



# **3253 Analytic Techniques and Machine Learning**

## **Module 8: Dimensionality Reduction**



# Course Plan

## Module Titles

Module 1 – Introduction to Machine Learning

Module 2 – End to End Machine Learning Project

Module 3 – Classification

Module 4 – Clustering and Unsupervised Learning

Module 5 – Training Models and Feature Selection

Module 6 – Support Vector Machines

Module 7 – Decision Trees and Ensemble Learning

**Current Focus: Module 8 – Dimensionality Reduction**

Module 9 – Introduction to TensorFlow

Module 10 – Introduction to Deep Learning and Deep Neural Networks

Module 11 – Distributing TensorFlow, CNNs and RNNs

Module 12 – Final Assignment and Presentations (no content)



# Learning Outcomes for this Module

- Be aware of “The Curse of Dimensionality” and strategies for minimizing it
- Apply dimensionality reduction techniques such as
  - Principal Component Analysis (PCA)
  - Kernel PCA
  - Local Linear Embedding



# Topics for this Module

- **8.1** The “curse” of dimensionality
- **8.2** Dimensionality reduction using projection
- **8.3** Dimensionality reduction using manifolds
- **8.4** Principal Component Analysis (PCA)
- **8.5** Local Linear Embedding (LLE)
- **8.6** Resources and Wrap-up



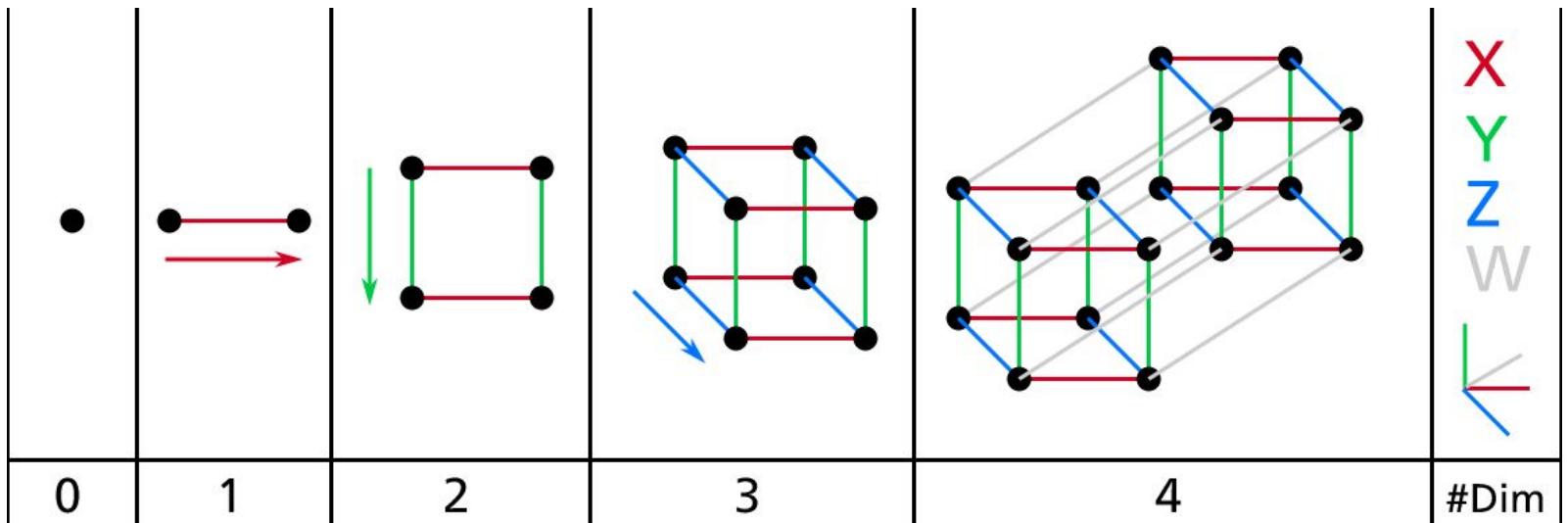
## Module 8 – Section 1

# The “Curse” of Dimensionality

# Introduction

- Machine Learning problems involve thousands or even millions of features for each training instance:
  - Too many features makes training extremely slow, it can also make it much harder to find a good solution
  - This problem is often referred to as the “curse” of dimensionality
- It is often possible to reduce the number of features considerably, turning an intractable problem into a tractable one.
- Dimensionality reduction is also very useful for data visualization

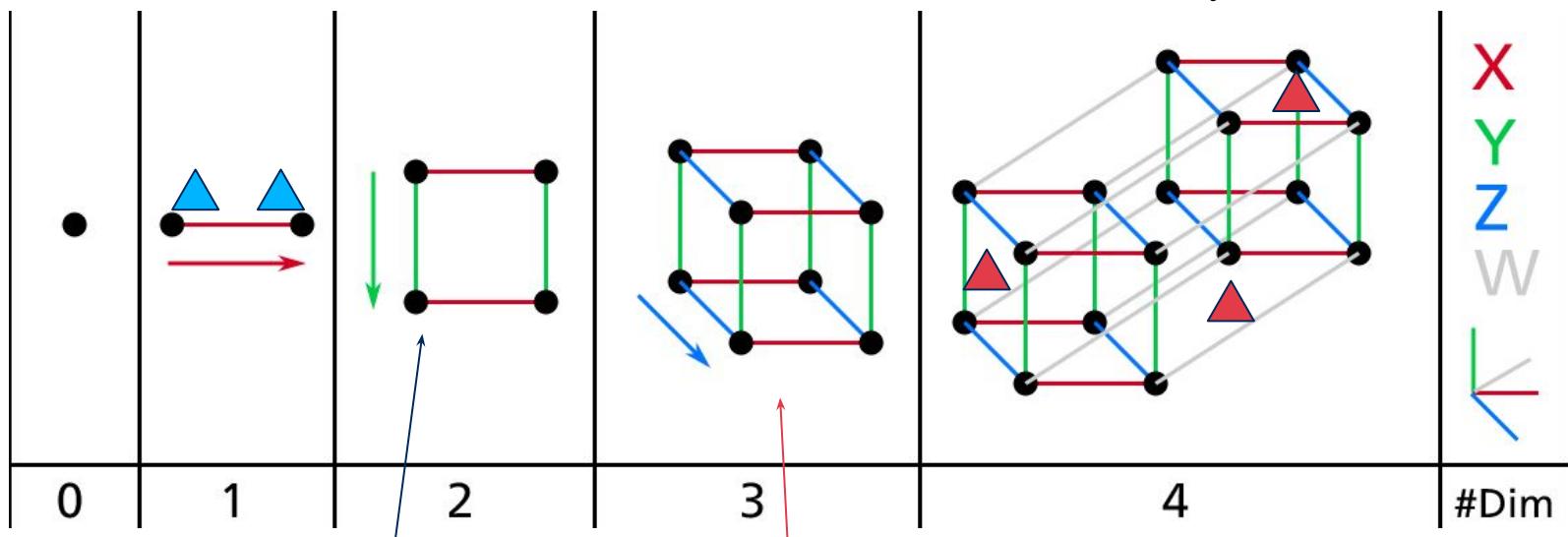
# N-Dimensions



Even a basic 4D hypercube is incredibly hard to picture in our mind

# N-Dimensions

Blue triangles part of a 1 feature space are comparatively very close



within a square, distance between two random points will be, on average 0.52

within a cube, distance between two random points will be, on average 0.66

# Curse of Dimensionality: Sparsity

- Things behave very differently in high-dimensional space.
  - Probability of a random point being close to the border:
    - In a  $1 \times 1$  square, there is about a 0.4% chance of the point being located less than 0.001 from a border.
    - For a 10,000-dimensional unit hypercube, this probability is greater than 99.999999%.
    - Most points in a high-dimensional hypercube are very close to the border.
  - Two random chosen points inside a cube:
    - In a unit square, the distance between these two points will be, on average, roughly 0.52.
    - In a unit 3D cube, the average distance will be roughly 0.66.
    - In a 1,000,000-dimensional hypercube will be about 408.25
    - High-dimensional datasets are at risk of being very sparse: most training instances are likely to be far away from each other.

