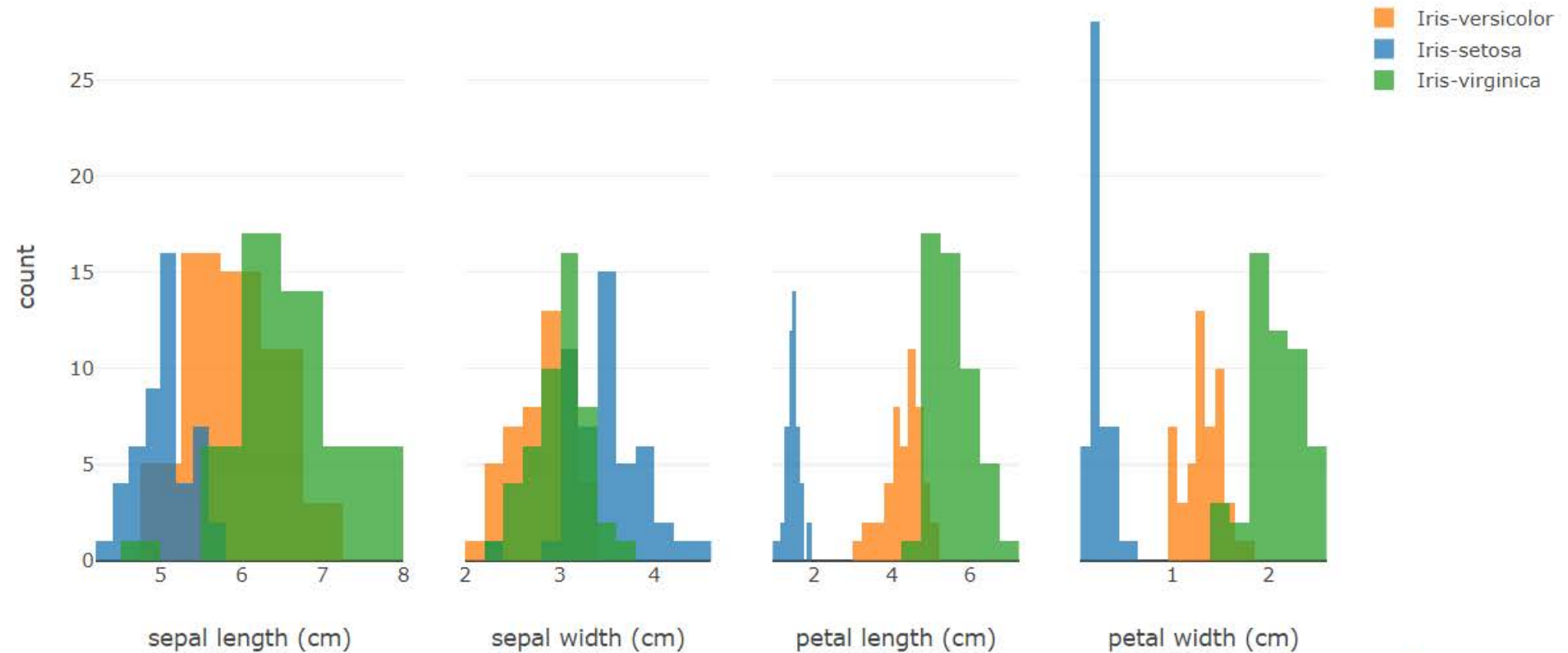


```
fig = go.Figure(data=data, layout=layout)
iplot(fig)
```

