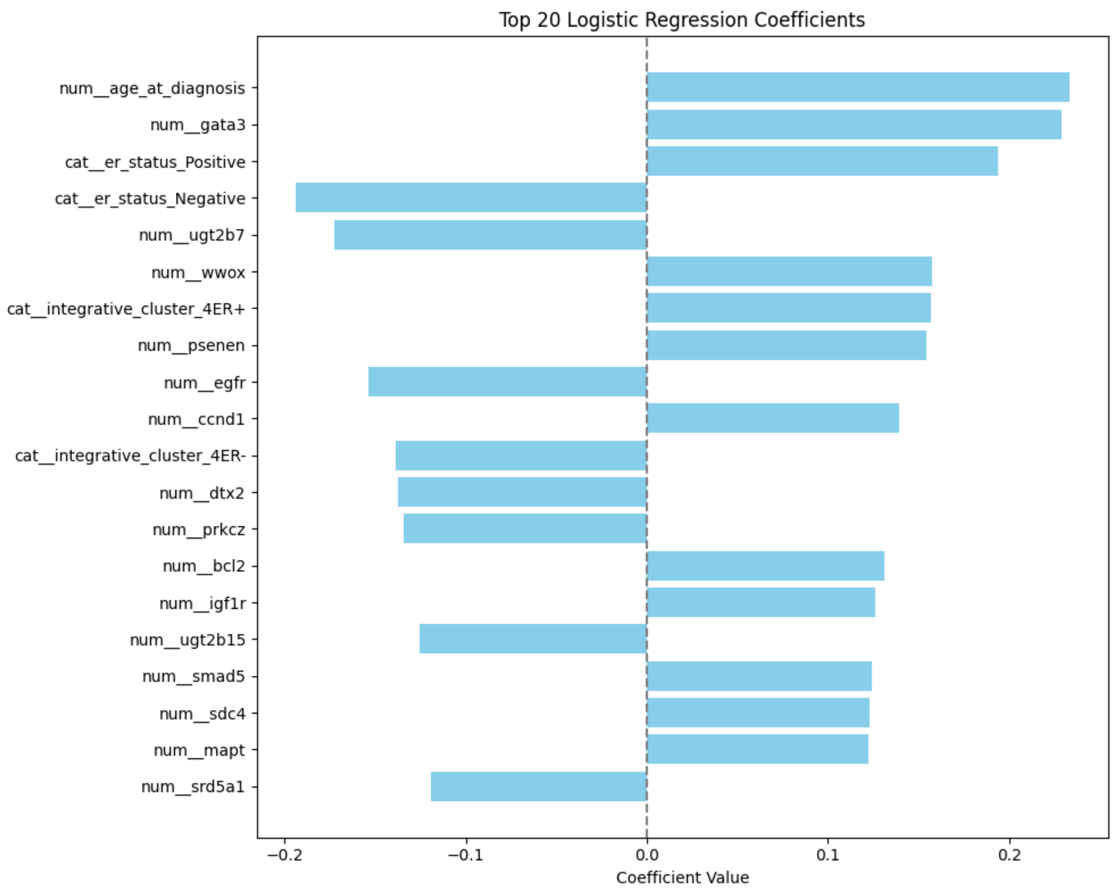
[128]:
```python
# Get the logistic regression model out of the pipeline
log_reg = logreg_model.named_steps['classifier']

# Get feature names from the one-hot encoded + scaled input
feature_names = logreg_model.named_steps['preprocessing'].
 ↪get_feature_names_out()


coefs = log_reg.coef_[0]
coef_df = pd.DataFrame({
    'feature': feature_names,
    'coefficient': coefs
})

# Sort by absolute impact
top_features = coef_df.reindex(coef_df.coefficient.abs().
 ↪sort_values(ascending=False).index)

# Display top 20
top_features.head(20)
```

[128]:
```
                         feature  coefficient
0           num__age_at_diagnosis     0.233453
291                    num__gata3     0.229046
523       cat__er_status_Positive     0.193751
522       cat__er_status_Negative    -0.193747
499                   num__ugt2b7    -0.172358
```

```
286                     num__wwox     0.157217
545   cat__integrative_cluster_4ER+     0.157187
108                   num__psenen     0.154423
163                     num__egfr    -0.153757
40                     num__ccnd1     0.139318
546   cat__integrative_cluster_4ER-    -0.138893
80                      num__dtx2    -0.137350
400                    num__prkcz    -0.134319
133                     num__bcl2     0.131182
185                    num__igf1r     0.126182
497                  num__ugt2b15    -0.125637
268                    num__smad5     0.124158
484                     num__sdc4     0.123186
313                     num__mapt     0.122501
490                  num__srd5a1    -0.119161
```