# More instances to help sparsity

- A new instance will likely be far away from any training instance, making predictions much less reliable than in lower dimensions, since they will be based on much larger extrapolations.
  - The more dimensions the training set has, the greater the risk of overfitting it.
- One solution to the curse of dimensionality could be to increase the size of the training set to reach a sufficient density of training instances.
  - In practice, the number of training instances required to reach a given density grows exponentially with the number of dimensions.

# Curse of Dimensionality (cont'd)

one-dimensional  
cube

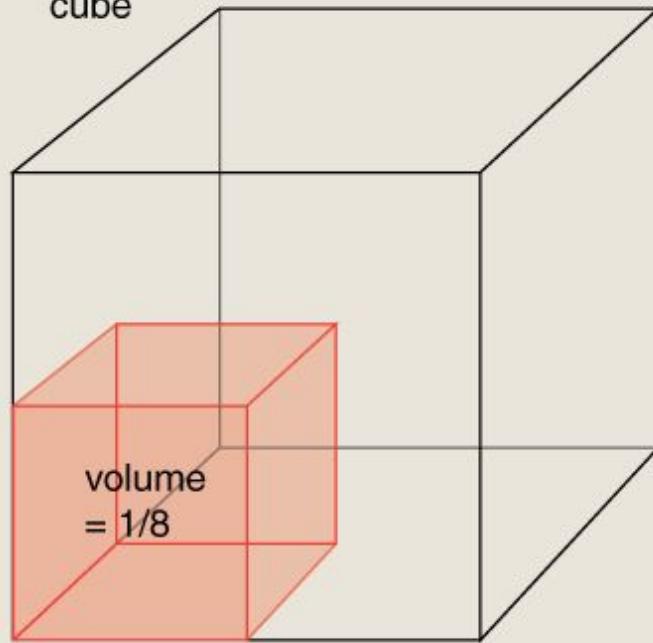


volume = 1/2

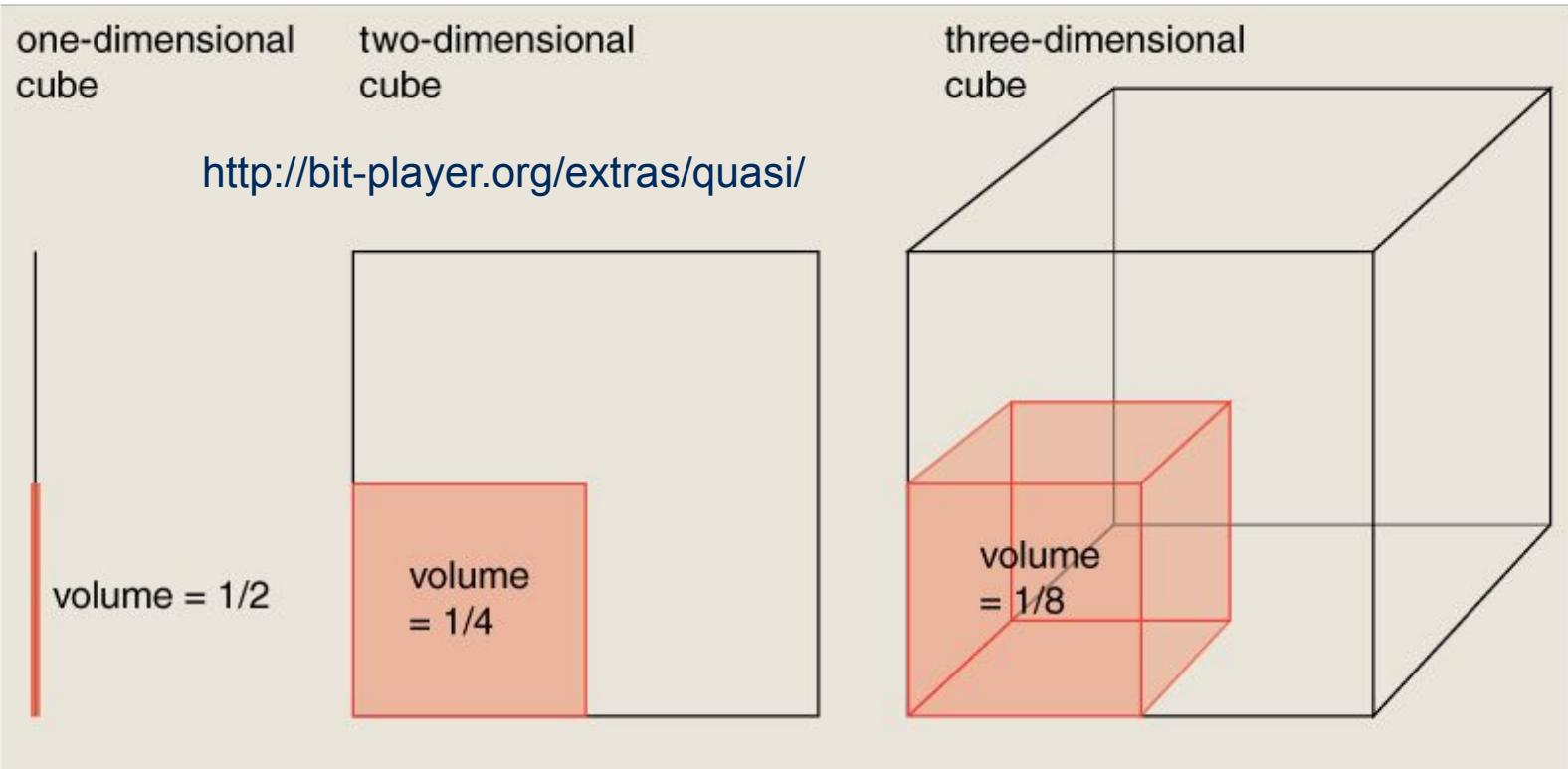
two-dimensional  
cube



three-dimensional  
cube



<http://bit-player.org/extras/quasi/>



- As dimensions grow, fewer observations per region
- The volume of the unit sphere tends to zero as the dimensionality of the sphere increases



