Importing Libraries

In [1]:
```
# Basic Libraries for EDA and handling data
import pandas as pd
import seaborn as sns
import numpy as np
import matplotlib.pyplot as plt

# Importing libraries for standardising and spliting data
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split

# Libraries for supervised learning
from sklearn.ensemble import RandomForestClassifier
from sklearn.svm import SVC

# Libraries for unsupervised learning
from sklearn.cluster import KMeans
from sklearn.mixture import GaussianMixture

# Libraries for visualising the resultant decision trees and plots
from sklearn.tree import plot_tree
from mlxtend.plotting import plot_decision_regions

# Libraries for measuring the accuracy of the trained models
from sklearn.metrics import accuracy_score, classification_report
from sklearn.metrics import confusion_matrix, ConfusionMatrixDisplay
from sklearn.metrics import silhouette_score
```

EDA

In [2]:
```
# Loading dataset
df = pd.read_csv('data.csv')
df.head()
```

Out[2]:

	Pelvic Incidence	Pelvic Tilt	Lumbar Lordosis Angle	Sacral Slope	Pelvic Radius	Grade of Spondylolisthesis	Class
0	63.03	22.55	39.61	40.48	98.67	-0.25	AB
1	39.06	10.06	25.02	29.00	114.41	4.56	AB
2	68.83	22.22	50.09	46.61	105.99	-3.53	AB
3	69.30	24.65	44.31	44.64	101.87	11.21	AB
4	49.71	9.65	28.32	40.06	108.17	7.92	AB

In [3]:
```
total_len = df.shape[0]
abnormal_len = df[df["Class"] == "AB"].shape[0]

print(f"Percentage of data in abnormal category: {(abnormal_len/total_len
```

```
Percentage of data in abnormal category: 67.74%
```

In [4]:
```python
df["Class"].unique()
```

Out[4]:
```
array(['AB', 'NO'], dtype=object)
```

In [5]:
```python
df.loc[df["Class"]=='NO', "Class"] = 0 # Normal
df.loc[df["Class"]=='AB', "Class"] = 1 # Abnormal
```

In [6]:
```python
df["Class"] = df["Class"].astype(int)
```

In [7]:
```python
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 310 entries, 0 to 309
Data columns (total 7 columns):
 #   Column                        Non-Null Count  Dtype  
---  ------                        --------------  -----  
 0   Pelvic Incidence              310 non-null    float64
 1   Pelvic Tilt                   310 non-null    float64
 2   Lumbar Lordosis Angle         310 non-null    float64
 3   Sacral Slope                  310 non-null    float64
 4   Pelvic Radius                 310 non-null    float64
 5   Grade of Spondylolisthesis    310 non-null    float64
 6   Class                         310 non-null    int64  
dtypes: float64(6), int64(1)
memory usage: 17.1 KB
```

In [8]:
```python
df.describe()
```

Out[8]:

	Pelvic Incidence	Pelvic Tilt	Lumbar Lordosis Angle	Sacral Slope	Pelvic Radius	Grac Spondylolisth
count	310.000000	310.000000	310.000000	310.000000	310.000000	310.00(
mean	60.496484	17.542903	51.930710	42.953871	117.920548	26.29(
std	17.236109	10.008140	18.553766	13.422748	13.317629	37.558
min	26.150000	-6.550000	14.000000	13.370000	70.080000	-11.06(
25%	46.432500	10.667500	37.000000	33.347500	110.710000	1.60(
50%	58.690000	16.360000	49.565000	42.405000	118.265000	11.765
75%	72.880000	22.120000	63.000000	52.692500	125.467500	41.285
max	129.830000	49.430000	125.740000	121.430000	163.070000	418.54(

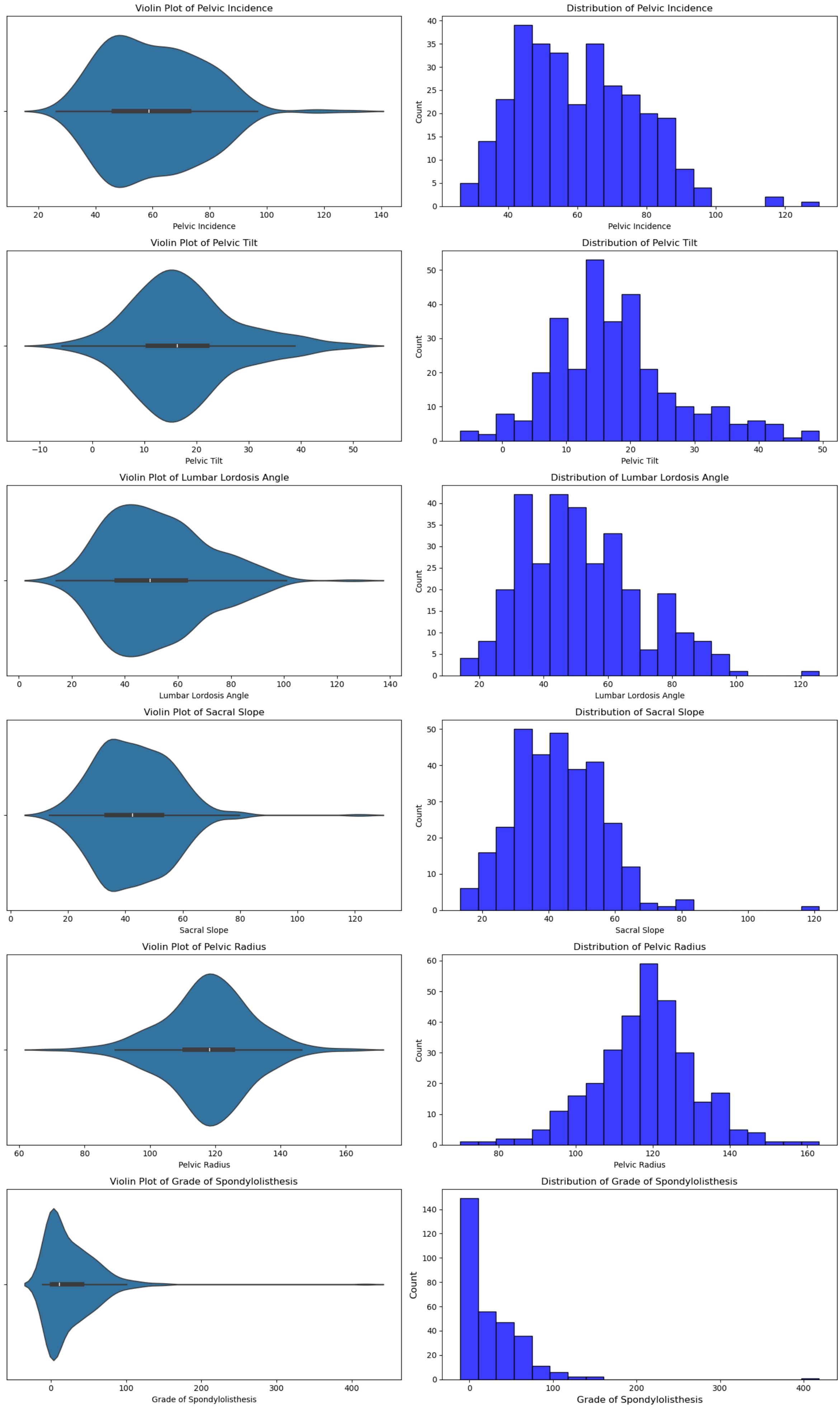
In [9]:
```python
print(df.isnull().sum()) # No missing values
```

```
Pelvic Incidence              0
Pelvic Tilt                   0
Lumbar Lordosis Angle         0
Sacral Slope                  0
Pelvic Radius                 0
Grade of Spondylolisthesis    0
Class                         0
dtype: int64
```