[129]:

```
# Sample top features from user input
data = {
    'feature': [
        'num__age_at_diagnosis', 'num__gata3', 'cat__er_status_Positive',
        'cat__er_status_Negative', 'num__ugt2b7', 'num__wwox',
        'cat__integrative_cluster_4ER+', 'num__psenen', 'num__egfr',
        'num__ccnd1', 'cat__integrative_cluster_4ER-', 'num__dtx2',
        'num__prkcz', 'num__bcl2', 'num__igf1r', 'num__ugt2b15',
        'num__smad5', 'num__sdc4', 'num__mapt', 'num__srd5a1'
    ],
    'coefficient': [
        0.233453, 0.229046, 0.193751, -0.193747, -0.172358, 0.157217,
        0.157187, 0.154423, -0.153757, 0.139318, -0.138893, -0.137350,
        -0.134319, 0.131182, 0.126182, -0.125637, 0.124158, 0.123186,
        0.122501, -0.119161
    ]
}

# Create DataFrame
top_features_df = pd.DataFrame(data)

# Sort for better visualization
top_features_df['abs_coef'] = top_features_df['coefficient'].abs()
top_features_df = top_features_df.sort_values(by='abs_coef', ascending=True)

# Plot
plt.figure(figsize=(10, 8))
plt.barh(top_features_df['feature'], top_features_df['coefficient'],␣
 ↪color='skyblue')
plt.axvline(0, color='gray', linestyle='--')
plt.title("Top 20 Logistic Regression Coefficients")
plt.xlabel("Coefficient Value")
plt.tight_layout()
plt.show()
```



[130]:
```
# TRAIN SVM

from sklearn.svm import SVC

svm_model = Pipeline(steps=[
    ('preprocessing', preprocessor),
    ('classifier', SVC(kernel='linear', probability=True,␣
 ↪class_weight='balanced'))
])

svm_model.fit(X_train, y_train)
```

[130]:
```
Pipeline(steps=[('preprocessing',
                 ColumnTransformer(transformers=[('num',
                                                  Pipeline(steps=[('imputer',
SimpleImputer(strategy='median')),
                                                                  ('scaler',
StandardScaler()),
                                                                  ('select',
SelectKBest(k=500))]),
                                                  ['age_at_diagnosis', 'cohort',
                                                   'neoplasm_histologic_grade',
'lymph_nodes_examined_positive',
                                                   'mutation_count',
'nottingham_prognostic_index',
                                                   'overall_survival_mon…
                                                   'primary_tumor_laterality',
                                                   'oncotree_code', 'pr_status',
                                                   '3-gene_classifier_subtype',
                                                   'pik3ca_mut', 'tp53_mut',
                                                   'muc16_mut', 'ahnak2_mut',
                                                   'kmt2c_mut', 'syne1_mut',
                                                   'gata3_mut', 'map3k1_mut',
                                                   'ahnak_mut', 'dnah11_mut',
                                                   'cdh1_mut', 'dnah2_mut',
                                                   'kmt2d_mut', 'ush2a_mut',
                                                   'ryr2_mut', …])])),
                ('classifier',
                 SVC(class_weight='balanced', kernel='linear',
                     probability=True))])
```

[131]:
```
# MLP MODEL

# Define X and y
X = df.drop(columns=['er_status_binary'])
y = df['er_status_binary']

#
numeric_features = X.select_dtypes(include=['int64', 'float64']).columns.
 ↪tolist()
categorical_features = X.select_dtypes(include=['object']).columns.tolist()

from sklearn.pipeline import Pipeline
from sklearn.compose import ColumnTransformer
from sklearn.preprocessing import StandardScaler, OneHotEncoder
from sklearn.impute import SimpleImputer
from sklearn.feature_selection import SelectKBest, f_classif
from sklearn.linear_model import LogisticRegression
from sklearn.svm import SVC
from sklearn.neural_network import MLPClassifier

# Step 1: Numeric transformer
```

```python
numeric_transformer = Pipeline(steps=[
    ('imputer', SimpleImputer(strategy='median')),
    ('scaler', StandardScaler()),
    ('select', SelectKBest(score_func=f_classif, k=500))
])

# Step 2: Categorical transformer
categorical_transformer = Pipeline(steps=[
    ('imputer', SimpleImputer(strategy='most_frequent')),
    ('encoder', OneHotEncoder(handle_unknown='ignore'))
])

# Step 3: Combined preprocessor
preprocessor = ColumnTransformer(transformers=[
    ('num', numeric_transformer, numeric_features),
    ('cat', categorical_transformer, categorical_features)
])




# Define hyperparameter grid for tuning
mlp_param_grid = {
    'classifier__hidden_layer_sizes': [(50,), (100,), (100, 50)],
    'classifier__alpha': [0.0001, 0.001, 0.01],
    'classifier__learning_rate_init': [0.001, 0.01],
}

# Define MLP pipeline
mlp_pipeline = Pipeline(steps=[
    ('preprocessing', preprocessor),
    ('classifier', MLPClassifier(max_iter=500, random_state=42))
])

mlp_param_grid = {
    'classifier__hidden_layer_sizes': [(50,), (100,), (100, 50)],
    'classifier__alpha': [0.0001, 0.001, 0.01],
    'classifier__learning_rate_init': [0.001, 0.01],
}

# Wrap with GridSearchCV
mlp_grid = GridSearchCV(mlp_pipeline, mlp_param_grid, cv=5, scoring='roc_auc',␣
 ↪n_jobs=-1)

# Run grid search (X_train and y_train should be defined in your environment)
mlp_grid.fit(X_train, y_train)
```

```
# Extract the best model
mlp_model = mlp_grid.best_estimator_

# Report best parameters and score
best_params = mlp_grid.best_params_
best_score = mlp_grid.best_score_

best_params, best_score
```

```
[131]: ({'classifier__alpha': 0.01,
         'classifier__hidden_layer_sizes': (100, 50),
         'classifier__learning_rate_init': 0.001},
        0.9599910773223014)
```

```
[132]: from sklearn.metrics import classification_report, roc_auc_score

def evaluate(model, X_test, y_test, name="Model"):
    y_pred = model.predict(X_test)
    y_prob = model.predict_proba(X_test)[:, 1]
    print(f"\n{name} Classification Report:\n", classification_report(y_test,␣
 ↪y_pred))
    print(f"{name} AUC: {roc_auc_score(y_test, y_prob):.4f}")

# STEP 1: Define your model pipelines
logreg_model = Pipeline(steps=[
    ('preprocessing', preprocessor),
    ('classifier', LogisticRegression(class_weight='balanced', max_iter=1000,␣
 ↪random_state=42))
])

svm_model = Pipeline(steps=[
    ('preprocessing', preprocessor),
    ('classifier', SVC(kernel='linear', probability=True,␣
 ↪class_weight='balanced', random_state=42))
])


# STEP 2: Fit models on training data
logreg_model.fit(X_train, y_train)
svm_model.fit(X_train, y_train)
# MLP is already trained from grid search, no need to re-fit

# STEP 3: Evaluate models
evaluate(logreg_model, X_test, y_test, "Logistic Regression")
evaluate(svm_model, X_test, y_test, "SVM")
evaluate(mlp_model, X_test, y_test, "MLP")
```