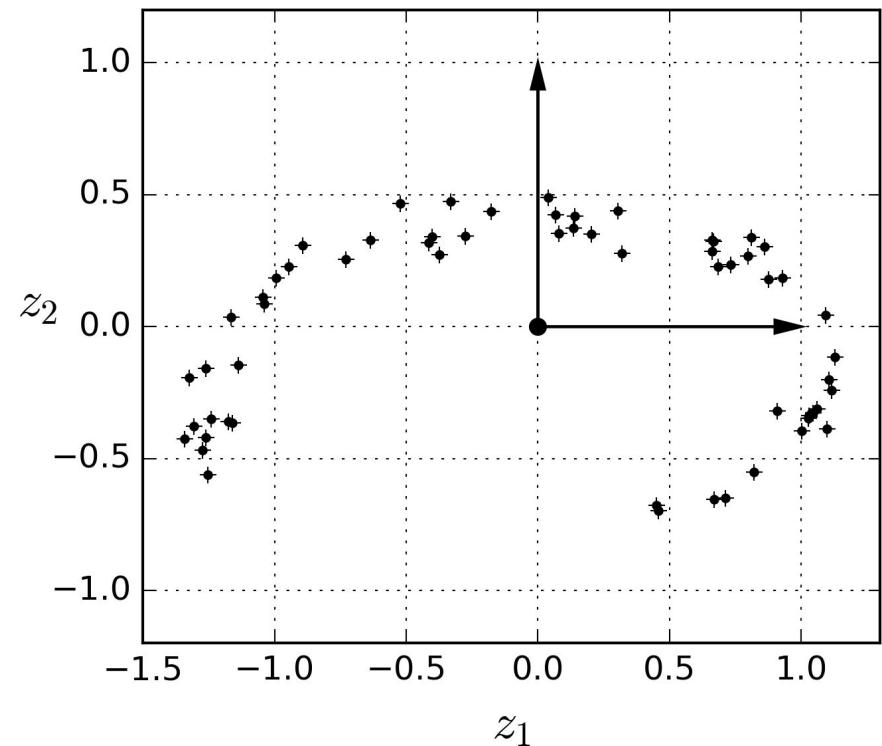
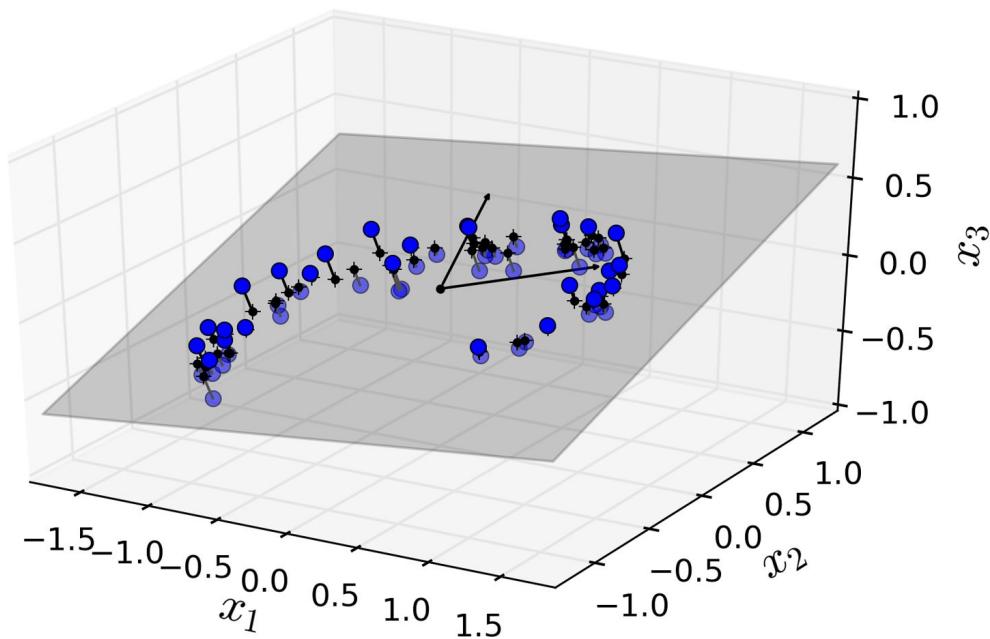
## Module 9 – Section 2

# Dimensionality Reduction using Projection

# Dimensionality Reduction – Projection

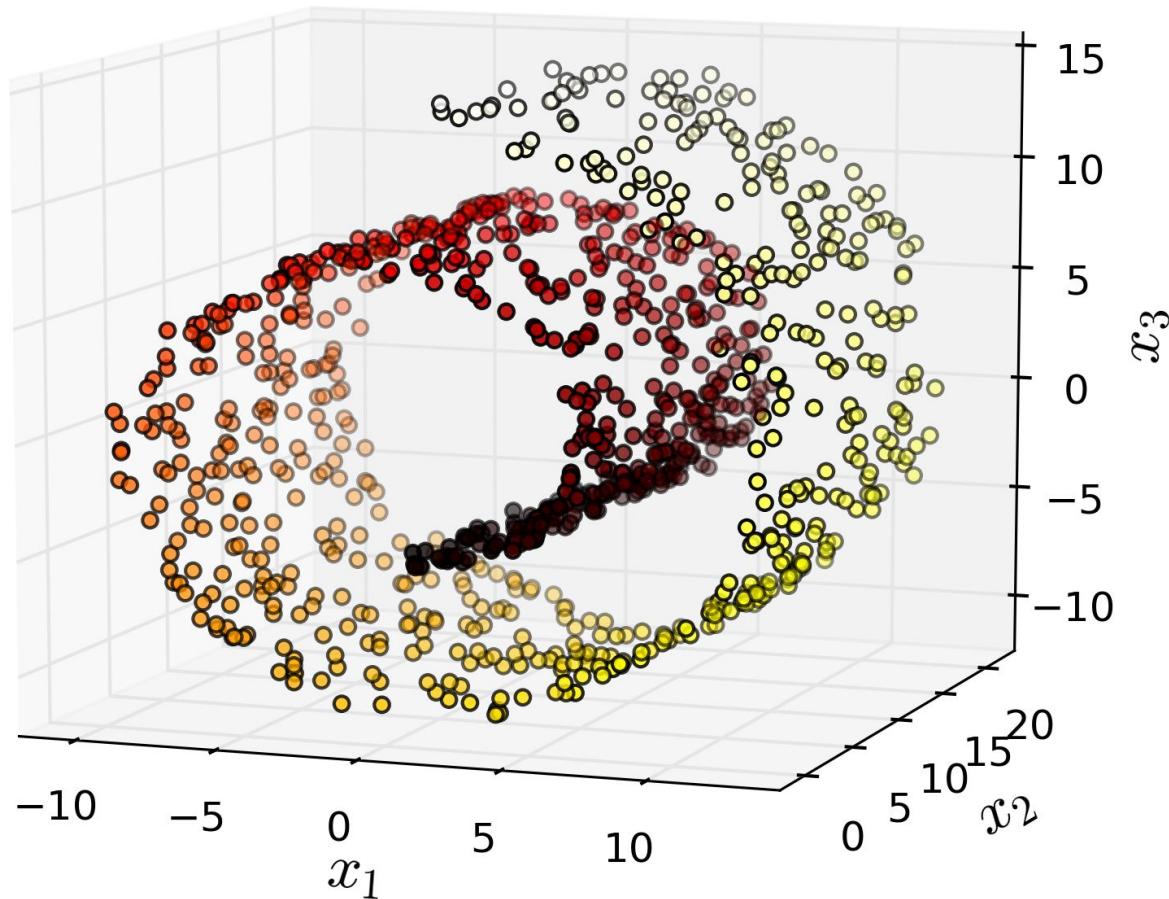
- A technique to reduce dimensionality
- Data is not spread out uniformly across all dimensions.
  - Many features are almost constant, while others are highly correlated
  - All training instances actually lie within a much lower-dimensional subspace of the high-dimensional space.
- If we project every training instance perpendicularly onto this subspace, we get the new 2D dataset
  - We have just reduced the dataset's dimensionality from 3D to 2D.

# Dimensionality Reduction – Projection (cont'd)



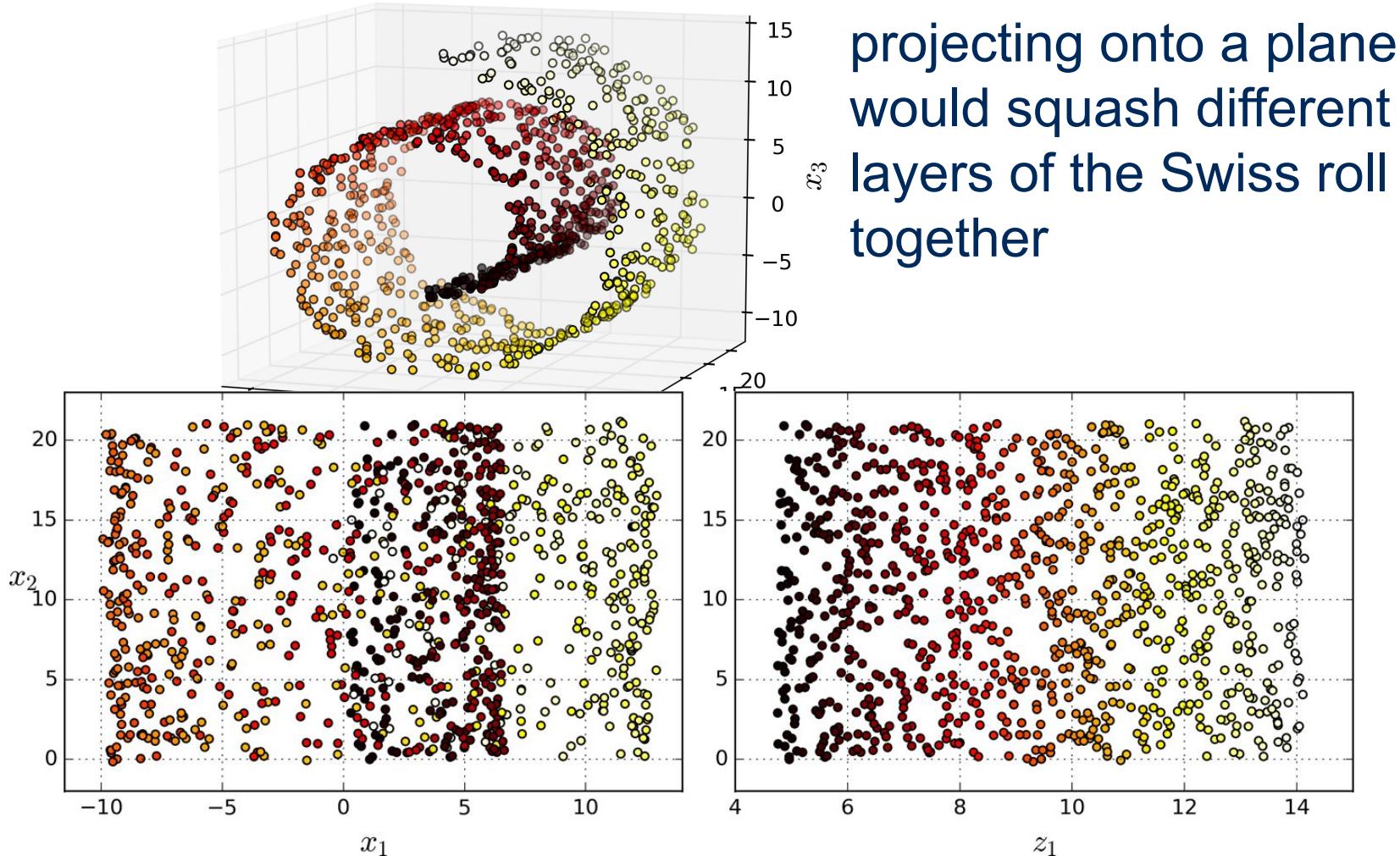
Reduction of feature space from 3 to 2

# Dimensionality Reduction – Projection (cont'd)



But... does it always  
work?

# Dimensionality Reduction – Projection (cont'd)





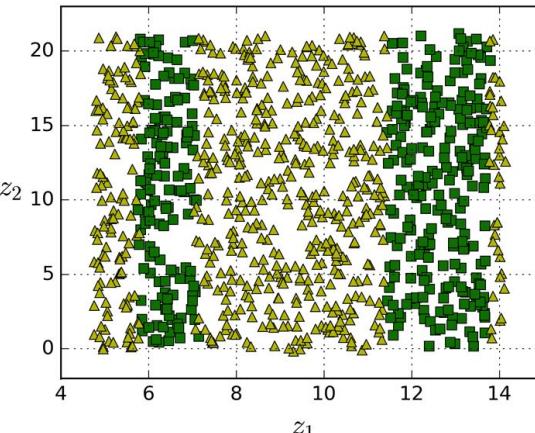
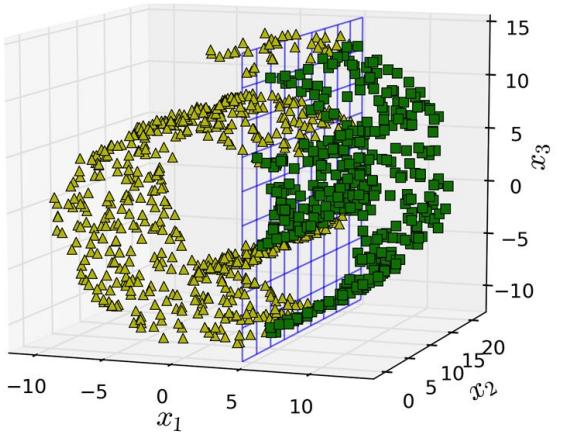
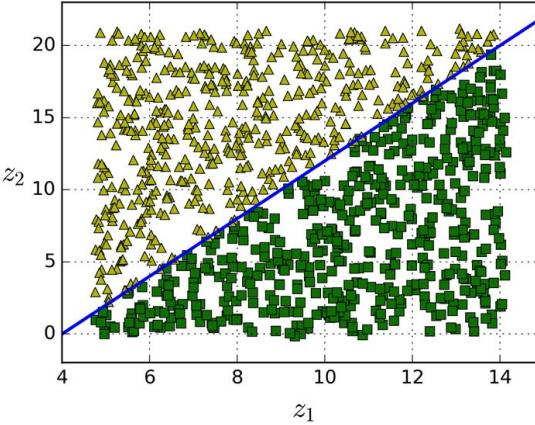
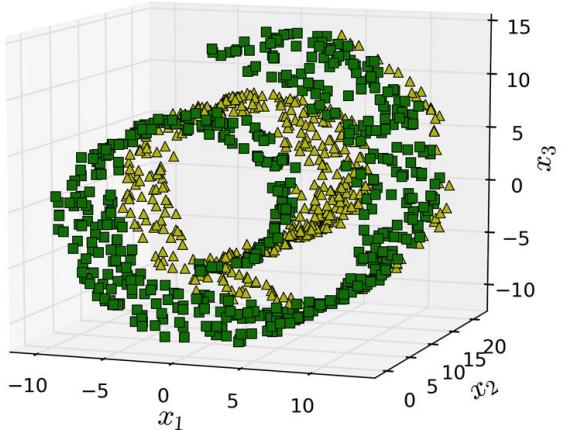
## Module 8 – Section 3

# Dimensionality Reduction using Manifolds

# Manifold Learning

- A d-dimensional manifold is a part of an n-dimensional space (where  $d < n$ ) that locally resembles a d-dimensional hyperplane.
  - In the case of the Swiss roll,  $d = 2$  and  $n = 3$ : it locally resembles a 2D plane, but it is rolled in the third dimension.
- Most real-world high-dimensional datasets lie close to a much lower-dimensional manifold.
- The task at hand (e.g., classification or regression) will be simpler if expressed in the lower-dimensional space of the manifold.

# Manifold Learning (cont'd)



If you reduce the dimensionality of your training set before training a model, it will definitely speed up training, However, it may not always lead to a better or simpler solution; it all depends on the dataset.



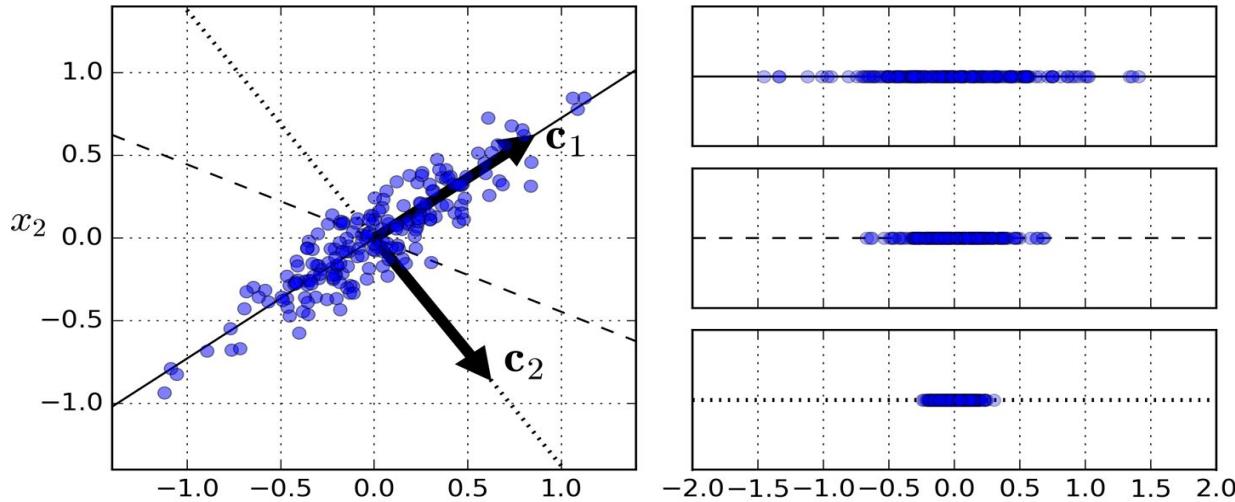
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## Module 8 – Section 4

# Principal Component Analysis (PCA)

# PCA

- Principal Component Analysis (PCA)
- Is a **linear transformation** and assumes it can create a linear model of data (from N dimension to d)
- Vanilla PCA **fails** to model non-linear relationship
- First it identifies the hyperplane that lies closest to the data, and then it projects the data onto it.



The projection onto the  $z_1$  solid line preserves the maximum variance, while the projection onto the dotted line preserves very little variance.

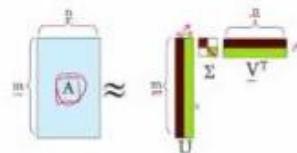
# PCA (cont'd)

- PCA Minimizes MSE: The main axis of PCA minimizes the mean squared distance between the original dataset and its projection onto that axis
- The unit vector that defines the  $i^{th}$  axis is called the  $i^{th}$  principal component (PC)
- How to find the PCs?
  - Use the matrix factorization technique called Singular Value Decomposition (SVD). SVD decomposes a matrix  $X$  into the product of three matrices  $U \cdot \Sigma \cdot V^T$ , where **V contains all the principal components** that we are looking for

---

## Singular Value Decomposition

$$A \approx U \Sigma V^T = \sum_i \sigma_i u_i \circ v_i^T$$



# Projecting down n to d using PCA

- The dimensionality of the dataset can be reduced by projecting n dimensions onto the hyperplane defined by the first d principal components

$$\mathbf{X}_{d\text{-proj}} = \mathbf{X} \cdot \mathbf{W}_d$$

```
X_centered = X - X.mean(axis=0)
U, s, Vt = np.linalg.svd(X_centered)
c1 = Vt.T[:, 0]
c2 = Vt.T[:, 1]
```

`W2 = Vt.T[:, :2]`      W2 has the first 2 components from PCA

`X2D = X_centered.dot(W2)` ← X2D is the data in 2 (lower) dimensions

# PCA sklearn

```
from sklearn.decomposition import PCA  
  
pca = PCA(n_components = 2)  
X2D = pca.fit_transform(X)
```

**components\_**: After fitting the PCA transformer to the dataset, you can access the principal components using the components\_ variable

**explained\_variance\_ratio\_ variable**: Indicates the proportion of the dataset's variance that lies along the axis of each principal component.

```
>>> pca.explained_variance_ratio_  
array([ 0.84248607,  0.14631839])
```

# Choosing n-dimensions

Choose the number of dimensions that add up to a sufficiently large portion of the variance

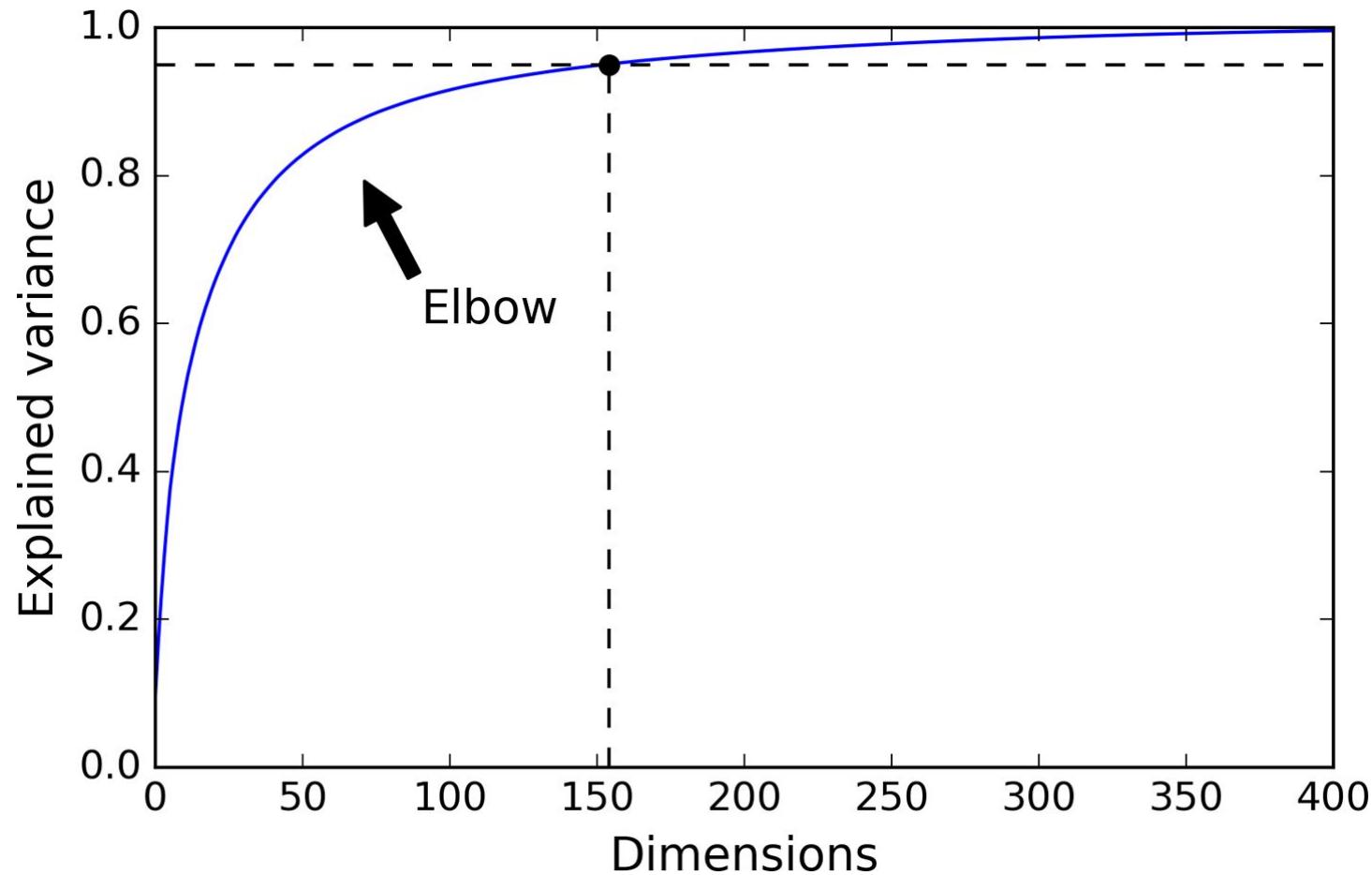
Example: Preserve 95% Variance

```
pca = PCA()  
pca.fit(X_train)  
cumsum = np.cumsum(pca.explained_variance_ratio_ )  
d = np.argmax(cumsum >= 0.95) + 1
```

Alternatively:

```
pca = PCA(n_components=0.95)  
X_reduced = pca.fit_transform(X_train)
```

# Choosing n-dimensions (cont'd)



**Hands-On: Lets see it in action [here](#)**

# PCA for Compression

- Example: PCA on MNIST (95% variance):
  - 150 features, instead of the original 784 features
- The dataset is now less than 20% of its original size! This can speed up a classification algorithm (such as an SVM classifier) tremendously.

# PCA for Compression (cont'd)

```
pca = PCA(n_components = 154)  
X_reduced = pca.fit_transform(X_train)  
X_recovered = pca.inverse_transform(X_reduced)
```

Original

1 4 0 1 7  
8 3 0 5 1  
0 2 7 7 6  
3 2 0 6 2  
4 5 8 3 4

Compressed

1 4 0 1 7  
8 3 0 5 1  
0 2 7 7 6  
3 2 0 6 2  
4 5 8 3 4

# Flavors of PCA

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scikit-learn 0.24.2 Other versions

Please cite us if you use the software.

[sklearn.decomposition.PCA](#)  
Examples using [sklearn.decomposition.PCA](#)

**See also:**

[KernelPCA](#)  
Kernel Principal Component Analysis.

[SparsePCA](#)  
Sparse Principal Component Analysis.

[TruncatedSVD](#)  
Dimensionality reduction using truncated SVD.

[IncrementalPCA](#)  
Incremental Principal Component Analysis.

## sklearn.decomposition.PCA

```
class sklearn.decomposition.PCA(n_components=None, *, copy=True, whiten=False, svd_solver='auto', tol=0.0, iterated_power='auto', random_state=None)
```

Principal component analysis (PCA).

Linear dimensionality reduction using Singular Value Decomposition of the data to project it to a lower dimensional input data is centered but not scaled for each feature before applying the SVD.

It uses the LAPACK implementation of the full SVD or a randomized truncated SVD by the method of Halko et al. 2009 depending on the shape of the input data and the number of components to extract.

<https://scikit-learn.org/stable/modules/generated/sklearn.decomposition.PCA.html>

# Incremental PCA

- Split the training set into mini-batches and feed an IPCA algorithm one mini-batch at a time
  - Useful for large datasets or online PCA

```
from sklearn.decomposition import IncrementalPCA

n_batches = 100
inc_pca = IncrementalPCA(n_components=154)
for X_batch in np.array_split(X_train, n_batches):
    inc_pca.partial_fit(X_batch)

X_reduced = inc_pca.transform(X_train)
```

# Randomized PCA

- Stochastic algorithm that quickly finds an approximation of the first d principal components (i.e., finds estimate for W)
  - Its computational complexity is  $O(m \times d^2) + O(d^3)$ , instead of  $O(m \times n^2) + O(n^3)$ , so it is dramatically faster than the previous algorithms when d is much smaller than n.

```
rnd_pca = PCA(n_components=154, svd_solver="randomized")
X_reduced = rnd_pca.fit_transform(X_train)
```

$$\mathbf{X}_{d\text{-proj}} = \mathbf{X} \cdot \mathbf{W}_d$$

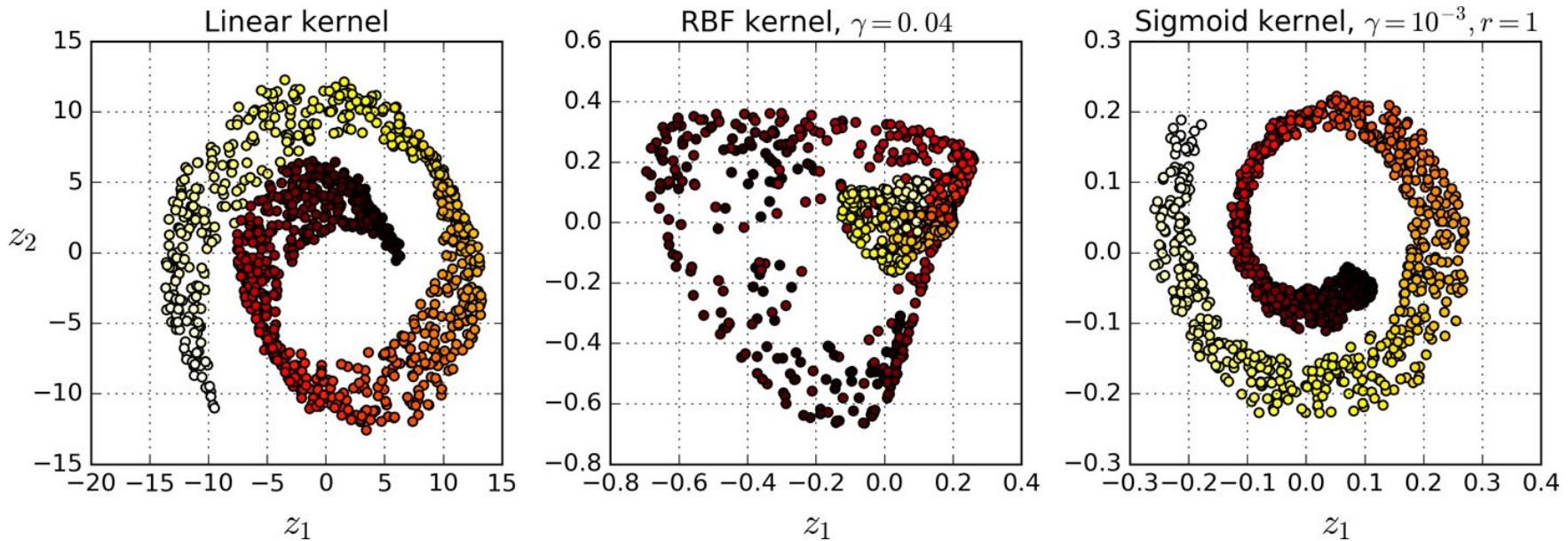
# Kernel PCA

- Recall that a linear decision boundary in the high-dimensional feature space corresponds to a complex nonlinear decision boundary in the *original space*.
- It is often good at preserving clusters of instances after projection, or sometimes even unrolling datasets that lie close to a twisted manifold.

```
from sklearn.decomposition import KernelPCA

rbf_pca = KernelPCA(n_components = 2, kernel="rbf", gamma=0.04)
X_reduced = rbf_pca.fit_transform(X)
```

# Kernel PCA (cont'd)



Swiss roll, reduced to two dimensions using :

- linear kernel (equivalent to simply using the PCA class)
- RBF kernel
- sigmoid kernel (Logistic).

# Kernel PCA (cont'd)

```
from sklearn.decomposition import KernelPCA

rbf_pca = KernelPCA(n_components = 2, kernel="rbf", gamma=0.04)
X_reduced = rbf_pca.fit_transform(X)
```

# Selecting Kernel and Hyperparameters

- Dimensionality reduction is often a preparation step for a supervised learning task:
- Use a grid search to select the kernel and hyperparameters that lead to the best performance on that task. A simple workflow would be as below (this is an example):
  - Reduce dimensionality to two dimensions using kernel PCA
  - Apply Logistic Regression for classification.
  - Uses GridSearchCV to find the best kernel and gamma value for kPCA in order to get the best classification accuracy at the end of the pipeline

# Selecting Kernel and Hyperparameters (cont'd)

```
from sklearn.model_selection import GridSearchCV
from sklearn.linear_model import LogisticRegression
from sklearn.pipeline import Pipeline

clf = Pipeline([
    ("kpca", KernelPCA(n_components=2)),
    ("log_reg", LogisticRegression())
])

param_grid = [
    {"kpca__gamma": np.linspace(0.03, 0.05, 10),
     "kpca__kernel": ["rbf", "sigmoid"]}
]

grid_search = GridSearchCV(clf, param_grid, cv=3)
grid_search.fit(X, y)

>>> print(grid_search.best_params_)
{'kpca__gamma': 0.04333333333333335, 'kpca__kernel': 'rbf'}
```



## Module 9 – Section 5

# Local Linear Embedding (LLE)

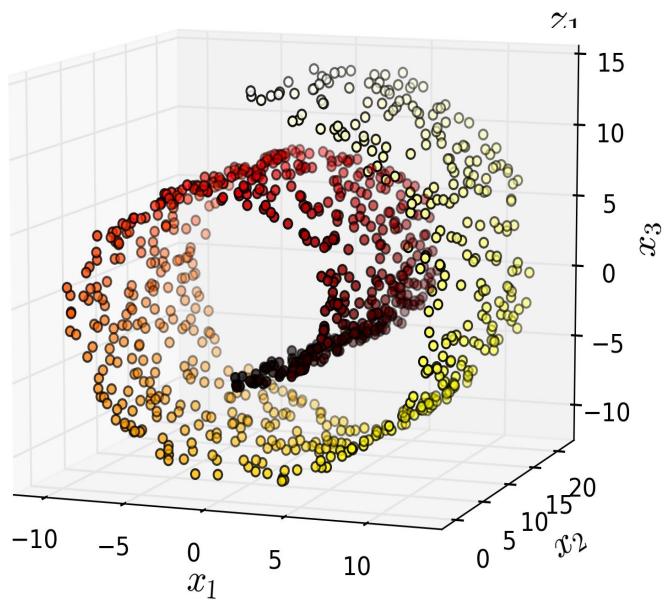
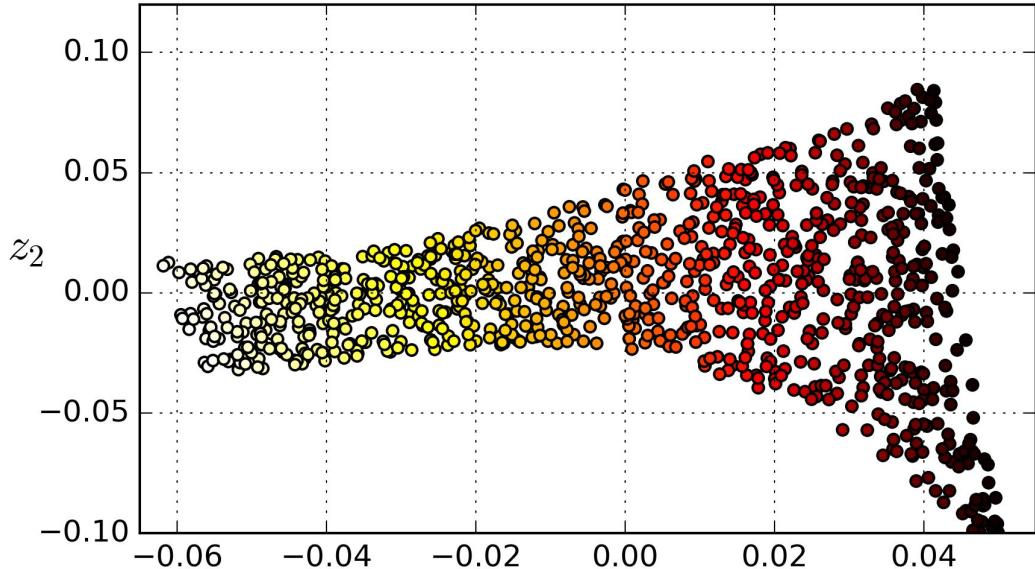
# Local Linear Embedding (LLE)

- LLE works by first measuring how each training instance linearly relates to its closest neighbors (c.n.), and then looking for a low-dimensional representation of the training set where these local relationships are best preserved
  - Particularly good at unrolling twisted manifolds, especially when there is not too much noise.

```
from sklearn.manifold import LocallyLinearEmbedding  
  
lle = LocallyLinearEmbedding(n_components=2, n_neighbors=10)  
X_reduced = lle.fit_transform(X)
```

# Local Linear Embedding (cont'd)

Unrolled Swiss roll using LLE



The Swiss roll is completely unrolled and the distances between instances are locally well preserved.

