(Non-linear) dimensionality reduction

Jiří Kléma

Department of Computer Science,
Czech Technical University in Prague

http://cw.felk.cvut.cz/wiki/courses/b4m36san/start

Outline

- motivation, task definition,
- linear approaches such as PCA
  - and its non-linearization: kernel PCA,
- distance preserving approaches
  - multidimensional scaling,
  - Isomap,
  - locally linear embedding,
  - tSNE,
- self-organizing maps
  - a vector quantization approach,
  - their relation to k-means clustering,

Task definition

- Input: $\mathbf{X} = \{\mathbf{x_i}\}_{i=1}^{m} \subset \mathcal{X}$ of dimension D (typically $\mathbb{R}^D$),
- assumed: $\mathbf{X}$ at least approximately lies on a manifold with $d < D$,
- output:
  - a transformed space $\mathcal{T}$ of dimension L,
  - dimensionality reduction mapping $\mathbf{F} : \mathcal{X} \to \mathcal{T}$,
  - reconstruction mapping $\mathbf{f} : \mathcal{T} \to \mathcal{M} \subset \mathcal{X}$,
- such that:
  - $L < D$, L is as small as possible, at best $L = d$ (the intrinsic dimension),
  - the manifold approximately contains all the sample points

$$\{\mathbf{x_i}\}_{i=1}^{m} \underset{\sim}{\subseteq} \mathcal{M} \overset{def}{=} f(\mathcal{T}),$$

  - or alternatively, the reconstruction error of the sample is small

$$E_d(\mathbf{X}) \overset{def}{=} \sum_{i=1}^{m} d(\mathbf{x_i}, \mathbf{f}(\mathbf{F}(\mathbf{x_i})).$$

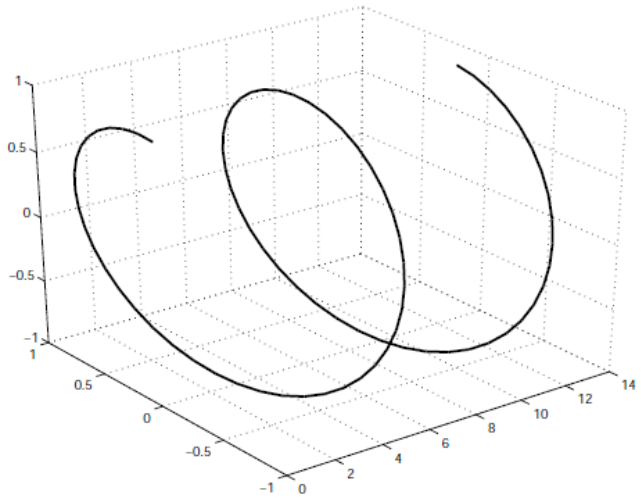
Manifold learning

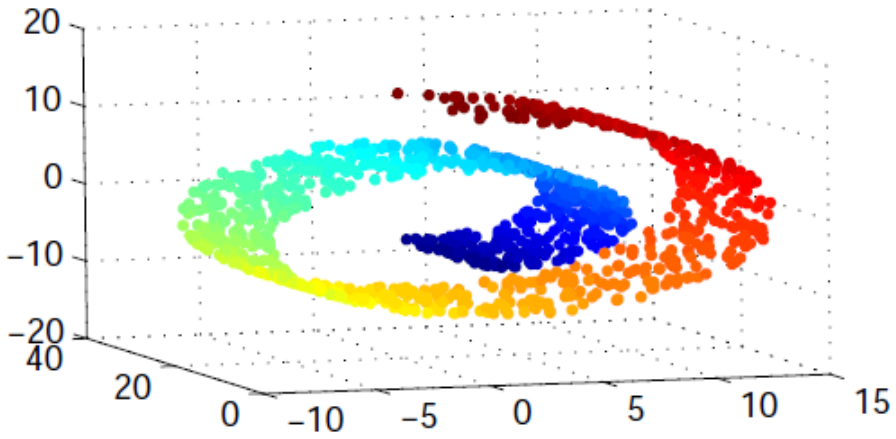
:: Manifold

- a topological space that on a small enough scale resembles the Euclidean space,
- globally typically nonlinear,

:: Learning

- identify a manifold dimension (it is embedded in a space of a higher dimension),
- project the problem (objects) into the low dimensional space – nonlinear dimension reduction,
- linear analogy: PCA or factor analysis.

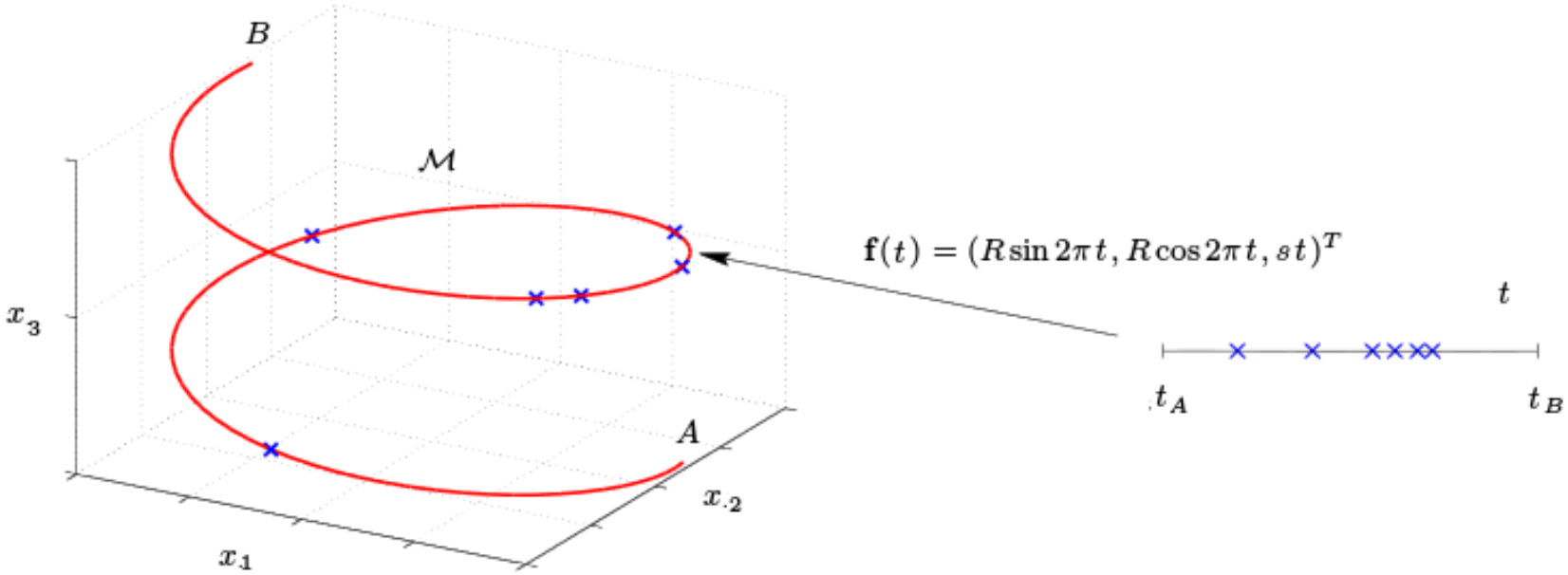




Cayton: Algorithms for Manifold Learning.

