```
In [2]: import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.cluster import KMeans
from sklearn.preprocessing import StandardScaler
from sklearn.decomposition import PCA
from scipy.stats import mode
from sklearn.metrics import accuracy_score
# Step 1: Read CSV file from device
df = pd.read_csv("Breast Cancer Wisconsin.csv")
# Step 2: Preprocess the dataset
df = df.drop(columns=['id', 'Unnamed: 32'], errors='ignore')
if 'diagnosis' in df.columns:
     diagnosis = df['diagnosis'].map({'M': 1, 'B': 0})  # 1: Malignant, 0: Benign
     df = df.drop(columns=['diagnosis'])
else:
     diagnosis = None
# Step 3: Standardize features
scaler = StandardScaler()
scaled_data = scaler.fit_transform(df)
# Step 4: Apply K-Means Clustering
kmeans = KMeans(n_clusters=2, random_state=42)
kmeans.fit(scaled_data)
labels = kmeans.labels_
# Step 5: PCA for Visualization
pca = PCA(n_components=2)
pca_data = pca.fit_transform(scaled_data)
# Prepare data for plotting
vis_df = pd.DataFrame({
     'PCA1': pca_data[:, 0],
     'PCA2': pca_data[:, 1],
     'Cluster': labels
})
if diagnosis is not None:
     vis_df['Actual'] = diagnosis
      # Map cluster numbers to label names based on majority
     cluster_map = {}
     for cluster in [0, 1]:
          majority = mode(diagnosis[labels == cluster], keepdims=True).mode[0]
          cluster_map[cluster] = 'Predicted Malignant' if majority == 1 else 'Predicted Benign'
     vis_df['Cluster_Label'] = vis_df['Cluster'].map(cluster_map)
     # Map actual labels to strings
     vis_df['Actual_Label'] = vis_df['Actual'].map({1: 'Actual Malignant', 0: 'Actual Benign'})
      # Calculate accuracy by comparing predicted labels with actual labels
      # Map the predicted clusters to actual labels (Malignant or Benign)
     predicted_labels = np.array([1 if cluster == 0 else 0 for cluster in labels]) # Map cluster 0 to Malignant, 1 to Benign
     accuracy = accuracy_score(diagnosis, predicted_labels)
     print(f"Accuracy: {accuracy * 100:.2f}%")
 # Step 6: Plotting
plt.figure(figsize=(10, 6))
# Plot predicted clusters (colored)
sns.scatterplot(
     data=vis_df,
     x='PCA1'
     y='PCA2'
     hue='Cluster_Label',
     palette={'Predicted Malignant': 'red', 'Predicted Benign': 'blue'},
     s=100,
     alpha=0.6,
     legend='full'
 # Plot actual values (black shapes)
if diagnosis is not None:
     sns.scatterplot(
          data=vis df,
          x='PCA1'
          y='PCA2',
          style='Actual Label',
          markers={'Actual Malignant': 'X', 'Actual Benign': 'o'},
          color='black',
          s=50,
          alpha=0.5,
          legend='brief'
plt.title("K-Means Clustering on Breast Cancer Dataset (PCA Projection)")
plt.xlabel("Principal Component 1")
plt.ylabel("Principal Component 2")
plt.legend(title="Legend", bbox_to_anchor=(1.05, 1), loc='upper left')
plt.grid(True)
plt.tight_layout()
plt.show()
/home/ailba/anaconda3/lib/python3.10/site-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 10 t
o 'auto' in 1.4. Set the value of `n_init` explicitly to suppress the warning
  warnings.warn(
Exception ignored on calling ctypes callback function: <function _ThreadpoolInfo._find_modules_with_dl_iterate_phdr.<locals>.match_module_callback at
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Accuracy: 91.04%
                        K-Means Clustering on Breast Cancer Dataset (PCA Projection)
                                                                                                                                          Legend
     12.5
                                                                                                                                       Predicted Malignant
```