However, compared to original roll (lower plot), distances are not preserved on a larger scale: the left part of the unrolled Swiss roll is squeezed, while the right part is stretched.

# Local Linear Embedding (cont'd)

- For each training instance  $\mathbf{x}^{(i)}$ , the algorithm identifies its  **$k$  closest neighbors**, then tries to **reconstruct**  $\mathbf{x}^{(i)}$  as a **linear** function of these neighbors.
- It finds the weights  $w_{i,j}$  such that the squared distance between  $\mathbf{x}^{(i)}$  and

$$\sum_{j=1}^m w_{i,j} \mathbf{x}^{(j)}$$

is as small as possible, assuming  $w_{i,j} = 0$  if  $\mathbf{x}^{(j)}$  is not one of the  $k$  closest neighbors of  $\mathbf{x}^{(i)}$

## How LLE works – STEP 1

- In the first step, we calculate the weights that best represents the relationships between instances.

$$\hat{\mathbf{W}} = \underset{\mathbf{W}}{\operatorname{argmin}} \sum_{i=1}^m \| \mathbf{x}^{(i)} - \sum_{j=1}^m w_{i,j} \mathbf{x}^{(j)} \|^2$$

subject to  $\begin{cases} w_{i,j} = 0 & \text{if } \mathbf{x}^{(j)} \text{ is not one of the } k \text{ c.n. of } \mathbf{x}^{(i)} \\ \sum_{j=1}^m w_{i,j} = 1 & \text{for } i = 1, 2, \dots, m \end{cases}$

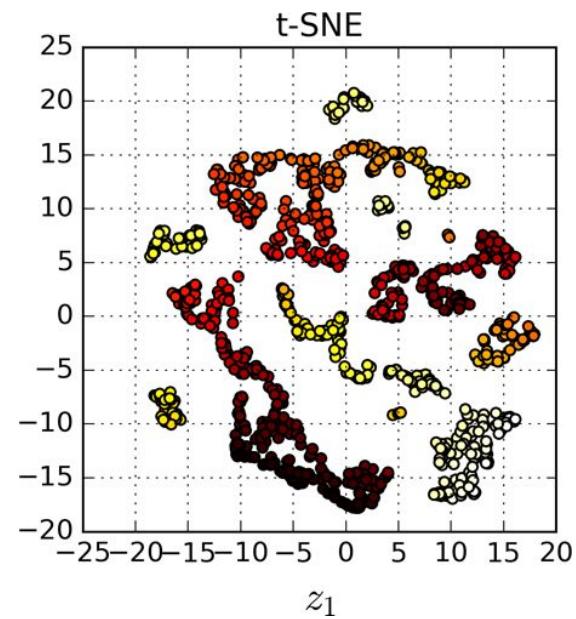
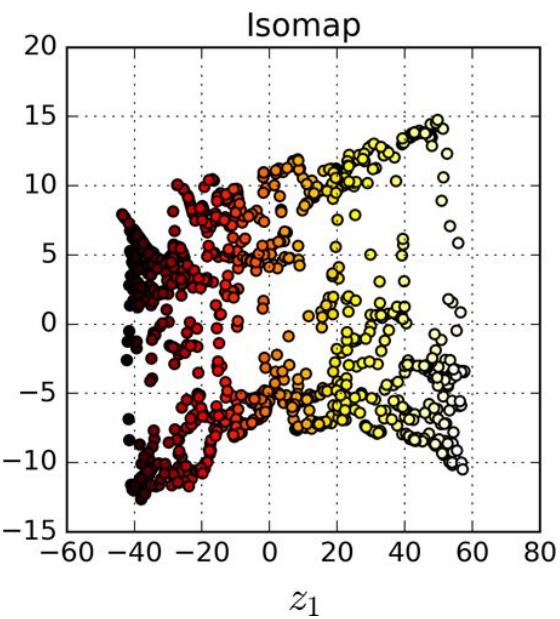
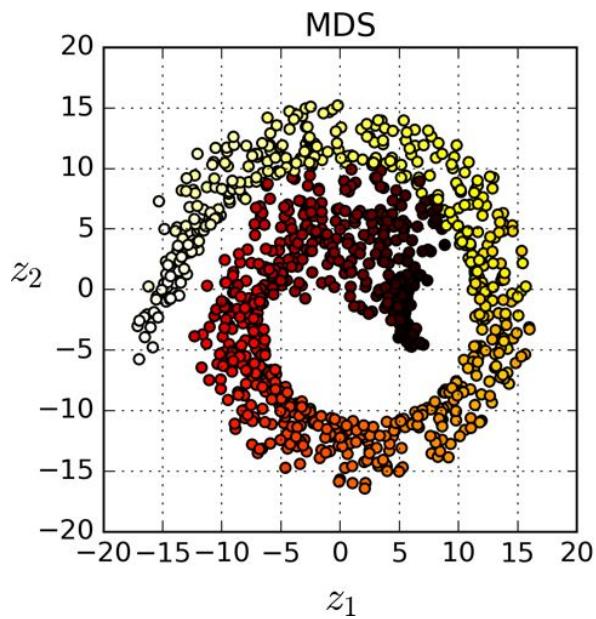
- $\hat{\mathbf{W}}$  (W hat) will be the weights for such a representation

## How LLE works – STEP 2

- The second step is to map the training instances into a d-dimensional space (where  $d < n$ ) while preserving these local relationships as much as possible.
- If  $\mathbf{z}^{(i)}$  is the image of  $\mathbf{x}^{(i)}$  in this d-dimensional space, then we want the squared distance between  $\sum_{j=1}^m \hat{w}_{i,j} \mathbf{z}^{(j)}$  to be as small as possible.

$$\hat{\mathbf{Z}} = \operatorname{argmin}_{\mathbf{Z}} \sum_{i=1}^m \| \mathbf{z}^{(i)} - \sum_{j=1}^m \hat{w}_{i,j} \mathbf{z}^{(j)} \|^2$$

# Other Methods



# PCA for Noise Reduction



<https://jakevdp.github.io/PythonDataScienceHandbook/05.09-principal-component-analysis.html>



## Module 9 – Section 6

# Resources and Wrap-up

# Resources

- Hands-On Machine Learning with Scikit-Learn and Tensorflow:
  - Chapter 8

# Assessment

- See Jupyter Notebook

# Next Class

- Introduction to Tensorflow

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