Classification

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I. Unsupervised Clustering Method /Supervised Classification Method

Unsupervised clustering, exemplified by methods like K-means, explores data without labeled outcomes, grouping similar points based on feature similarities alone. It's ideal for discovering hidden patterns when no prior classification exists. Supervised classification, like k-nearest neighbors (KNN) and decision trees, requires labeled data to predict the category of new observations. With a defined target outcome, supervised methods typically outperform unsupervised ones, making accurate predictions when classes are known in advance.

II. Exploratory Data Analysis

The dataset created by Dr. Henrique da Mota consists of six biomechanical attributes, specifically designed to classify orthopedic patients into two categories: normal and abnormal. These features include pelvic incidence, pelvic tilt, lumbar lordosis angle, sacral slope, pelvic radius, and grade of spondylolisthesis. This dataset reveals a total of **310 entries**, with **100** being classified as **normal** and **210** as **abnormal**, indicating a dataset with complete information and no missing values.

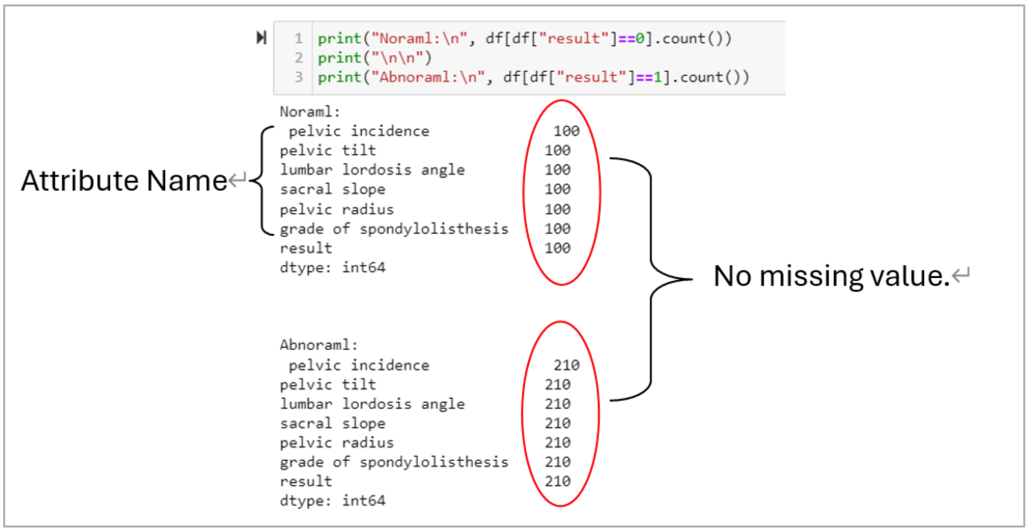


Figure 1: Dataset information

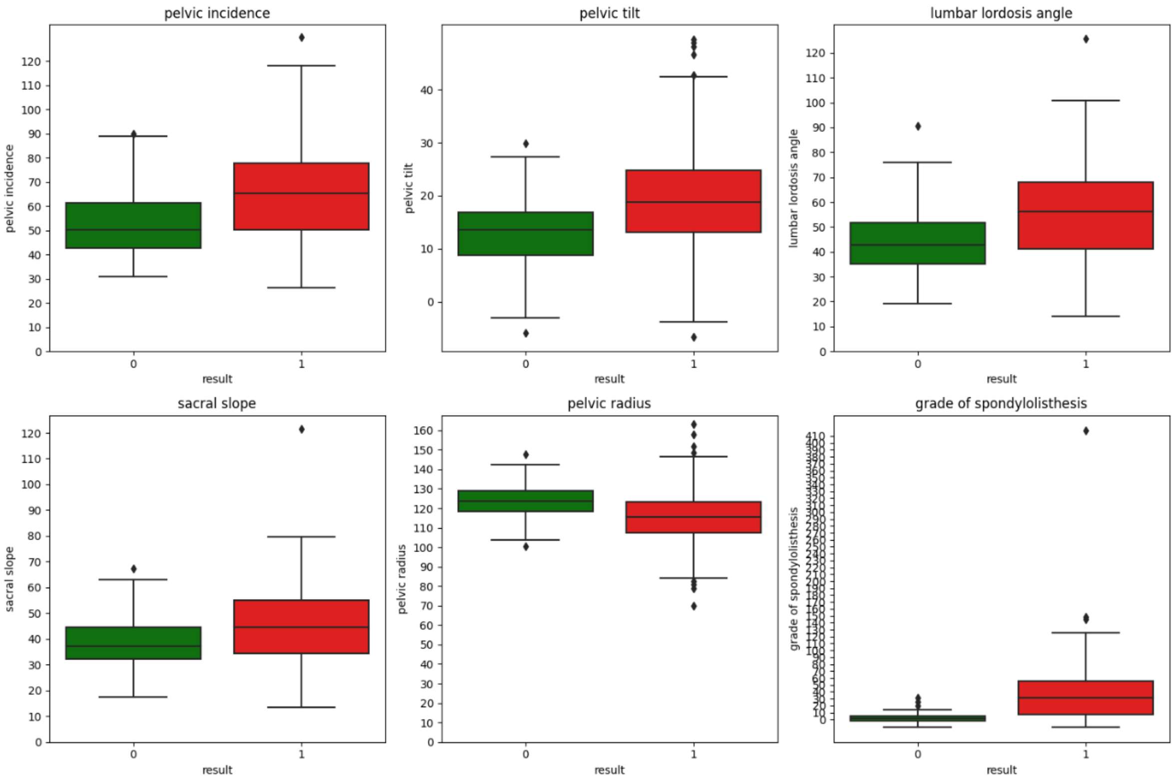


Figure 2: Box plots for all features

The graphical representation through box plots, depicted in Figure 2, uses green to signify the normal (0) category, and red to represent the abnormal (1) category. Table 1 summarizes the interquartile ranges (25th to 75th percentiles) for each biomechanical feature, comparing patients classified as normal versus abnormal.

Feature	Normal IQR	versus	Abnormal IQR
Pelvic Incidence	42.8 - 61.4	<	50.1 - 77.6
Pelvic Tilt	8.8 - 16.8	<	13.0 - 24.8
Lumbar Lordosis Angle	35.0 - 51.6	<	41.2 - 68.1
Sacral Slope	32.3 - 44.6	<	34.4 - 55.1
Pelvic Radius	118.2 - 129.0	>	107.3 - 123.1
Grade of Spondylolisthesis	-1.5 - 4.97	<	7.3 - 55.4

Table 1: IQR of features classified as normal and abnormal people.

It is noteworthy that the "**grade of spondylolisthesis**" exhibits a stark distinction between the normal and abnormal groups, with **little to no overlap in the data**. This clear demarcation emphasizes the importance of the grade of spondylolisthesis as a potentially critical feature in diagnosing abnormal conditions in orthopedic patients. Moreover, except for the **pelvic radius** feature for patients with **abnormalities is slightly lower than that of normal individuals**, other features of abnormal patients tend to have higher measurements compared to normal individuals.

III. Results and Discussion

A. Supervised Classification Results

Two unsupervised machine learning methods were employed: a **decision tree** and **KNN**. The decision tree was selected for its ability to reveal the most significant features that influence the classification between the two classes. KNN was chosen for its efficacy in classification problems where the decision boundary is not linear, as it can capture the complexity of the feature space. In this case, cross-validation was used to determine the optimal K value, which was found to be **7**, as it yielded the highest accuracy.

