



TEXAS TECH UNIVERSITY

# Kernelized Principal Component Analysis

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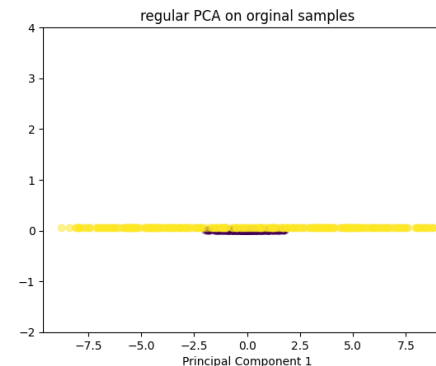
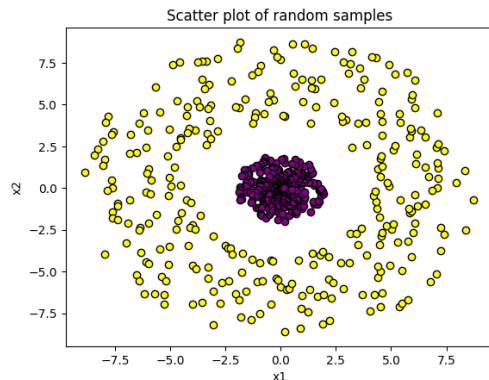
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# Kernel PCA

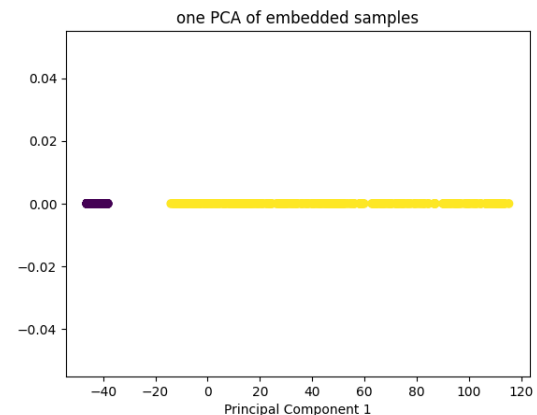
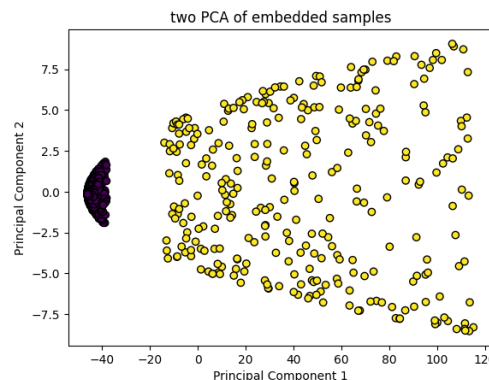
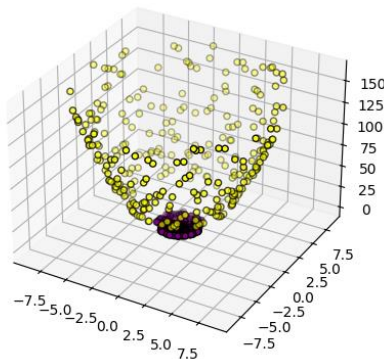


## ■ Definition:

- Given a set of samples in the original space, we project each sample onto a new embedding of higher dimensionality. We perform PCA in this higher dimension. The result is a non-linear projection of samples in the dimension of required principal components.



samples embedded in a higher dimension





# Kernel PCA Basics

- Computing the mean

- Original space:

$$\mu = \frac{1}{N} \sum_{k=1}^N x^k$$

- Embedded space:

$$\bar{\Phi} = \frac{1}{N} \sum_{k=1}^N \Phi(x^k)$$

- Covariance matrix

- Original space:

$$\Sigma(x^k - \mu)(x^k - \mu)^T$$

- Embedded space:

$$\Sigma_{\Phi} = (\Phi(x^k) - \bar{\Phi}) (\Phi(x^k) - \bar{\Phi})^T$$

- Projection

- Original space:

$$y^k = (x^k - \mu)^T e$$

- Embedded space:

$$\Phi(y^k) = (\Phi(x^k) - \bar{\Phi})^T e_{\Phi}$$



# Kernel PCA Mathematical Foundation

- The choice of embedding has significant impact on computational complexity.  
Example: polynomial embedding.

$$\Phi[x_1, x_2, \dots, x_d] = [x_1^n, x_1^{n-1}x_2, \dots, x_1^{n-1}x_d, \dots, x_1^{n-2}x_2^2, \dots, x_d^n]$$

- $\Phi[X]$  is an  $[m \times n]$  matrix where  $m$  is the number of features/dimensions in the embedded space.
- Increasing the degree of the polynomial,  $n$ , increases  $m$ .

$$m = \binom{d+n-1}{d}$$

- If  $m$  is large the computation is impractical.  $\Sigma_\Phi$  is an  $[m \times m]$  matrix.

$$\Sigma_\Phi = \Phi\Phi^T$$

- How can we achieve efficient PCA in the embedded space?
- If we proceed and try to find the eigenvectors:

$$\Phi\Phi^T e = \lambda e$$

$$\text{For all } \lambda > 0: \quad \Phi \frac{(\Phi^T e)}{\lambda} = e,$$

$$\text{let } \frac{(\Phi^T e)}{\lambda} = w$$



# Kernel PCA Mathematical Foundation

- The result is  $\Phi w = e$  this tells us that the eigenvectors we want,  $e$ , is always a linear combination of the columns of the embedded data matrix.

- Eigenvectors of  $\Sigma_\Phi$  that correspond to  $\lambda > 0$  are in the column span of  $\Phi$ .

$$w = \lambda^{-1} \Phi^T e$$

- $w$  is the vector of coefficients.

- If we take the definition of  $w$

$$\begin{aligned} \Phi^T \Phi w &= \Phi^T \Phi (\lambda^{-1} \Phi^T e) \\ &= \Phi^T e \end{aligned}$$

$$\Phi^T \Phi w = \lambda w$$

- Initially  $\Phi \Phi^T$  was too large  $[m \times m]$  but now we have  $\Phi^T \Phi$  which is  $[n \times n]$ , where  $n \ll m$

- Instead of computing eigenvectors of  $\Sigma_\Phi$ ;  $\Phi \Phi^T e = \lambda e$ , we can find eigenvectors  $w$ , since the eigenvalues  $\lambda$  are essentially the same where  $\Phi^T \Phi w = \lambda w$

$$\text{Note: } \|w\|^2 = w^T w = u^T \Phi \Phi^T u \left( \frac{1}{\lambda^2} \right) = u^T (\lambda u) \left( \frac{1}{\lambda^2} \right) = \frac{1}{\lambda}$$



# Kernel PCA Mathematical Foundation

- Solving the eigen problem  $\Phi^T \Phi w = \lambda w$ , we get  $w$  and  $\lambda$ . This will yield  $\|w\|^2 = 1$  since the norm of symmetric
- We then normalize  $w$  so that  $\|w\|^2 = \frac{1}{\lambda}$  then  $e$  the eigenvector we want is equal to  $\Phi w = e$ .

$$\tilde{w} = \frac{1}{\sqrt{\lambda}}$$

- If we define our  $K = \Phi^T \Phi$  as our Kernel matrix, we can find the projection  $y$  of the original data  $x$

$$\begin{aligned} y &= e^T \Phi \\ y &= w^T \Phi^T \Phi; \quad e = \Phi w \\ y &= \tilde{w}^T K \end{aligned}$$



# Kernel PCA Algorithm

1. Given samples  $[x_1, x_2, \dots, x_n]$ , a Kernel function  $K(x, y)$ , and number of principal components  $d$ .
2. Calculate  $K_{ij} = K(x_i, x_j)$ ,  $\tilde{K} = JKJ^T$  :
3. Perform an Eigen Decomposition of  $\tilde{K} \approx W\Lambda W^{-1}$  for the top  $d$  eigenvectors.
4.  $Y = \tilde{W}^T K$



# Kernel PCA extensions

- Kernel recompositing of original samples
  - Unlike standard PCA, the transformed data in the higher-dimensional space cannot be directly mapped back to the original feature space.
- Kernelizing Out of sample data:
  - If we want to project a new data point, we can use the kernel trick to calculate the kernel between the new data point and all the samples:

$$y^* = w^T K_x$$

$$\text{Where } K_x = [K(x, x_1), K(x, 2), \dots K(x, n)]^T$$

- Using Label-Based Weights
  - One way of improving the separation of data points belonging to different classes is to modify the kernel matrix by using the labels.
  - A weight,  $\alpha_{ij}$ , proportional to the difference in label values, can be inserted into the kernel function.

$$K_{ij} = \exp(-\alpha_{ij}\gamma\|x_i - x_j\|^2)$$

- An embedding exist for any random Kernel.