Sparse Projections of Medical Images onto Manifolds George H. Chen, Christian Wachinger, Polina Golland ^A

Motivation

Manifold learning in medical imaging

 \rightarrow e.g., segmentation, registration, computational anatomy, classification, detection, respiratory gating

Some applications demand fast projection to manifold



Results

KRR vs. our method

(λ =0.1, σ =4, ε =0.003)

Our method

ctors

Synthetic data

- 1000-pt Swiss roll \rightarrow 2D (Hessian eigenmaps)
- Kernel: $\mathbb{K}(x, x') = \exp(-\|x x'\|_2^2 / \sigma^2)$

Projected support vectors (λ =0.1, σ =4, ε =0.003)



Higher λ or σ result in fewer support vectors



 \mathbb{R}^d to manifold in \mathbb{R}^p

Embedding y_1, y_2, \dots, y_n

Input points x_1, x_2, \dots, x_n



Main idea







support vectors seems to scale with "complexity" of embedding, not number of training data points (λ =0.1, σ =4, ε =0.003)

# pts in Swiss roll	1000	2000	3000	4000
# support vectors	161	174	163	170

Respiratory gating for ultrasound



- 640x480 images \rightarrow 1D (Laplacian eigenmaps)
- 1D manifold enables tracking patient breathing cycle
- Train on first 200 frames of sequence, embed rest using sparse projection, correlate with embedding of full seq. (repeat with 5 seq's of lengths 354, 335, 298, 371, 298)

Trade off correlation coefficient & computational complexity

- Use any manifold learning algorithm to embed input points $x_1, x_2, ..., x_n \in \mathbb{R}^d \text{ to } y_1, y_2, ..., y_n \in \mathbb{R}^p \ (d \gg p)$
- Compute "good" projection f that maps \mathbb{R}^d to \mathbb{R}^p and depends on only a few of $x_1, x_2, ..., x_n$ (support vectors)
- Computational cost proportional to # support vectors!
- Trade off projection accuracy with computational cost

Sparse Kernel Ridge Regression

II: reproducing kernel Hilbert space of functions $\mathbb{R}^d \to \mathbb{R}^p$ $\mathbb{K}(x, x')$: kernel for \mathbb{H} specifying how similar $x, x' \in \mathbb{R}^d$ are





support vectors similar between embedding of first 200 frames and embedding of full seq. (λ =0.1, ε =0.001)

		Seq 1	Seq 2	Seq 3	Seq 4	Seq 5
# support vectors	First 200 frames	79	99	51	53	41
	Full seq.	73	100	61	45	50



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