

In [2]: # Kindly use the Jupyter Notebook to run this program.

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.datasets import load_iris
from sklearn.decomposition import PCA
from sklearn.preprocessing import StandardScaler
```

In [4]: # Load Iris dataset  
iris = load\_iris()  
X = iris.data # Feature matrix (4D)  
y = iris.target # Labels  
target\_names = iris.target\_names  
  
print("✅ Iris dataset loaded successfully.")

✅ Iris dataset loaded successfully.

In [6]: # Standardize features to have mean=0 and variance=1  
scaler = StandardScaler()  
X\_std = scaler.fit\_transform(X)

In [8]: # Reduce dimensions to 2 using PCA  
pca = PCA(n\_components=2)  
X\_pca = pca.fit\_transform(X\_std)  
  
# Create DataFrame with PCA results  
df\_pca = pd.DataFrame(data=X\_pca, columns=['PC1', 'PC2'])  
df\_pca['Species'] = y

In [13]: # Define species names and colors  
species\_labels = ['Setosa', 'Versicolor', 'Virginica']  
colors = ['brown', 'hotpink', 'purple']  
  
# Plot the PCA results  
plt.figure(figsize=(7, 5))  
for i, color in zip(np.unique(y), colors):  
 plt.scatter(df\_pca[df\_pca['Species'] == i]['PC1'],  
 df\_pca[df\_pca['Species'] == i]['PC2'],  
 c=color, label=species\_labels[i], edgecolor='k', alpha=0.7)  
  
plt.xlabel('Principal Component 1 (PC1)')  
plt.ylabel('Principal Component 2 (PC2)')  
plt.title('🌸 PCA Visualization of Iris Dataset')  
plt.legend()  
plt.grid(True)  
plt.tight\_layout()  
plt.show()

```
/var/folders/p2/mlmtsgwx3l39qzybtsj493s40000gn/T/ipykernel_2048/2430915314.py:17: UserWarning:
Glyph 127800 (\N{CHERRY BLOSSOM}) missing from font(s) DejaVu Sans.
  plt.tight_layout()
/opt/anaconda3/lib/python3.12/site-packages/IPython/core/pylabtools.py:170: UserWarning: Glyph
127800 (\N{CHERRY BLOSSOM}) missing from font(s) DejaVu Sans.
  fig.canvas.print_figure(bytes_io, **kw)
```

PCA Visualization of Iris Dataset