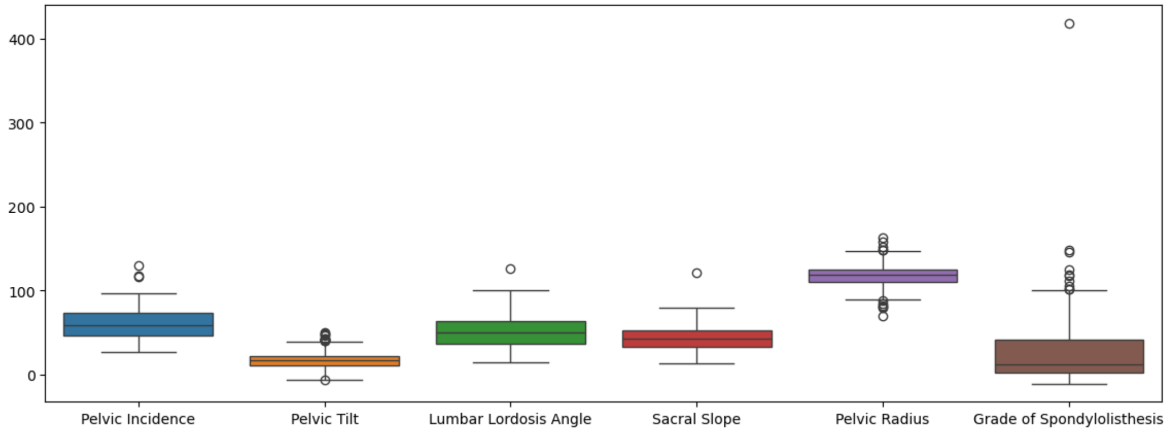
In [10]:
```
print(df.duplicated().sum())  # No duplicate entries
```

```
0
```

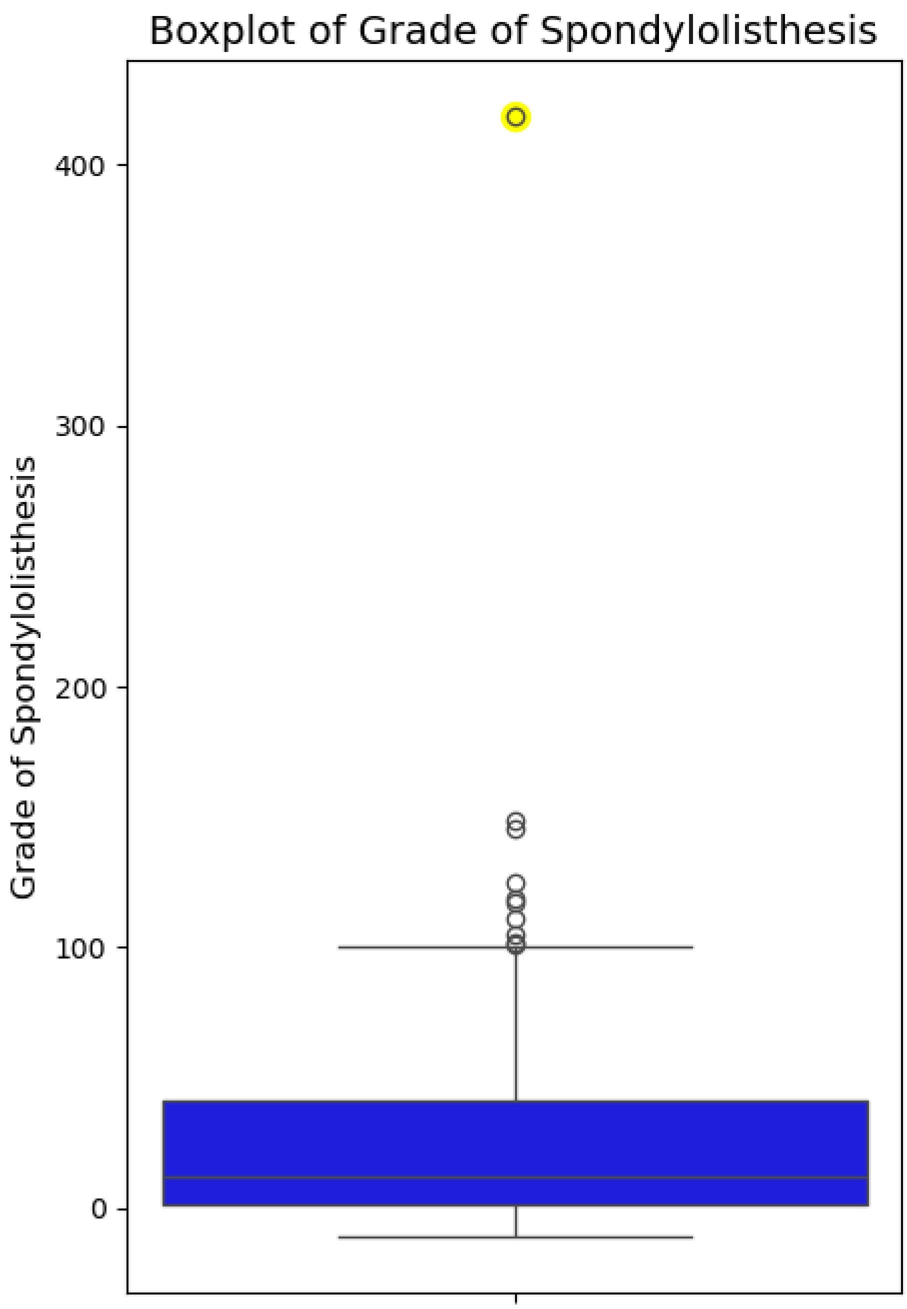
In [11]:
```
feature_columns = [
            'Pelvic Incidence',
            'Pelvic Tilt',
            'Lumbar Lordosis Angle',
            'Sacral Slope',
            'Pelvic Radius',
            'Grade of Spondylolisthesis'
        ]

fig, ax = plt.subplots(len(feature_columns),2, figsize=(15,25))

for idx, col in enumerate(feature_columns):
    ax[idx][0].set_title(f"Violin Plot of {col}")
    sns.violinplot(x=df[col], ax=ax[idx][0])

    sns.histplot(df[col], bins=20, color="blue", ax=ax[idx][1])
    ax[idx][1].set_title(f"Distribution of {col}")
    plt.xlabel(col, fontsize=12)
    plt.ylabel("Count", fontsize=12)

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


Violin Plot of Pelvic Incidence
Pelvic Incidence
Distribution of Pelvic Incidence
Count
Pelvic Incidence
Violin Plot of Pelvic Tilt
Pelvic Tilt
Distribution of Pelvic Tilt
Count
Pelvic Tilt
Violin Plot of Lumbar Lordosis Angle
Lumbar Lordosis Angle
Distribution of Lumbar Lordosis Angle
Count
Lumbar Lordosis Angle
Violin Plot of Sacral Slope
Sacral Slope
Distribution of Sacral Slope
Count
Sacral Slope
Violin Plot of Pelvic Radius
Pelvic Radius
Distribution of Pelvic Radius
Count
Pelvic Radius
Violin Plot of Grade of Spondylolisthesis
Grade of Spondylolisthesis
Distribution of Grade of Spondylolisthesis
Count
Grade of Spondylolisthesis

In [12]:
```
plt.figure(figsize=(14,5))
sns.boxplot(data=df[feature_columns])
plt.show()
```



In [13]:
```
max = df["Grade of Spondylolisthesis"].max()

plt.figure(figsize=(5, 8))
sns.boxplot(y=df["Grade of Spondylolisthesis"], color="blue")

# Highlighting extreme outlier
plt.scatter(0, max, color="yellow", s=100)

plt.title("Boxplot of Grade of Spondylolisthesis", fontsize=14)
plt.ylabel("Grade of Spondylolisthesis", fontsize=12)
plt.show()
```



In [14]:
```
# Creating function to determine number of outliers

df_numeric = df.iloc[:, :-1]

def count_outliers(data):
    Q1 = data.quantile(0.25)
    Q3 = data.quantile(0.75)
    IQR = Q3 - Q1

    # Outlier thresholds- if a value is more than 1.5 times the IQR away
    lower_bound = Q1 - 1.5 * IQR
    upper_bound = Q3 + 1.5 * IQR

    # Separating counts for low and high outliers
    low_outliers = (data < lower_bound).sum()
    high_outliers = (data > upper_bound).sum()

    return pd.Series({"Low Outliers": low_outliers, "High Outliers": high

# Applying function to all numerical columns(so excluding Class)
```

```
outlier_counts = df_numeric.apply(count_outliers)

print("Outlier counts for each variable:")
outlier_counts
```

Outlier counts for each variable:

Out[14]:

	Pelvic Incidence	Pelvic Tilt	Lumbar Lordosis Angle	Sacral Slope	Pelvic Radius	Grade of Spondylolisthesis
Low Outliers	0	1	0	0	6	0
High Outliers	3	12	1	1	5	10
Total Outliers	3	13	1	1	11	10

In [15]:

```
# Counting number of outliers per row
outlier_counts = df_numeric.apply(count_outliers)

outlier_mask = (df_numeric < (df_numeric.quantile(0.25) - 1.5 * (df_numer
               (df_numeric > (df_numeric.quantile(0.75) + 1.5 * (df_numer

# Filtering rows with at least one outlier
outliers_df = df[outlier_mask.sum(axis=1) > 0].copy()

# Adding 'Outlier Count' column (for display)
outliers_df["Outlier Count"] = outlier_mask.sum(axis=1)

print("Outliers found in the dataset:")
outliers_df[["Outlier Count", "Class"] + df_numeric.columns.tolist()]
```

Outliers found in the dataset:

Out[15]:

	Outlier Count	Class	Pelvic Incidence	Pelvic Tilt	Lumbar Lordosis Angle	Sacral Slope	Pelvic Radius	Grade of Spondylolisthesis
9	1	1	36.69	5.01	41.95	31.68	84.24	0.66
51	1	1	74.43	41.56	27.70	32.88	107.95	5.00
65	1	1	83.93	41.29	62.00	42.65	115.01	26.59
71	1	1	86.90	32.93	47.79	53.97	135.08	101.72
75	3	1	70.22	39.82	68.12	30.40	148.53	145.38
76	1	1	86.75	36.04	69.22	50.71	139.41	110.86
83	1	1	81.10	24.79	77.89	56.31	151.84	65.21
84	1	1	76.33	42.40	57.20	33.93	124.27	50.13
85	1	1	45.44	9.91	45.00	35.54	163.07	20.32
95	1	1	57.52	33.65	50.91	23.88	140.98	148.75
112	1	1	42.02	-6.55	67.90	48.58	111.59	27.34
115	3	1	129.83	8.40	48.38	121.43	107.69	418.54
122	1	1	80.07	48.07	52.40	32.01	110.71	67.73
136	1	1	88.02	39.84	81.77	48.18	116.60	56.77
141	2	1	89.50	48.90	72.00	40.60	134.63	118.35
143	1	1	60.63	20.60	64.54	40.03	117.23	104.86
145	1	1	85.64	42.69	78.75	42.95	105.14	42.89
155	1	1	66.80	14.55	72.08	52.25	82.46	41.69
162	2	1	118.14	38.45	50.84	79.70	81.02	74.04
163	1	1	115.92	37.52	76.80	78.41	104.70	81.20
167	1	1	72.34	16.42	59.87	55.92	70.08	12.07
173	1	1	50.83	9.06	56.30	41.76	79.00	23.04
179	1	1	68.72	49.43	68.06	19.29	125.02	54.69
180	1	1	37.90	4.48	24.71	33.42	157.85	33.61
190	1	1	43.72	9.81	52.00	33.91	88.43	40.88
191	1	1	86.47	40.30	61.14	46.17	97.40	55.75
192	1	1	74.47	33.28	66.94	41.19	146.47	124.98
197	2	1	58.83	37.58	125.74	21.25	135.63	117.31
202	2	1	76.31	41.93	93.28	34.38	132.27	101.22
206	1	1	95.48	46.55	59.00	48.93	96.68	77.28
304	1	0	45.08	12.31	44.58	32.77	147.89	-8.94

In [16]:

```
ax = sns.heatmap(df.corr(), linewidth=0.5, annot=True, cmap="coolwarm")
```

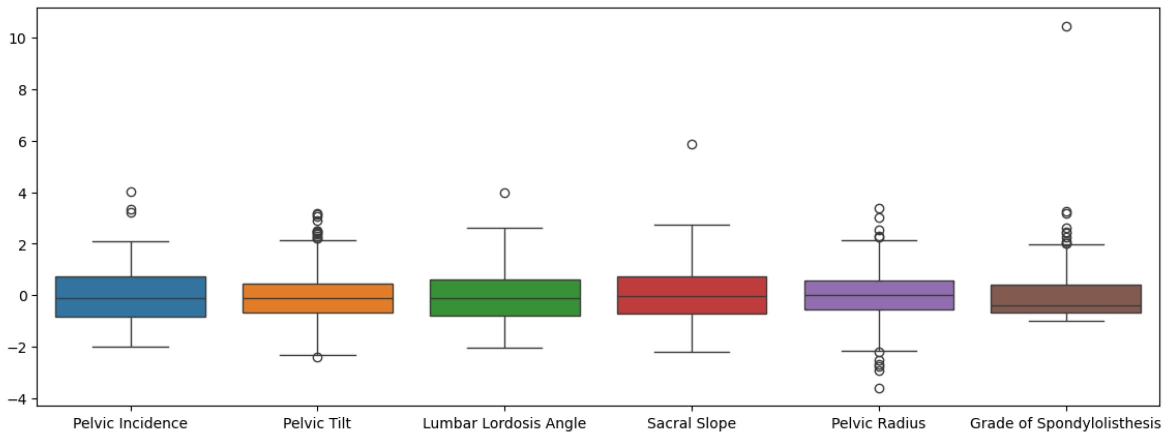
```python
plt.show()
```

In [17]:
```python
# Applying Standardisation
scaler = StandardScaler()
df_scaled = pd.DataFrame(scaler.fit_transform(df.iloc[:, :-1]), columns=f

# Adding back 'Class' column
df_scaled["Class"] = df["Class"]

# Displaying first few rows to check standardisation worked
df_scaled.head()
```

Out[17]:

	Pelvic Incidence	Pelvic Tilt	Lumbar Lordosis Angle	Sacral Slope	Pelvic Radius	Grade of Spondylolisthesis	Class
0	0.147227	0.501111	-0.665128	-0.184602	-1.447831	-0.707946	
1	-1.245707	-0.748891	-1.452763	-1.041250	-0.264028	-0.579673	
2	0.484273	0.468085	-0.099370	0.272823	-0.897295	-0.795417	
3	0.511586	0.711280	-0.411401	0.125820	-1.207159	-0.402332	
4	-0.626819	-0.789923	-1.274614	-0.215943	-0.733337	-0.490069	

In [18]:
```python
plt.figure(figsize=(14,5))
sns.boxplot(data=df_scaled[feature_columns])
plt.show()
```



In [19]:
```
# Applying previously defined function to standardised data
outlier_counts = df_scaled.apply(count_outliers)

print("Outlier counts for each variable:")
print(outlier_counts)
```

```
Outlier counts for each variable:
                Pelvic Incidence  Pelvic Tilt  Lumbar Lordosis Angle  \
Low Outliers                   0            1                      0
High Outliers                  3           12                      1
Total Outliers                 3           13                      1