Distribution of the different Iris flower features



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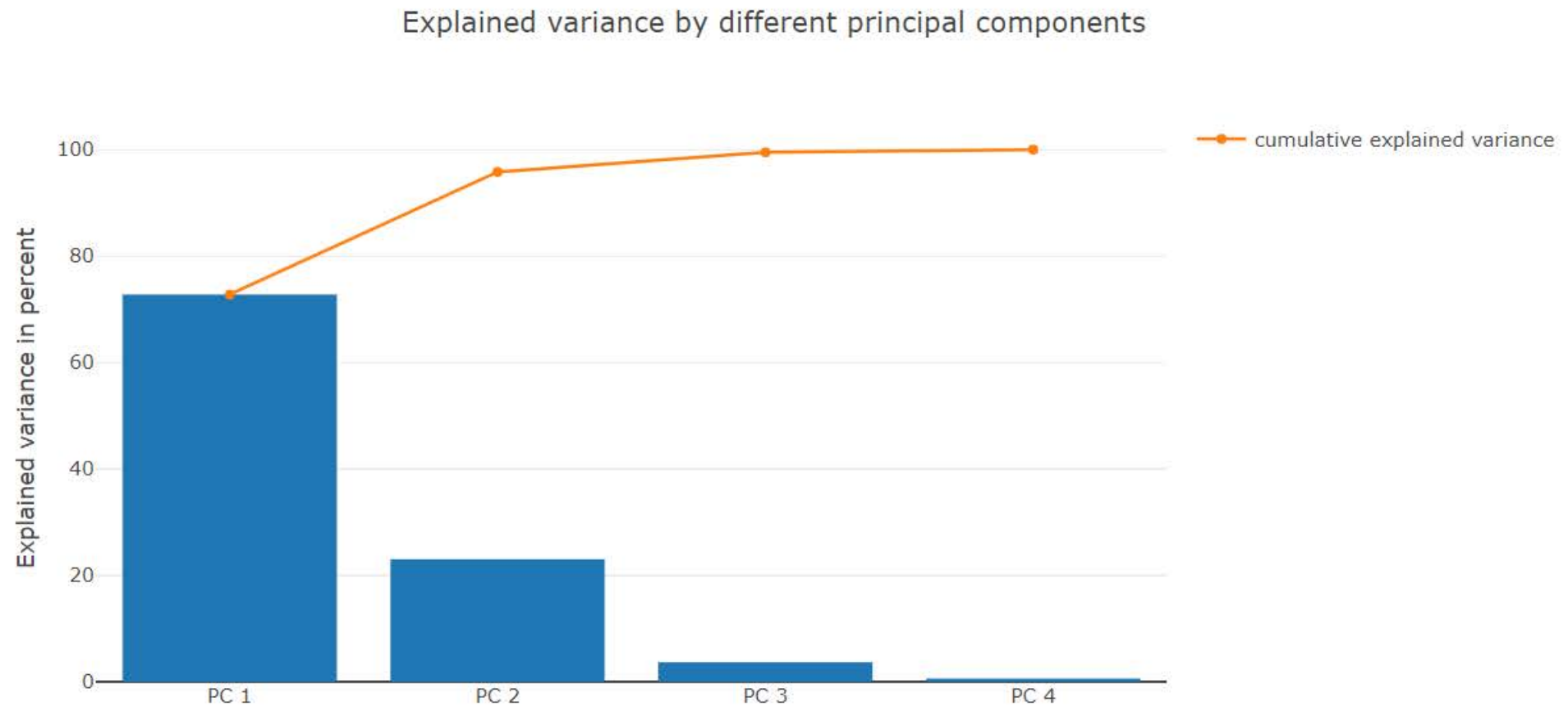
Standardize (scale, transform) the data

```
In [47]: from sklearn.preprocessing import StandardScaler
X_std = StandardScaler().fit_transform(X)
```

Perform eigen-decomposition on the covariance matrix

```
title='Explained variance by different principal components')
```

```
fig = Figure(data=data, layout=layout)  
iplot(fig)
```