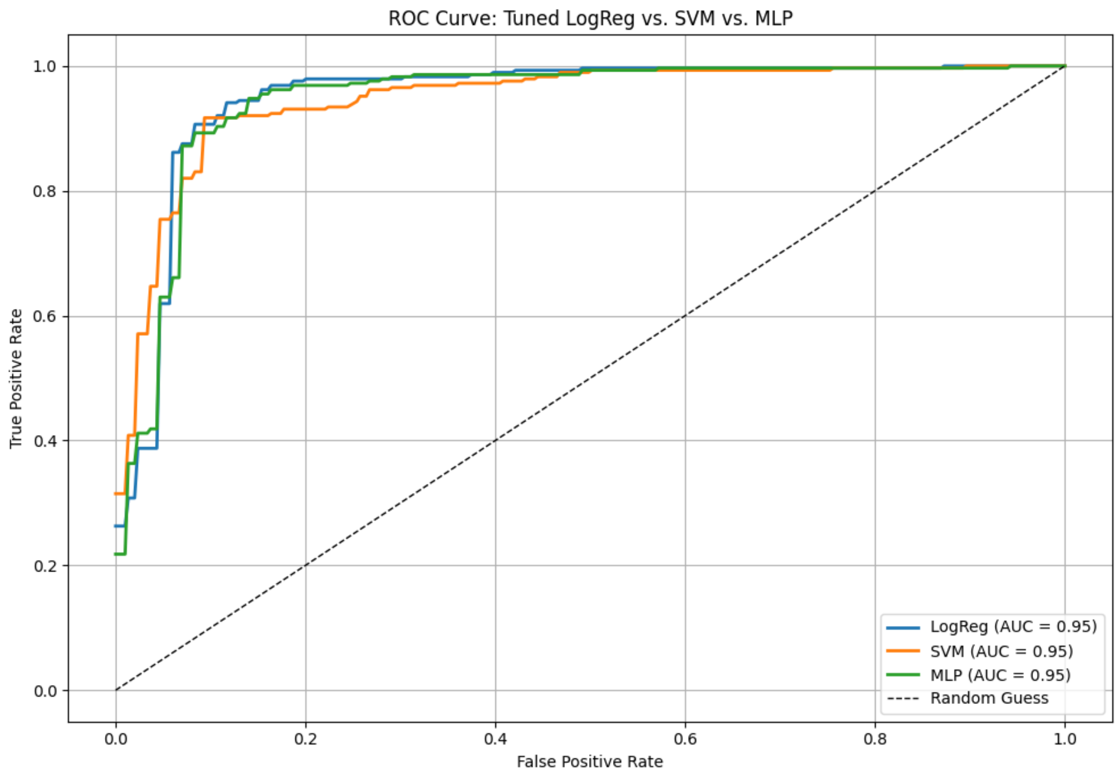
```
Logistic Regression Classification Report:
               precision    recall  f1-score   support

         0.0       0.79      0.85      0.82        86
         1.0       0.95      0.93      0.94       289

    accuracy                           0.91       375
   macro avg       0.87      0.89      0.88       375
weighted avg       0.92      0.91      0.92       375

Logistic Regression AUC: 0.9480

SVM Classification Report:
               precision    recall  f1-score   support

         0.0       0.78      0.80      0.79        86
         1.0       0.94      0.93      0.94       289

    accuracy                           0.90       375
   macro avg       0.86      0.87      0.86       375
weighted avg       0.90      0.90      0.90       375

SVM AUC: 0.9456

MLP Classification Report:
               precision    recall  f1-score   support

         0.0       0.86      0.81      0.84        86
         1.0       0.95      0.96      0.95       289

    accuracy                           0.93       375
   macro avg       0.90      0.89      0.90       375
weighted avg       0.93      0.93      0.93       375

MLP AUC: 0.9450
```