                Sacral Slope  Pelvic Radius  Grade of Spondylolisthesis  C
lass
Low Outliers               0              6                           0
0
High Outliers              1              5                          10
0
Total Outliers             1             11                          10
0
```

Due to the outliers found in the EDA, standardisation was chosen. Outliers still exist when standardisation is used but they won't distort the scale like min-max scaling would. Min-max scaling is heavily influenced by outliers as one extreme value(e.g. the one in the Grade of Spondylolisthesis column) causes scale to be stretched and all other values to be compressed together. As clustering algorithms are distance based, standardisation prevents features with larger values from dominating the algorithm- k-means clustering and hierarchical clustering are both sensitive to outliers, as is SVM.

Machine Learning

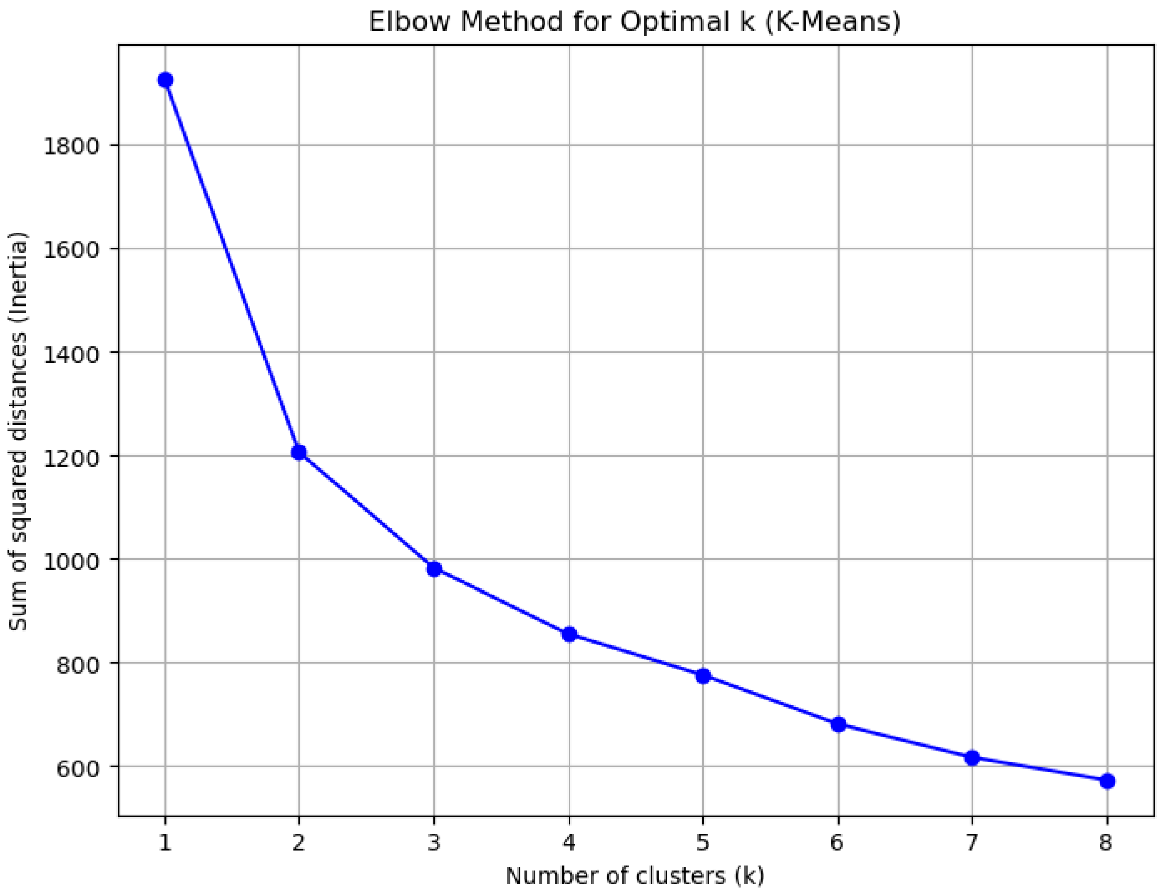
Unsupervised Learning

In this project three unsupervised clustering models are used to discover structure in the data by organising them into groups whose members are similar:

- Naive K-Means Clustering
- Model-Based Clustering (GMM)

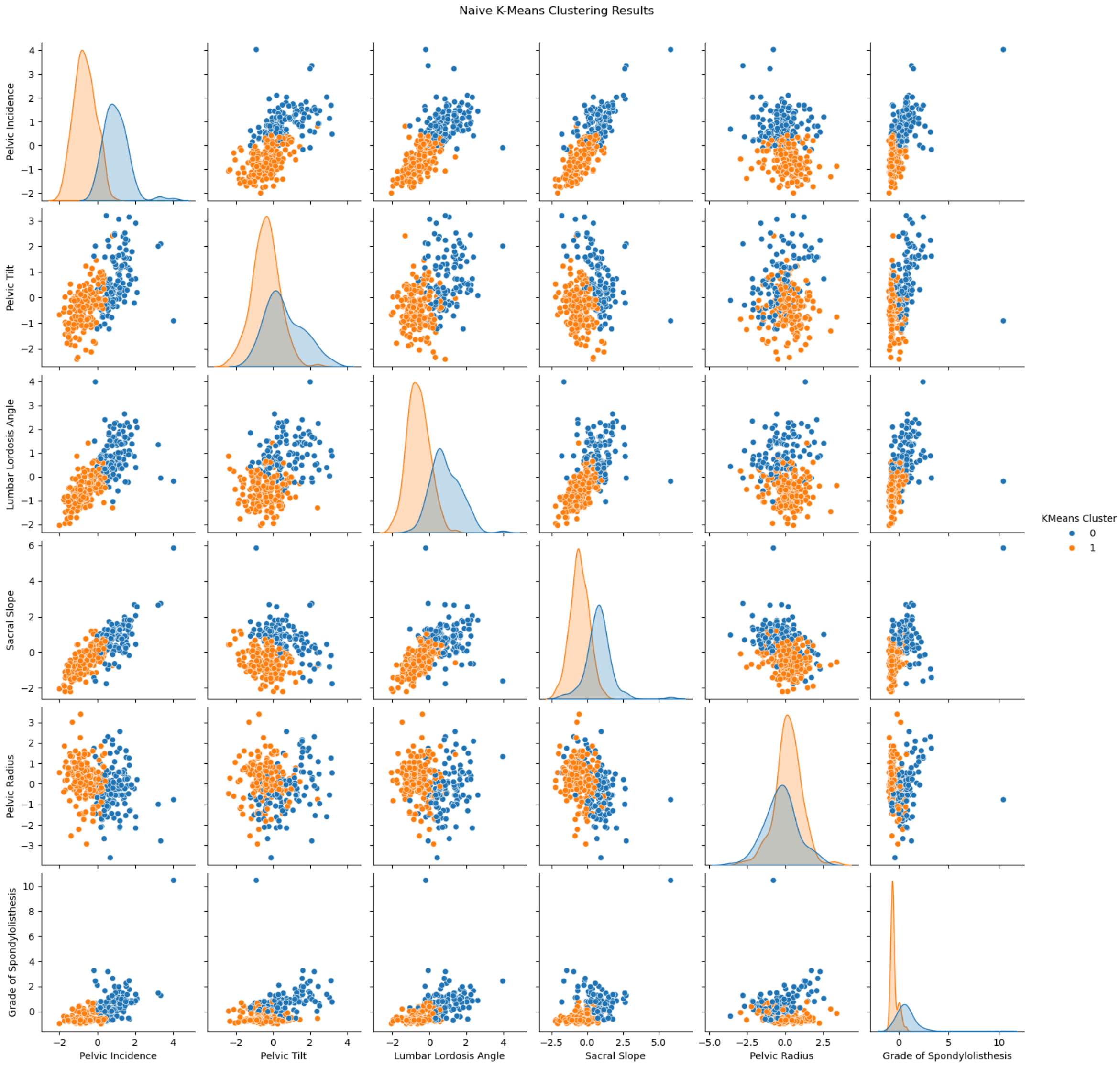
K-Means Method

In [20]:
```
# Determine Optimal K using Elbow Method for K-Means
kMin = 1
kMax = 8
repsPerK = 10

kValues = np.arange(kMin, kMax + 1)
SumOfSquares = np.zeros(len(kValues))

for i, k in enumerate(kValues):
    kmeans = KMeans(n_clusters=k, n_init=repsPerK, random_state=42)
    kmeans.fit(df_scaled)
    SumOfSquares[i] = kmeans.inertia_

# Plotting the Elbow Method
plt.figure(figsize=(8, 6))
plt.plot(kValues, SumOfSquares, 'bo-')
plt.xlabel('Number of clusters (k)')
plt.ylabel('Sum of squared distances (Inertia)')
plt.title('Elbow Method for Optimal k (K-Means)')
plt.grid(True)
plt.show()
```



In [21]:
```
# Applying Naive K-Means with Optimal K
optimal_k = 2
kmeans = KMeans(n_clusters=optimal_k, n_init=repsPerK, random_state=42)
df_scaled['KMeans Cluster'] = kmeans.fit_predict(df_scaled[feature_column

# Visualising K-Means Clustering
sns.pairplot(df_scaled.drop("Class", axis=1), hue='KMeans Cluster', diag_
```

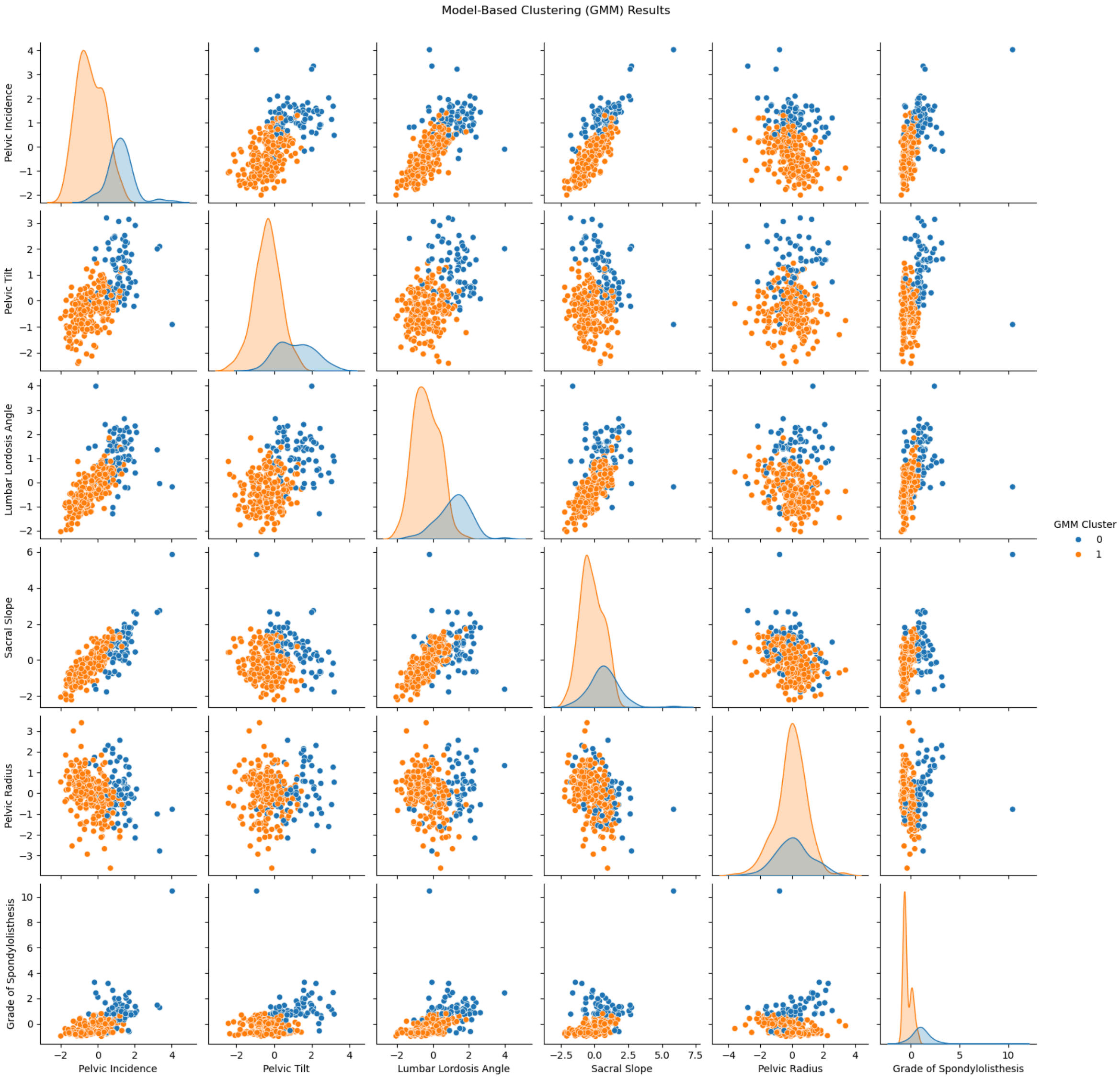
```
plt.suptitle('Naive K-Means Clustering Results', y=1.02)
plt.show()
```



Model-Based Clustering (GMM)

Applying a Gaussian Mixture Model (GMM) with 2 clusters

In [22]:
```
# Model-Based Clustering (Gaussian Mixture Model)
gmm = GaussianMixture(n_components=optimal_k, random_state=42)
df_scaled['GMM Cluster'] = gmm.fit_predict(df_scaled[feature_columns])

# Visualising GMM Clustering
sns.pairplot(df_scaled.drop(["Class", "KMeans Cluster"], axis=1), hue='GM
plt.suptitle('Model-Based Clustering (GMM) Results', y=1.02)
plt.show()
```



Evaluating Models using silhouette scores:

In [23]:
```
# Silhouette Scores to Evaluate Cluster Quality
for method in ['KMeans Cluster', 'GMM Cluster']:
    score = silhouette_score(df_scaled[feature_columns], df_scaled[method
    print(f'Silhouette Score for {method}: {score:.4f}')
```

```
Silhouette Score for KMeans Cluster: 0.3629
Silhouette Score for GMM Cluster: 0.3656
```

GMM has the highest silhouette score (0.3656), suggesting it is the most effective model among the three. The K-Means score is also decent (0.3629), indicating that this method is not far behind.

GMM scores the highest, we experiment with k values for GMM method:

In [24]:
```
# Experimenting with k values
for k in range(2, 6):
    gmm = GaussianMixture(n_components=k, random_state=42)
    cluster_labels = gmm.fit_predict(df_scaled[feature_columns])
    score = silhouette_score(df_scaled[feature_columns], cluster_labels)
    print(f'Silhouette Score for GMM with {k} clusters: {score:.4f}')
```

```
Silhouette Score for GMM with 2 clusters: 0.3656
Silhouette Score for GMM with 3 clusters: 0.2264
Silhouette Score for GMM with 4 clusters: 0.1942
Silhouette Score for GMM with 5 clusters: 0.1266
```

The highest score is with clusters, reinforcing the decision to use k = 2. Increasing the number of clusters reduces the silhouette score, indicating poorer clustering quality with more clusters. This behaviour suggests that the data might not naturally separate into more than 2 clusters.

In [25]:
```
clusters = ["KMeans Cluster", "GMM Cluster"]

for cls_type in clusters:
    print(cls_type)
    total = df_scaled.shape[0]
    first_cluster = df_scaled[df_scaled[cls_type]==1].shape[0]
    print(f"Percentage of datapoints in first cluster: {(first_cluster/to
    print(f"Percentage of datapoints in second cluster: {((total - first_
```

```
KMeans Cluster
Percentage of datapoints in first cluster: 59.35%
Percentage of datapoints in second cluster: 40.65%

GMM Cluster
Percentage of datapoints in first cluster: 75.81%
Percentage of datapoints in second cluster: 24.19%
```

Supervised Learning

Scaling and Splitting Data

In [26]:
```
# Feature selection
X = df_scaled[feature_columns]
y = df_scaled["Class"]
```

In [27]:
```
# Split data into train and test sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,
```

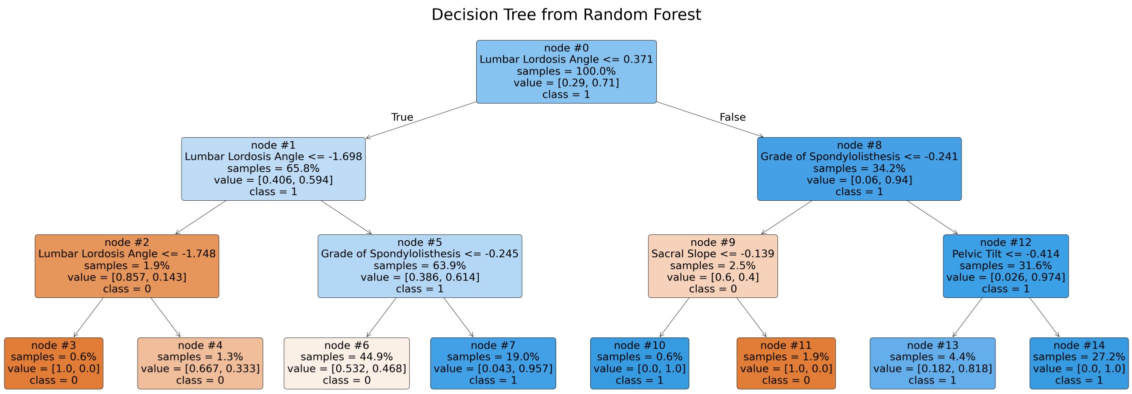
Random Forest

In [28]:
```
# Train Random Forest Classifier
rf_model = RandomForestClassifier(n_estimators=200, random_state=46, max_
rf_model.fit(X_train, y_train)
y_pred_rf = rf_model.predict(X_test)
```

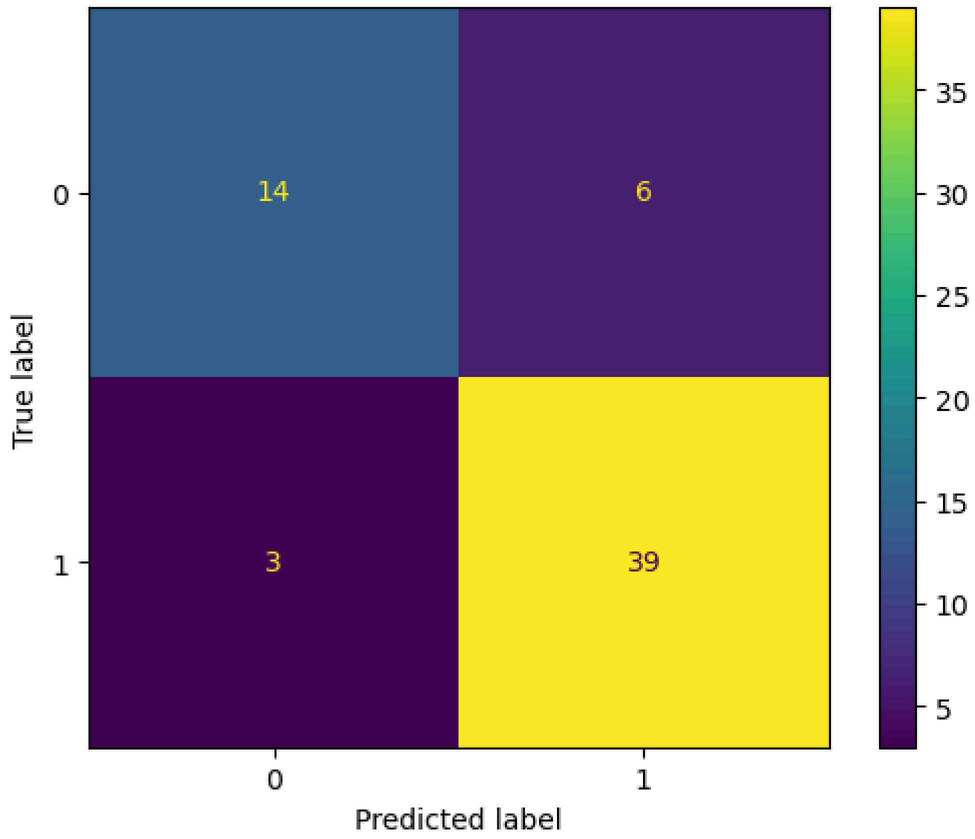
In [29]:
```
# Evaluate models
print("Random Forest Accuracy:", accuracy_score(y_test, y_pred_rf))
print("Random Forest Classification Report:\n", classification_report(y_t
```

```
Random Forest Accuracy: 0.8548387096774194
Random Forest Classification Report:
              precision    recall  f1-score   support

           0       0.82      0.70      0.76        20
           1       0.87      0.93      0.90        42

    accuracy                           0.85        62
   macro avg       0.85      0.81      0.83        62
weighted avg       0.85      0.85      0.85        62
```

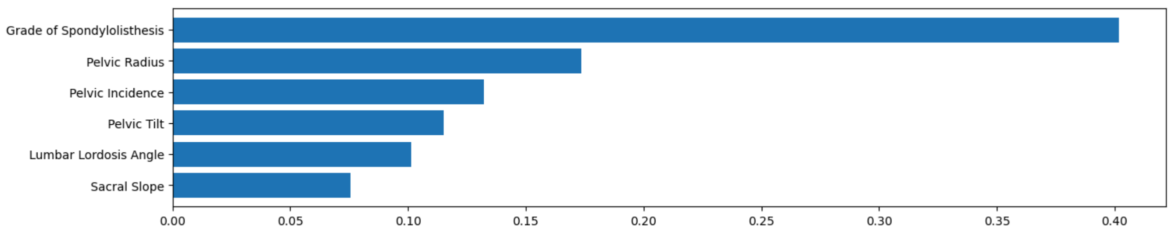
In [30]:
```python
# Visualisation: Plot one of the trees from the Random Forest
# Set figure size
fig, ax = plt.subplots(figsize=(60, 20))
plot_tree(
    rf_model.estimators_[0],
    feature_names=X.columns,
    class_names=["0", "1"],
    filled=True,
    fontsize=30,  # Adjust font size for readability
    rounded=True,  # Rounded boxes for better aesthetics
    proportion=True,  # Show proportions instead of absolute values
    impurity=False,  # Hide impurity to make it cleaner
    node_ids=True,  # Show node IDs
    ax=ax
)
plt.title("Decision Tree from Random Forest", fontsize=45)
plt.show()
```



In [31]:
```python
cm = confusion_matrix(y_test, y_pred_rf, labels=rf_model.classes_, sample
disp = ConfusionMatrixDisplay(confusion_matrix=cm,
                              display_labels=rf_model.classes_)
disp.plot()
plt.show()
```



In [32]:
```
importances = rf_model.feature_importances_
indices = np.argsort(importances)

fig, ax = plt.subplots(figsize=(15,3))
ax.barh(range(len(importances)), importances[indices])
ax.set_yticks(range(len(importances)))
_ = ax.set_yticklabels(np.array(X_train.columns)[indices])
```



Comparisons and Discussion

In [33]:
```
outlier_indices = outliers_df.index

# Select the GMM cluster assignments for data points found to be outliers
outlier_clusters = df_scaled.loc[outlier_indices, "GMM Cluster"]
# Count how many outliers are in each cluster
outlier_cluster_counts = outlier_clusters.value_counts()

print(outlier_cluster_counts) # 22 of the outliers are in cluster 0, we c
```

```
GMM Cluster
0    22
1     9
Name: count, dtype: int64
```

In [34]:
```
df_scaled["GMM Cluster"] = df_scaled["GMM Cluster"].apply(lambda x: 1 if
```

In [35]:
```python
# Count number of data points in each GMM cluster
cluster_counts = df_scaled["GMM Cluster"].value_counts()
print(cluster_counts) # 235 in abnormal, 75 in normal
```

```
GMM Cluster
0    235
1     75
Name: count, dtype: int64
```

In [36]:
```python
test_indices = X_test.index
print(test_indices)
```

```
Index([  4, 230, 102,  41, 212,  95, 262, 224, 273,  11, 171, 294, 130, 30
1,
       174, 136, 247, 134, 100, 173, 297,  61, 161, 103,  26,   0, 135, 12
2,
       239, 142,  62,  27,  71,  98, 207, 211, 270,  36,  14, 292, 123, 23
1,
       233, 150,  40,  32, 284, 203, 302,  80, 194, 162,  47, 261, 205, 28
1,
        89,  34, 141,  51, 131, 296],
      dtype='int64')
```

In [37]:
```python
df_test_scaled = df_scaled.loc[test_indices]  # Keep only test set rows
print(df_test_scaled)
```

