```
In [1]:
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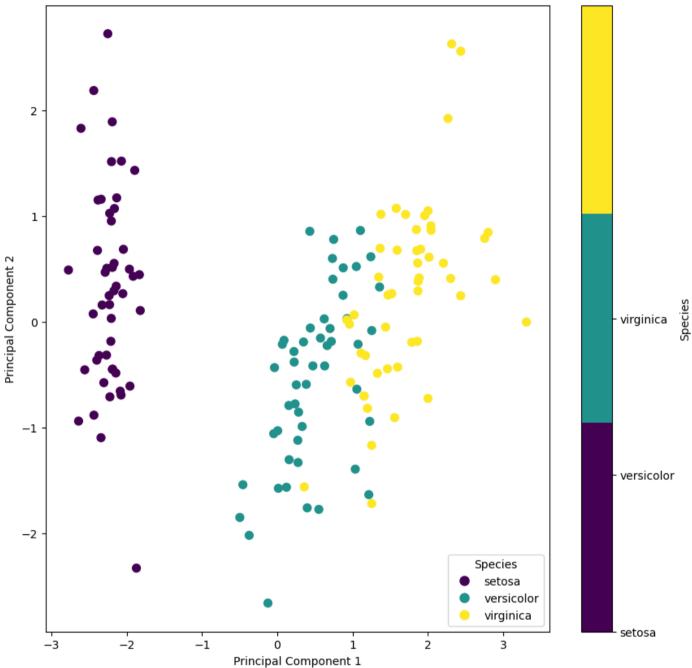
```
import pandas as pd
import numpy as np
from sklearn.decomposition import PCA
import matplotlib.pyplot as plt
from sklearn.preprocessing import StandardScaler
# Load the dataset
df = pd.read csv("IRIS DATASET.csv")
# Define feature columns and target column
features = ['sepal length', 'sepal width', 'petal length', 'petal width']
targetcolumn = 'species'
# Extract features and target from the dataframe
x = df[features].values
y = df[targetcolumn].values
# Standardize the data
scaler = StandardScaler()
x scaled = scaler.fit transform(x)
# Perform PCA
pca model = PCA(n components=2)
x pca = pca model.fit transform(x scaled)
# Check the shape of the transformed data
print(f"Original shape: {x.shape}")
print(f"Transformed shape: {x pca.shape}")
# Create a mapping of species to integers
species mapping = {species: idx for idx, species in enumerate(np.unique(y))}
# Map the target values to integers
y mapped = np.array([species mapping[species] for species in y])
# Define the colormap
cmap = plt.get_cmap('viridis', len(species_mapping))
# Plotting the PCA results
plt.figure(figsize=(10, 10))
scatter = plt.scatter(x_pca[:, 0], x_pca[:, 1], c=y_mapped, cmap=cmap, s=50)
plt.xlabel("Principal Component 1")
plt.ylabel("Principal Component 2")
plt.title("PCA of Iris Dataset")
# Create a legend manually with specific colors
handles = []
for species, idx in species mapping.items():
    handles.append(plt.Line2D([0], [0], marker='o', color='w', markerfacecolor=cmap(idx /
plt.legend(handles=handles, title='Species')
# Colorbar to show the color mapping
cbar = plt.colorbar(scatter)
cbar.set label('Species')
cbar.set ticks(np.linspace(0, 1, len(species mapping)))
cbar.set_ticklabels(list(species_mapping.keys()))
```

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plt.show()

# Explained variance
explained_variance = pca_model.explained_variance_ratio_
print(f"Explained variance by each component: {explained_variance}")
```

Original shape: (150, 4)
Transformed shape: (150, 2)





Explained variance by each component: [0.72770452 0.23030523]