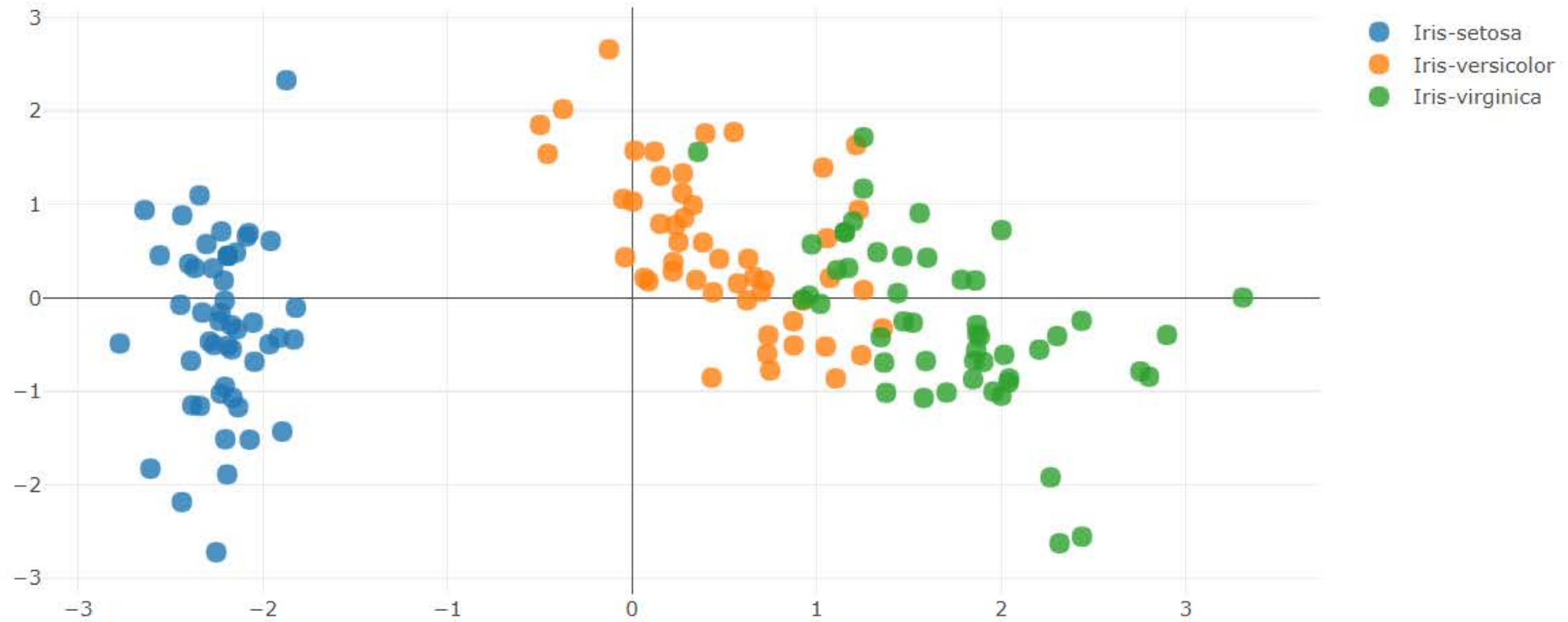


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Now reduce the 4D feature space to 2D feature space by selecting the top 2 eigenvalues and corresponding eigenvectors

```
In [57]: matrix_w = np.hstack((eig_pairs[0][1].reshape(4,1),  
                                eig_pairs[1][1].reshape(4,1)))  
  
print('Matrix W:\n', matrix_w)
```

```
fig = Figure(data=data, layout=layout)
iplot(fig)
```

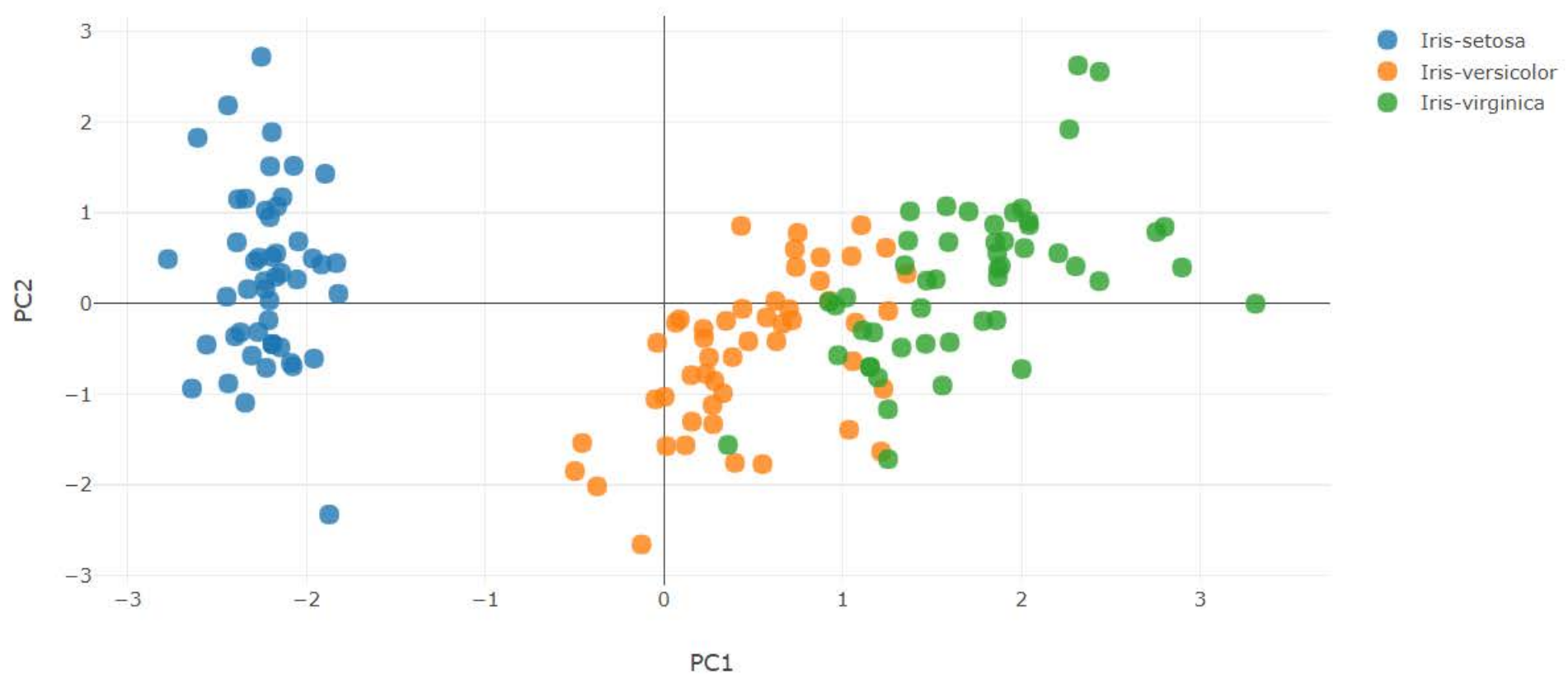


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As an alternative method use sklearn

```
In [60]: from sklearn.decomposition import PCA as sklearnPCA
sklearn_pca = sklearnPCA(n_components=2)
Y_sklearn = sklearn_pca.fit_transform(X_std)
```

```
traces.append(trace)  
data = Data(traces)  
layout = Layout(xaxis=XAxis(title='PC1', showline=False),  
                yaxis=YAxis(title='PC2', showline=False))  
fig = Figure(data=data, layout=layout)  
iplot(fig)
```



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In []: