


```

# Centering and standardizing the data
# Subtract the mean from each feature and divide it by its standard
# Subtracting the mean --> centers the data
# Dividing by the standard deviation --> ensures proper scaling.

featuresStandardized = (features - np.mean(features, axis=0)) / np.

```

The next step is to compute the covariance matrix. The covariance matrix is essentially helpful as it helps visualize mathematically the relations between data and shows how features are correlated to each other. Helps in finding the direction having the most variation.

```

# Computing the covariance matrix:

covarianceMatrix = np.cov(featuresStandardized.T)

# Can also be written as covarianceMatrix = np.cov(featuresStandard
# This point just aims to explain that every column is a feature, n

print(covarianceMatrix)

 2.27079511e-01  3.95694673e-01 -1.03935708e-01 -1.00215889e-03
 9.95457402e-01  3.65741024e-01  1.00176056e+00  9.79299180e-01
 2.37191461e-01  5.30339746e-01  6.19432713e-01  8.17759288e-01
 2.69967228e-01  1.39201504e-01]
 [ 9.42739295e-01  3.44150782e-01  9.43207466e-01  9.60902082e-01
 2.07082304e-01  5.10500995e-01  6.77177350e-01  8.11055024e-01
 1.77505338e-01 -2.32262646e-01  7.52871625e-01 -8.33414586e-02
 7.31999440e-01  8.12836496e-01 -1.82516245e-01  1.99722335e-01
 1.88684259e-01  3.42873752e-01 -1.10537008e-01 -2.27761757e-02
 9.85746984e-01  3.46451160e-01  9.79299180e-01  1.00176056e+00
 2.09513547e-01  4.39067932e-01  5.44287093e-01  7.48734680e-01
 2.09513722e-01  7.97872577e-02]
 [ 1.19826732e-01  7.76398084e-02  1.50814456e-01  1.23740409e-01
 8.06742020e-01  5.66536837e-01  4.49612218e-01  4.53550155e-01
 4.27426215e-01  5.05831058e-01  1.42168410e-01 -7.37873381e-02
 1.30283361e-01  1.25610187e-01  3.15011078e-01  2.27794574e-01
 1.68777943e-01  2.15729735e-01 -1.26840915e-02  1.70868612e-01
 2.16955724e-01  2.25826298e-01  2.37191461e-01  2.09513547e-01
 1.00176056e+00  5.69186845e-01  5.19436186e-01  5.48655147e-01
 4.94707764e-01  6.18711558e-01]
 [ 4.14190751e-01  2.78318729e-01  4.56576647e-01  3.91097651e-01
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 4.76657749e-01  3.61467607e-01  5.30339746e-01  4.39067932e-01
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 6.15522263e-01  8.11881713e-01]

```

```
[ 5.27839123e-01  3.01555198e-01  5.64872009e-01  5.13508396e-01
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 4.41247742e-01  6.03510257e-01  -3.04669411e-02  2.15582894e-01
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 5.48655147e-01  8.02490717e-01  8.56939906e-01  1.00176056e+00
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 7.01057885e-01  3.34606745e-01  9.47092790e-02  -1.28440488e-01
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 1.98136040e-01  1.43367633e-01  3.90088053e-01  1.11289544e-01
 2.43957953e-01  2.33437721e-01  2.69967228e-01  2.09513722e-01
 4.94707764e-01  6.15522263e-01  5.33457264e-01  5.03413227e-01
 1.00176056e+00  5.38795122e-01]
[ 7.07832563e-03  1.19415220e-01  5.11083511e-02  3.74417763e-03
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 4.39185353e-01  7.68647654e-01  4.96466850e-02  -4.57349464e-02
 8.55829815e-02  1.75701742e-02  1.01658978e-01  5.92013208e-01
 4.40102736e-01  3.11201479e-01  7.82169401e-02  5.92369136e-01
 9.36565772e-02  2.19508204e-01  1.39201504e-01  7.97872577e-02
 6.18711558e-01  8.11881713e-01  6.87719567e-01  5.12013995e-01
 5.38795122e-01  1.00176056e+00]]
```

Eigenvalue Decomposition:

Theoretically, after implementing PCA, the most axis containing the most variance of the data is the set of eigenvectors.

Given that the covariance matrix is a square symmetric matrix, and according to the spectral theorem, there exists an orthogonal set of eigenvectors as a basis.

This means that for a covariance matrix of dimension 30, the data can be represented using a set of 30 dimensions, each orthogonal to one another (right angles from one another). The eigenvalues on the other hand portray the variance inherent in each direction.

If the eigenvectors are sorted with the highest eigenvalues, the n new dimensions can be represented with the highest n eigenvectors.

```
# Compute eigenvalues and eigenvectors:  
  
eigenvalues, eigenvectors = np.linalg.eig(covarianceMatrix)  
  
# Sort the eigenvectors by the highest eigenvalues  
# np.argsort(eigenvalues)[::-1] returns the indices of the highest  
eigenvectors = eigenvectors[np.argsort(eigenvalues)[::-1]]
```

Explained Variance Ratio:

"Variance Ratio refers to the ratio of variance explained by each principal component in a Principal Component Analysis (PCA). It is used to determine the optimal number of dimensions needed to explain the variance in a dataset, with the total ratio summing up to 1." <https://www.sciencedirect.com/topics/computer-science/variance-ratio>

```
# Simplified previous operations to a class.  
  
class PCA:  
    def __init__(self, numberOfPrincipleComponents=2):  
        self.numberOfPrincipleComponents = numberOfPrincipleComponents  
        self.eigenvectors = None  
        self.eigenvalues = None  
        self.mean = None  
        self.std = None  
        self.covarianceMatrix = None  
        self.explainedVarianceRatio = None  
        self.pca = None  
        self.reconstructed = None  
  
    def fit(self, features):  
        self.mean = np.mean(features, axis=0)  
        self.std = np.std(features, axis=0)  
  
        # Precautionary step to ensure no features having a standard deviation of 0  
        self.std[self.std == 0] = 1  
  
        standardized = (features - self.mean) / self.std  
        self.covarianceMatrix = np.cov(standardized.T)  
        eigenvalues, eigenvectors = np.linalg.eig(self.covarianceMatrix)  
        # By default, np.argsort sorts in ascending order. For this mode, we want descending order.  
        sortedIndices = np.argsort(eigenvalues)[::-1]  
        self.eigenvalues = eigenvalues[sortedIndices]  
        # Sorts columns, not rows.  
        self.eigenvectors = eigenvectors[:,sortedIndices]
```

```
totalVariance = np.sum(eigenvalues)
self.explainedVarianceRatio = self.eigenvalues / totalVariance

return self

def project(self, features):
    standardized = (features - self.mean) / self.std
    # The np.dot function projects the input data onto the provided
    pca = np.dot(standardized, self.eigenvectors[:, :self.numberOfPr
    self.pca = pca
    return pca

def reconstruct(self, projectedFeatures):
    # Reconstruct the data after projecting it on the principle axes
    reconstructed = np.dot(projectedFeatures, self.eigenvectors[:, ::
    self.reconstructed = reconstructed
    return reconstructed

def reconstructionError(self, features):
    # Calculating the error in the reconstructed data
    projectedData = self.project(features)
    reconstructedData = self.reconstruct(projectedData)

    error = np.mean((features - reconstructedData)**2)

    print(f"Reconstruction Error using MSE:{error:.3f}")
    return error

...def plot(self, target):
....# Plotting a scatter plot
....plt.figure()
....color=['r','g']
....names=['Malignant', 'Benign']
....for i in range(len(color)):
....    plt.scatter(self.pca[target==i,0], self.pca[target==i,1], c=co
....    plt.title("PCA Plot of Two Components")
....    plt.xlabel(f"Principal Component 1 With Explained Variance of:{s
....    plt.ylabel(f"Principal Component 2 With Explained Variance of:{s
....    plt.legend()

    plt.figure()
    # Plot a bar chart for the explained variance of all features in
    barComponents=np.arange(1, len(self.explainedVarianceRatio)+1)
    plt.bar(barComponents, self.explainedVarianceRatio, align='center

    plt.ylabel('Explained Variance Ratio')
    plt.xlabel('Principle Component Index')
```

```
    plt.xlabel('Principal Component 1'),  
    plt.title('Variance Ratio Plot')
```

```
# Testing PCA class:
```

```
pca = PCA(numberOfPrincipleComponents=2)  
pca.fit(features)  
pca.project(features)  
pca.plot(target)  
reconstructionError = pca.reconstructionError(features)
```

Reconstruction Error using MSE: 809.793