```
     Pelvic Incidence  Pelvic Tilt  Lumbar Lordosis Angle  Sacral Slope  \
4           -0.626819    -0.789923              -1.274614     -0.215943   
230          0.297154     0.560159               0.574897     -0.036107   
102          0.575509    -0.407617               0.500399      1.042911   
41          -0.816844    -0.915024              -1.235745     -0.365931   
212         -0.937716    -0.859980              -0.271581     -0.562184   
..                ...          ...                    ...           ...   
34          -0.052096     1.446869              -0.289935     -1.145719   
141          1.685439     3.138225               1.083432     -0.175648   
51           0.809698     2.403636              -1.308084     -0.751721   
131          0.539479    -0.376592               0.327648      0.973513   
296         -1.210840    -0.133397              -0.823843     -1.455395   

     Pelvic Radius  Grade of Spondylolisthesis  Class  KMeans Cluster  \
4        -0.733337                   -0.490069      1               1   
230       0.467012                   -0.810084      0               1   
102      -1.171811                   -0.020181      1               0   
41       -0.183553                   -0.646610      1               1   
212       0.849830                   -0.568206      0               1   
..             ...                         ...    ...             ...   
34        0.106005                   -0.662077      1               1   
141       1.256715                    2.454868      1               0   
51       -0.749883                   -0.567940      1               1   
131       0.075921                   -0.223657      1               0   
296       1.052897                   -0.833819      0               1   

     GMM Cluster  
4              0  
230            0  
102            0  
41             0  
212            0  
..           ...  
34             0  
141            1  
51             1  
131            0  
296            0  

[62 rows x 9 columns]
```

In [38]:

```
df_test_scaled["RF_Prediction"] = y_pred_rf
```

In [45]:

```
# Similarities in test set

# Similarity between GMM and Class Labels
gmm_similarity_test = (df_test_scaled["Class"] == df_test_scaled["GMM Clu

# Similarity between RF and Class Labels
rf_similarity_test = (df_test_scaled["Class"] == df_test_scaled["RF_Predi

# Similarity between GMM and RF Labels
gmm_rf_similarity_test = (df_test_scaled["GMM Cluster"] == df_test_scaled

print(f"Similarity between GMM and True Labels: {gmm_similarity_test:.2%}
print(f"Similarity between RF and True Labels: {rf_similarity_test:.2%}")
print(f"Similarity between GMM and RF Labels: {gmm_rf_similarity_test:.2%
```

```
Similarity between GMM and True Labels: 54.84%
Similarity between RF and True Labels: 85.48%
Similarity between GMM and RF Labels: 56.45%
```

In [40]:

```
# Similarity between GMM and Class Labels- whole dataset
gmm_similarity = (df_scaled["Class"] == df_scaled["GMM Cluster"]).mean()
print(f"Similarity between GMM and True Labels: {gmm_similarity:.2%}")
```

```
Similarity between GMM and True Labels: 54.52%
```

In [41]:

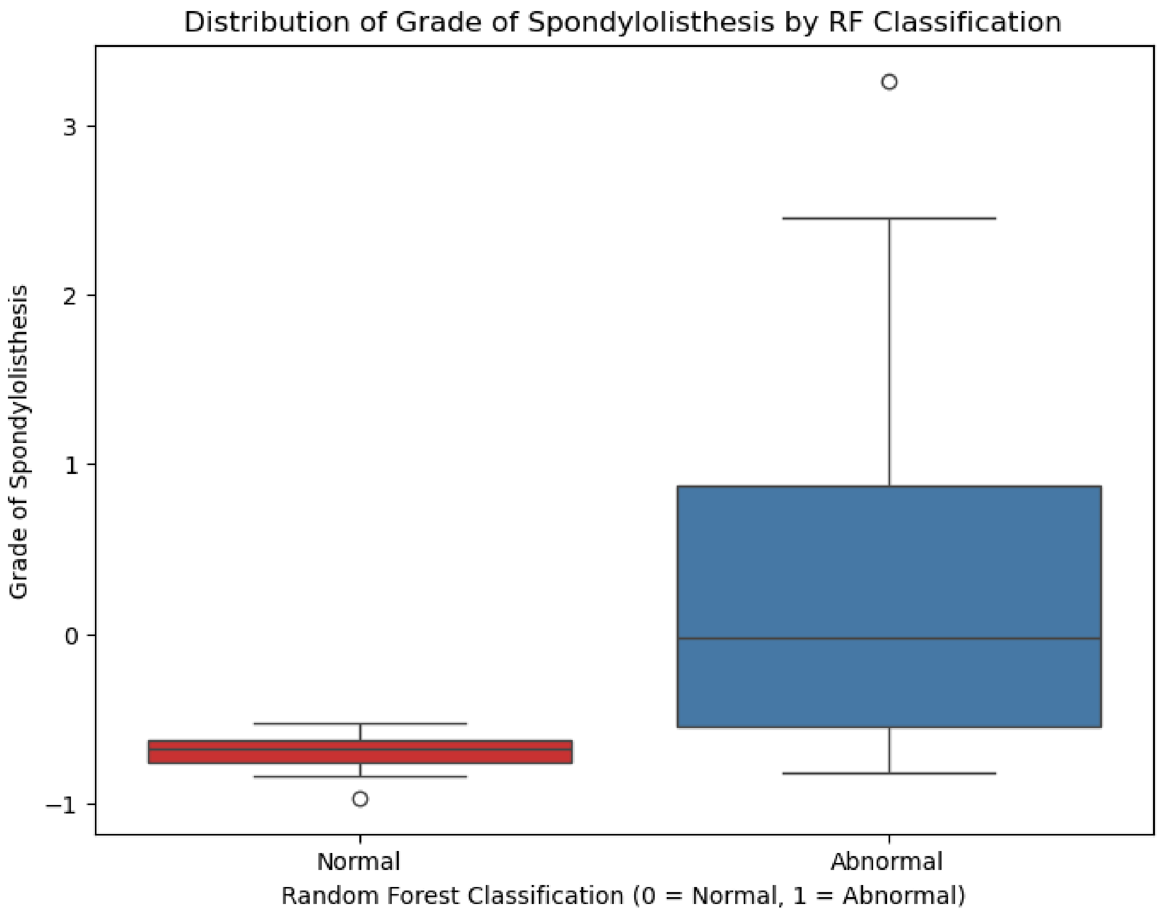
```
# Count occurrences of '1' (abnormal) for test set
rf_count = df_test_scaled["RF_Prediction"].value_counts()[1]
gmm_count = df_test_scaled["GMM Cluster"].value_counts()[1]
true_count = df_test_scaled["Class"].value_counts()[1]

# Print results
print(f"Number of abnormal cases in Actual Class: {true_count}")
print(f"Number of abnormal cases in Random Forest: {rf_count}")
print(f"Number of abnormal cases in GMM Clustering: {gmm_count}")
```

```
Number of abnormal cases in Actual Class: 42
Number of abnormal cases in Random Forest: 45
Number of abnormal cases in GMM Clustering: 18
```

In [42]:

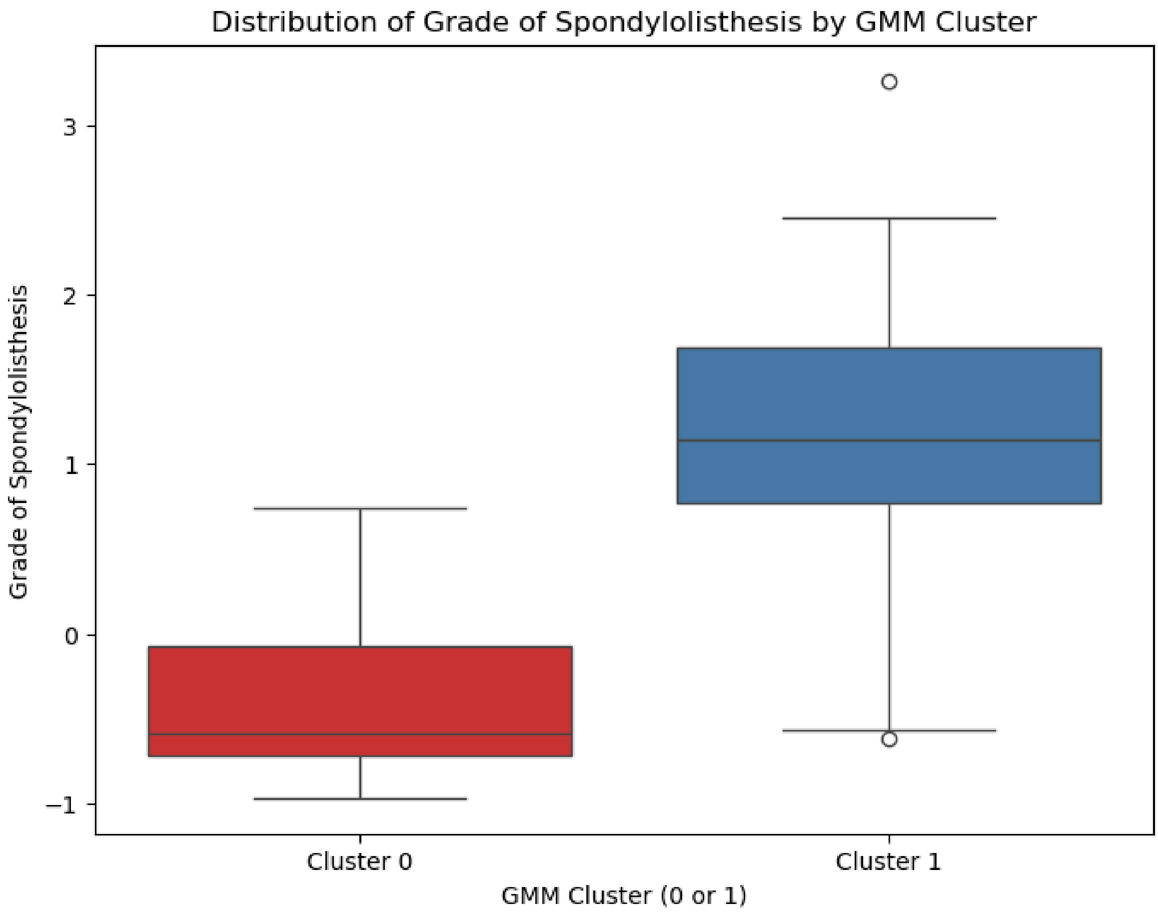
```
plt.figure(figsize=(8,6))
sns.boxplot(x=df_test_scaled["RF_Prediction"], y=df_test_scaled["Grade of

plt.xlabel("Random Forest Classification (0 = Normal, 1 = Abnormal)")
plt.ylabel("Grade of Spondylolisthesis")
plt.title("Distribution of Grade of Spondylolisthesis by RF Classificatio
plt.xticks([0,1], ["Normal", "Abnormal"])
plt.show()
```

```
/var/folders/3f/ll25jtyn6lb30vmzj6d4dfsm0000gn/T/ipykernel_3018/299157802
2.py:2: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be remove
d in v0.14.0. Assign the `x` variable to `hue` and set `legend=False` for
the same effect.

  sns.boxplot(x=df_test_scaled["RF_Prediction"], y=df_test_scaled["Grade o
f Spondylolisthesis"], palette="Set1")
```

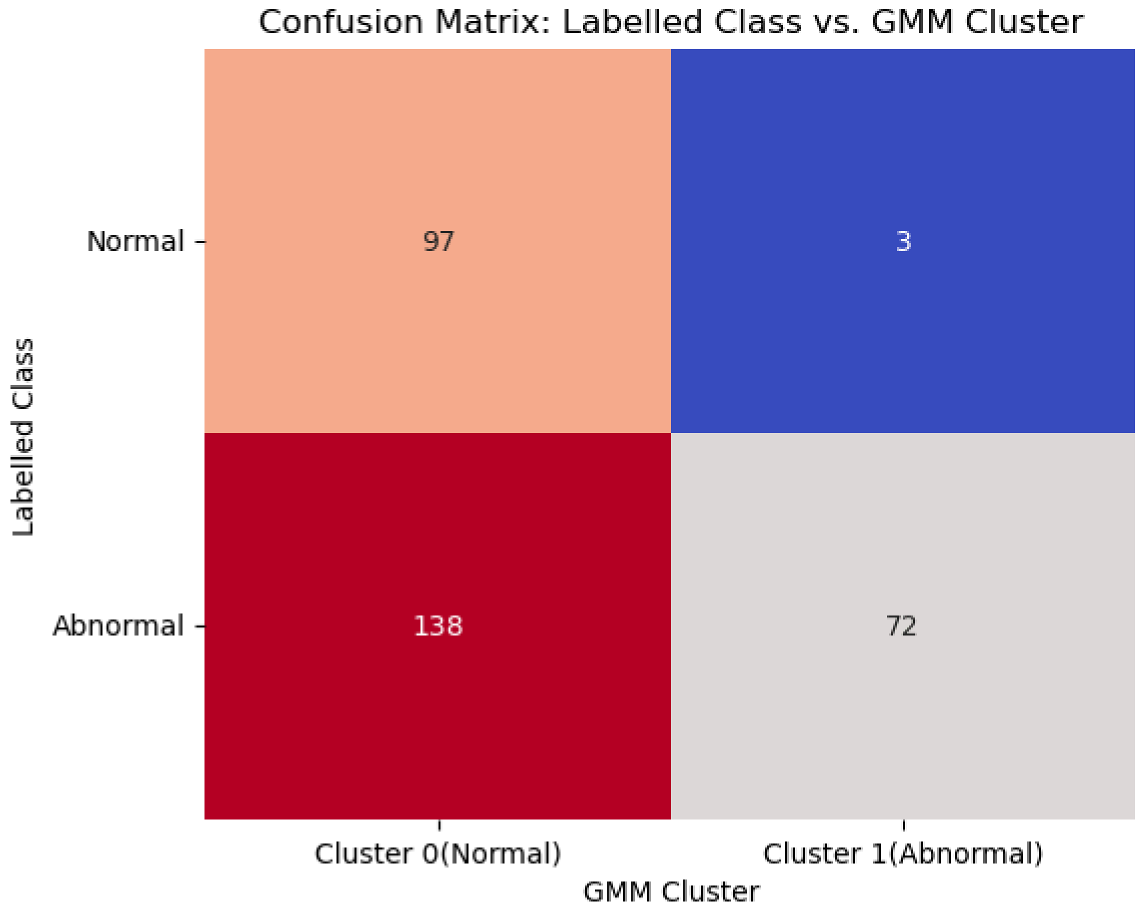


In [43]:
```
plt.figure(figsize=(8,6))
sns.boxplot(x=df_test_scaled["GMM Cluster"], y=df_test_scaled["Grade of S

plt.xlabel("GMM Cluster (0 or 1)")
plt.ylabel("Grade of Spondylolisthesis")
plt.title("Distribution of Grade of Spondylolisthesis by GMM Cluster")
plt.xticks([0,1], ["Cluster 0", "Cluster 1"])
plt.show()
```

```
/var/folders/3f/ll25jtyn6lb30vmzj6d4dfsm0000gn/T/ipykernel_3018/116962275.
py:2: FutureWarning:

Passing `palette` without assigning `hue` is deprecated and will be remove
d in v0.14.0. Assign the `x` variable to `hue` and set `legend=False` for
the same effect.

  sns.boxplot(x=df_test_scaled["GMM Cluster"], y=df_test_scaled["Grade of
Spondylolisthesis"], palette="Set1")
```



In [44]:
```
cluster_comparison = pd.crosstab(df_scaled["Class"], df_scaled["GMM Clust
# Good at identifying abnormal with very few false positives

plt.figure(figsize=(6,5))
sns.heatmap(cluster_comparison, annot=True, fmt="d", cmap="coolwarm", cba

plt.xlabel("GMM Cluster")
plt.ylabel("Labelled Class")
plt.title("Confusion Matrix: Labelled Class vs. GMM Cluster")
plt.xticks(ticks=[0.5,1.5], labels=["Cluster 0(Normal)", "Cluster 1(Abnor
plt.yticks(ticks=[0.5,1.5], labels=["Normal", "Abnormal"], rotation=0)

plt.show()
```


Confusion Matrix: Labelled Class vs. GMM Cluster
Normal
Abnormal
Labelled Class
97
3
138
72
Cluster 0(Normal)
Cluster 1(Abnormal)
GMM Cluster

In [ ]: