SDMA: Semi-Definite Manifold Alignment

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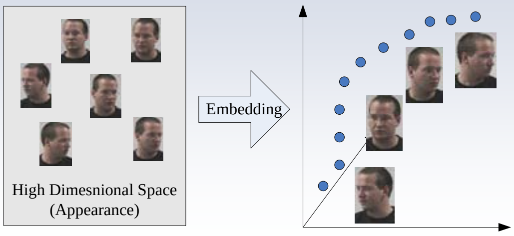
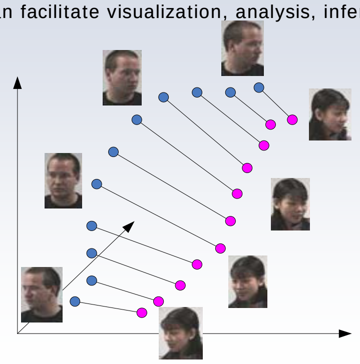
In many problems, samples in high-dimension feature spaces actually lie on a low-dimensional manifold. We can use **Embedding** algorithms to reveal and visualize these structures.



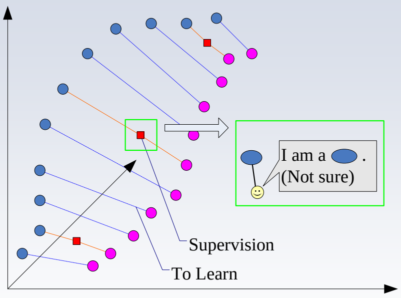
Manifold Embedding

How to further utilize this structural information? One choice is **Manifold Alignment (MA)**, which aims at finding correspondences — pairs of samples that have the same underlying parameter(s) — between manifolds given the premise that these manifolds share the same structure. MA can facilitate visualization, analysis, inference, etc.



Manifold Alignment

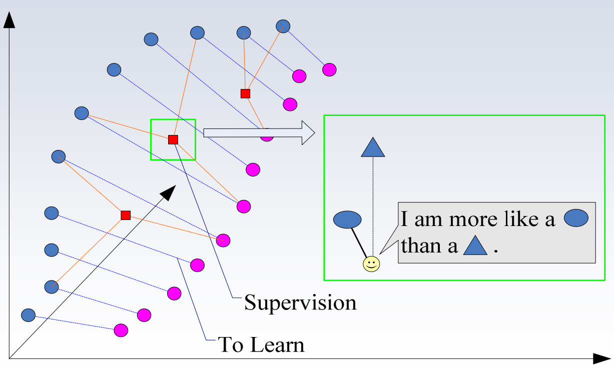
Manifold Alignment is often achieved in a semi-supervised and transductive way. Traditionally, pair-wise correspondences are used as supervision.



Traditional Semi-supervised Manifold Alignment

Possible problems of traditional alignment:
- Its hard/expensive to find accurate pairs in large datasets.
- "Correspondence" is sometimes not well defined.
- Exact correspondence may not even exist.

SDMA: Supervise manifold alignment by relative comparisons



Problem Formulation

- Use Manifold Regularization to capture the underlying manifold structures.
- Use Euclidean distance in the embedded space to represent similarity.

Symbols:

$\mathbf{X}=[\mathbf{x}_1,\mathbf{x}_2,\cdots,\mathbf{x}_n]$	$\mathbf{H}=[\mathbf{h}_1,\mathbf{h}_2,\cdots,\mathbf{h}_n]$	$\mathbf{M}$	T
Raw samples	Embedded samples	Regularization	Supervision tuple set
$\mathbf{K}=\mathbf{H}^T\mathbf{H}$	$E=\{\varepsilon_c, c=1,2,\cdots C\}$	α	
Sample kernel matrix	Margin of constraints	Constant	

The quadratic formulation:

$$\min_{\mathbf{H}} trace(\mathbf{HMH}^T)$$
$$s.t.\begin{cases}\forall\{\mathbf{x}_i,\mathbf{x}_j,\mathbf{x}_k\}\in T, \|\mathbf{h}_i-\mathbf{h}_j\|\le\|\mathbf{h}_i-\mathbf{h}_k\| \\ \text{Translation, scale, and rotation invariance.}\end{cases}$$

The quadratic formulation leads to a **non-convex** *Quadratically Constrained Quadratic Programming* (QCQP) problem. To make it tractable, we apply the semi-definite relaxation and deal with the data kernel matrix instead.

The semi-definite formulation (**SDMA**):

$$\min_{\mathbf{K},E} trace(\mathbf{MK})+\alpha\sum_{\varepsilon_c\in E}\varepsilon_c$$
$$s.t.\begin{cases}\forall\{\mathbf{x}_i,\mathbf{x}_j,\mathbf{x}_k\}\in T, -2\mathbf{K}_{ij}+2\mathbf{K}_{ik}+\mathbf{K}_{jj}-\mathbf{K}_{kk}\le\varepsilon_c \\ \mathbf{K}\text{ is positive semi-definite.} \\ \forall\varepsilon_c\in E, \varepsilon_c\le 0 \\ \text{Translation, scale, and rotation invariance.}\end{cases}$$

This is a standard **convex** *Semi-Definite Programming* (SDP) problem, which can be readily solved.

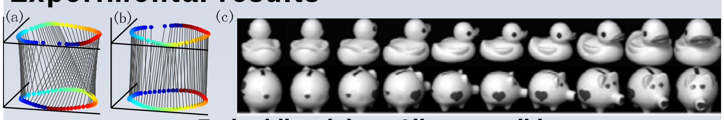
Pros

- Flexible supervision. Relative comparisons are easy and cheap to obtain. Traditional pair-wise supervision can also be easily integrated.
- Widely applicable. SDMA is able to utilize comparisons among any three samples, and can be used to facilitate single manifold embedding or multiple manifolds alignment.

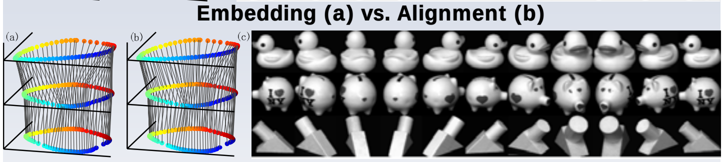
Cons

- Compared to pair-wise constraints in traditional methods, SDMA requires more relative comparison constraints, which are "weaker", to achieve satisfactory performance.
- Computationally expensive. The semi-definite relaxation step inevitably increases the number of variables. Alternative optimization techniques can be used to solve this problem.

Experimental results



Embedding (a) vs. Alignment (b)



Alignment of 3 manifolds

Alignment of head poses

Alignment of facial expressions