AAM-IPL-Wk-5-SVM-ProjectName-Full-Code-V4

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1 AAM-IPL Week-4 SVM - Breast Cancer Diagnosis

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Project Implementation Details: As published in the project announcement in AAM-IPL Online Classroom

This project implements a Support Vector Machine (SVM) classifier to predict the class of breast cancer from the provided dataset. The dataset is loaded - `load_breast_cancer()`- from sklearn. The breast cancer dataset consists of 569 samples, each representing a patient with a set of features.

The dataset is used for training a SVM classifier and evaluate its performance using various metrics such as accuracy, precision, recall, F1-score. Additionally, various other classifiers, such as Logistic Regression, Naive Bayes, and K-Nearest Neighbors are also implemented and evaluated for comparison.

AAM-IPL of GPREC is brought to you by Brillium Technologies.

[1]:
```
# Importing necessary libraries for breast cancer SVM classifier
from sklearn import datasets
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.metrics import accuracy_score
from sklearn.svm import SVC
import pandas as pd # for dataframe manipulation
from pandas.plotting import parallel_coordinates # for parallel coordinates␣
↪plot of breast cancer data set
import matplotlib.pyplot as plt # for plotting graphs
from sklearn.manifold import TSNE # for t-SNE plot
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import auc, confusion_matrix, precision_score,␣
↪recall_score, roc_curve
from sklearn.model_selection import cross_val_score
from sklearn.metrics import f1_score
from sklearn.linear_model import LogisticRegression
from sklearn.naive_bayes import GaussianNB
from sklearn.neighbors import KNeighborsClassifier
```

```
from sklearn.tree import DecisionTreeClassifier
import seaborn as sns
from collections import Counter
import numpy as np
from sklearn.metrics import accuracy_score, f1_score, roc_curve, auc,␣
 ↪precision_recall_curve, confusion_matrix, ConfusionMatrixDisplay
from matplotlib.colors import ListedColormap
import seaborn as sns
from matplotlib.offsetbox import TextArea, DrawingArea, OffsetImage,␣
 ↪AnnotationBbox
import matplotlib.image as mpimg
from matplotlib.transforms import Affine2D
from matplotlib.offsetbox import OffsetImage, AnnotationBbox
from scipy.ndimage import rotate
from PIL import Image
```

[2]:
```
# Create virtual environment
# !python -m venv venv
# Activate virtual environment
# !source venv/bin/activate
```

[2]:
```
# Define name, email, plot watermarks etc.
name = "Venkateswar Reddy Melachervu"
email = "venkat.reddy.gf@gprec.ac.in"

# Load your watermark image (assuming it's in the same directory)
aam_ipl_wama_image = plt.imread('AAM-IPL-Watermark-for-Plots.png')

# Function to add a diagonal watermark
def add_aam_ipl_wama_revised(ax, watermark_image, zoom, alpha=0.3,␣
 ↪rotation_angle=45):
    """
    Adds an image watermark diagonally to the provided axis.

    Parameters:
    - ax: The axis to add the watermark to.
    - watermark_image: The image to use as the watermark.
    - alpha: The transparency level for the watermark.
    - zoom: The scale of the watermark image.
    - rotation_angle: The angle to rotate the watermark (default is 45 degrees).
    """
    imagebox = OffsetImage(watermark_image, alpha=alpha, zoom=zoom)

    # Create a transformation for diagonal placement
    trans_data = Affine2D().rotate_deg(rotation_angle) + ax.transData
    ab = AnnotationBbox(imagebox, (0.5, 0.5), frameon=False, xycoords='axes␣
 ↪fraction', boxcoords="axes fraction", pad=0, transform=trans_data)
```

```
    # Add watermark image to the axis
    ax.add_artist(ab)

# Load the breast cancer dataset from sklearn
bcancer = datasets.load_breast_cancer()
X = bcancer.data
Y = bcancer.target


# Print the description/meta data
print(bcancer.DESCR)

# Scale the data using standard scaler
scaler = StandardScaler()
standard_scaled_X = scaler.fit_transform(X)

# Display column/feature names in the breast cancer dataset
df = pd.DataFrame(data=X, columns=bcancer.feature_names)
df['target'] = Y

# Set display option to show all columns
pd.set_option('display.max_columns', None)
pd.set_option('display.width', 1000)
print('Breast Cancer Data Set Details:')
print(f'\tComprises of {df.shape[0]} data sample vectors')
print(f'\tEach vector is of {df.shape[1]-1} features/dimensions and a target␣
 ↪scalar response.')

# Count the data samples for each target value
target_counts = df['target'].value_counts()

# Print the counts separately
count_0 = target_counts[0]
count_1 = target_counts[1]

print(f"\tNumber of samples with target value 1 - \"Benign/Non-cancerous␣
 ↪Tumors\": {count_1}")
print(f"\tNumber of samples with target value 0 - \"Malignant/Cancerous␣
 ↪Tumors\": {count_0}")
print(f"\tTotal number of data samples - \"Breast Cancer\" data set: {count_0}")

# Capitalize the first letter of each word in the feature names
df.columns = [col.title() for col in df.columns]

# Filter out the 'Target' column after capitalizing
feature_columns = [col for col in df.columns if col != 'Target']
```

```python
# Convert to list
column_names = feature_columns
print(f"\tThe feature names are:")
print(f'\t{column_names}')
```

```
.. _breast_cancer_dataset:

Breast cancer wisconsin (diagnostic) dataset
--------------------------------------------

**Data Set Characteristics:**

:Number of Instances: 569

:Number of Attributes: 30 numeric, predictive attributes and the class

:Attribute Information:
    - radius (mean of distances from center to points on the perimeter)
    - texture (standard deviation of gray-scale values)
    - perimeter
    - area
    - smoothness (local variation in radius lengths)
    - compactness (perimeter^2 / area - 1.0)
    - concavity (severity of concave portions of the contour)
    - concave points (number of concave portions of the contour)
    - symmetry
    - fractal dimension ("coastline approximation" - 1)

    The mean, standard error, and "worst" or largest (mean of the three
    worst/largest values) of these features were computed for each image,
    resulting in 30 features.  For instance, field 0 is Mean Radius, field
    10 is Radius SE, field 20 is Worst Radius.

    - class:
            - WDBC-Malignant
            - WDBC-Benign

:Summary Statistics:

===================================== ====== ======
                                        Min    Max
===================================== ====== ======
radius (mean):                        6.981  28.11
texture (mean):                       9.71   39.28
perimeter (mean):                     43.79  188.5
area (mean):                          143.5  2501.0
smoothness (mean):                    0.053  0.163
```

```
compactness (mean):                     0.019  0.345
concavity (mean):                       0.0    0.427
concave points (mean):                  0.0    0.201
symmetry (mean):                        0.106  0.304
fractal dimension (mean):               0.05   0.097
radius (standard error):                0.112  2.873
texture (standard error):               0.36   4.885
perimeter (standard error):             0.757  21.98
area (standard error):                  6.802  542.2
smoothness (standard error):            0.002  0.031
compactness (standard error):           0.002  0.135
concavity (standard error):             0.0    0.396
concave points (standard error):        0.0    0.053
symmetry (standard error):              0.008  0.079
fractal dimension (standard error):     0.001  0.03
radius (worst):                         7.93   36.04
texture (worst):                        12.02  49.54
perimeter (worst):                      50.41  251.2
area (worst):                           185.2  4254.0
smoothness (worst):                     0.071  0.223
compactness (worst):                    0.027  1.058
concavity (worst):                      0.0    1.252
concave points (worst):                 0.0    0.291
symmetry (worst):                       0.156  0.664
fractal dimension (worst):              0.055  0.208
==================================== ====== ======

:Missing Attribute Values: None

:Class Distribution: 212 - Malignant, 357 - Benign

:Creator:  Dr. William H. Wolberg, W. Nick Street, Olvi L. Mangasarian

:Donor: Nick Street

:Date: November, 1995

This is a copy of UCI ML Breast Cancer Wisconsin (Diagnostic) datasets.
https://goo.gl/U2Uwz2

Features are computed from a digitized image of a fine needle
aspirate (FNA) of a breast mass.  They describe
characteristics of the cell nuclei present in the image.

Separating plane described above was obtained using
Multisurface Method-Tree (MSM-T) [K. P. Bennett, "Decision Tree
Construction Via Linear Programming." Proceedings of the 4th
Midwest Artificial Intelligence and Cognitive Science Society,
```

pp. 97-101, 1992], a classification method which uses linear
programming to construct a decision tree. Relevant features
were selected using an exhaustive search in the space of 1-4
features and 1-3 separating planes.

The actual linear program used to obtain the separating plane
in the 3-dimensional space is that described in:
[K. P. Bennett and O. L. Mangasarian: "Robust Linear
Programming Discrimination of Two Linearly Inseparable Sets",
Optimization Methods and Software 1, 1992, 23-34].

This database is also available through the UW CS ftp server:

ftp ftp.cs.wisc.edu
cd math-prog/cpo-dataset/machine-learn/WDBC/

.. dropdown:: References

  - W.N. Street, W.H. Wolberg and O.L. Mangasarian. Nuclear feature extraction
    for breast tumor diagnosis. IS&T/SPIE 1993 International Symposium on
    Electronic Imaging: Science and Technology, volume 1905, pages 861-870,
    San Jose, CA, 1993.
  - O.L. Mangasarian, W.N. Street and W.H. Wolberg. Breast cancer diagnosis and
    prognosis via linear programming. Operations Research, 43(4), pages 570-577,
    July-August 1995.
  - W.H. Wolberg, W.N. Street, and O.L. Mangasarian. Machine learning techniques
    to diagnose breast cancer from fine-needle aspirates. Cancer Letters 77
(1994)
    163-171.

Breast Cancer Data Set Details:
        Comprises of 569 data sample vectors
        Each vector is of 30 features/dimensions and a target scalar response.
        Number of samples with target value 1 - "Benign/Non-cancerous Tumors":
357
        Number of samples with target value 0 - "Malignant/Cancerous Tumors":
212
        Total number of data samples - "Breast Cancer" data set: 212
        The feature names are:
        ['Mean Radius', 'Mean Texture', 'Mean Perimeter', 'Mean Area', 'Mean
Smoothness', 'Mean Compactness', 'Mean Concavity', 'Mean Concave Points', 'Mean
Symmetry', 'Mean Fractal Dimension', 'Radius Error', 'Texture Error', 'Perimeter
Error', 'Area Error', 'Smoothness Error', 'Compactness Error', 'Concavity
Error', 'Concave Points Error', 'Symmetry Error', 'Fractal Dimension Error',
'Worst Radius', 'Worst Texture', 'Worst Perimeter', 'Worst Area', 'Worst
Smoothness', 'Worst Compactness', 'Worst Concavity', 'Worst Concave Points',
'Worst Symmetry', 'Worst Fractal Dimension']

[3]:
```
# Display the first row of the data set
print('First row of standard scaled data sample in the Breast Cancer data set␣
 ↪is:')
first_sample = df.iloc[0]
for idx, (feature, value) in enumerate(first_sample.items(), start=1):
    print(f"{idx}. {feature:<30} {value:.6f}")
```

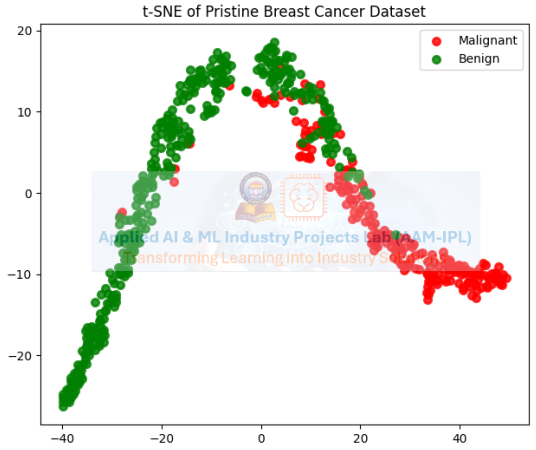
```
First row of standard scaled data sample in the Breast Cancer data set is:
1. Mean Radius                    17.990000
2. Mean Texture                   10.380000
3. Mean Perimeter                 122.800000
4. Mean Area                      1001.000000
5. Mean Smoothness                0.118400
6. Mean Compactness               0.277600
7. Mean Concavity                 0.300100
8. Mean Concave Points            0.147100
9. Mean Symmetry                  0.241900
10. Mean Fractal Dimension         0.078710
11. Radius Error                   1.095000
12. Texture Error                  0.905300
13. Perimeter Error                8.589000
14. Area Error                     153.400000
15. Smoothness Error               0.006399
16. Compactness Error              0.049040
17. Concavity Error                0.053730
18. Concave Points Error           0.015870
19. Symmetry Error                 0.030030
20. Fractal Dimension Error        0.006193
21. Worst Radius                   25.380000
22. Worst Texture                  17.330000
23. Worst Perimeter                184.600000
24. Worst Area                     2019.000000
25. Worst Smoothness               0.162200
26. Worst Compactness              0.665600
27. Worst Concavity                0.711900
28. Worst Concave Points           0.265400
29. Worst Symmetry                 0.460100
30. Worst Fractal Dimension        0.118900
31. Target                         0.000000
```

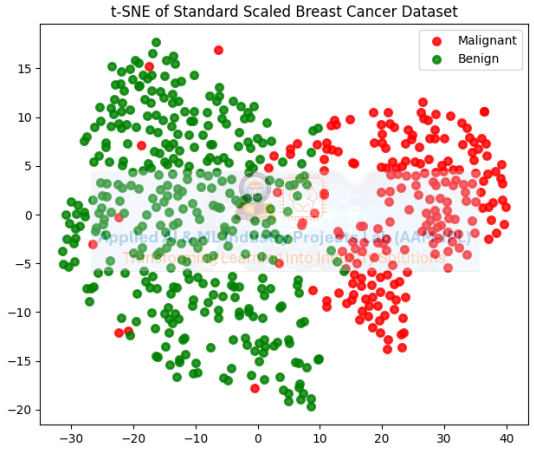
[5]:
```
# Lets plot t-SNE - t-distributed stochastic neighbor embedding plot of the␣
 ↪breast cancer data set - visual dimensionality reduction technique
import os
logical_cores = os.cpu_count()
os.environ['LOKY_MAX_CPU_COUNT'] = str(logical_cores)

# Perform t-SNE on pristine data
```

```
tsne_pristine = TSNE(n_components=2, random_state=42)
X_tsne_pristine = tsne_pristine.fit_transform(X)

# Perform t-SNE on standard scaled data
tsne_scaled = TSNE(n_components=2, random_state=42)
X_tsne_scaled = tsne_scaled.fit_transform(standard_scaled_X)

# Print the derived X and Y values
print("t-SNE on Pristine Data (first 5 points):")
print(X_tsne_pristine[:5])
print("\nt-SNE on Standard Scaled Data (first 5 points):")
print(X_tsne_scaled[:5])

# Define colors and line width for the plot
colors = ['red', 'green']
lw = 2

# Plot t-SNE results
fig, axes = plt.subplots(1, 2, figsize=(16, 6))

# t-SNE on pristine data
axes[0].set_title('t-SNE of Pristine Breast Cancer Dataset')
for color, i, target_name in zip(colors, [0, 1], bcancer.target_names):
    axes[0].scatter(X_tsne_pristine[Y == i, 0], X_tsne_pristine[Y == i, 1],␣
 ↪color=color, alpha=.8, lw=lw, label=target_name.capitalize())
axes[0].legend(loc='best', shadow=False, scatterpoints=1)

# t-SNE on standard scaled data
axes[1].set_title('t-SNE of Standard Scaled Breast Cancer Dataset')
for color, i, target_name in zip(colors, [0, 1], bcancer.target_names):
    axes[1].scatter(X_tsne_scaled[Y == i, 0], X_tsne_scaled[Y == i, 1],␣
 ↪color=color, alpha=.8, lw=lw, label=target_name.capitalize())
axes[1].legend(loc='best', shadow=False, scatterpoints=1)

# Add watermark with the loaded image
add_aam_ipl_wama_revised(axes[0], aam_ipl_wama_image, 0.3)
add_aam_ipl_wama_revised(axes[1], aam_ipl_wama_image, 0.3)

plt.show()
```

```
t-SNE on Pristine Data (first 5 points):
[[ 42.337463  -12.640097 ]
 [ 42.50024    -9.92803  ]
 [ 37.894382  -10.039126 ]
 [-17.654438    1.4511237]
 [ 36.764866   -7.9306464]]
```

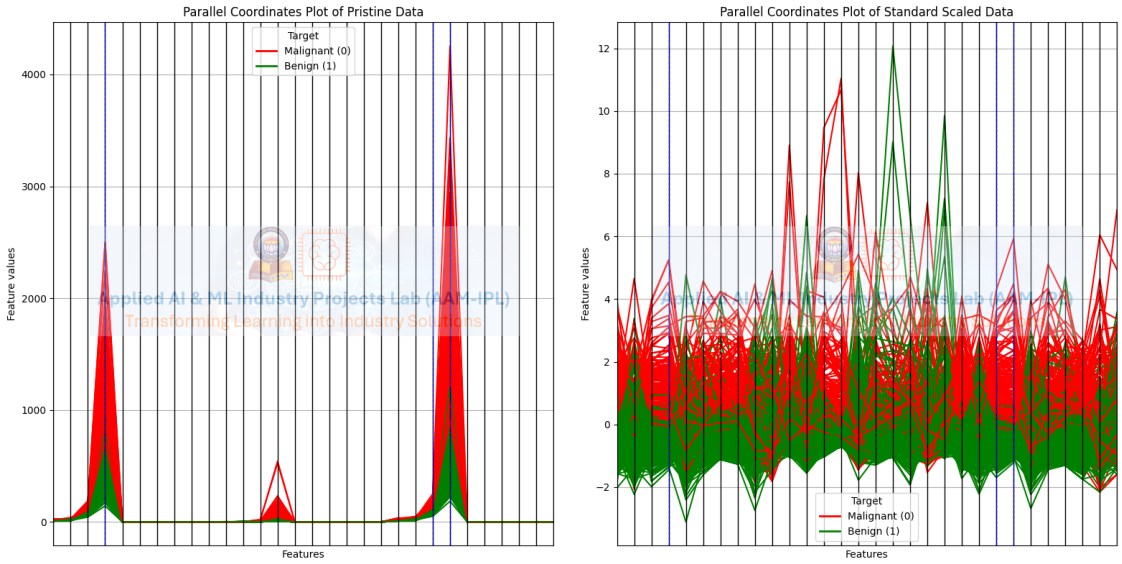
```
t-SNE on Standard Scaled Data (first 5 points):
[[ 37.784595    1.2305161]
 [ 23.71192     7.3292117]
 [ 31.739286    3.551559 ]
 [ 20.865301  -13.742583 ]
 [ 26.342352   -1.7316735]]
```





[6]:
```
# Parallel coordinates plot of the breast cancer data set for pristine and standard scaled data

# Create DataFrames from the data
df_pristine = pd.DataFrame(data=X, columns=bcancer.feature_names)
df_pristine['target'] = Y

df_scaled = pd.DataFrame(data=standard_scaled_X, columns=bcancer.feature_names)
df_scaled['target'] = Y

# Convert target to string for color coding
df_pristine['target'] = df_pristine['target'].astype(str)
df_scaled['target'] = df_scaled['target'].astype(str)

# Define colors for each class explicitly
color_dict = {'0': 'red', '1': 'green'}
# Create a colormap from the color dictionary
cmap = plt.cm.colors.ListedColormap([color_dict['0'], color_dict['1']])

# Identify features with mean value above 100 - Exclude the 'target' column
mean_values = df_pristine.drop('target', axis=1).mean()
features_above_100 = mean_values[mean_values > 100].index

# Create subplots for parallel coordinates
```

```
fig, axes = plt.subplots(1, 2, figsize=(16, 8))

# Parallel coordinates plot for pristine data
parallel_coordinates(df_pristine, 'target', colormap=cmap, ax=axes[0])
axes[0].set_title('Parallel Coordinates Plot of Pristine Data')
axes[0].set_xlabel('Features')
axes[0].set_ylabel('Feature values')

# Highlight the dominant features
for feature in features_above_100:
    axes[0].axvline(df_pristine.columns.get_loc(feature), color='blue',␣
 ↪linestyle='--', linewidth=1)

# Parallel coordinates plot for standard scaled data
parallel_coordinates(df_scaled, 'target', colormap=cmap, ax=axes[1])
axes[1].set_title('Parallel Coordinates Plot of Standard Scaled Data')
axes[1].set_xlabel('Features')
axes[1].set_ylabel('Feature values')

# Highlight the dominant features
for feature in features_above_100:
    axes[1].axvline(df_scaled.columns.get_loc(feature), color='blue',␣
 ↪linestyle='--', linewidth=1)

# Add custom legend
handles = [plt.Line2D([0], [0], color=color_dict['0'], lw=2), plt.Line2D([0],␣
 ↪[0], color=color_dict['1'], lw=2)]
axes[0].legend(handles, ['Malignant (0)', 'Benign (1)'], title='Target')
axes[1].legend(handles, ['Malignant (0)', 'Benign (1)'], title='Target')

# Remove x-axis labels
axes[0].set_xticks([])
axes[1].set_xticks([])

# Add watermark to both plots
add_aam_ipl_wama_revised(axes[0], aam_ipl_wama_image, 0.4)
add_aam_ipl_wama_revised(axes[1], aam_ipl_wama_image, 0.4)

plt.tight_layout()
plt.show()
```



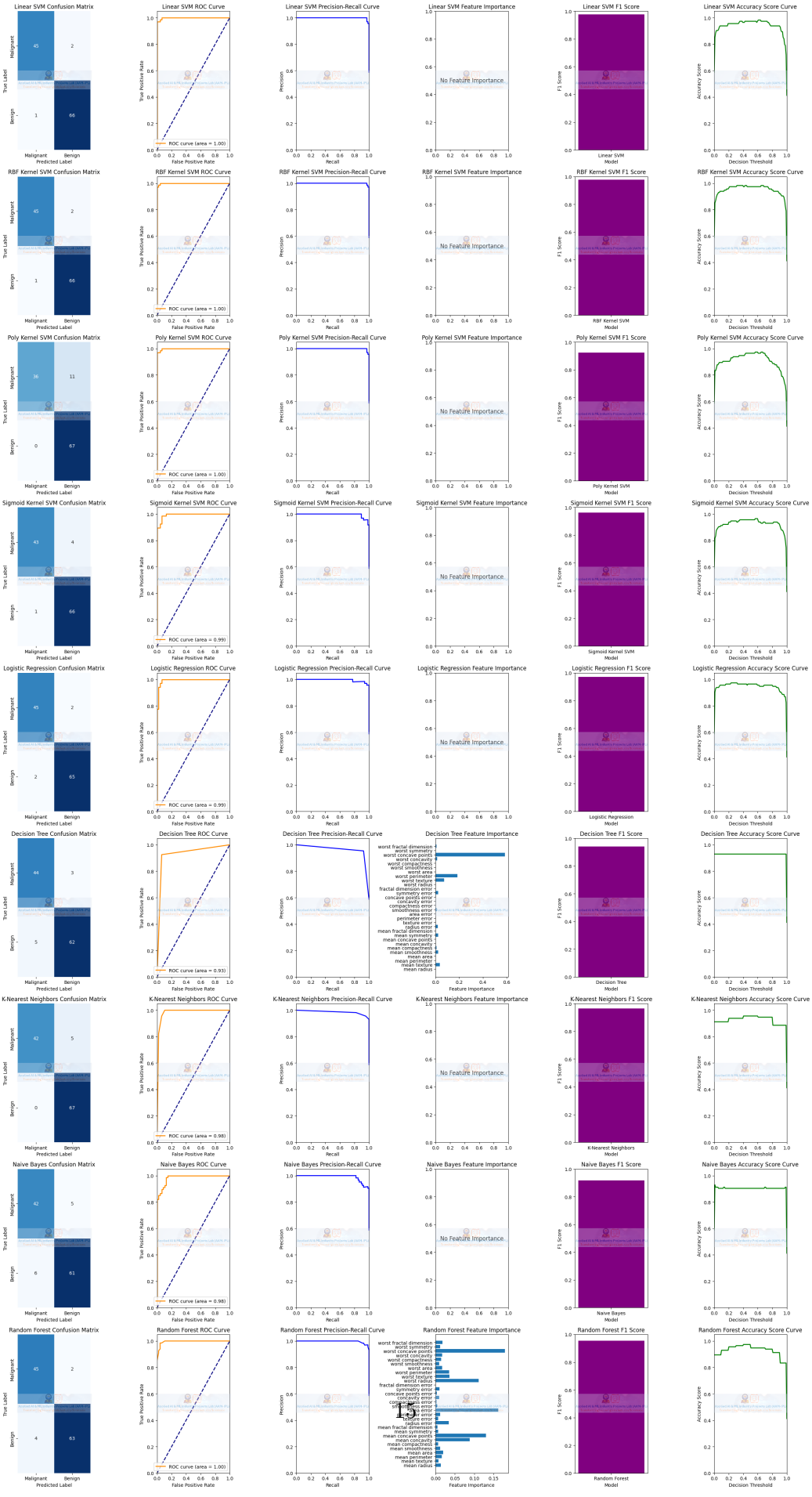
[7]:
```
# Plot curves for all classifiers - accuracy, confusion matrix, ROC curve, PR curve, feature importance, F1 score

# Define the formulae as strings
precision_formula = "Precision = True Positives / (True Positives + False Positives)"
recall_formula = "Recall = True Positives / (True Positives + False Negatives)"
f1_score_formula = "F1 Score = 2 * (Precision * Recall) / (Precision + Recall)"

# Print the formulae
print(precision_formula)
print(recall_formula)
print(f1_score_formula, '\n')

# Define a dictionary of models
models = {
    'Linear SVM': SVC(kernel='linear', random_state=0, probability=True),
    'RBF Kernel SVM': SVC(kernel='rbf', random_state=0, probability=True),
    'Poly Kernel SVM': SVC(kernel='poly', degree=3, random_state=0, probability=True),
    'Sigmoid Kernel SVM': SVC(kernel='sigmoid', random_state=0, probability=True),
    'Logistic Regression': LogisticRegression(max_iter=10000, random_state=0),
    'Decision Tree': DecisionTreeClassifier(criterion='entropy', random_state=0),
    'K-Nearest Neighbors': KNeighborsClassifier(n_neighbors=5, metric='minkowski', p=2),
    'Naive Bayes': GaussianNB(),
```

```
    'Random Forest': RandomForestClassifier(n_estimators=10,␣
 ↪criterion='entropy', random_state=0)
}

# Initialize plot
fig, axs = plt.subplots(len(models), 6, figsize=(24, len(models) * 5))
fig.subplots_adjust(hspace=0.5)

# Split the data
X_train, X_test, Y_train, Y_test = train_test_split(standard_scaled_X, Y,␣
 ↪test_size=0.2, random_state=0)

# Loop through models
for idx, (name, model) in enumerate(models.items()):
    # Train model
    model.fit(X_train, Y_train)

    # Predict results
    Y_pred = model.predict(X_test)
    Y_proba = model.predict_proba(X_test)[:, 1] if hasattr(model,␣
 ↪'predict_proba') else None
    accuracy = accuracy_score(Y_test, Y_pred)
    print(f"{name} Accuracy Score: {100 * accuracy:.2f}%")

    # Compute metrics
    cm = confusion_matrix(Y_test, Y_pred)
    fpr, tpr, _ = roc_curve(Y_test, Y_proba) if Y_proba is not None else ([],␣
 ↪[], [])
    roc_auc = auc(fpr, tpr) if Y_proba is not None else None
    precision, recall, _ = precision_recall_curve(Y_test, Y_proba) if Y_proba␣
 ↪is not None else ([], [], [])
    f1 = f1_score(Y_test, Y_pred)

    # Plot Accuracy Score curve
    if Y_proba is not None:
        thresholds = np.linspace(0, 1, 100)
        accuracy_scores = [accuracy_score(Y_test, (Y_proba > threshold).
 ↪astype(int)) for threshold in thresholds]
        axs[idx, 5].plot(thresholds, accuracy_scores, color='green', lw=2)
        axs[idx, 5].set_xlim([0.0, 1.0])
        axs[idx, 5].set_ylim([0.0, 1.05])
        axs[idx, 5].set_xlabel('Decision Threshold')
        axs[idx, 5].set_ylabel('Accuracy Score')
        axs[idx, 5].set_title(f'{name} Accuracy Score Curve')
    else:
```

```
        axs[idx, 5].text(0.5, 0.5, 'No Accuracy Curve',␣
↪horizontalalignment='center', verticalalignment='center', fontsize=12)
        axs[idx, 5].set_title(f'{name} Accuracy Score Curve')

    # Plot confusion matrix
    sns.heatmap(cm, annot=True, fmt='d', cmap='Blues', ax=axs[idx, 0],␣
↪cbar=False, xticklabels=['Malignant', 'Benign'], yticklabels=['Malignant',␣
↪'Benign'])
    axs[idx, 0].set_xlabel('Predicted Label')
    axs[idx, 0].set_ylabel('True Label')
    axs[idx, 0].set_title(f'{name} Confusion Matrix')

    # Plot ROC curve
    if Y_proba is not None:
        axs[idx, 1].plot(fpr, tpr, color='darkorange', lw=2, label=f'ROC curve␣
↪(area = {roc_auc:.2f})')
        axs[idx, 1].plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')
        axs[idx, 1].set_xlim([0.0, 1.0])
        axs[idx, 1].set_ylim([0.0, 1.05])
        axs[idx, 1].set_xlabel('False Positive Rate')
        axs[idx, 1].set_ylabel('True Positive Rate')
        axs[idx, 1].set_title(f'{name} ROC Curve')
        axs[idx, 1].legend(loc='lower right')
    else:
        axs[idx, 1].text(0.5, 0.5, 'No ROC Curve',␣
↪horizontalalignment='center', verticalalignment='center', fontsize=12)
        axs[idx, 1].set_title(f'{name} ROC Curve')

    # Plot Precision-Recall curve
    if Y_proba is not None:
        axs[idx, 2].plot(recall, precision, color='blue', lw=2)
        axs[idx, 2].set_xlim([0.0, 1.0])
        axs[idx, 2].set_ylim([0.0, 1.05])
        axs[idx, 2].set_xlabel('Recall')
        axs[idx, 2].set_ylabel('Precision')
        axs[idx, 2].set_title(f'{name} Precision-Recall Curve')
    else:
        axs[idx, 2].text(0.5, 0.5, 'No PR Curve', horizontalalignment='center',␣
↪verticalalignment='center', fontsize=12)
        axs[idx, 2].set_title(f'{name} Precision-Recall Curve')

    # Plot feature importance for models that have it
    if hasattr(model, 'feature_importances_'):
        importances = model.feature_importances_
        axs[idx, 3].barh(range(len(importances)), importances, align='center')
        axs[idx, 3].set_yticks(range(len(importances)))
        axs[idx, 3].set_yticklabels(bcancer.feature_names)
```

```
        axs[idx, 3].set_xlabel('Feature Importance')
        axs[idx, 3].set_title(f'{name} Feature Importance')
    else:
        axs[idx, 3].text(0.5, 0.5, 'No Feature Importance',␣
↪horizontalalignment='center', verticalalignment='center', fontsize=12)
        axs[idx, 3].set_title(f'{name} Feature Importance')

    # Plot F1 Score
    axs[idx, 4].bar(name, f1, color='purple')
    axs[idx, 4].set_ylim([0, 1])
    axs[idx, 4].set_xlabel('Model')
    axs[idx, 4].set_ylabel('F1 Score')
    axs[idx, 4].set_title(f'{name} F1 Score')

   # Add watermark to all subplots
    for ax in axs[idx, :]:
        add_aam_ipl_wama_revised(ax, aam_ipl_wama_image, 0.15)

plt.tight_layout()
plt.show()
```

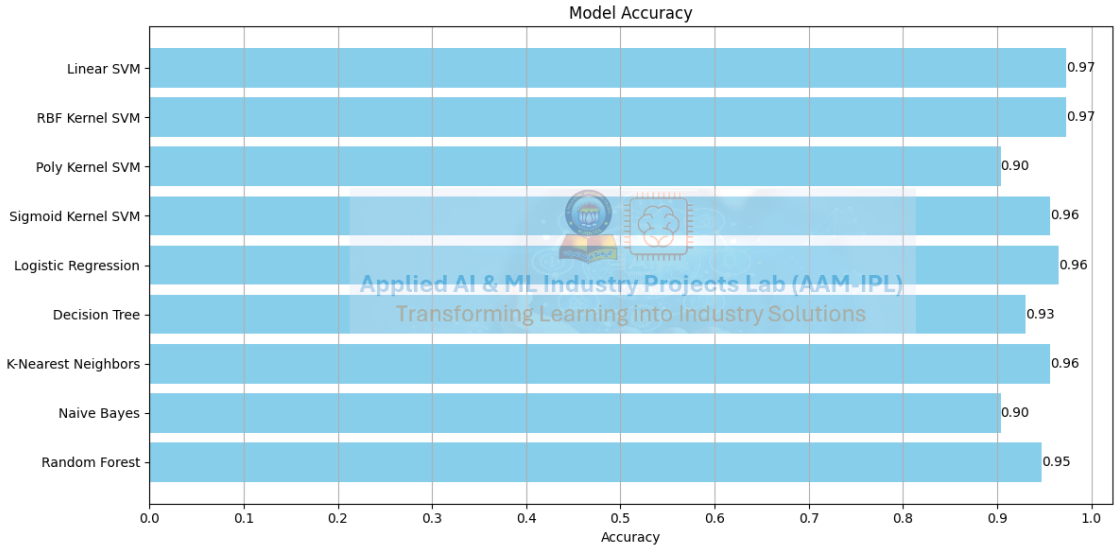
```
Precision = True Positives / (True Positives + False Positives)
Recall = True Positives / (True Positives + False Negatives)
F1 Score = 2 * (Precision * Recall) / (Precision + Recall)

Linear SVM Accuracy Score: 97.37%
RBF Kernel SVM Accuracy Score: 97.37%
Poly Kernel SVM Accuracy Score: 90.35%
Sigmoid Kernel SVM Accuracy Score: 95.61%
Logistic Regression Accuracy Score: 96.49%
Decision Tree Accuracy Score: 92.98%
K-Nearest Neighbors Accuracy Score: 95.61%
Naive Bayes Accuracy Score: 90.35%
Random Forest Accuracy Score: 94.74%
```

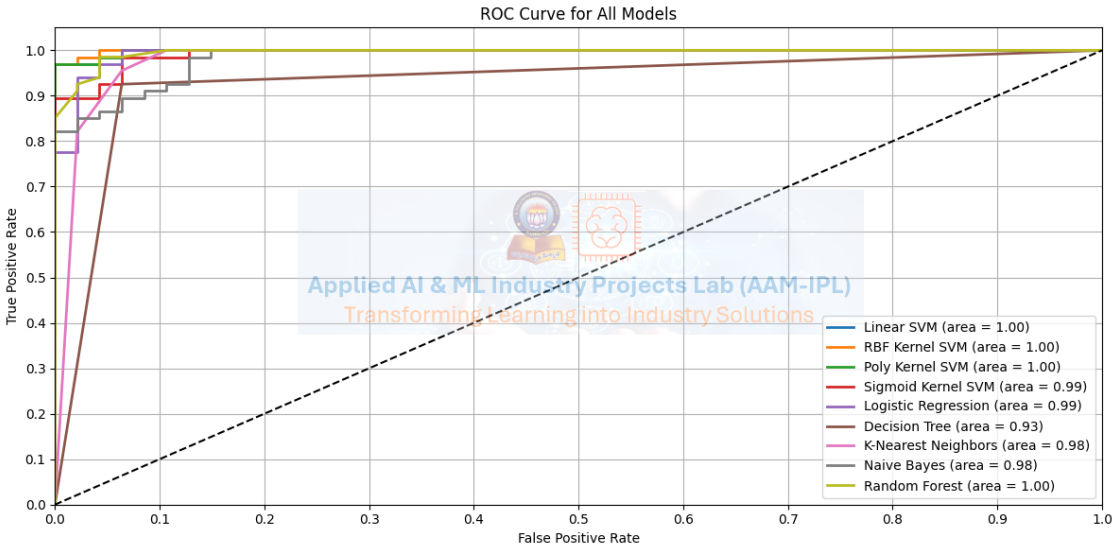

Linear SVM Confusion Matrix
Linear SVM ROC Curve
Linear SVM Precision-Recall Curve
Linear SVM Feature Importance
Linear SVM F1 Score
Linear SVM Accuracy Score Curve
RBF Kernel SVM Confusion Matrix
RBF Kernel SVM ROC Curve
RBF Kernel SVM Precision-Recall Curve
RBF Kernel SVM Feature Importance
RBF Kernel SVM F1 Score
RBF Kernel SVM Accuracy Score Curve
Poly Kernel SVM Confusion Matrix
Poly Kernel SVM ROC Curve
Poly Kernel SVM Precision-Recall Curve
Poly Kernel SVM Feature Importance
Poly Kernel SVM F1 Score
Poly Kernel SVM Accuracy Score Curve
Sigmoid Kernel SVM Confusion Matrix
Sigmoid Kernel SVM ROC Curve
Sigmoid Kernel SVM Precision-Recall Curve
Sigmoid Kernel SVM Feature Importance
Sigmoid Kernel SVM F1 Score
Sigmoid Kernel SVM Accuracy Score Curve
Logistic Regression Confusion Matrix
Logistic Regression ROC Curve
Logistic Regression Precision-Recall Curve
Logistic Regression Feature Importance
Logistic Regression F1 Score
Logistic Regression Accuracy Score Curve
Decision Tree Confusion Matrix
Decision Tree ROC Curve
Decision Tree Precision-Recall Curve
Decision Tree Feature Importance
Decision Tree F1 Score
Decision Tree Accuracy Score Curve
K-Nearest Neighbors Confusion Matrix
K-Nearest Neighbors ROC Curve
K-Nearest Neighbors Precision-Recall Curve
K-Nearest Neighbors Feature Importance
K-Nearest Neighbors F1 Score
K-Nearest Neighbors Accuracy Score Curve
Naive Bayes Confusion Matrix
Naive Bayes ROC Curve
Naive Bayes Precision-Recall Curve
Naive Bayes Feature Importance
Naive Bayes F1 Score
Naive Bayes Accuracy Score Curve
Random Forest Confusion Matrix
Random Forest ROC Curve
Random Forest Precision-Recall Curve
Random Forest Feature Importance
Random Forest F1 Score
Random Forest Accuracy Score Curve
No Feature Importance
True Label
Predicted Label
Malignant
Benign
True Positive Rate
False Positive Rate
Precision
Recall
F1 Score
Accuracy Score
Decision Threshold
Feature Importance
Model
Linear SVM
RBF Kernel SVM
Poly Kernel SVM
Sigmoid Kernel SVM
Logistic Regression
Decision Tree
K-Nearest Neighbors
Naive Bayes
Random Forest

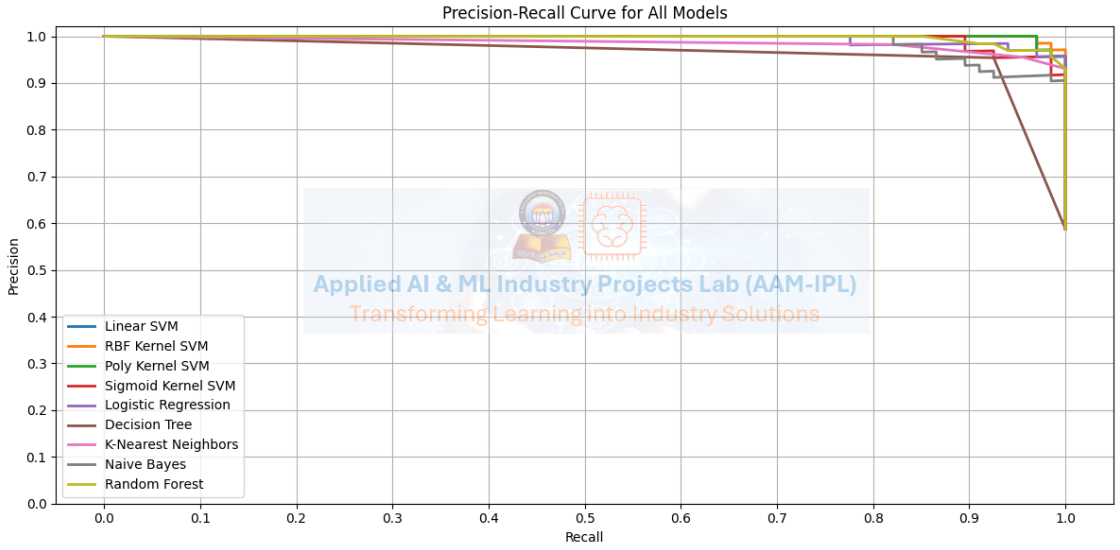
[8]:
```
# Plot relative performance plots of all models - accuracy, ROC curve, PR␣
 ↪curve, F1 score

# Define a dictionary of models
models = {
    'Linear SVM': SVC(kernel='linear', random_state=0, probability=True),
    'RBF Kernel SVM': SVC(kernel='rbf', random_state=0, probability=True),
    'Poly Kernel SVM': SVC(kernel='poly', degree=3, random_state=0,␣
 ↪probability=True),
    'Sigmoid Kernel SVM': SVC(kernel='sigmoid', random_state=0,␣
 ↪probability=True),
    'Logistic Regression': LogisticRegression(max_iter=10000, random_state=0),
    'Decision Tree': DecisionTreeClassifier(criterion='entropy',␣
 ↪random_state=0),
    'K-Nearest Neighbors': KNeighborsClassifier(n_neighbors=5,␣
 ↪metric='minkowski', p=2),
    'Naive Bayes': GaussianNB(),
    'Random Forest': RandomForestClassifier(n_estimators=10,␣
 ↪criterion='entropy', random_state=0)
}

# Split the data
X_train, X_test, Y_train, Y_test = train_test_split(standard_scaled_X, Y,␣
 ↪test_size=0.2, random_state=0)

# Initialize dictionaries to store metrics
accuracy_scores = {}
f1_scores = {}
roc_data = {}
prc_data = {}

# Calculate metrics
for name, model in models.items():
    model.fit(X_train, Y_train)
    Y_pred = model.predict(X_test)
    Y_proba = model.predict_proba(X_test)[:, 1] if hasattr(model,␣
 ↪'predict_proba') else None

    # Accuracy
    accuracy = accuracy_score(Y_test, Y_pred)
    accuracy_scores[name] = accuracy

    # F1 Score
    f1 = f1_score(Y_test, Y_pred)
```

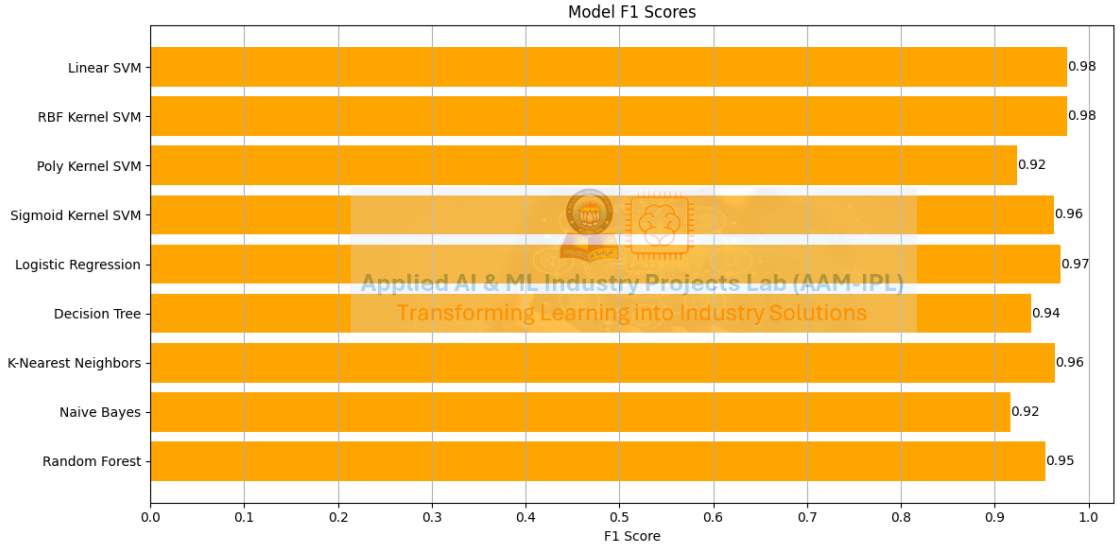
```
    f1_scores[name] = f1

    # ROC Curve
    if Y_proba is not None:
        fpr, tpr, _ = roc_curve(Y_test, Y_proba)
        roc_auc = auc(fpr, tpr)
        roc_data[name] = (fpr, tpr, roc_auc)

        # Precision-Recall Curve
        precision, recall, _ = precision_recall_curve(Y_test, Y_proba)
        prc_data[name] = (precision, recall)

# Plot Accuracy Scores
plt.figure(figsize=(12, 6))
bars = plt.barh(list(accuracy_scores.keys()), list(accuracy_scores.values()),␣
 ↪color='skyblue')
plt.xlabel('Accuracy')
plt.title('Model Accuracy')
plt.gca().invert_yaxis()
plt.grid(axis='x')
# Set x-axis ticks
plt.xticks(np.arange(0, 1.1, 0.1))
add_aam_ipl_wama_revised(plt.gca(), aam_ipl_wama_image, 0.4)

# Add value labels to each bar
for bar in bars:
    plt.text(bar.get_width(), bar.get_y() + bar.get_height()/2,
             f'{bar.get_width():.2f}', va='center', ha='left')
plt.tight_layout()
plt.show()

# Plot ROC Curves
plt.figure(figsize=(12, 6))
for name, (fpr, tpr, roc_auc) in roc_data.items():
    plt.plot(fpr, tpr, lw=2, label=f'{name} (area = {roc_auc:.2f})')
plt.plot([0, 1], [0, 1], 'k--')
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('ROC Curve for All Models')
plt.legend(loc='lower right')
plt.grid()
# Set x-axis ticks
plt.xticks(np.arange(0, 1.1, 0.1))
# Set y-axis ticks
plt.yticks(np.arange(0, 1.1, 0.1))
```

```
add_aam_ipl_wama_revised(plt.gca(), aam_ipl_wama_image, 0.4)
plt.tight_layout()
plt.show()

# Plot Precision-Recall Curves
plt.figure(figsize=(12, 6))
for name, (precision, recall) in prc_data.items():
    plt.plot(recall, precision, lw=2, label=name)
plt.xlabel('Recall')
plt.ylabel('Precision')
plt.title('Precision-Recall Curve for All Models')
plt.legend(loc='best')
plt.grid()
# Set x-axis ticks
plt.xticks(np.arange(0, 1.1, 0.1))
# Set y-axis ticks
plt.yticks(np.arange(0, 1.1, 0.1))
add_aam_ipl_wama_revised(plt.gca(), aam_ipl_wama_image, 0.4)
plt.tight_layout()
plt.show()

# Plot F1 Scores
plt.figure(figsize=(12, 6))
bars = plt.barh(list(f1_scores.keys()), list(f1_scores.values()),␣
 ↪color='orange')
plt.xlabel('F1 Score')
plt.title('Model F1 Scores')
plt.gca().invert_yaxis()
plt.grid(axis='x')
# Set x-axis ticks
plt.xticks(np.arange(0, 1.1, 0.1))
add_aam_ipl_wama_revised(plt.gca(), aam_ipl_wama_image, 0.4)
# Add value labels to each bar
for bar in bars:
    plt.text(bar.get_width(), bar.get_y() + bar.get_height()/2,
             f'{bar.get_width():.2f}', va='center', ha='left')
plt.tight_layout()
plt.show()
```





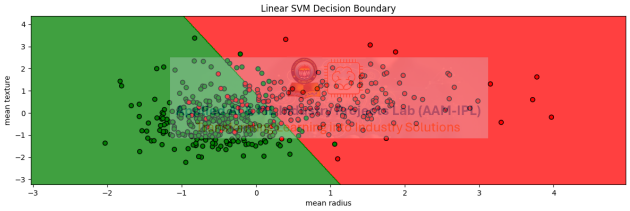


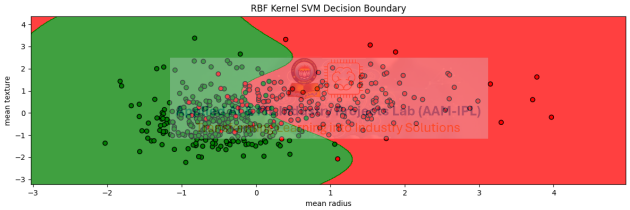


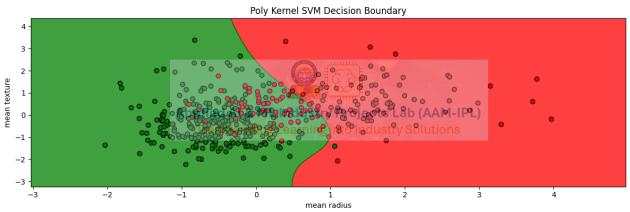
[9]:
```
# Plot decision boundaries
# Define a dictionary of models
models = {
    'Linear SVM': SVC(kernel='linear', random_state=0),
    'RBF Kernel SVM': SVC(kernel='rbf', random_state=0),
    'Poly Kernel SVM': SVC(kernel='poly', degree=3, random_state=0),
    'Sigmoid Kernel SVM': SVC(kernel='sigmoid', random_state=0),
    'Logistic Regression': LogisticRegression(max_iter=10000, random_state=0),
    'Decision Tree': DecisionTreeClassifier(criterion='entropy',␣
 ↪random_state=0),
```

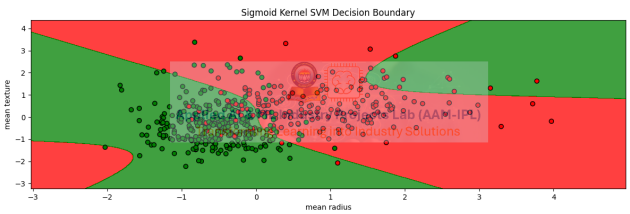
```
    'K-Nearest Neighbors': KNeighborsClassifier(n_neighbors=5,␣
 ↪metric='minkowski', p=2),
    'Naive Bayes': GaussianNB(),
    'Random Forest': RandomForestClassifier(n_estimators=10,␣
 ↪criterion='entropy', random_state=0)
}

# Initialize plot
fig, axs = plt.subplots(len(models), 1, figsize=(12, len(models) * 4))
fig.subplots_adjust(hspace=0.5)

# Split the data
X_train, X_test, Y_train, Y_test = train_test_split(standard_scaled_X, Y,␣
 ↪test_size=0.2, random_state=0)

# Select two features for decision boundary plot
feature1, feature2 = 0, 1  # example feature indices, change as needed

# Loop through models
for idx, (name, model) in enumerate(models.items()):
    # Train and plot decision boundary on two features
    X_train_2d = X_train[:, [feature1, feature2]]
    X_test_2d = X_test[:, [feature1, feature2]]
    model_2d = model.__class__(**model.get_params())  # Create a new instance␣
 ↪with the same parameters
    model_2d.fit(X_train_2d, Y_train)

    X_set, y_set = X_train_2d, Y_train
    X1, X2 = np.meshgrid(np.arange(start=X_set[:, 0].min() - 1, stop=X_set[:,␣
 ↪0].max() + 1, step=0.01),
                         np.arange(start=X_set[:, 1].min() - 1, stop=X_set[:,␣
 ↪1].max() + 1, step=0.01))
    Z = model_2d.predict(np.array([X1.ravel(), X2.ravel()]).T).reshape(X1.shape)

    # Plot the decision boundary
    axs[idx].contourf(X1, X2, Z, alpha=0.75, cmap=ListedColormap(('red',␣
 ↪'green')))
    axs[idx].scatter(X_set[:, 0], X_set[:, 1], c=y_set,␣
 ↪cmap=ListedColormap(('red', 'green')), edgecolor='k')
    axs[idx].set_xlim(X1.min(), X1.max())
    axs[idx].set_ylim(X2.min(), X2.max())
    axs[idx].set_xlabel(bcancer.feature_names[feature1])
    axs[idx].set_ylabel(bcancer.feature_names[feature2])
    axs[idx].set_title(f'{name} Decision Boundary')

    # Add watermark to the current subplot
```

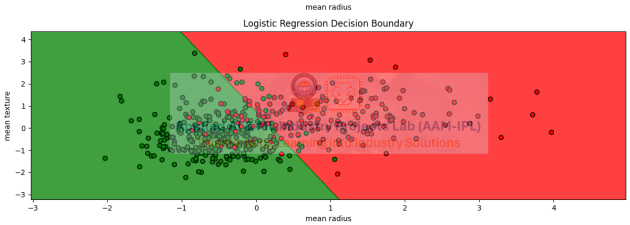
```
    add_aam_ipl_wama_revised(axs[idx], aam_ipl_wama_image, 0.4)

plt.tight_layout()
plt.show()
```

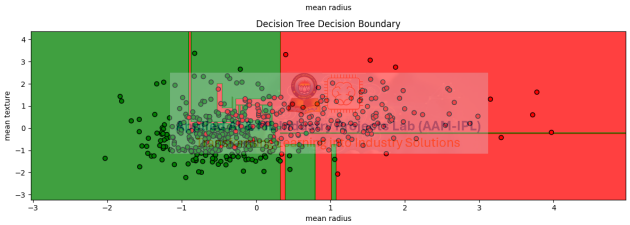

Linear SVM Decision Boundary
mean texture
mean radius

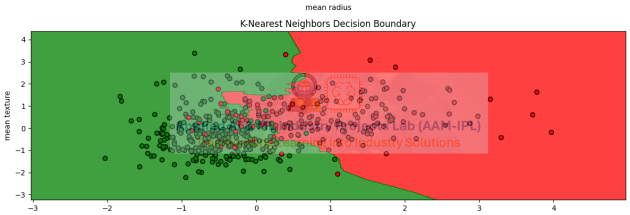

RBF Kernel SVM Decision Boundary
mean texture
mean radius

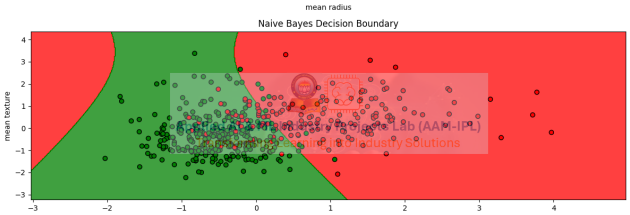

Poly Kernel SVM Decision Boundary
mean texture
mean radius

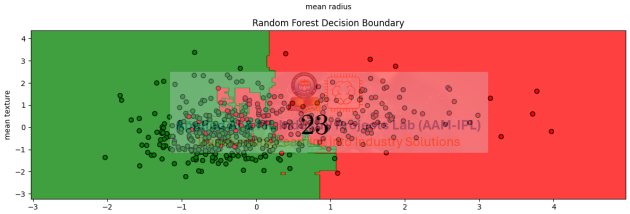

Sigmoid Kernel SVM Decision Boundary
mean texture
mean radius


Logistic Regression Decision Boundary
mean texture
mean radius


Decision Tree Decision Boundary
mean texture
mean radius


K-Nearest Neighbors Decision Boundary
mean texture
mean radius


Naive Bayes Decision Boundary
mean texture
mean radius


Random Forest Decision Boundary
mean texture
mean radius

[11]:
```
!jupyter nbconvert --to pdf AAM-IPL-Wk-5-SVM-ProjectName-Full-Code-V4.ipynb
```

```
C:\Program Files\Python313\Scripts\jupyter-nbconvert.EXE\__main__.py:4:
DeprecationWarning: Parsing dates involving a day of month without a year
specified is ambiguious
and fails to parse leap day. The default behavior will change in Python 3.15
to either always raise an exception or to use a different default year (TBD).
To avoid trouble, add a specific year to the input & format.
See https://github.com/python/cpython/issues/70647.
[NbConvertApp] Converting notebook AAM-IPL-Wk-5-SVM-ProjectName-Full-
Code-V4.ipynb to pdf
[NbConvertApp] Support files will be in AAM-IPL-Wk-5-SVM-ProjectName-Full-
Code-V4_files\
[NbConvertApp] Making directory .\AAM-IPL-Wk-5-SVM-ProjectName-Full-
Code-V4_files
[NbConvertApp] Writing 106321 bytes to notebook.tex
[NbConvertApp] Building PDF
[NbConvertApp] Running xelatex 3 times: ['xelatex', 'notebook.tex', '-quiet']
[NbConvertApp] Running bibtex 1 time: ['bibtex', 'notebook']
[NbConvertApp] WARNING | b had problems, most likely because there were no
citations
[NbConvertApp] PDF successfully created
[NbConvertApp] Writing 3496329 bytes to AAM-IPL-Wk-5-SVM-ProjectName-Full-
Code-V4.pdf
```