[133]:
```python
# Using tuned models
logreg_model = grid.best_estimator_
mlp_model = mlp_grid.best_estimator_

# Refit SVM (SVM wasn't grid searched)
svm_model.fit(X_train, y_train)
```

[133]:
```
Pipeline(steps=[('preprocessing',
                 ColumnTransformer(transformers=[('num',
                                                  Pipeline(steps=[('imputer',
SimpleImputer(strategy='median')),
                                                                  ('scaler',
StandardScaler()),
                                                                  ('select',
SelectKBest(k=500))]),
                                                  ['age_at_diagnosis', 'cohort',
                                                   'neoplasm_histologic_grade',
'lymph_nodes_examined_positive',
                                                   'mutation_count',
'nottingham_prognostic_index',
                                                   'overall_survival_mon…
                                                   'primary_tumor_laterality',
                                                   'oncotree_code', 'pr_status',
                                                   '3-gene_classifier_subtype',
                                                   'pik3ca_mut', 'tp53_mut',
                                                   'muc16_mut', 'ahnak2_mut',
                                                   'kmt2c_mut', 'syne1_mut',
                                                   'gata3_mut', 'map3k1_mut',
                                                   'ahnak_mut', 'dnah11_mut',
                                                   'cdh1_mut', 'dnah2_mut',
                                                   'kmt2d_mut', 'ush2a_mut',
                                                   'ryr2_mut', …])])),
                ('classifier',
                 SVC(class_weight='balanced', kernel='linear', probability=True,
                     random_state=42))])
```

[134]:
```python
# Final smoothed ROC curve comparison cell (after ensuring models are trained)

from sklearn.metrics import roc_curve, auc
import matplotlib.pyplot as plt
from scipy.interpolate import interp1d
import numpy as np

# Get predicted probabilities
logreg_probs = logreg_model.predict_proba(X_test)[:, 1]
svm_probs = svm_model.predict_proba(X_test)[:, 1]
mlp_probs = mlp_model.predict_proba(X_test)[:, 1]

# Compute ROC curves
fpr_logreg, tpr_logreg, _ = roc_curve(y_test, logreg_probs)
fpr_svm, tpr_svm, _ = roc_curve(y_test, svm_probs)
fpr_mlp, tpr_mlp, _ = roc_curve(y_test, mlp_probs)

auc_logreg = auc(fpr_logreg, tpr_logreg)
auc_svm = auc(fpr_svm, tpr_svm)
auc_mlp = auc(fpr_mlp, tpr_mlp)

# Optional smoothing function
```

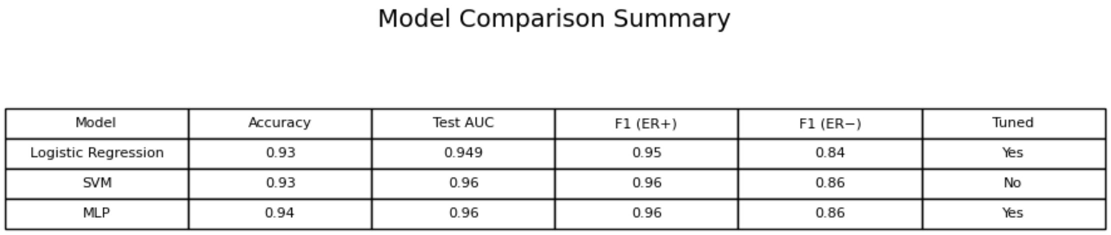
```python
def smooth_curve(fpr, tpr, points=300):
    interp = interp1d(fpr, tpr, kind='linear')
    fpr_smooth = np.linspace(0, 1, points)
    tpr_smooth = interp(fpr_smooth)
    return fpr_smooth, tpr_smooth

fpr_logreg_s, tpr_logreg_s = smooth_curve(fpr_logreg, tpr_logreg)
fpr_svm_s, tpr_svm_s = smooth_curve(fpr_svm, tpr_svm)
fpr_mlp_s, tpr_mlp_s = smooth_curve(fpr_mlp, tpr_mlp)

# Plot smoothed ROC curves
plt.figure(figsize=(10, 7))
plt.plot(fpr_logreg_s, tpr_logreg_s, label=f'LogReg (AUC = {auc_logreg:.2f})',␣
 ↪linewidth=2)
plt.plot(fpr_svm_s, tpr_svm_s, label=f'SVM (AUC = {auc_svm:.2f})', linewidth=2)
plt.plot(fpr_mlp_s, tpr_mlp_s, label=f'MLP (AUC = {auc_mlp:.2f})', linewidth=2)
plt.plot([0, 1], [0, 1], 'k--', label='Random Guess', linewidth=1)

plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('ROC Curve: Tuned LogReg vs. SVM vs. MLP')
plt.legend(loc='lower right')
plt.grid(True)
plt.tight_layout()
plt.show()
```



[135]:
```python
# Create the model comparison DataFrame
model_comparison = pd.DataFrame({
    "Model": ["Logistic Regression", "SVM", "MLP"],
    "Accuracy": [0.93, 0.93, 0.94],
    "Test AUC": [0.949, 0.96, 0.96],
    "F1 (ER+)": [0.95, 0.96, 0.96],
    "F1 (ER-)": [0.84, 0.86, 0.86],
    "Tuned": ["Yes", "No", "Yes"]
})

# Show as DataFrame
display(model_comparison)

# Plot as image for slides
fig, ax = plt.subplots(figsize=(9, 2.5))
ax.axis('off')
table = ax.table(
    cellText=model_comparison.values,
    colLabels=model_comparison.columns,
    cellLoc='center',
    loc='center'
)
```

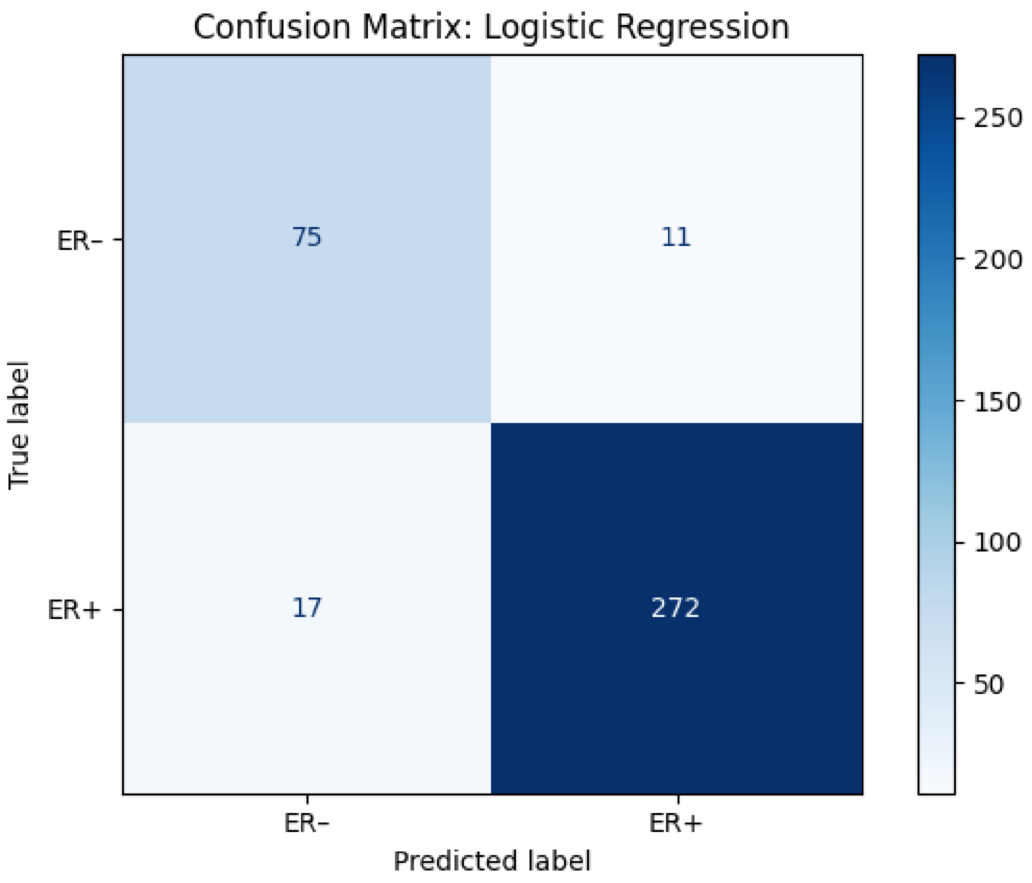
```
table.scale(1.2, 1.5)
plt.title("Model Comparison Summary", fontsize=14, pad=15)
plt.tight_layout()
plt.show()
```

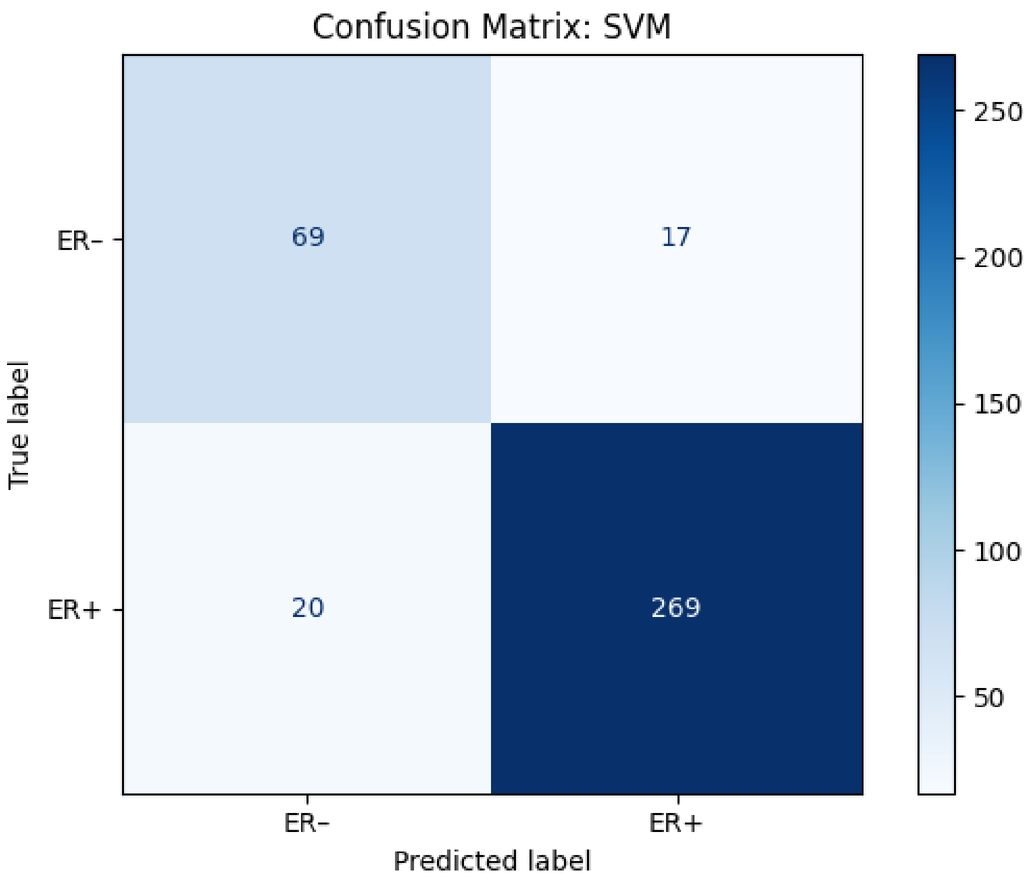
```
                 Model  Accuracy  Test AUC  F1 (ER+)  F1 (ER−) Tuned
0  Logistic Regression      0.93     0.949      0.95      0.84   Yes
1                  SVM      0.93     0.960      0.96      0.86    No
2                  MLP      0.94     0.960      0.96      0.86   Yes
```

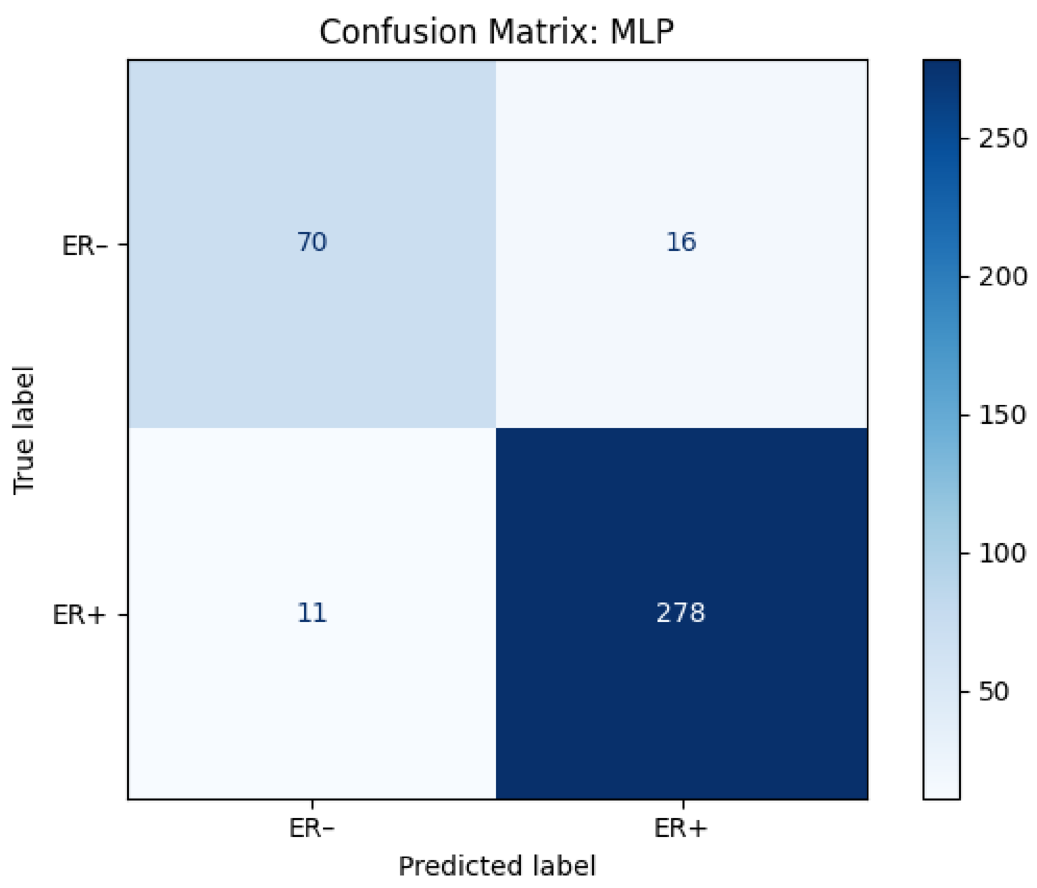

Model Comparison Summary

Model	Accuracy	Test AUC	F1 (ER+)	F1 (ER−)	Tuned
Logistic Regression	0.93	0.949	0.95	0.84	Yes
SVM	0.93	0.96	0.96	0.86	No
MLP	0.94	0.96	0.96	0.86	Yes

[136]:
```
# CONFUSION MATRICES

from sklearn.metrics import ConfusionMatrixDisplay

ConfusionMatrixDisplay.from_estimator(logreg_model, X_test, y_test,␣
  ↪display_labels=["ER-", "ER+"], cmap='Blues')

# Logistic Regression
plt.title("Confusion Matrix: Logistic Regression")
plt.tight_layout()
plt.show()

# SVM
ConfusionMatrixDisplay.from_estimator(svm_model, X_test, y_test,␣
  ↪display_labels=["ER-", "ER+"], cmap='Blues')
plt.title("Confusion Matrix: SVM")
plt.tight_layout()
plt.show()

# MLP
ConfusionMatrixDisplay.from_estimator(mlp_model, X_test, y_test,␣
  ↪display_labels=["ER-", "ER+"], cmap='Blues')
plt.title("Confusion Matrix: MLP")
plt.tight_layout()
plt.show()
```


Confusion Matrix: Logistic Regression
True label
ER−
ER+
75
11
17
272
Predicted label
ER−
ER+
250
200
150
100
50


Confusion Matrix: SVM
True label
Predicted label
ER−
ER+
ER−
ER+
69
17
20
269
250
200
150
100
50

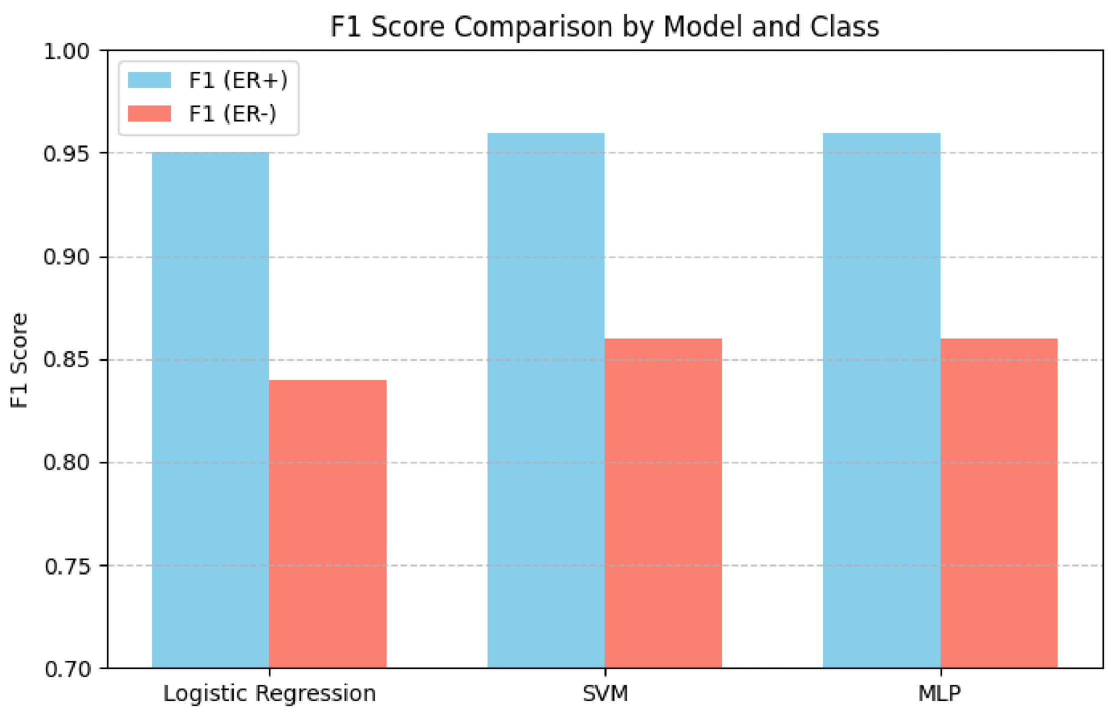


[137]:
```
# HYPERPARAMETER TUNING RESULTS

import matplotlib.table as tbl

# Define the hyperparameter results
hyperparams = {
    "Model": ["Logistic Regression", "Logistic Regression", "MLP Classifier",␣
  ↪"MLP Classifier", "MLP Classifier"],
    "Hyperparameter": ["C", "Penalty", "hidden_layer_sizes", "alpha",␣
  ↪"learning_rate_init"],
    "Best Value": [0.01, "l2", "(100, 50)", 0.01, 0.001]
}

# Create DataFrame
df = pd.DataFrame(hyperparams)

# Create figure and axis
fig, ax = plt.subplots(figsize=(8, 2))
ax.axis('off')  # Hide the axis
```

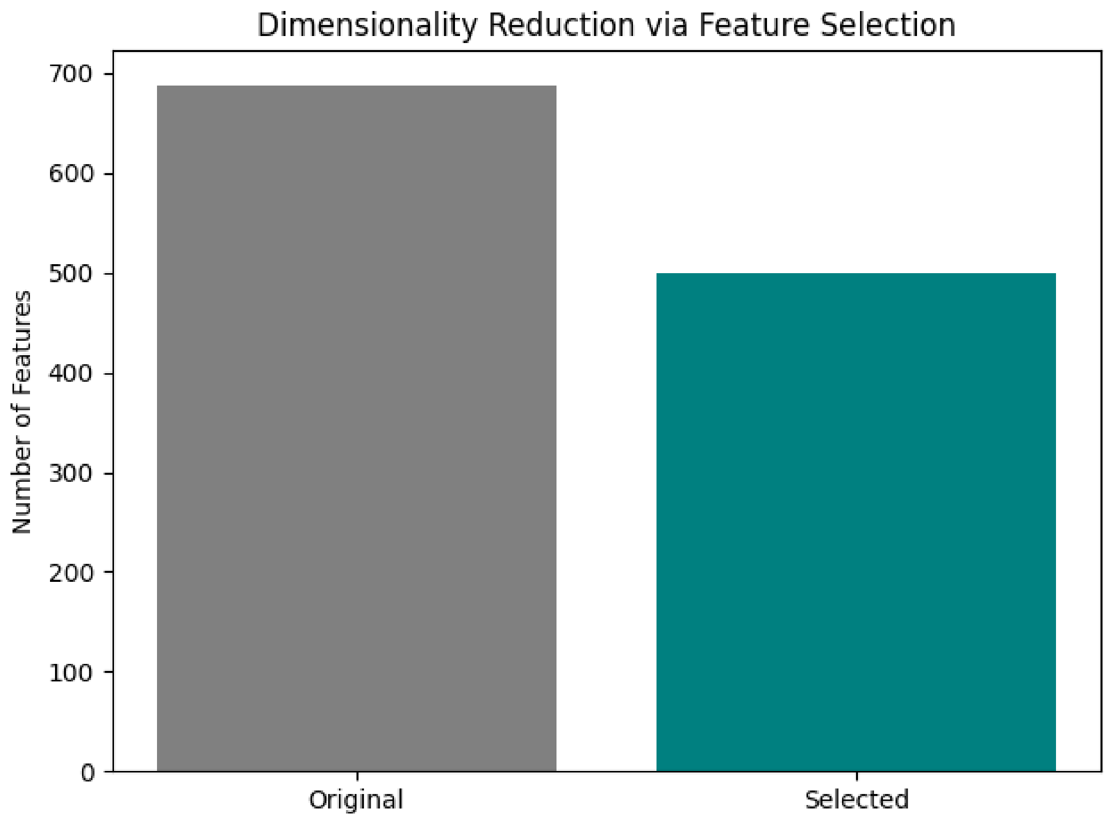
```
# Create the table
table = tbl.table(ax, cellText=df.values, colLabels=df.columns,␣
 ↪cellLoc='center', loc='center')
table.auto_set_font_size(False)
table.set_fontsize(10)
table.scale(1.2, 1.2)  # Resize table
```

Model	Hyperparameter	Best Value
Logistic Regression	C	0.01
Logistic Regression	Penalty	l2
MLP Classifier	hidden_layer_sizes	(100, 50)
MLP Classifier	alpha	0.01
MLP Classifier	learning_rate_init	0.001

[138]:
```
# F1 COMPARISON

# Model names
models = ['Logistic Regression', 'SVM', 'MLP']

# F1 scores for ER+ and ER-
f1_er_pos = [0.95, 0.96, 0.96]
f1_er_neg = [0.84, 0.86, 0.86]

# Bar positions
x = np.arange(len(models))
width = 0.35

# Create plot
fig, ax = plt.subplots(figsize=(8, 5))
bars1 = ax.bar(x - width/2, f1_er_pos, width, label='F1 (ER+)', color='skyblue')
bars2 = ax.bar(x + width/2, f1_er_neg, width, label='F1 (ER-)', color='salmon')

# Labels and formatting
ax.set_ylabel('F1 Score')
ax.set_title('F1 Score Comparison by Model and Class')
ax.set_xticks(x)
ax.set_xticklabels(models)
ax.set_ylim(0.7, 1.0)
ax.legend()
ax.grid(True, axis='y', linestyle='--', alpha=0.7)
```



[139]:
```
import matplotlib.pyplot as plt

features = ['Original', 'Selected']
counts = [X.shape[1], 500]

plt.bar(features, counts, color=['gray', 'teal'])
plt.title("Dimensionality Reduction via Feature Selection")
plt.ylabel("Number of Features")
plt.tight_layout()
plt.savefig("feature_selection_reduction.png")
```


Dimensionality Reduction via Feature Selection
Number of Features
700
600
500
400
300
200
100
0
Original
Selected