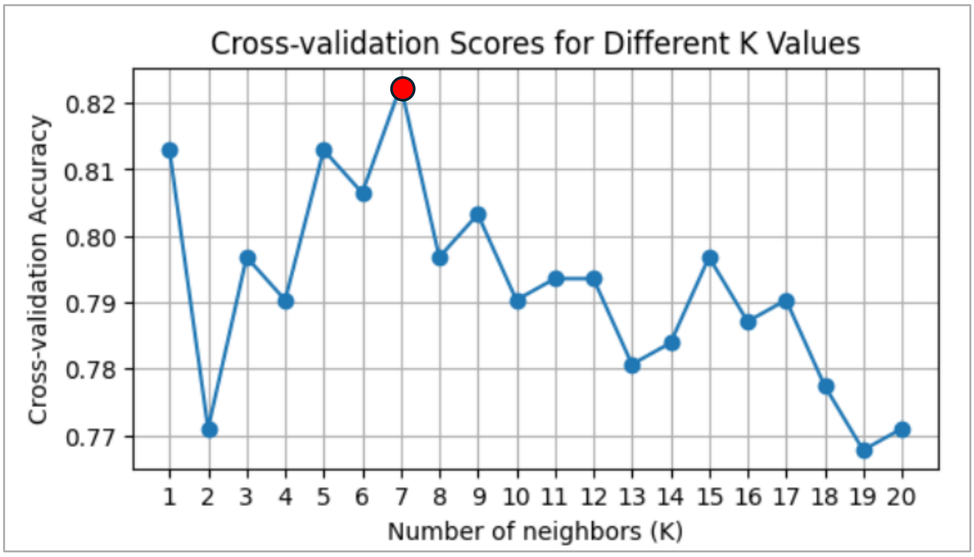


Figure 3:Cross-validation Scores for Different K values

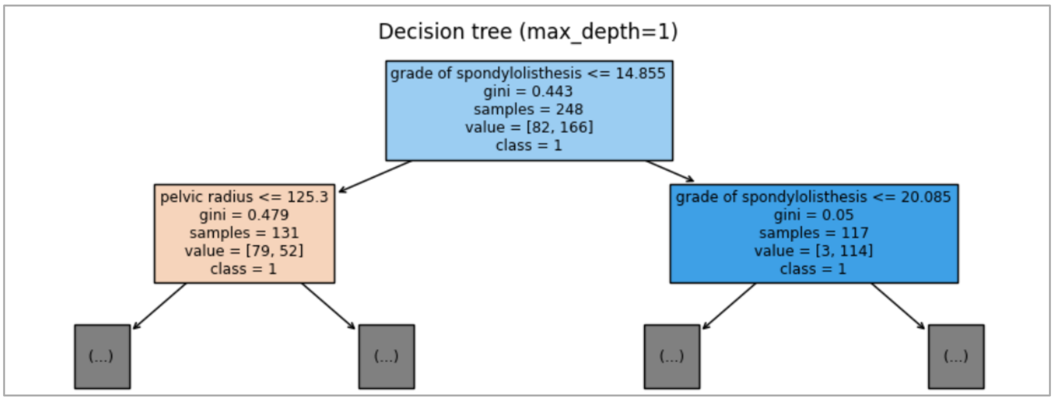


Figure 4: Decision tree (max_depth=1)

The initial levels of the decision tree indicate the importance of the feature "**grade of spondylolisthesis**," with a primary node cutoff at **≤ 14.855**. The secondary nodes focus on **"pelvic radius" ≤ 125.3** and **"grade of spondylolisthesis" ≤ 20.085**. These findings corroborate the inferences made during the exploratory data analysis, which suggested that "grade of spondylolisthesis" and "pelvic radius" are critical in differentiating between the two classes.

To evaluate model performance, a confusion matrix, and accuracy rates were employed. The confusion matrix is crucial in medical diagnostic problems since it allows for the minimization of false negatives, which are significantly more consequential in clinical settings. A false negative, or failing to identify a patient with the condition, could lead to a lack of necessary treatment and worsen the patient's prognosis.

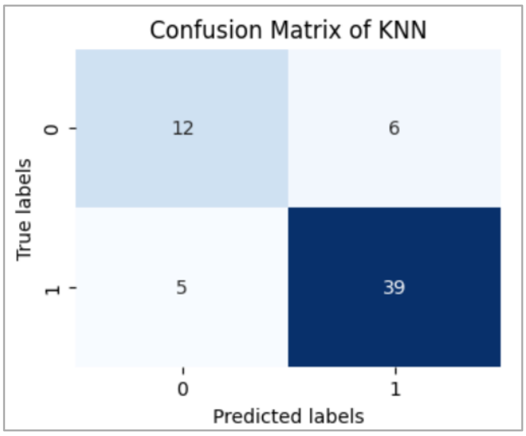


Figure 5(A) Confusion matrix of KNN

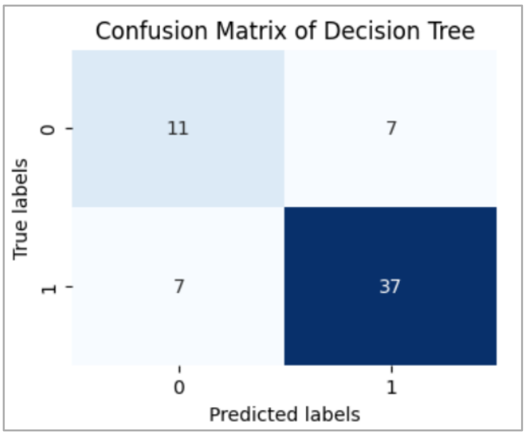


Figure 5(B) Confusion matrix of Decision tree

The comparison of model accuracies is as follows:

Model	Accuracy
Decision Tree	0.77
KNN	0.82

Comparing the confusion matrices and accuracy rates between models, KNN outperforms the decision tree. KNN's effectiveness may lie in its capacity to capture intricate patterns within the data.

B. Unsupervised Clustering Results

I chose the K Means algorithm to cluster my data, evaluating its performance using the Adjusted Rand Index and the Silhouette Score, which turned out to be 0.11 and 0.45, respectively. These results were disappointing, indicating a poor clustering outcome.

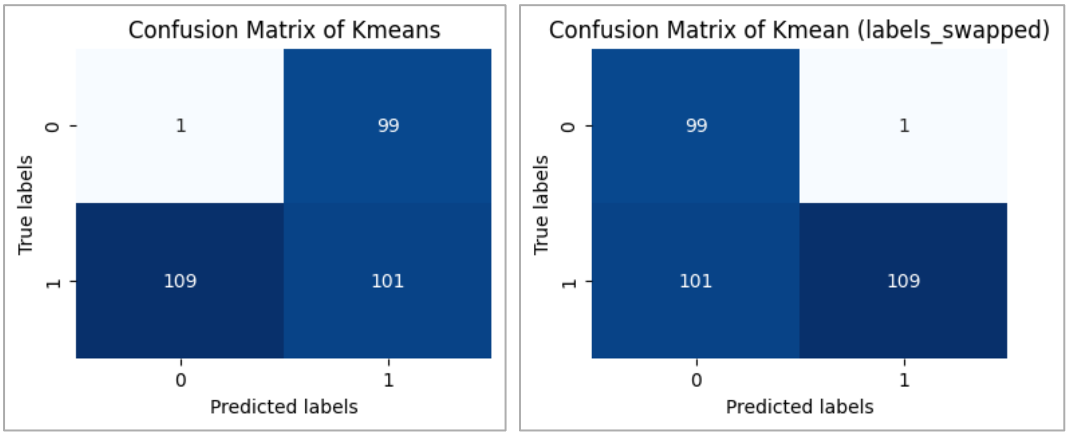


Figure 6(A) Confusion matrix of Kmeans

Figure 6(B) Confusion matrix of Kmeans(labels_swapped)

Upon reviewing the confusion matrix in Figure 6(A) and 6(B), I observed that the True Positives (TP) and True Negatives (TN) were lower than the False Positives (FP) and False Negatives (FN), suggesting the clusters were inverted. After swapping the labels, it appeared that 207 out of 300 instances were correctly classified. However, the presence of nearly one-third as False Negatives underscores a significant issue in correctly identifying patients.

Figure 7 illustrates feature interactions among actual and predicted clusters, revealing inadequate separation. Despite evident distinctions, the overlap indicates insufficient separation.

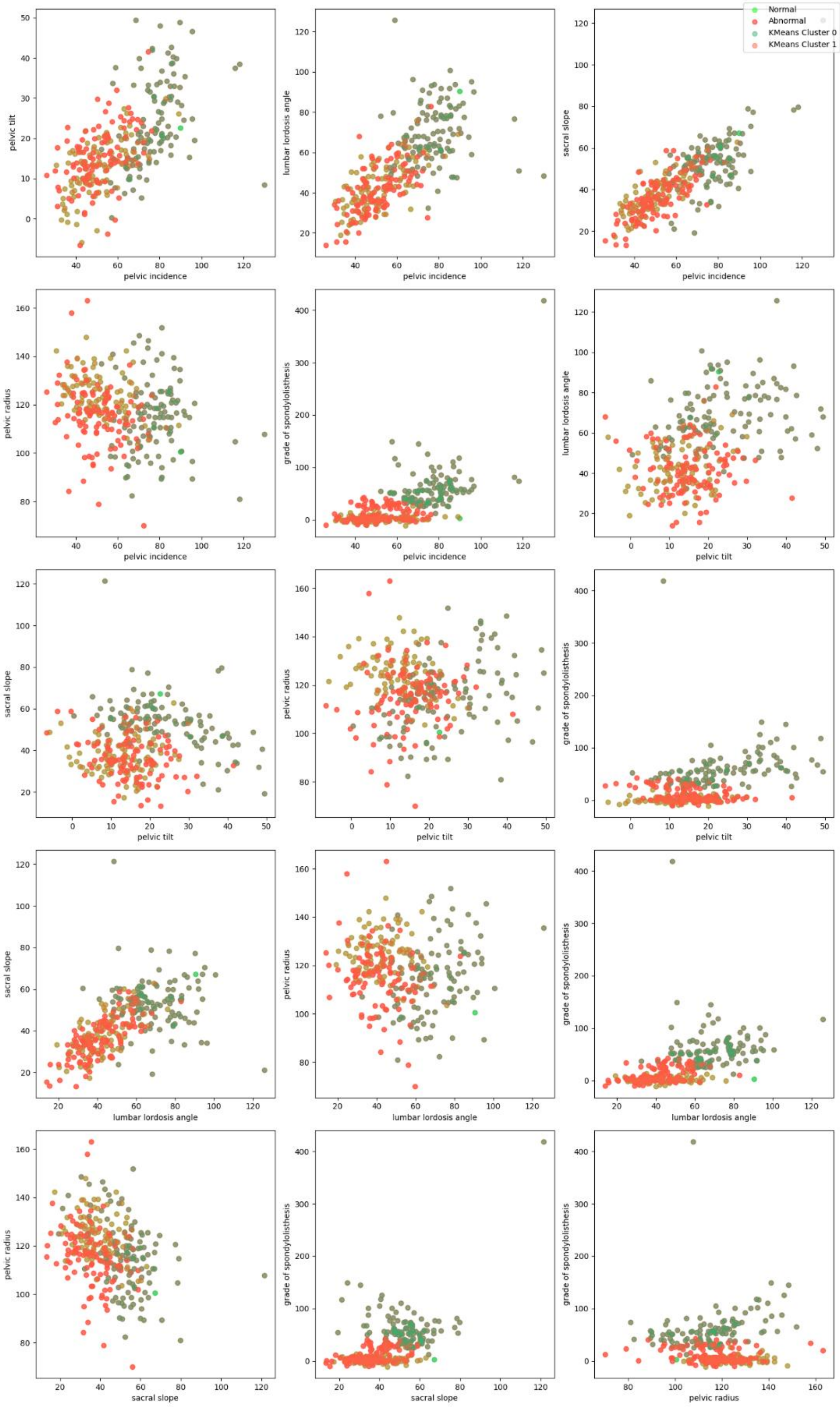


Figure 7: Interaction among features by actual and predicted clusters.

C. **Comparison and Integration:**

The comparison between supervised and unsupervised learning methods in this coursework highlights distinct advantages and challenges. While the decision tree and KNN demonstrated effective class differentiation, with KNN slightly outperforming the decision tree due to its ability to navigate complex data patterns. Conversely, the K Means algorithm, despite its appeal for not needing labeled data, struggled with accurately clustering the data, as indicated by low Adjusted Rand Index and Silhouette Score values.

IV. Appendix

2024/3/10 下午6:19 SML_0311 - Jupyter Notebook

In [209]:

```
import pandas as pd

path  = "C:\\Users\\user\\Desktop\\sml_due0311\\vertebral_column_data.csv"
df = pd.read_csv(path)

df["result"].replace({"AB": 1, "NO": 0}, inplace=True)
y =  df["result"]

df1 = df.drop(["result"], axis=1 )
df1.count()

df1.head()
```

Out[209]:

	pelvic incidence	pelvic tilt	lumbar lordosis angle	sacral slope	pelvic radius	grade of spondylolisthesis
0	63.03	22.55	39.61	40.48	98.67	-0.25
1	39.06	10.06	25.02	29.00	114.41	4.56
2	68.83	22.22	50.09	46.61	105.99	-3.53
3	69.30	24.65	44.31	44.64	101.87	11.21
4	49.71	9.65	28.32	40.06	108.17	7.92

In [210]:

```
df1.columns.tolist()
```

Out[210]:

```
['pelvic incidence',
 'pelvic tilt',
 'lumbar lordosis angle',
 'sacral slope',
 'pelvic radius',
 'grade of spondylolisthesis']
```

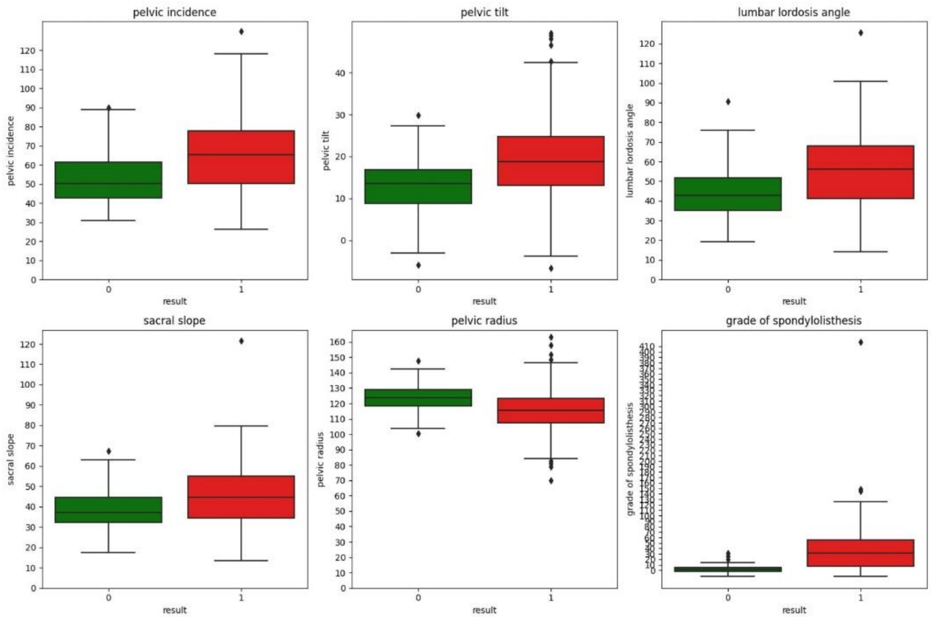
In [211]:

```
print("Noraml:\n", df[df["result"]==0].count())
print("\n\n")
print("Abnoraml:\n", df[df["result"]==1].count())
```

```
Noraml:
 pelvic incidence              100
pelvic tilt                   100
lumbar lordosis angle         100
sacral slope                  100
pelvic radius                 100
grade of spondylolisthesis    100
result                        100
dtype: int64



Abnoraml:
 pelvic incidence              210
pelvic tilt                   210
lumbar lordosis angle         210
sacral slope                  210
pelvic radius                 210
grade of spondylolisthesis    210
result                        210
dtype: int64
```

In [212]:

```python
import seaborn as sns
import matplotlib.pyplot as plt

# Create a figure with multiple subplots
fig, axes = plt.subplots(nrows=2, ncols=3, figsize=(15, 10))

# Draw box plots for six different columns
for i, column in enumerate(df.columns[:6]):
    sns.boxplot(x="result", y=column, data=df, ax=axes[i//3, i%3], palette=['green', 'red'])
    axes[i//3, i%3].set_title(column)
    axes[i//3, i%3].set_yticks(range(0, int(df[column].max())+1, 10))  # Set y-axis ticks every 10 units

# Automatically adjust subplot layout
plt.tight_layout()

# Show the plot
plt.show()

```



IQR

Abnormal

- **Pelvic Incidence**: 50.1 - 77.6
- **Pelvic Tilt**: 13.0 - 24.8
- **Lumbar Lordosis Angle**: 41.2 - 68.1
- **Sacral Slope**: 34.4 - 55.1
- **Pelvic Radius**: 107.3 - 123.1
- **Grade of Spondylolisthesis**: 7.3 - 55.4

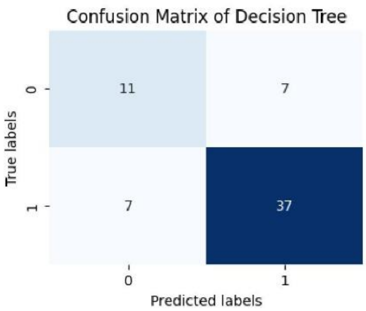
Normal

- **Pelvic Incidence**: 42.8 - 61.4
- **Pelvic Tilt**: 8.8 - 16.8
- **Lumbar Lordosis Angle**: 35.0 - 51.6
- **Sacral Slope**: 32.3 - 44.6
- **Pelvic Radius**: 118.2 - 129.0
- **Grade of Spondylolisthesis**: -1.5 - 4.97

In [213]:

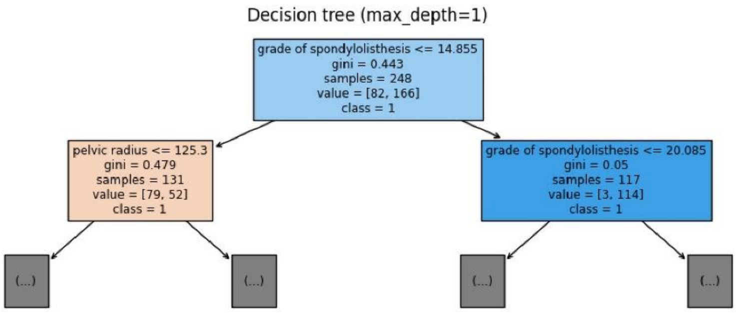
```python
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import accuracy_score, confusion_matrix
import matplotlib.pyplot as plt
import seaborn as sns

# Split the data into training and testing sets (80% train, 20% test)
X_train, X_test, y_train, y_test = train_test_split(df1, y, test_size=0.2, random_state=42)

# Initialize the Decision Tree classifier
tree = DecisionTreeClassifier(random_state=42)

# Fit the classifier to the training data
tree.fit(X_train, y_train)

# Predict on the test set
y_pred = tree.predict(X_test)

# Calculate accuracy
accuracy = accuracy_score(y_test, y_pred)
print("Accuracy:", accuracy)

# Calculate confusion matrix
cm = confusion_matrix(y_test, y_pred)

# Plot confusion matrix
plt.figure(figsize=(4, 3))
sns.heatmap(cm, annot=True, fmt="d", cmap="Blues", cbar=False)
plt.xlabel("Predicted labels")
plt.ylabel("True labels")
plt.title("Confusion Matrix of Decision Tree")
plt.show()
```

```
Accuracy: 0.7741935483870968
```



In [214]:

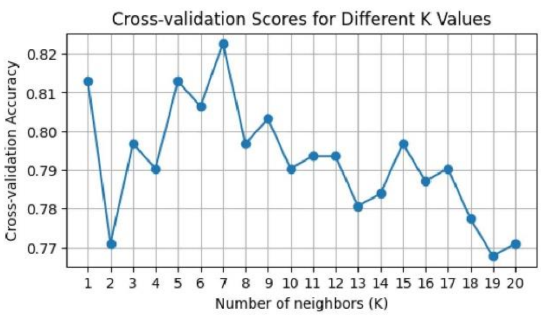
```
from sklearn.tree import plot_tree

# Initialize the Decision Tree classifier
tree = DecisionTreeClassifier(random_state=42)

# Fit the classifier to the data
tree.fit(X_train, y_train)

# Convert class names to string array
class_names = [str(c) for c in y]

# Plot the first three levels of the decision tree
plt.figure(figsize=(12, 4))
plot_tree(tree, max_depth=1, feature_names=df1.columns, class_names=class_names, filled=True)
plt.title("Decision tree (max_depth=1)")
plt.show()


```



In [215]:

```
from sklearn.model_selection import cross_val_score
import numpy as np

# Range of K values to test
k_values = range(1, 21)

# Perform cross-validation for each K value
cv_scores = []
for k in k_values:
    knn = KNeighborsClassifier(n_neighbors=k)
    scores = cross_val_score(knn, df1, y, cv=5, scoring='accuracy')  # 5-fold cross-validation
    cv_scores.append(np.mean(scores))

# Find the best K value
best_k = k_values[np.argmax(cv_scores)]
print("Best K value:", best_k)

# Plot cross-validation scores
plt.figure(figsize=(6, 3))
plt.plot(k_values, cv_scores, marker='o')
plt.xlabel('Number of neighbors (K)')
plt.ylabel('Cross-validation Accuracy')
plt.title('Cross-validation Scores for Different K Values')
plt.xticks(k_values)
plt.grid(True)
plt.show()

```

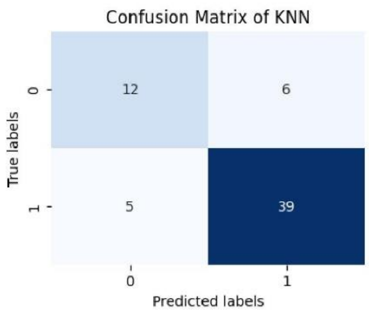
```
Best K value: 7
```



In [216]:

```
from sklearn.model_selection import train_test_split
from sklearn.neighbors import KNeighborsClassifier
from sklearn.metrics import accuracy_score, confusion_matrix
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns


# Split the data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(df1, y, test_size=0.2, random_state=42)
### 62 test datas in total

# Initialize the KNN classifier
knn = KNeighborsClassifier(n_neighbors=7)

# Train the classifier
knn.fit(X_train, y_train)

# Predict on the test set
y_pred = knn.predict(X_test)

# Calculate accuracy
accuracy = accuracy_score(y_test, y_pred)
print("Accuracy:", round(accuracy,2))

# Calculate confusion matrix
cm = confusion_matrix(y_test, y_pred)

# Plot confusion matrix
plt.figure(figsize=(4, 3))
sns.heatmap(cm, annot=True, fmt="d", cmap="Blues", cbar=False)
plt.xlabel("Predicted labels")
plt.ylabel("True labels")
plt.title("Confusion Matrix of KNN")
plt.show()

```

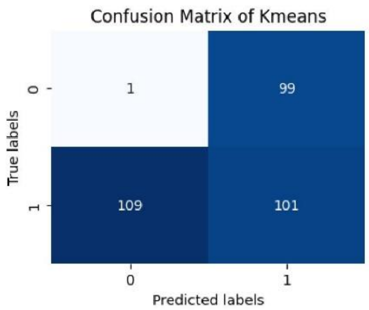
```
Accuracy: 0.82
```



In [217]:

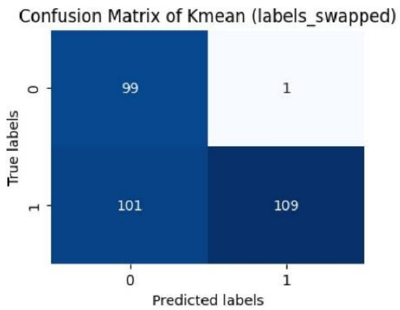
```python
from sklearn.cluster import KMeans
from sklearn.metrics import adjusted_rand_score, silhouette_score
from sklearn.metrics import confusion_matrix
# Initialize KMeans model
kmeans = KMeans(n_clusters=2, random_state=42)

# Fit KMeans model
kmeans.fit(df1)

# Get cluster labels
kmeans_labels = kmeans.labels_

# Calculate Adjusted Rand Index
ari = adjusted_rand_score(y, kmeans_labels)
print("Adjusted Rand Index:", round(ari,2))

# Calculate Silhouette Score
silhouette = silhouette_score(df1, kmeans_labels)
print("Silhouette Score:", round(silhouette,2))

# Calculate the confusion matrix
cm = confusion_matrix(y, kmeans_labels)

# Plot confusion matrix
plt.figure(figsize=(4, 3))
sns.heatmap(cm, annot=True, fmt="d", cmap="Blues", cbar=False)

plt.xlabel("Predicted labels")
plt.ylabel("True labels")
plt.title("Confusion Matrix of Kmeans")
plt.show()
```

```
D:\anaconda\envs\envs_notebook\lib\site-packages\sklearn\cluster\_kmeans.py:870: FutureWarning: The default value of `n
_init` will change from 10 to 'auto' in 1.4. Set the value of `n_init` explicitly to suppress the warning
  warnings.warn(

Adjusted Rand Index: 0.11
Silhouette Score: 0.45
```



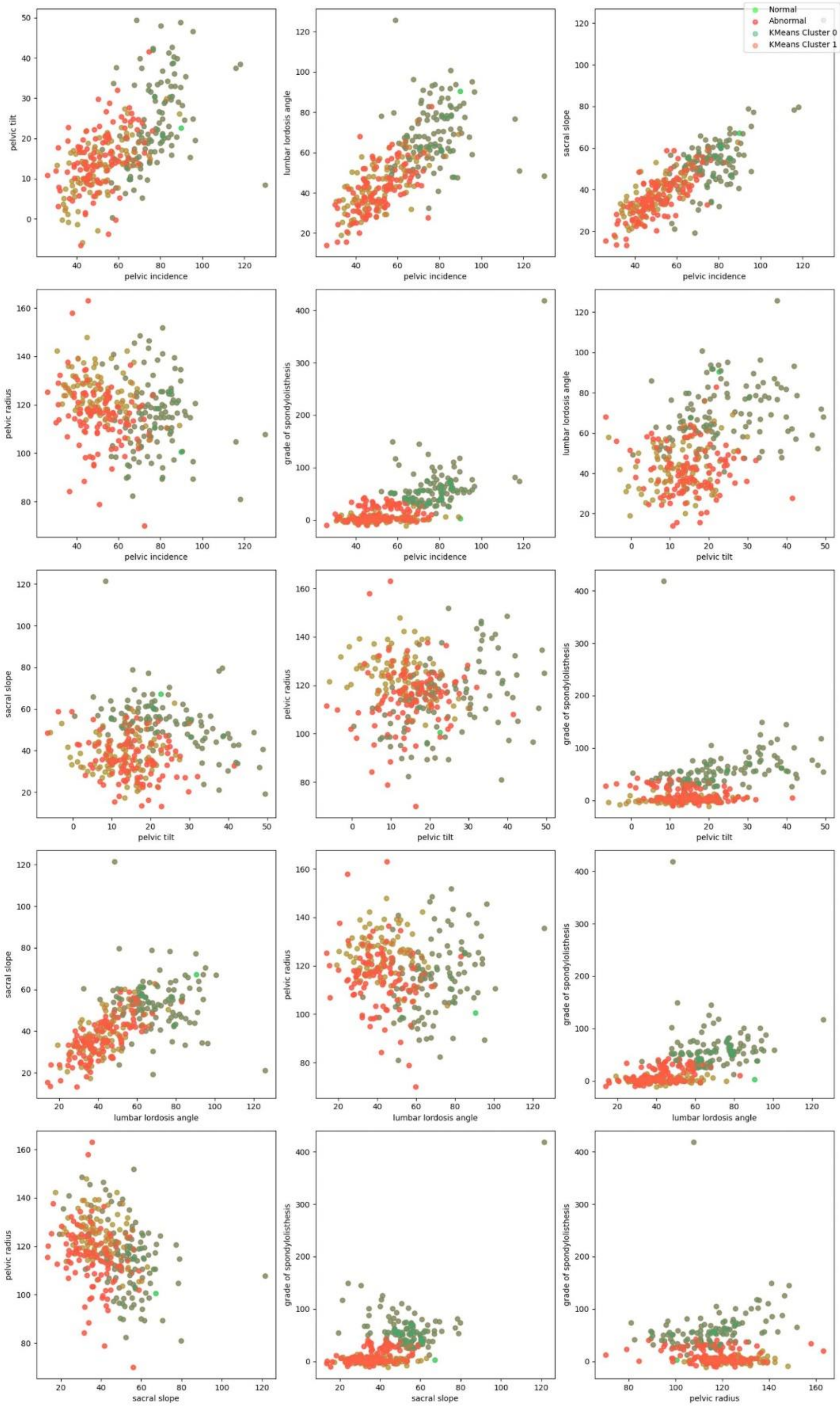
In [218]:

```python
# Swap cluster labels
kmeans_labels_swapped = 1 - kmeans_labels

cm_swapped = confusion_matrix(y, kmeans_labels_swapped)

plt.figure(figsize=(4, 3))
sns.heatmap(cm_swapped, annot=True, fmt="d", cmap="Blues", cbar=False)

plt.xlabel("Predicted labels")
plt.ylabel("True labels")
plt.title("Confusion Matrix of Kmean (labels_swapped)")
plt.show()

```



In [219]:

```
import matplotlib.pyplot as plt
from itertools import combinations

# Assuming df1 is your DataFrame, y is the actual labels, and kmeans_labels is from KMeans

features = df1.columns
feature_combinations = list(combinations(features, 2))

# Define the number of rows and columns for subplots
n_rows = (len(feature_combinations) + 2) // 3  # Adjusted to cover all combinations
n_cols = 3

# Create a figure with subplots
fig, axs = plt.subplots(n_rows, n_cols, figsize=(5*n_cols, 5*n_rows))

# Placeholder for the legend handles
handles = []

for idx, (feature1, feature2) in enumerate(feature_combinations):
    row = idx // n_cols
    col = idx % n_cols
    ax = axs[row, col]

    # Plot each combination for actual labels and KMeans labels
    scatter_y0 = ax.scatter(df1[feature1][y==0], df1[feature2][y==0], color='lime', label='Normal', alpha=0.5)
    scatter_y1 = ax.scatter(df1[feature1][y==1], df1[feature2][y==1], color='red', label='Abnormal', alpha=0.5)
    scatter_k0 = ax.scatter(df1[feature1][kmeans_labels==0], df1[feature2][kmeans_labels==0], color='mediumseagreen'
    scatter_k1 = ax.scatter(df1[feature1][kmeans_labels==1], df1[feature2][kmeans_labels==1], color='tomato', label=


    ax.set_xlabel(feature1)
    ax.set_ylabel(feature2)

    # Collect legend handles
    if idx == 0:
        handles.extend([scatter_y0, scatter_y1, scatter_k0, scatter_k1])

# Create a unified legend for the entire figure
fig.legend(handles, ['Normal', 'Abnormal', 'KMeans Cluster 0', 'KMeans Cluster 1'], loc='upper right')

# Adjust the layout
plt.tight_layout()
plt.show()

```


Normal
Abnormal
KMeans Cluster 0
KMeans Cluster 1
pelvic incidence
pelvic tilt
lumbar lordosis angle
sacral slope
pelvic radius
grade of spondylolisthesis