Example of a manifold and its mapping

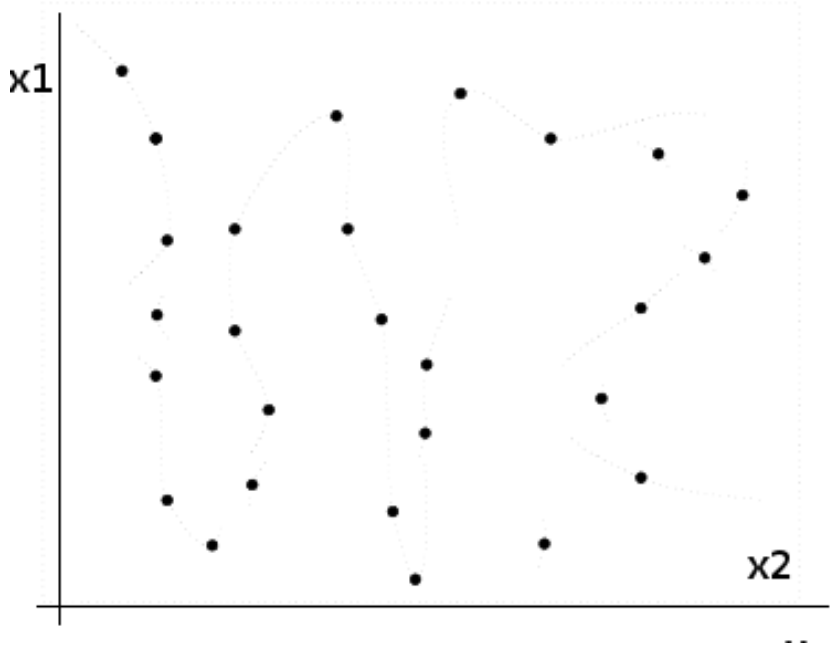
- A spiral of radius R and step s
  - 1D non-linear manifold in $\mathbb{R}^3$,
  - no noise, the given $f(t)$ guarantees zero reconstruction error.



Carreira-Perpinan: A Review of Dimension Reduction Techniques

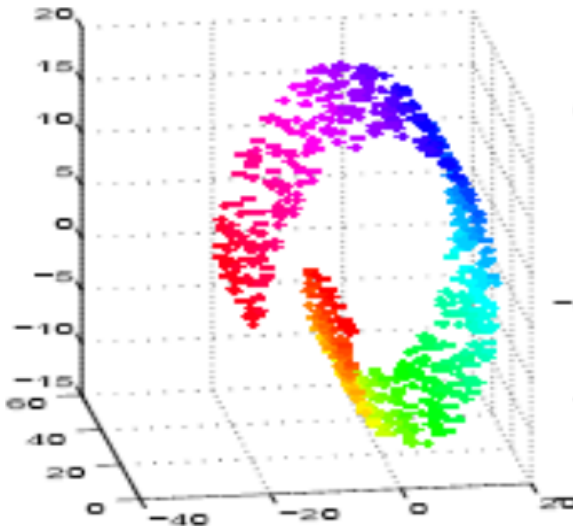
Intrinsic dimension

- the number of variables that **satisfactorilly** describe the phenomenon/data,
- when estimated from data, it is a vague number, it depends on
  - the minimum approximation quality criterion or alternatively,
  - smoothness of the manifold,
- it does not have to be a natural number (can be e.g., 1.4, consider fractals).

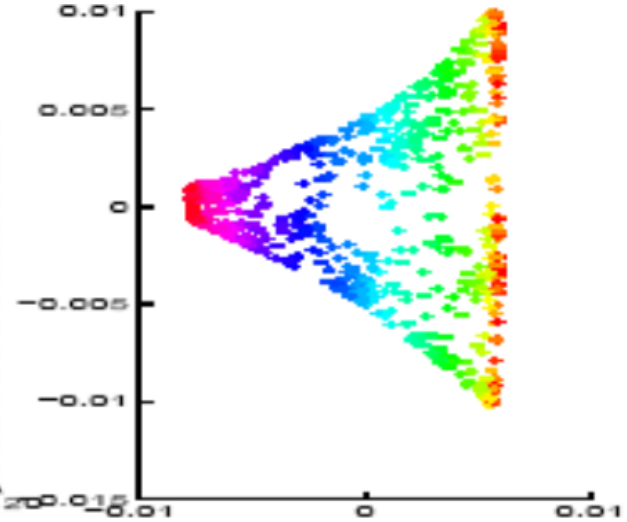


Motivation

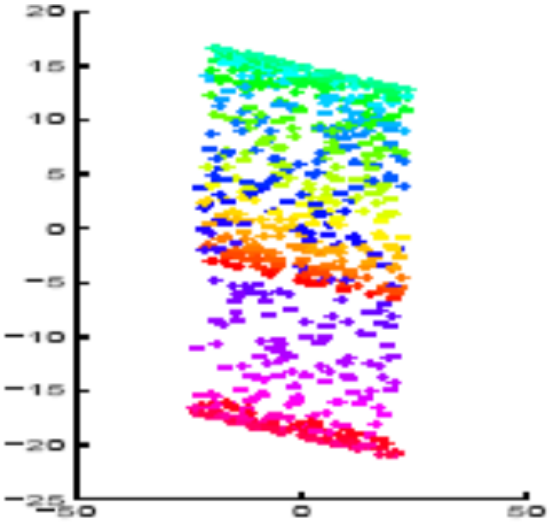
- Visualize the data and understand them (typically project into 2 or 3-D),
- compress the data to minimize storage and retrieval cost,
- identify hidden causes/latent variables that govern the process under study,
- learn in the lower-dimensional space
  - possibly obtain better results with fewer training samples in shorter time,
  - a lot of work has already been done during the projection.



Swiss roll



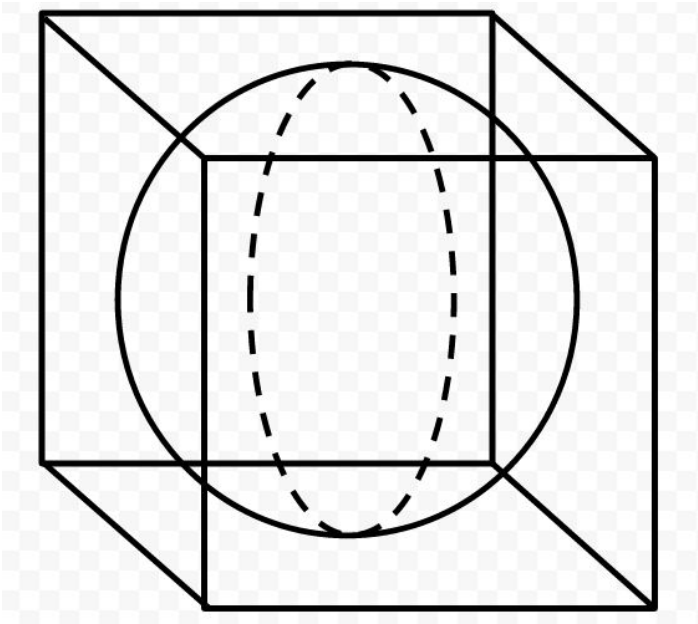
2D non-linear projection



2D linear projection

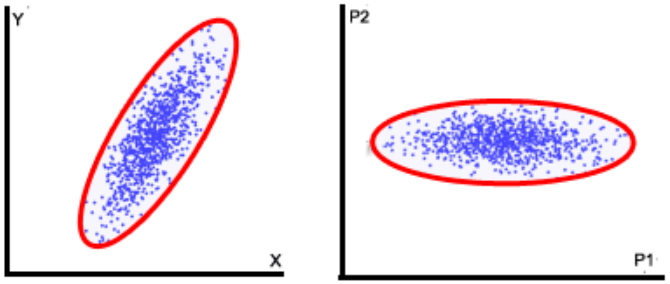
The challenges of high-dimensional spaces

- The curse of dimensionality
  - in the absence of **simplifying assumptions**, the sample size needed to estimate a function with D variables to a given **degree of accuracy** grows **exponentially** with D,
- the geometry of high-dimensional spaces
  - the empty space phenomenon,
  - guess what is the ratio of the volumes of unit hypersphere and unit hypercube ...



A brief review of PCA

- PCA could be seen as fitting a (hyper)ellipsoid to the data
  - the new axes have the direction of the highest variance,
  - they match the axes of the encapsulating/confidence ellipsoid.



- What happens in terms of covariances and redundancy?
  - left image: $\sigma_Y^2 > \sigma_{XY}^2 > \sigma_X^2$,
  - right image: $\sigma_{P1}^2 \gg \sigma_{P2}^2$, $\sigma_{P_1P_2}^2 = 0$,
  - in general, PCA **diagonalizes the covariance matrix**,
  - in other words, PCA removes linear relationship (redundancy) between variables.

A brief review of PCA

- For $\mathbf{X}$ with zero centered variables

$$\sum_{i=1}^{m} \mathbf{x_i} = 0$$

- the covariance matrix can be computed as follows

$$\mathbf{C_X} = \frac{1}{m} \sum_{i=1}^{m} \mathbf{x_i} \mathbf{x_i}^T = \frac{1}{m} \mathbf{X}^T \mathbf{X}$$

- by definition, PCA constructs a space transformation matrix $\mathbf{P}_{D \times D}$, such that

$$\mathbf{XP} = \mathbf{T} \text{ and } \mathbf{C_T} \text{ is a diagonal matrix}$$

- as $\mathbf{P}$ is not known, $\mathbf{C_T}$ cannot be calculated and diagonalized directly,
- instead, $\mathbf{C_T}$ can be expressed in terms of $\mathbf{C_X}$ and $\mathbf{P}$

$$\begin{aligned} \mathbf{C_T} &= \frac{1}{m} \mathbf{T}^T \mathbf{T} = \frac{1}{m} (\mathbf{XP})^T (\mathbf{XP}) = \\ &= \frac{1}{m} \mathbf{P}^T (\mathbf{X}^T \mathbf{X}) \mathbf{P} = \mathbf{P}^T \mathbf{C_X} \mathbf{P} \end{aligned}$$

A brief review of PCA

- any real symmetric matrix is diagonalized by a column matrix of its eigenvectors $\mathbf{E}$,
- $\mathbf{C_X}$ is real and symmetric, it follows that

$$\mathbf{C_X} = \mathbf{E}\mathbf{D}\mathbf{E}^T$$

- the only trick is to select $\mathbf{P}$ to be a matrix where each column $\mathbf{p_i}$ is an eigenvector of $\mathbf{C_X}$

$$\mathbf{P} = \mathbf{E}$$

- we also know that any orthogonal matrix has the same inverse and transpose,
- the above-selected $\mathbf{P}$ is necessarily orthogonal

$$\mathbf{P}^T\mathbf{P} = \mathbf{I} \Rightarrow \mathbf{P}^{-1} = \mathbf{P}^T$$

- then, it is easy to show that $\mathbf{P}$ diagonalizes $\mathbf{C_T}$

$$\begin{aligned}\mathbf{C_T} &= \mathbf{P}^T\mathbf{C_X}\mathbf{P} = \mathbf{P}^T(\mathbf{E}\mathbf{D}\mathbf{E}^T)\mathbf{P} = \\ &= (\mathbf{P}^T\mathbf{P})\mathbf{D}(\mathbf{P}^T\mathbf{P}) = (\mathbf{P}^{-1}\mathbf{P})\mathbf{D}(\mathbf{P}^{-1}\mathbf{P}) = \mathbf{D}\end{aligned}$$

- PCA is solved by finding the eigenvectors of $\mathbf{C_X}$.

A brief review of PCA

- what happens when D is large?
  - consider images, the color of each pixel is a feature, megapixel resolution,
  - large $\mathbf{C_X}$, unfeasible computation of its eigenvectors,
- provided that m is reasonable ($m \ll D$), we can employ the following trick,
- instead of the original eigenvector decomposition

$$\frac{1}{m}\mathbf{X}^T\mathbf{X}\mathbf{u_k} = \lambda_k\mathbf{u_k}$$

- we will consider

$$\frac{1}{m}\mathbf{X}\mathbf{X}^T\mathbf{v_k} = \gamma_k\mathbf{v_k}$$

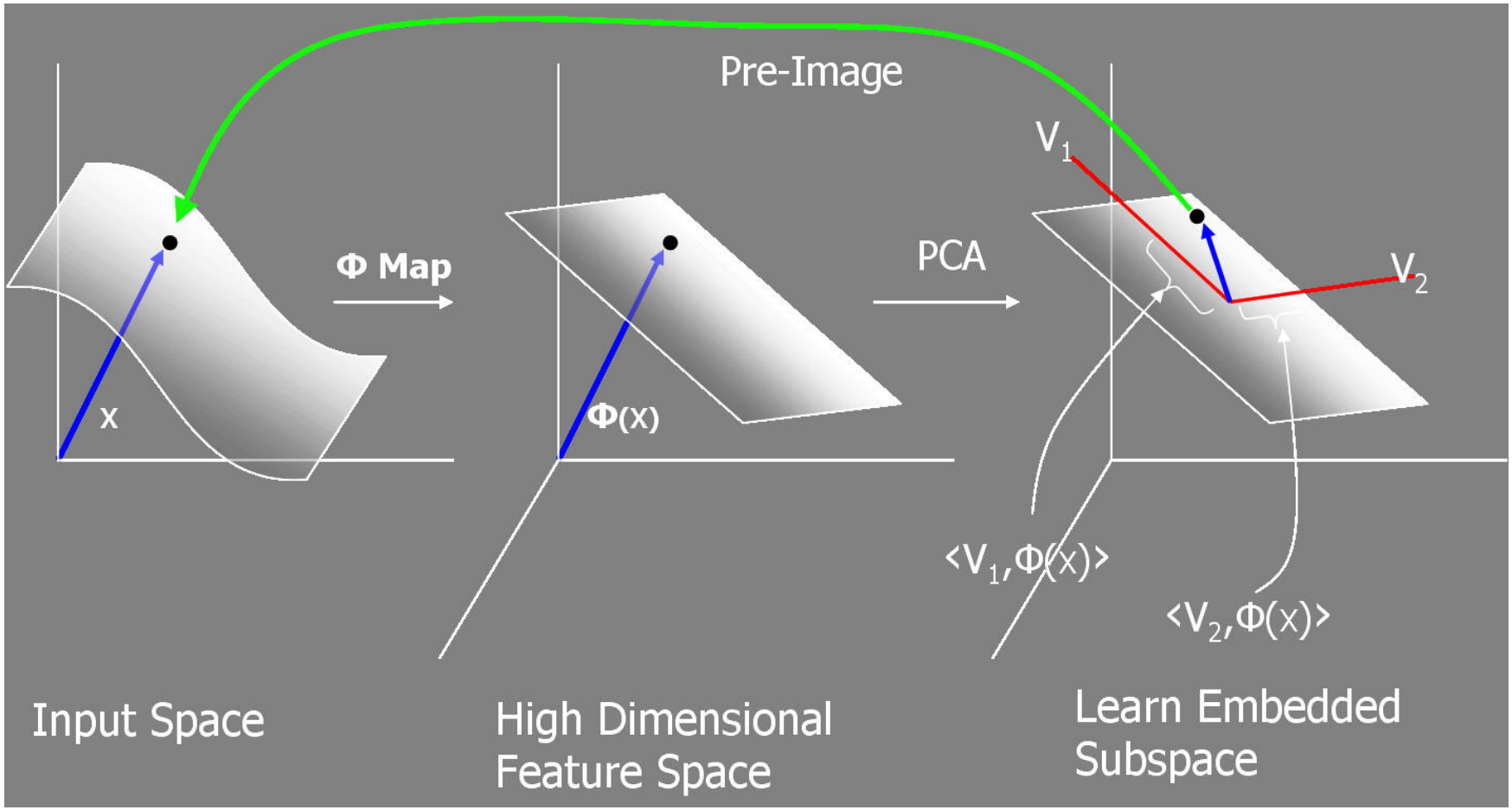
- and multiply both sides by $\mathbf{X}^T$

$$\frac{1}{m}\mathbf{X}^T\mathbf{X}\mathbf{X}^T\mathbf{v_k} = \gamma_k\mathbf{X}^T\mathbf{v_k}$$

- it is obvious that the substitution $\mathbf{X}^T\mathbf{v_k} = \mathbf{u_k}$ and $\gamma_k = \lambda_k$ matches the original eigenvector decomposition formula,
- PCA can be solved by decomposition of the $m \times m$ scalar-product matrix.

kernel PCA – the idea behind

- Introduce an intermediate feature space $\mathcal{U}$
  - $\mathcal{X} \to \mathcal{U} \to \mathcal{T}$, $\mathcal{U}$ linearizes the original manifold.



http://www.research.rutgers.edu

Why krenel in the method name?

- **feature space transformation** can capture non-linearity,
- a domain independent dimensionality reduction, only the transformation tuned for the domain
  - explicit transformation
    - get the object coordinates in the new feature space,
    - traditional PCA in the new space,
    - illustrative, but impractical,
  - implicit transformation
    - via similarity resp. kernel function $K : \mathcal{X} \times \mathcal{X} \to \mathbb{R}$,
    - purely a function of object pairs, no object coordinates in the new space,
    - very natural for clustering, similarity/distance its essential part anyway,
    - kernel trick analogy (SVM classification),
      - an implicit high-dimensional space, classes potentially easily separable,
    - very natural in clustering too, see kernel k-means later,
    - kernel PCA – kernel matrix $\to$ diagonalize $\to$ a low-dimensional feature space.

kernel PCA

- We choose a (non-linear) feature space transformation

$$\phi : \mathcal{X} \to \mathcal{U}$$

- the transformation is implicit, we only know the kernel function

$$\forall \mathbf{x_i}, \mathbf{x_j} \in \mathcal{X} : \mathbf{K}(\mathbf{x_i}, \mathbf{x_j}) := \langle \phi(\mathbf{x_i}), \phi(\mathbf{x_j}) \rangle = \phi(\mathbf{x_i})^T \phi(\mathbf{x_j})$$

- as with the PCA, we will assume the covariance matrix, now in the transformed space

$$\mathbf{C_U} = \frac{1}{m} \sum_{i=1}^{m} \phi(\mathbf{x_i}) \phi(\mathbf{x_i})^T$$

- note that the data are assumed to be centered

$$\sum_{i=1}^{m} \phi(\mathbf{x_i}) = 0$$

- similarly to PCA, we will find $\mathbf{C_U}$ eigenvectors $\mathbf{v}$ to decorrelate variables in $\mathcal{T}$

$$\mathbf{C_U v} = \lambda \mathbf{v} \to \frac{1}{m} \sum_{i=1}^{m} \phi(\mathbf{x_i}) \phi(\mathbf{x_i})^T \mathbf{v} = \lambda \mathbf{v}$$

kernel PCA

- $\phi(\mathbf{x_i})$ are not available, we need to replace them by $\mathbf{K}$,
- for $\lambda \geq 0$, $\mathbf{v}$'s are in the span of $\phi(\mathbf{x_i})$,
- they can be written as linear combination of the object images

$$\mathbf{v} = \sum_{i=1}^{m} \alpha_i \phi(\mathbf{x_i})$$

- we will substitute for $\mathbf{v}$ into the eigenvector formula (the last in the previous slide)

$$\lambda \sum_{j=1}^{m} \alpha_j \phi(\mathbf{x_j}) = \frac{1}{m} \sum_{i=1}^{m} \phi(\mathbf{x_i}) \phi(\mathbf{x_i})^T \sum_{j=1}^{m} \alpha_j \phi(\mathbf{x_j})$$

- and use the trick to introduce the dot product, we will multiply by $\phi(\mathbf{x_k})^T$

$$\lambda \sum_{j=1}^{m} \alpha_j \phi(\mathbf{x_k})^T \phi(\mathbf{x_j}) = \frac{1}{m} \sum_{j=1}^{m} \alpha_j \sum_{i=1}^{m} (\phi(\mathbf{x_k})^T \phi(\mathbf{x_i}))(\phi(\mathbf{x_i})^T \phi(\mathbf{x_j}))$$

- the kernel function replaces all the occurrences of ϕ, when iterating $\forall\ k = 1 \ldots m$ we obtain

$$\lambda \mathbf{K} \alpha = \frac{1}{m} \mathbf{K}^2 \alpha$$

- to diagonalize $\mathbf{C_T}$, we solve the eigenvalue problem for the kernel matrix

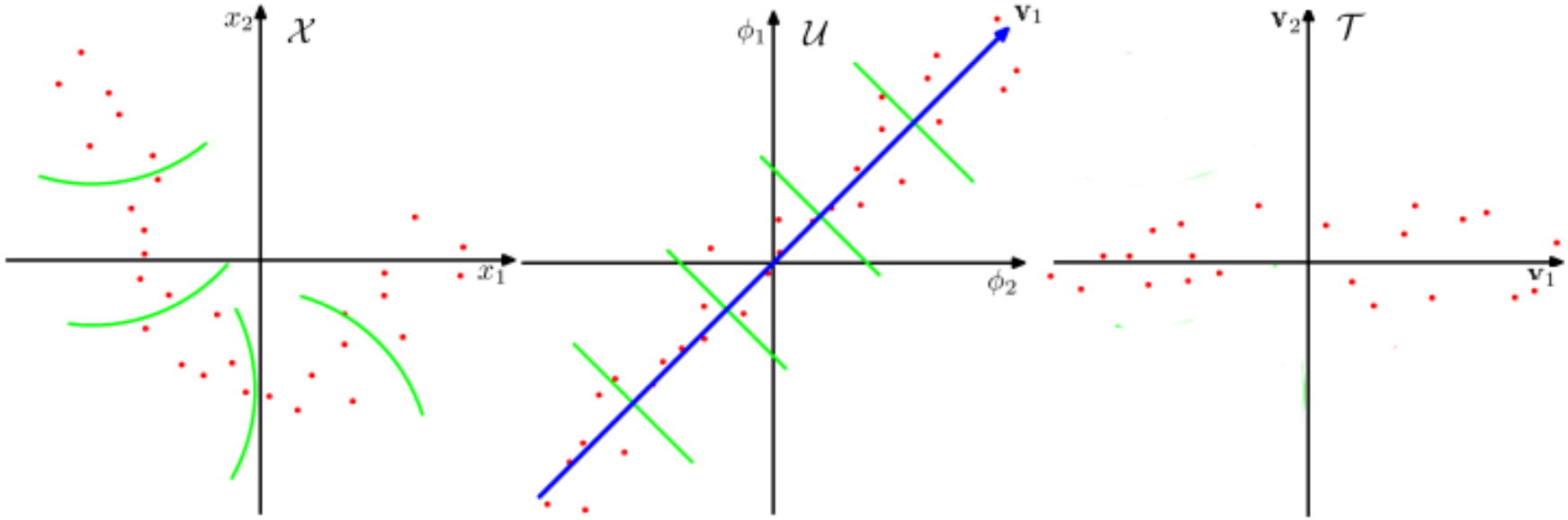
$$m\lambda\alpha = \mathbf{K}\alpha$$

kernel PCA

- the last issue is to extract the principal components, the final object images,
- i.e., the projections of $\phi(\mathbf{x_i})$ onto the eigenvectors in $\mathcal{U}$

$$t_{ik} = \mathbf{v_k}^T \phi(\mathbf{x_i}) = \sum_{j=1}^{m} \alpha_j \phi(\mathbf{x_j})^T \phi(\mathbf{x_i}) = \sum_{j=1}^{m} \alpha_j \mathbf{K}(\mathbf{x_i}, \mathbf{x_j})$$

- note that both the intermediate factors $\mathbf{v_k}$ and $\phi(\mathbf{x_i})$ remain implicit!



Bishop: Pattern Recognition and Machine Learning, modified

Remarks on kernel PCA

- kernel PCA works for non-linear manifolds
  - effectively compresses them,
- its complexity does not grow with the dimensionality of $\mathcal{U}$
  - one can work with a large number of components too, i.e., increase the dimension ($L > D$),
  - in PCA $L \leq D$
  - it can pay-off in subsequent classification,
- kernel matrix $\mathbf{K}$ grows quadratically with the number of data points m
  - for large data sets with small dimensionality ($m \gg D$) more expensive than PCA,
  - one may need to (properly) subsample the data,
- from the optimization point of view cannot get trapped in local minima,
- unlike PCA cannot reconstruct objects from their principal components
  - $\mathbf{f}$ is not available.

Multidimensional scaling (MDS)

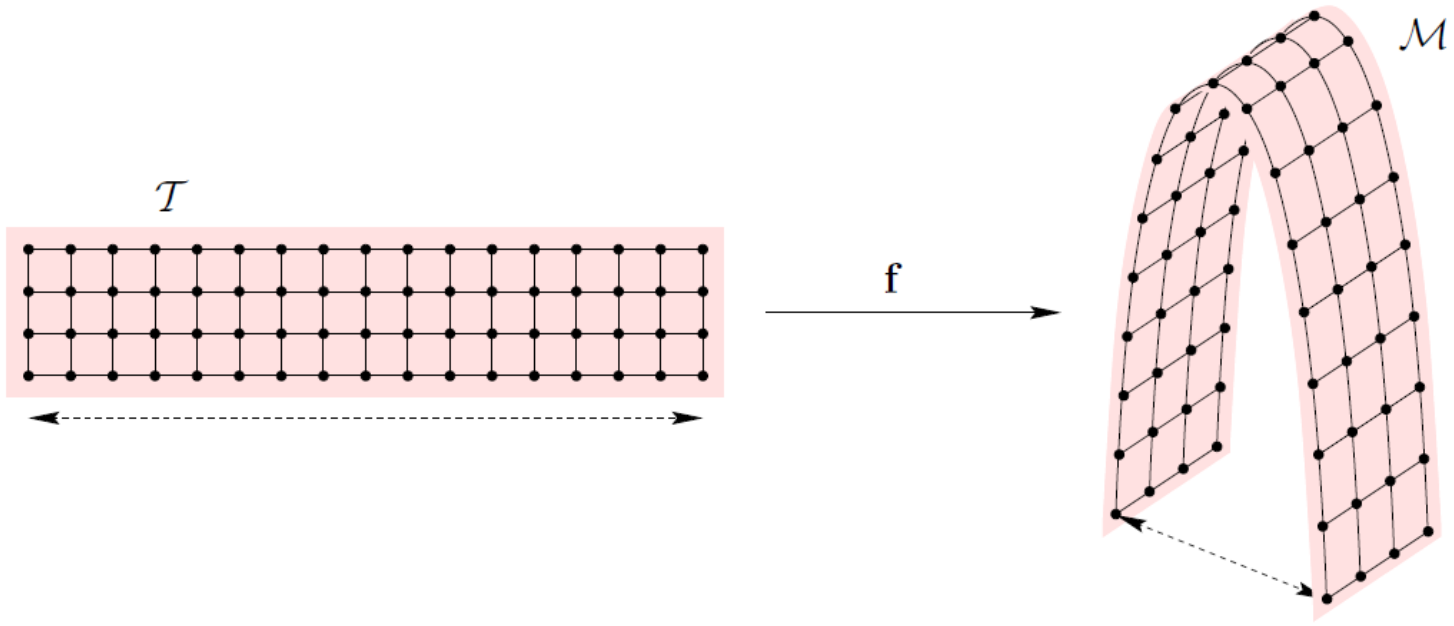
- The main idea
  - points close together in $\mathcal{X}$ should be mapped close together in $\mathcal{T}$,
- minimizes the **stress function**

$$stress(\mathbf{T}, f) = \sqrt{\frac{\sum_{i,j=1}^{m}(f(\delta_{ij}) - d_{ij})^2}{\sum_{i,j=1}^{m} d_{ij}^2}}$$

  - $\delta_{ij} = d_{\mathcal{X}}(\mathbf{x_i}, \mathbf{x_j})$, $d_{ij} = d_{\mathcal{T}}(\mathbf{t_i}, \mathbf{t_j})$ – typically Euclidean,
  - f is a proximity transformation function (e.g., identity, monotonic $\rightarrow$ metric, ordinal),
- whole class of methods that differ in
  - the method for calculation of proximities δ,
  - the parametrization of stress function,
  - the method that minimizes the stress function (e.g., gradient descent, Newton).

Geodesic distance

- What does Euclidean distance say about a non-linear manifold?
- We shall better preserve **geodesic distance** between points
  - a minimum of the length of a path joining both points that is contained in the manifold,
  - these paths are called geodesics,
- as a result, we unfold the manifold.



Carreira-Perpinan: A Review of Dimension Reduction Techniques

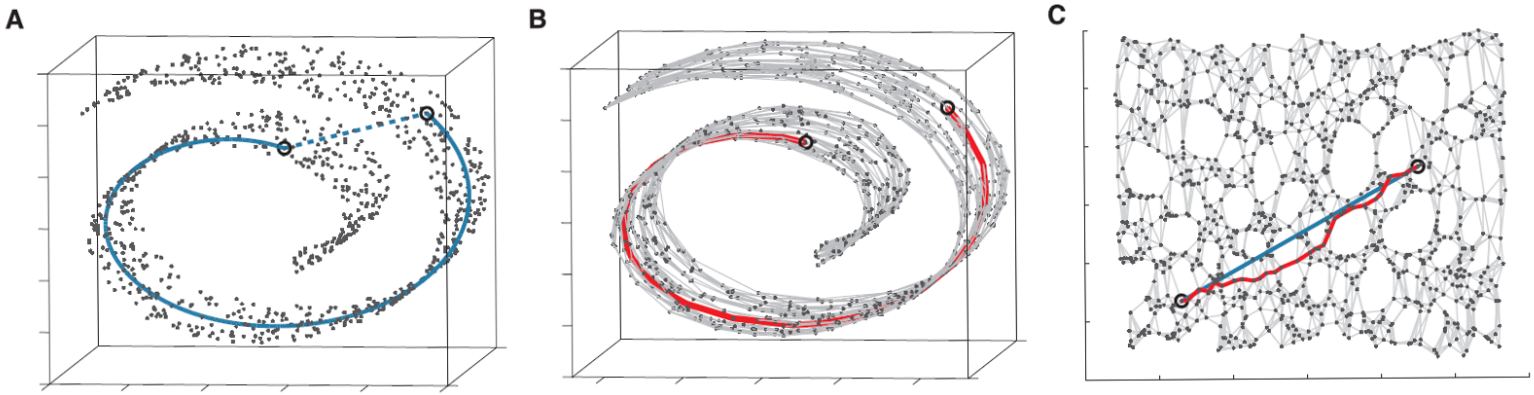
Isomap [Tenenbaum et al., 1998]

- Classical MDS with geodesic distance

(**A**) Euclidean vs geodesic distance to express intrinsic similarity in the input space,

(**B**) the neighborhood graph G ($K = 5$, $m = 1000$) and its shortest path (red) as an approximation to the true geodesic path,

(**C**) 2D embedding, which best preserves the shortest path distances in G, the straight lines in the embedding (blue) represent simpler and cleaner approximations to the true geodesic paths than do the corresponding graph paths.



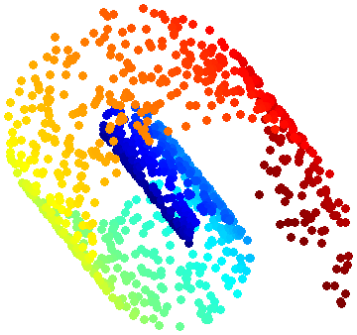
Tenenbaum et al.: A Global Geometric Framework for Nonlinear Dimensionality Reduction

Isomap [Tenenbaum et al., 1998]

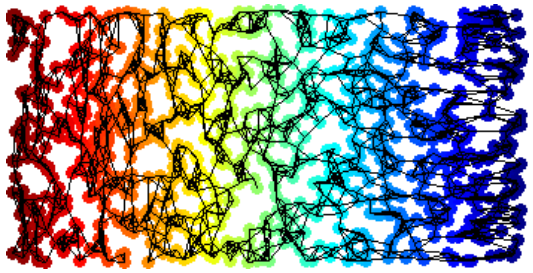
- The Isomap algorithm
  - determine the nearest neighbors
    - all points in a fixed radius or K-nearest neighbors,
  - construct a neighborhood graph
    - each point gets connected to its neighbors,
    - edge length equals the Euclidean distance between the points,
  - compute the shortest paths between all pairs of points
    - Floyd's or Dijkstra's algorithm ($\mathcal{O}(m^3)$ resp. $\mathcal{O}(Km^2 \log(m))$),
    - could be time consuming and result in a large non-sparse matrix,
    - use quantization to compress the graph,
  - construct a lower dimensional embedding
    - use classical MDS.

Isomap [Tenenbaum et al., 1998]

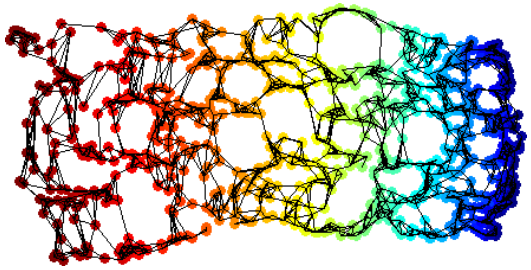
- Isomap has provable convergence guarantees,
- given the infinite (sufficient) input data, the method perfectly recovers the original distances
  - impractical concerning the next property,
  - otherwise, the geodesic distance can overestimate the true distance,
- cubic complexity in the number of objects can be too much
  - selection of M reference vectors can reduce the time to $\mathcal{O}(M^3)$,
  - we have to guarantee that the manifold is uniformly sampled,
- finding a proper value of K is not easy
  - too small/large K: insufficient graph/improper connections originate.



Swiss roll



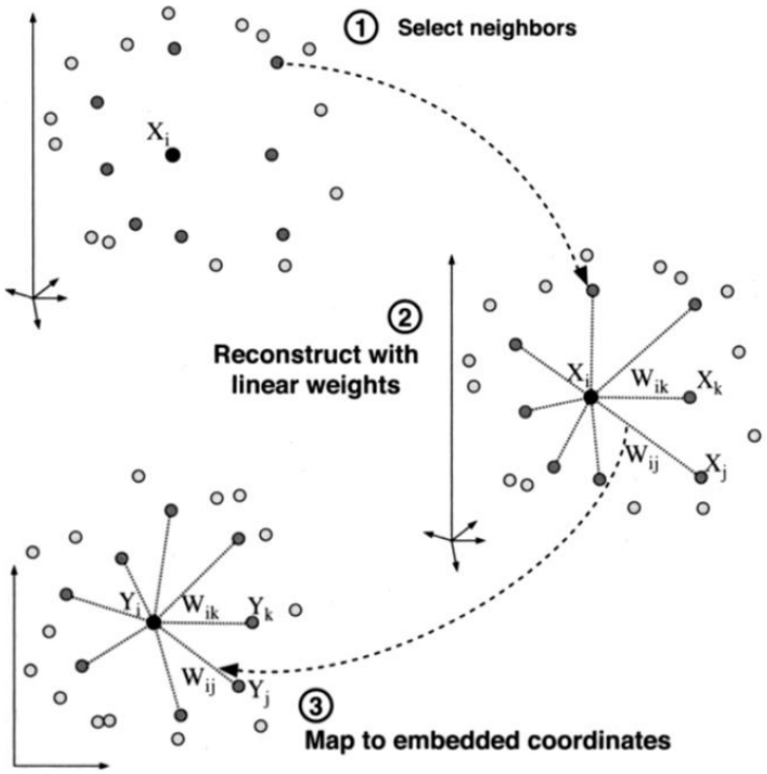
ideal projection



Isomap outcome

Locally Linear Embedding (LLE) [Roweis, Saul, 2000]

- Remember: manifold is a topological space that is **locally Euclidean**
  - we can locally fit (linear) models using Euclidean distance,
  - when compiled they create a global model.



Roweis, Saul: Nonlinear Dimensionality Reduction by LLE.

Locally Linear Embedding (LLE) [Roweis, Saul, 2000]

- The LLE algorithm
  - each data point and its neighbors lie close to a locally linear patch of the manifold,
  - each point can be written as a linear combination of its neighbors,
  - m local models, the weights chosen to minimize the reconstruction error

$$\hat{\mathbf{x}}_\mathbf{i} = \sum_{j \in \mathcal{N}(\mathbf{x_i})} w_{ij} \mathbf{x_j} \text{ such that } \sum_{i=1}^{m} ||\mathbf{x_i} - \hat{\mathbf{x}}_\mathbf{i}||^2 \text{ is minimized and } \sum_{j \in \mathcal{N}(\mathbf{x_i})} w_{ij} = 1$$

  - the same weights should reconstruct the point in L dimensions
    - the weights characterize the intrinsic geometric properties of each neighborhood,
  - global embedding fits the positions $\mathbf{t_i}$ in the low-dimensional space
    - we minimize the embedding cost function, the weights are fixed

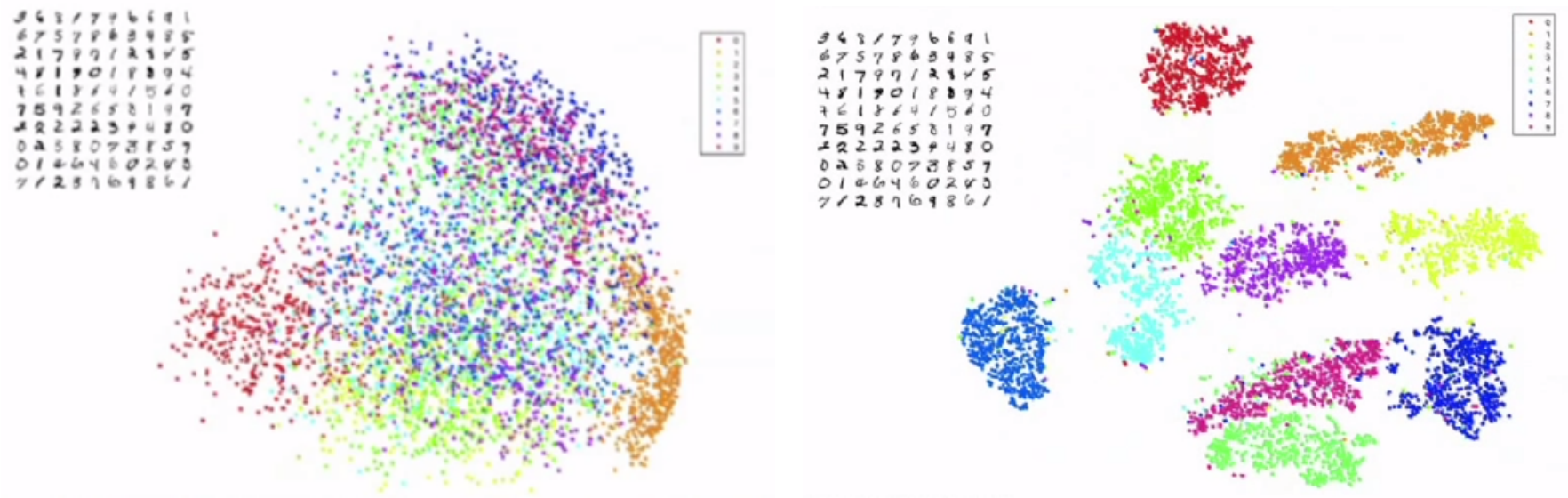
$$\hat{\mathbf{t}}_\mathbf{i} = \sum_{j \in \mathcal{N}(\mathbf{x_i})} w_{ij} \mathbf{t_j} \text{ such that } \sum_{i=1}^{m} ||\mathbf{t_i} - \hat{\mathbf{t}}_\mathbf{i}||^2 \text{ is minimized.}$$

Locally Linear Embedding (LLE) [Roweis, Saul, 2000]

- The ultimate case of piecewise linear modelling
  - approximation of the manifold by a combination of linear models,
  - in here, we have a linear model for each object,
- a special case of kernel PCA constructing a data-dependent kernel matrix
  - for some problems it is difficult to find a kernel for kernel PCA,
- advantages
  - efficient for large datasets, optimization does not involve local minima,
  - single parameter to tune (K),
  - invariant to scaling, rotation and translation,
- disadvantages
  - improper for representing future data,
  - can be unstable in sparse areas of the input space,
  - tends to collapse a lot of instances near the origin of $\mathcal{T}$.

t-Distributed Stochastic Neighbor Embedding (t-SNE)

- distance preserving visualization technique [van der Maaten, 2008] (like e.g., MDS),
- puts emphasis on preserving small pairwise distances between objects,
- large distances allowed to be modelled as being larger,
- as a result, two essential characteristics
  - the local data structures retained,
  - ability to reveal global structure such as the presence of clusters at several scales.



PCA tSNE

van der Maaten: Visualizing Data Using t-SNE, GoogletechTalks

t-Distributed Stochastic Neighbor Embedding (t-SNE)

- The key ideas are in the design of the stress function driving gradient descent search
  - convert Euclidean distances in both spaces into joint probabilities,
  - p_{ij} in the original space $\mathcal{X}$ and q_{ij} in the reduced space $\mathcal{T}$,
  - minimize their Kullback-Leibler divergence

$$S = KL(P||Q) = \sum_i \sum_{j \neq i} p_{ij} \log \frac{p_{ij}}{q_{ij}}$$

  .

- The first "trick" lies in asymmetry of KL divergence
  - large p_{ij} modeled by small $q_{ij} \rightarrow$ big penalty!
  - small p_{ij} modeled by large $q_{ij} \rightarrow$ small penalty!
  - tends to preserve large p_{ij}'s and thus small distances in the original space.

t-Distributed Stochastic Neighbor Embedding (t-SNE)

- The other "tricks" consist in definition of p_{ij} and q_{ij}
  - the empirical probability that an object j is a neighbor of an object i

$$p_{j|i} = \frac{\exp(-||\mathbf{x_i} - \mathbf{x_j}||^2/2\sigma_i)}{\sum_{k \neq i}(-||\mathbf{x_i} - \mathbf{x_k}||^2/2\sigma_i)}$$

  - i.e., it is normally distributed wrt their distance (and decreases quickly with it),
  - σ_i is the kernel bandwidth,
  - σ_i is locally adjusted so that a fixed number of objects falls in mode of the Gaussian,
  - the symmetric joint probability

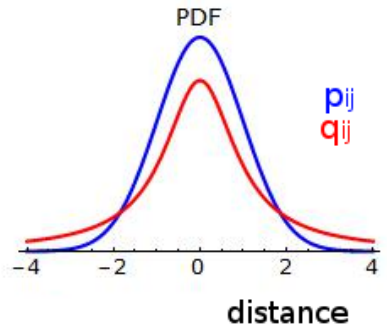
$$p_{ij} = \frac{p_{j|i} + p_{i|j}}{2m}$$

t-Distributed Stochastic Neighbor Embedding (t-SNE)

- In the reduced space $\mathcal{T}$ we permit higher probabilities for larger distances,
  - the normal distribution used in p_{ij} turns into the heavy-tailed t-distribution in q_{ij}

$$q_{ij} = \frac{(1 + ||\mathbf{t_i} - \mathbf{t_j}||^2)^{-1}}{\sum_{k \neq l}(1 + ||\mathbf{t_k} - \mathbf{t_l}||^2)^{-1}}$$

  - in KL divergence, p_{ij} and q_{ij} shall agree as much as possible, but they may map to different distances in both the spaces,
  - as a result, a moderate distance in the high-dimensional space can be faithfully modeled by a much larger distance in the map,
  - the reduced map gets insensitive to distant points (they can be placed to many places without big changes in q_{ij}).



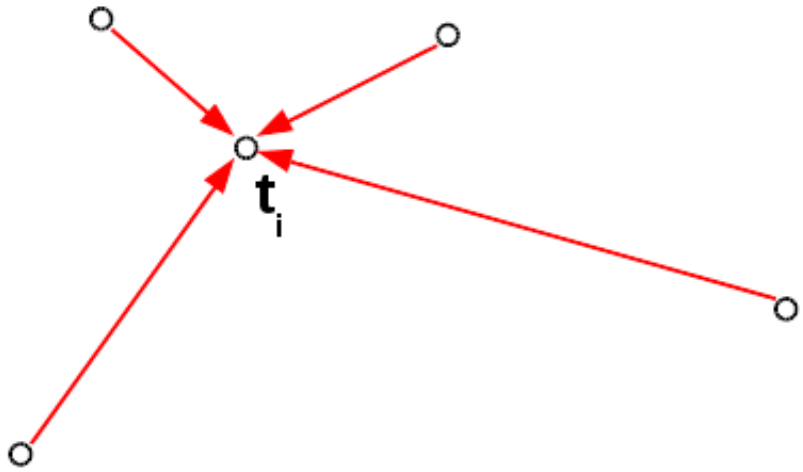
Tails in normal and student distributions.

t-Distributed Stochastic Neighbor Embedding (t-SNE)

- The overall picture
  - the gradient descent gradually minimizes the stress function for the individual objects

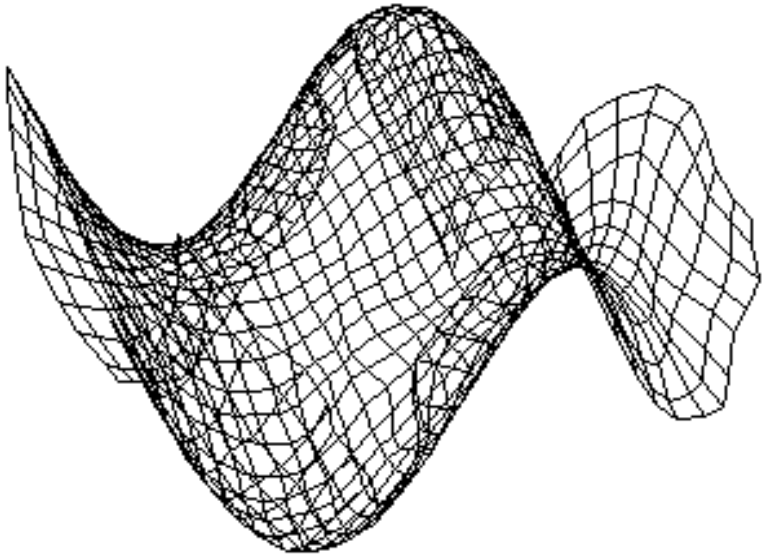
$$\frac{\partial S}{\partial \mathbf{t_i}} \propto \sum_{j \neq i} (p_{ij} - q_{ij})(1 + ||\mathbf{t_i} - \mathbf{t_j}||^2)^{-1}(\mathbf{t_i} - \mathbf{t_j})$$

  - all the other objects get connected via springs that are either stretched or compressed,
  - the resultant summed force tells us where to move the point in every gradient update.



Self-organizing map (SOM)

- unsupervised neural network producing a low dimensional (typically 2D) discretized map
  - the map is composed of neurons,
  - the neurons are mutually linked by a neighborhood relationship (e.g., make a grid),
  - the neurons compete for the right to respond to the individual input objects,
- the map preserves the topology of the input space
  - dimension reduction = the map from the position of the corresponding neuron in the input space to its (discrete) position in the grid.



Borgelt: XSOM visualization

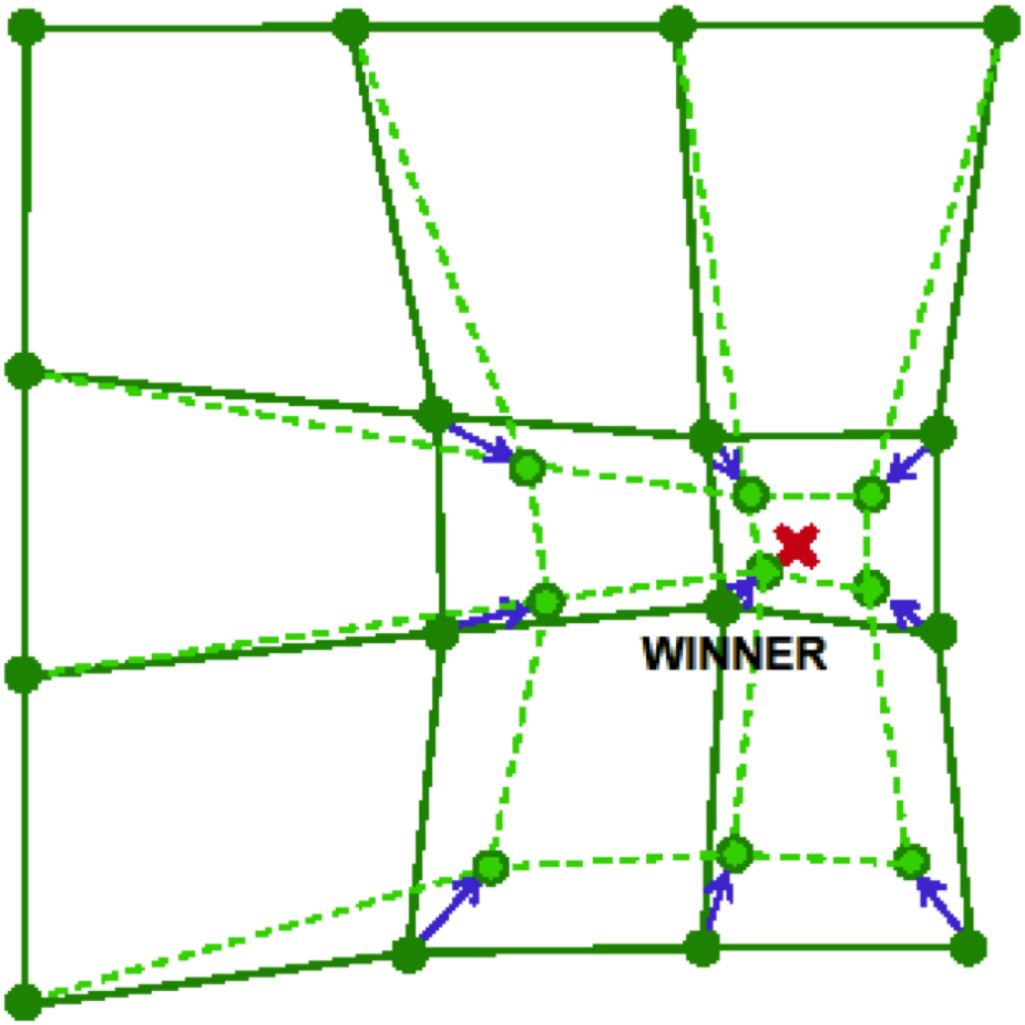
SOM learning algorithm

1. Initialize weight vectors of all the neurons $\mathbf{w}_i^0 \in \mathcal{X}\ (\mathbb{R}^D),\ \forall i = 1, \ldots, N$
   - randomly or rather sample evenly from the subspace spanned by the largest principal component eigenvectors,
2. resample the instance set $\mathbf{X}$
   - A: sample systematically, B: **permute** the instance set, C: randomly (bootstrap),
3. get the next instance $\mathbf{x}_i \in \mathbb{R}^D$ from the resample,
4. find the best matching unit (BMU), i.e., the neuron nearest to $\mathbf{x}_i$,
5. change the weights of neurons in the neighborhood of BMU (including BMU)

$$\mathbf{w}_i^{t+1} = \mathbf{w}_i^t + \alpha^t e^{-\frac{d(w_i^t, BMU)}{2(\sigma^t)^2}} (\mathbf{x}_i - \mathbf{w}_i^t)$$

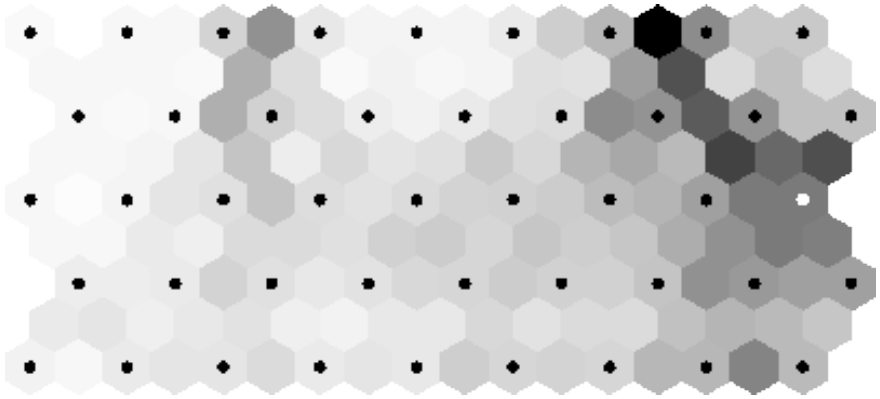
   - both the neighborhood size σ^t and the learning rate α^t decrease in time,
   - d is the distance in terms of the neighborhood relationship (e.g., the grid distance),
6. go to step 3 (or 2 when the sample is finished) until the given number of cycles is reached.

SOM learning algorithm – illustration

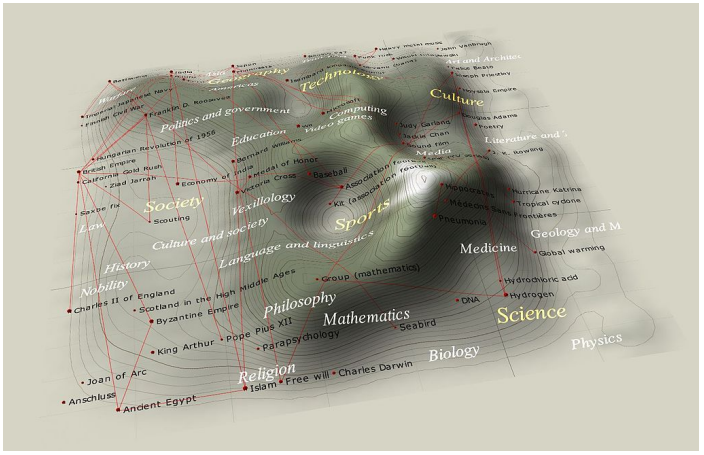


How to visualize and interpret SOM?

- U-matrix (unified distance matrix)
  - visualizes the distances between the neurons,
  - dark color between a pair of neurons corresponds to a large distance of their weight vectors,
  - light areas are candidate clusters while dark areas are interpreted as cluster separators.



Hollmen: U-matrix



Wikipedia articles

Relation to k-means

- The same **competitive learning** principle
  - the centroids/neurons compete for the right to respond to the individual input objects,
  - k-means employs the **winner takes all** principle (only the nearest centroid wins),
  - in SOM it is the BMU and its neighbors who win (for $\sigma \to 0$ equal to k-means),
- The same **vector quantization** approach
  - minimize the distance between objects and their representatives,
  - k-means concerns the nearest centroid only, SOM deals with the whole neighborhood,
- The main difference lies in
  - the most frequent way of using them (clustering versus dimensionality reduction),
  - k corresponds to the number of clusters, the number of neurons typically much larger.
- SOM can be seen as constrained k-means.

Summary – dimensionality reduction, manifold learning

- Difficult problem namely for the curse of dimensionality
  - huge sample sizes needed to guarantee reasonable parameter estimates, non-empty neighborhoods, etc.,
  - the intrinsic dimensionality estimation is not reliable,
- strong assumptions greatly simplify the task,
- the key role of PCA has not been undermined by any non-linear method yet
  - they work for well-sampled smooth manifolds, but not necessarily for real data,
  - besides the curse of dimensionality, the problems could be caused by insufficiency of objective functions or numerical problems during their optimization,
- there is a large pool of non-linear reduction methods,
- the key properties are effectivity and efficiency including convergence,
- other issues
  - setting hyperparameters?
  - implicit/explicit definition of $\mathbf{F}$ and $\mathbf{f}$,
  - additivity – can I drop a coordinate from L mapping to obtain $L-1$ mapping?

Recommended reading, lecture resources

:: Reading

- Jonathon Shlens: **A Tutorial on Principal Component Analysis.**
  - Google research, 2014,
  - http://arxiv.org/pdf/1404.1100.pdf,
- Scholkopf, Smola, Müller: **Kernel Principal Component Analysis.**
  - Artificial Neural Networks, 1997,
  - http://link.springer.com/chapter/10.1007/BFb0020217,
- Carreira-Perpinan: **A Review of Dimension Reduction Techniques.**
  - Tech. report, University of Sheffield, 1997,
  - http://www.pca.narod.ru/DimensionReductionBrifReview.pdf,
- van der Maaten, Hinton: **Visualizing High-Dimensional Data Using t-SNE.**
  - Journal of Machine Learning Research 9(Nov):2579-2605, 2008,
  - https://lvdmaaten.github.io/publications/papers/JMLR_2008.pdf.