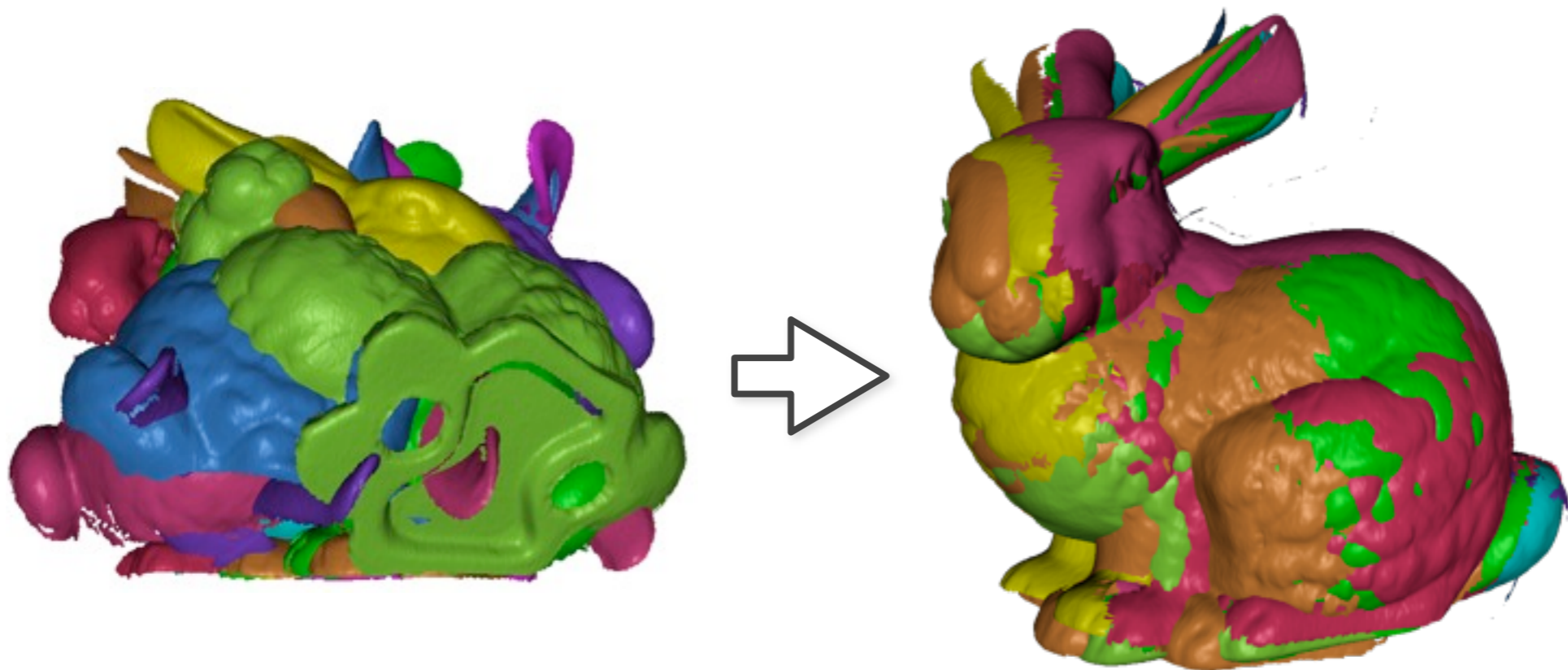


Robust Global Registration

Branch-and-bound



Niloy J. Mitra

Correspondence Problem Classification

How many meshes?

- **Two:** Pairwise registration
- **More than two:** multi-view registration

Initial registration available?

- **Yes:** Local optimization methods
- **No:** Global methods

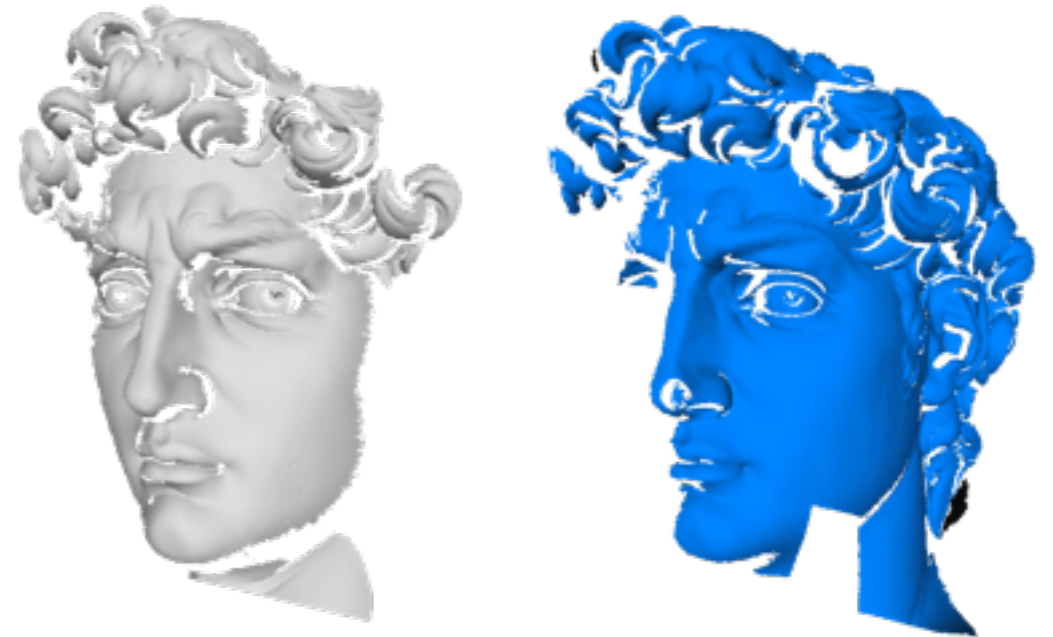
Class of transformations?

- **Rotation and translation:** Rigid-body
- **Non-rigid deformations**

Registration Problem

Given:

Two shapes **P** and **Q** which partially overlap.



Goal:

Using only *rigid transforms*, register **Q** against **P** by minimizing the squared distance between them.

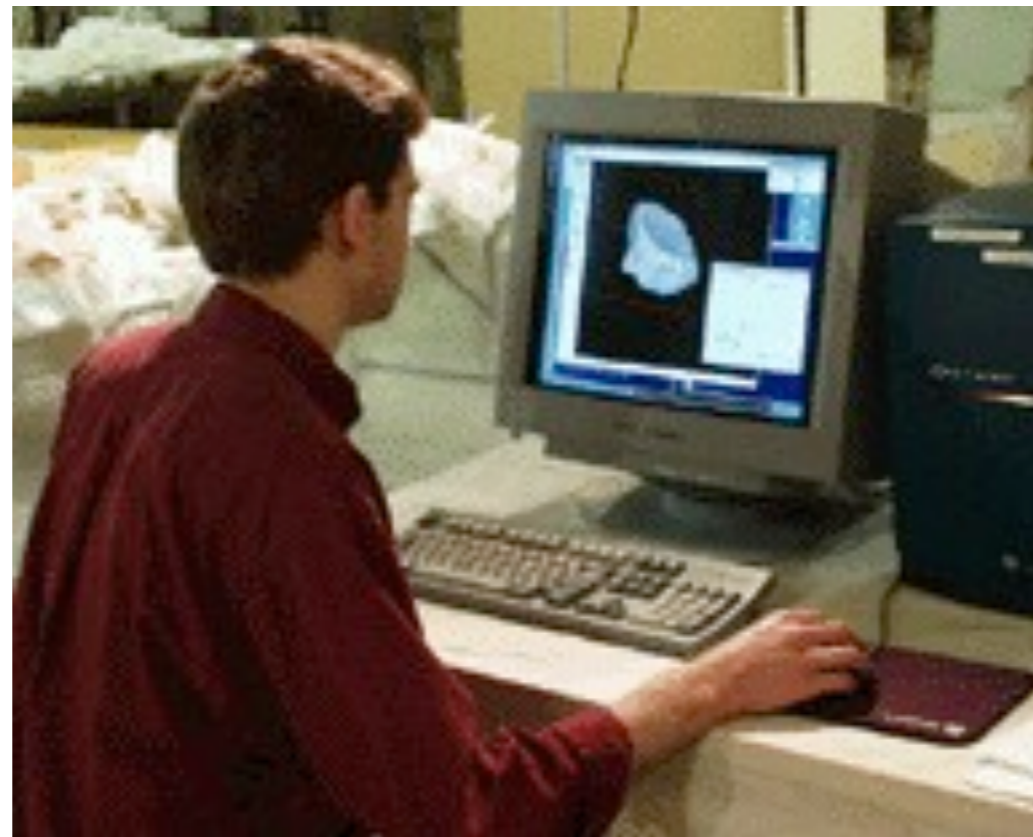
$$\text{Find } T \text{ s.t. } T(P) \approx Q$$



ICP for Refinement

When the input poses are *nearly* aligned

How to get initial alignment?



RANSAC styled Matching

How many (correct) point pairs uniquely determines a rigid transform?

Rigid transform can be specified with small number of points

- Try all possible transform bases
- Retain the one that aligns the most points

Guaranteed to find the correct transform

- But can be costly



Feature Points can Help

Improves correspondence search or used for feature extraction

- reduces the search space
- what are good features?



Registration Problem

Why it's hard

- Unknown areas of overlap
- Have to solve the correspondence problem

Why it's easy

- Rigid transform is specified by small number of points
- Prominent features are easy to identify

We only need to align a few points correctly!



Method Overview

1. Use descriptors to identify features

- Integral volume descriptor

2. Build correspondence search space

- Few correspondences for each feature

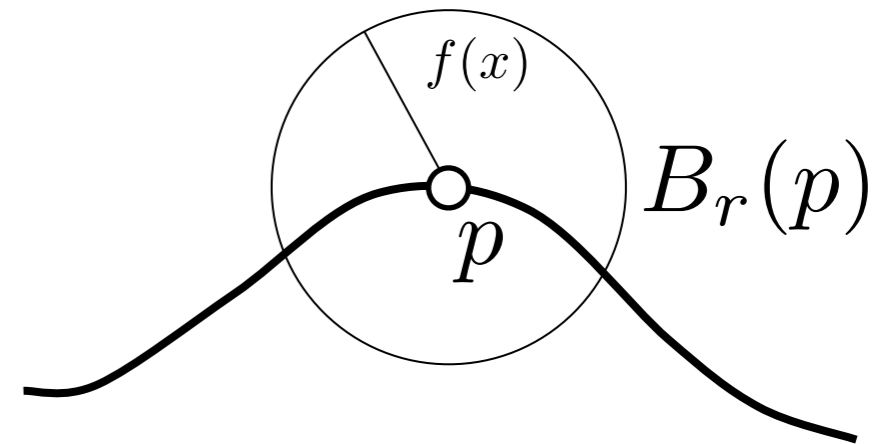
3. Efficiently explore search space

- Distance error metric
- Pruning algorithms



Integral Descriptors [Manay et al. 04]

$$F_r(p) = \int_{B_r(p) \cap S} f(x) dx$$



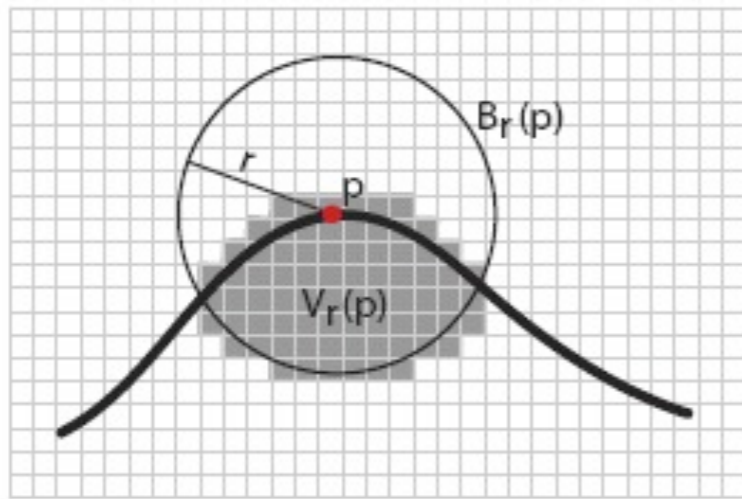
Multi-scale

Inherent smoothing



Efficient Computation

Approximate using a voxel grid



$$V(c) = (G_B * G_O)(c)$$

Convolution of occupancy grid with ball

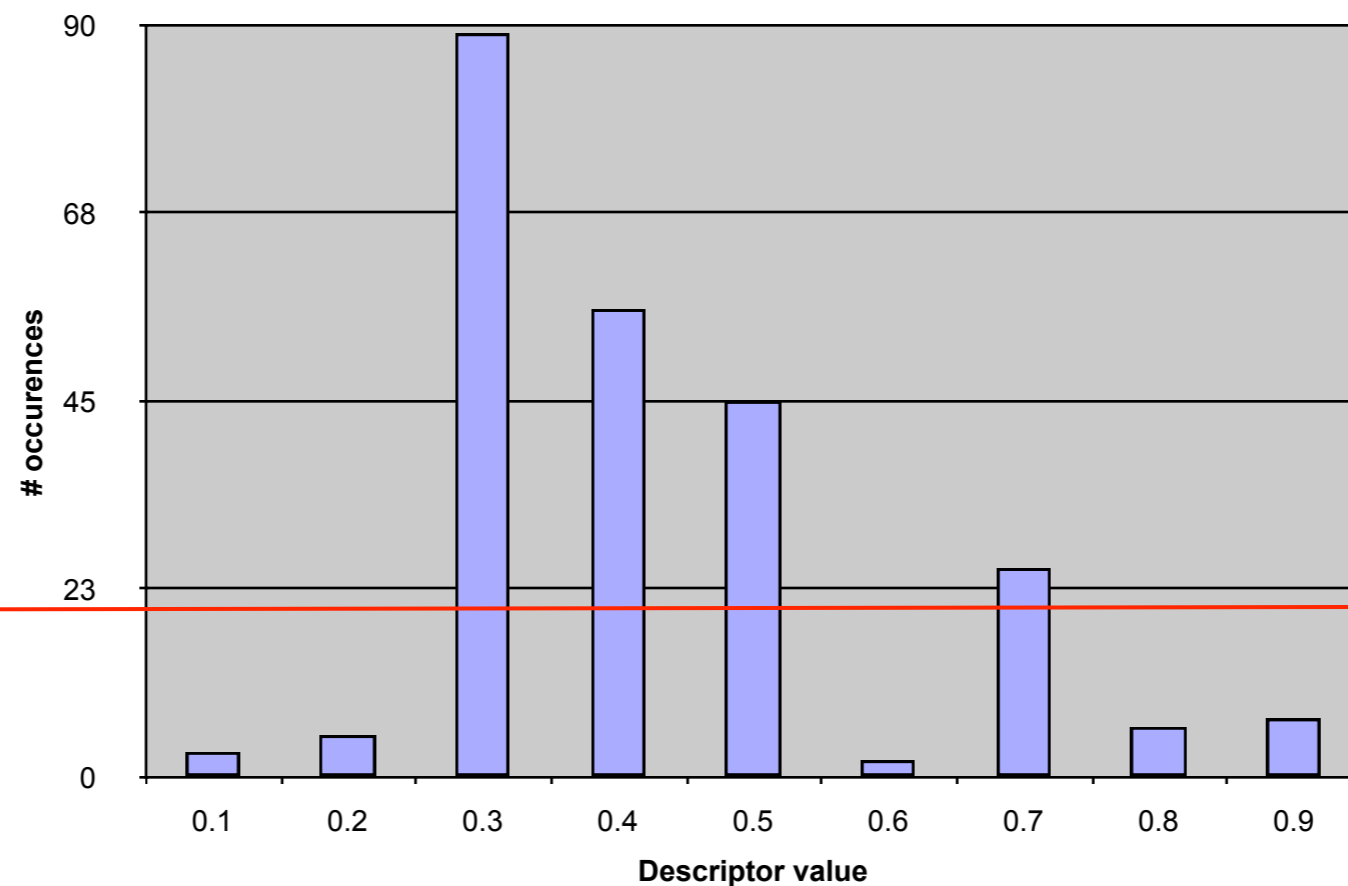


Which are good Feature Points?

Points with rare descriptor values

Rare in the data \Rightarrow rare in the model \Rightarrow few correspondences

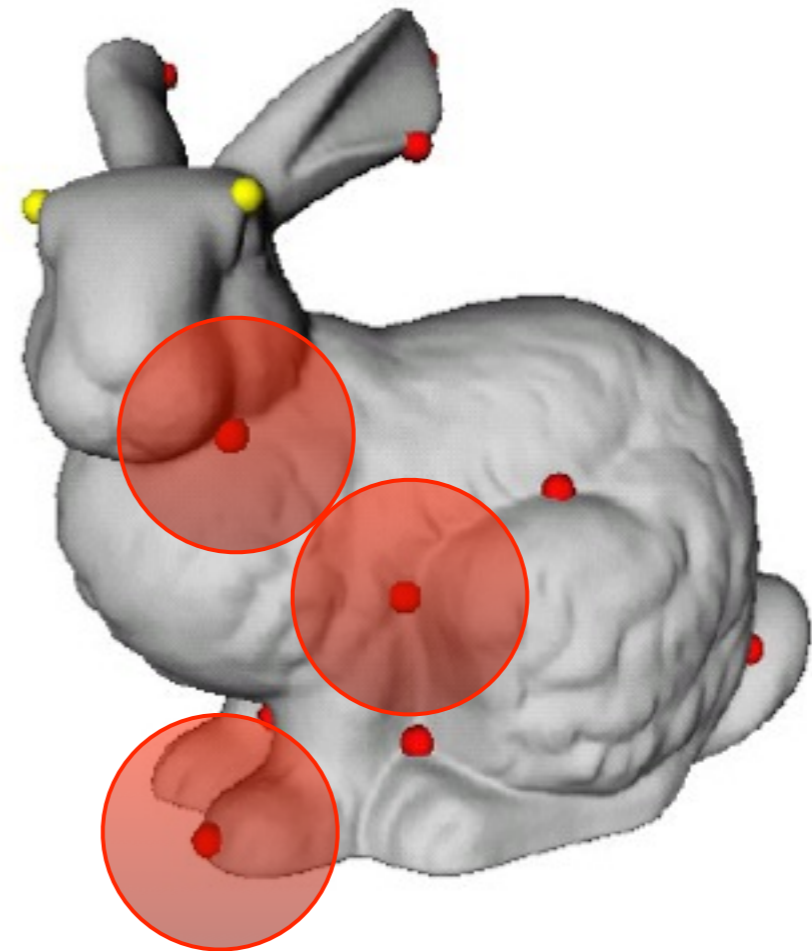
Works for any (stable) descriptor



Multi-scale Algorithm

Features should be *persistent over scale (r)* variations

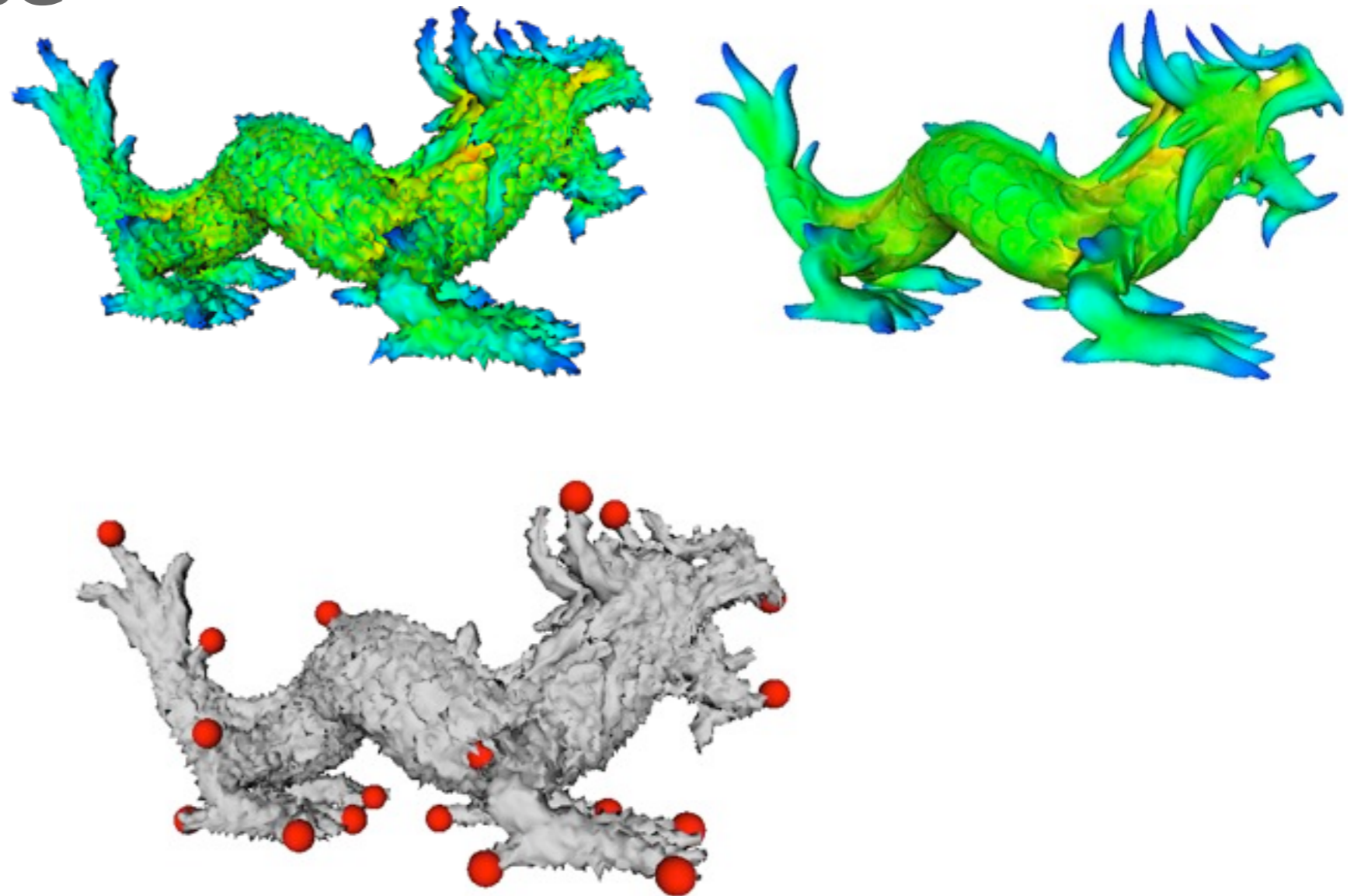
r=0.5	r=1	r=2	r=4	r=8
Y	Y	Y	N	N
N	N	Y	Y	Y
N	N	Y	N	N



Feature Properties

Sparse

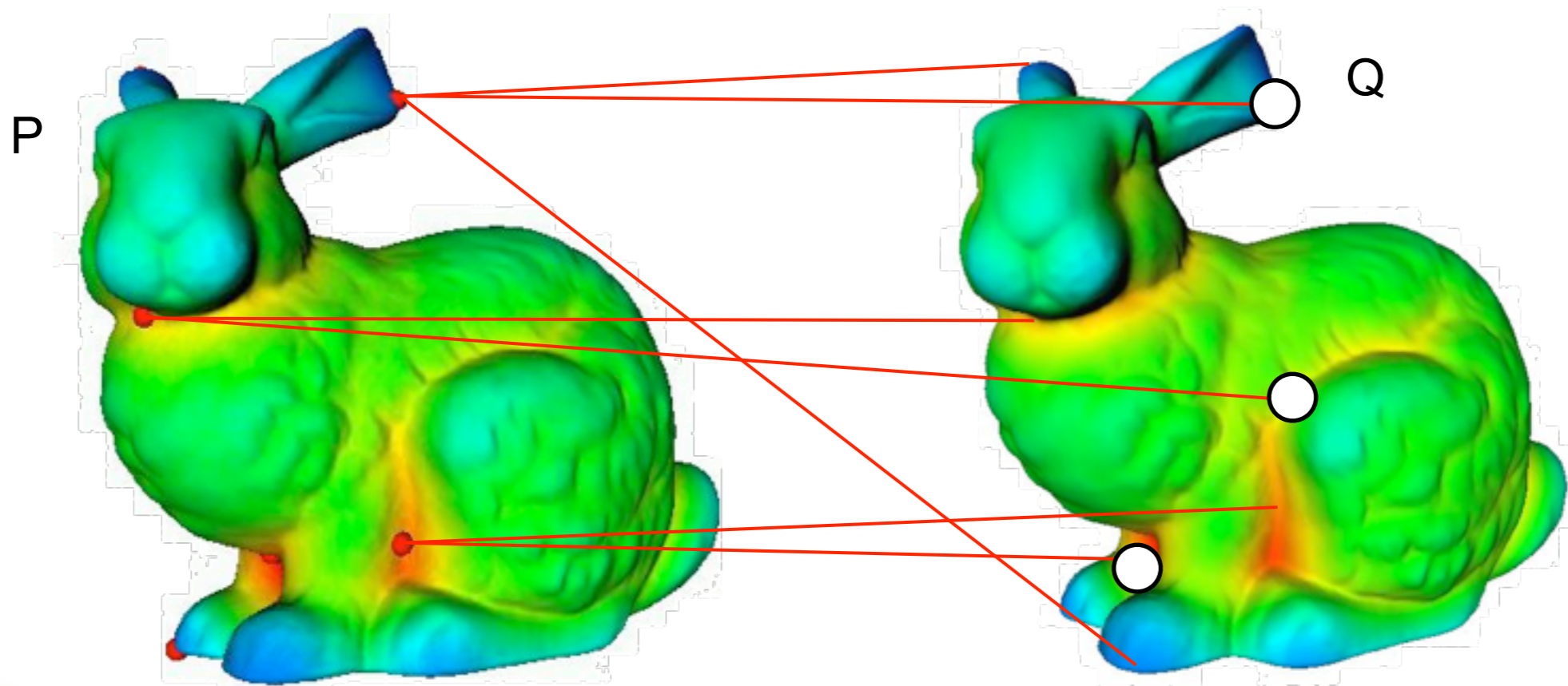
Robust to noise



Correspondence Space

Search the whole model for correspondences

- Range query for descriptor values
- Cluster and pick representatives



Evaluating Correspondences

Coordinate **root mean squared distance**

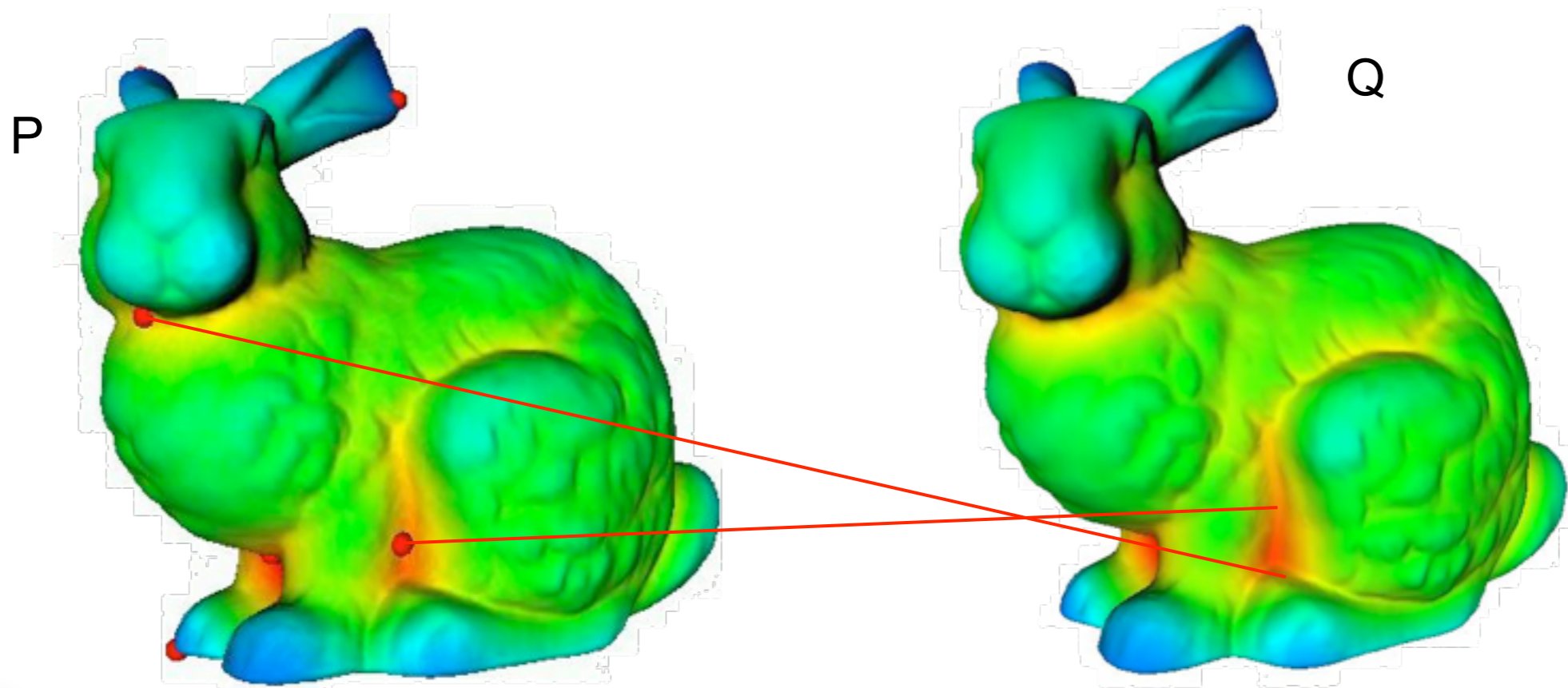
$$cRMS^2(\mathbf{P}, \mathbf{Q}) = \min_{\mathbf{R}, \mathbf{t}} \frac{1}{n} \sum_{i=1}^n \|\mathbf{R}\mathbf{p}_i + \mathbf{t} - \mathbf{q}_i\|^2$$

- Requires best aligning transform
- Looks at correspondences individually



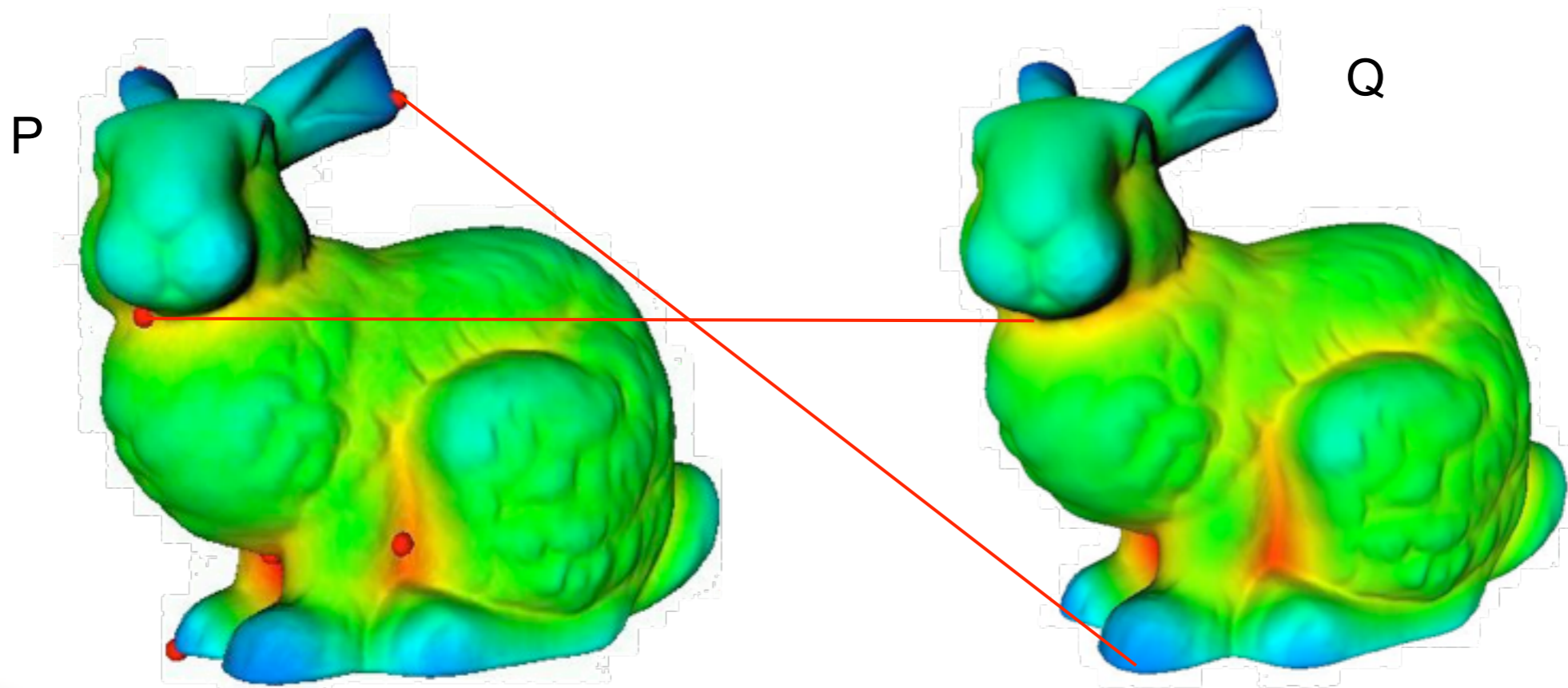
Rigidity Constraint

Pair-wise distances between features and correspondences should be *preserved*



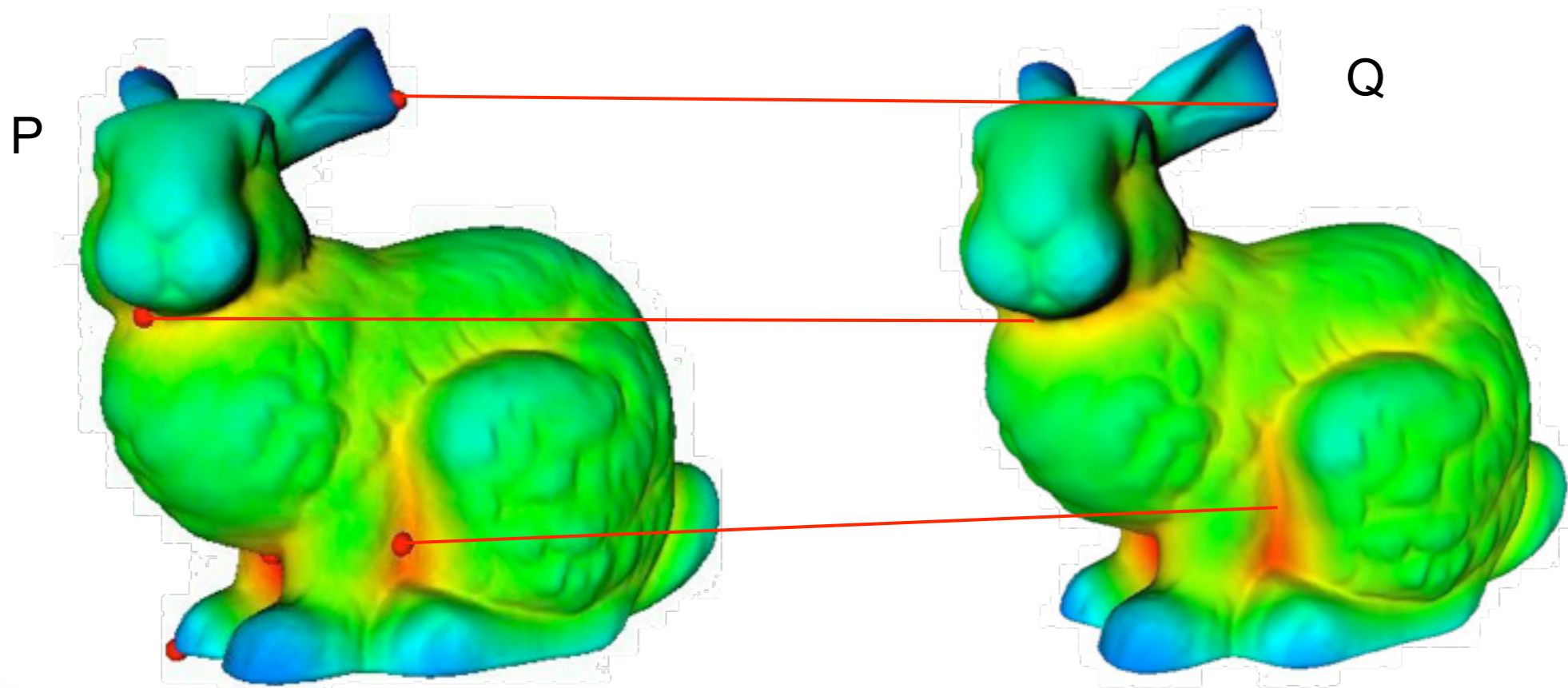
Rigidity Constraint

Pair-wise distances between features and correspondences should be *preserved*



Rigidity Constraint

Pair-wise distances between features and correspondences should be *preserved*



Evaluating Correspondences

Distance **root mean squared distance**

$$dRMS^2(\mathbf{P}, \mathbf{Q}) = \frac{1}{n^2} \sum_{i=1}^n \sum_{j=1}^n (\|\mathbf{p}_i - \mathbf{p}_j\| - \|\mathbf{q}_i - \mathbf{q}_j\|)^2$$

no dependence on (R, t)

Depends only on internal distance matrix

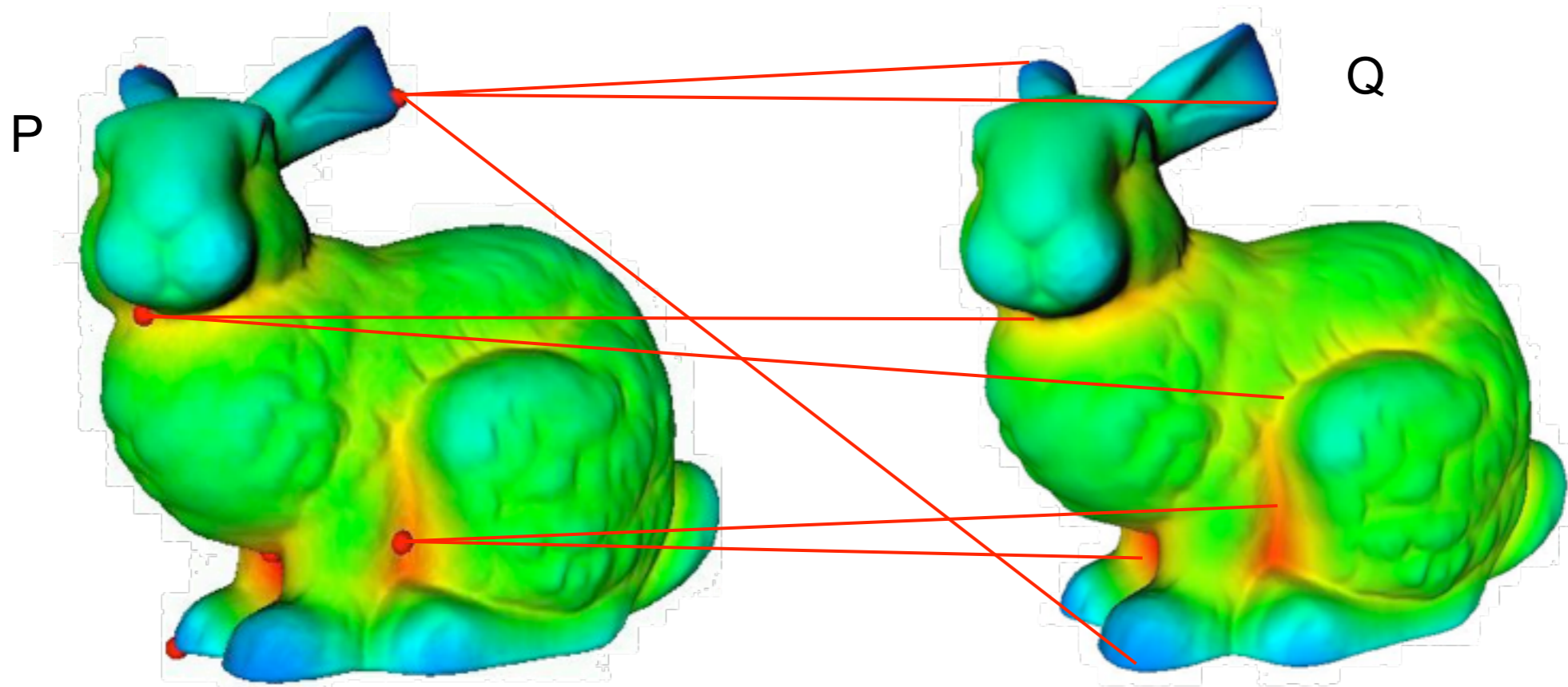
$$\frac{1}{k\sqrt{n}} cRMS(\mathbf{P}, \mathbf{Q}) \leq dRMS(\mathbf{P}, \mathbf{Q}) \leq \sqrt{2} cRMS(\mathbf{P}, \mathbf{Q})$$



Search Algorithm

Few features, each with few potential correspondences

- Minimize dRMS
- Exhaustive search still too expensive



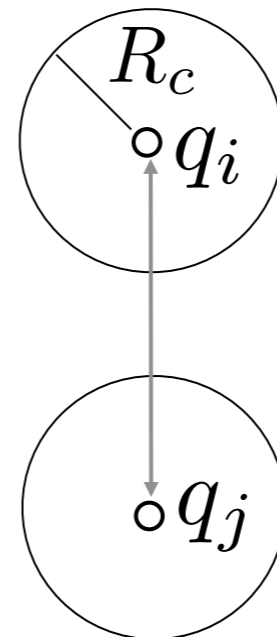
Search Algorithm

Branch and bound

Initial bound using greedy assignment

Discard partial correspondences that fail thresholding test

$$| \|p_i - p_j\| - \|q_i - q_j\| | \leq 2R_c$$



Search Algorithm

Branch and bound

Initial bound using greedy assignment

Discard partial correspondences that fail thresholding test

$$| \|p_i - p_j\| - \|q_i - q_j\| | \leq 2R_c$$

Prune if partial correspondence exceeds bound

Spaced out features make incorrect correspondences fail quickly

Since we explore the entire search space, we are guaranteed to find optimal alignment
(up to cluster size)



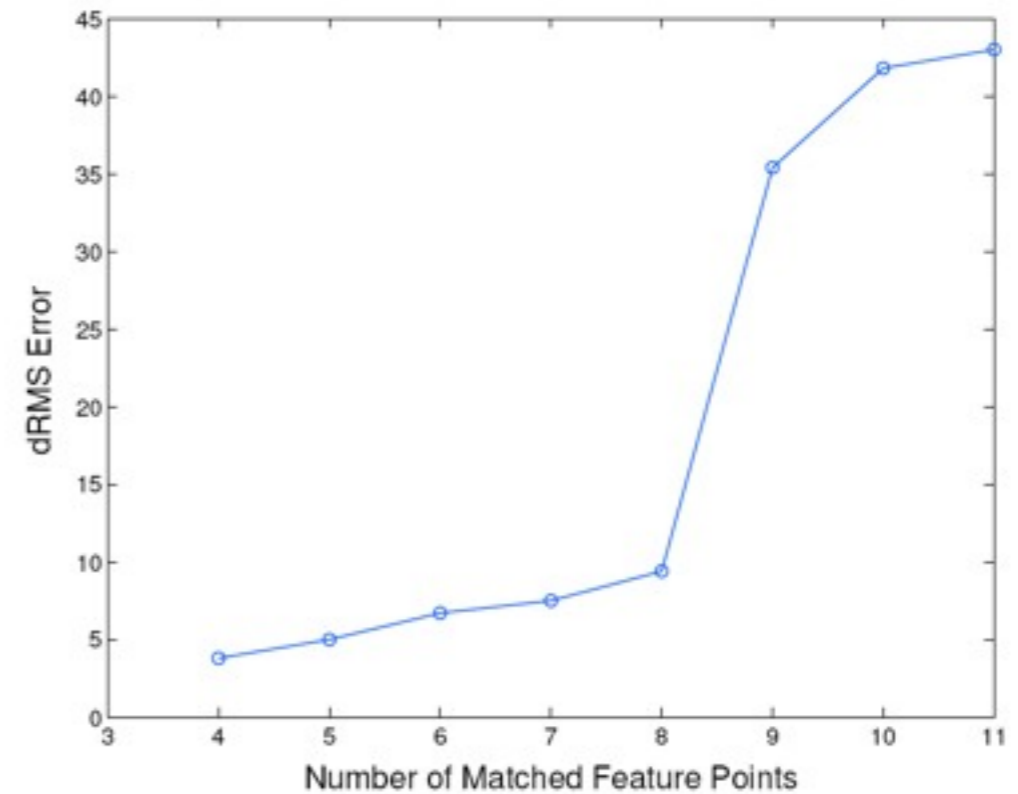
Greedy Initialization

(see paper)

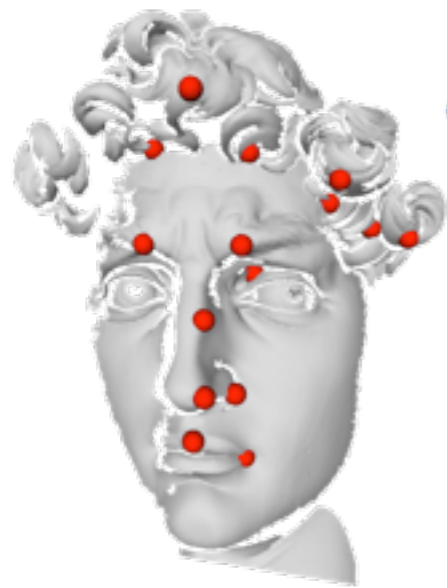


Partial Alignment

**Allow null correspondences,
while maximizing the number of matches points**



Alignment Results



input: 2 scans



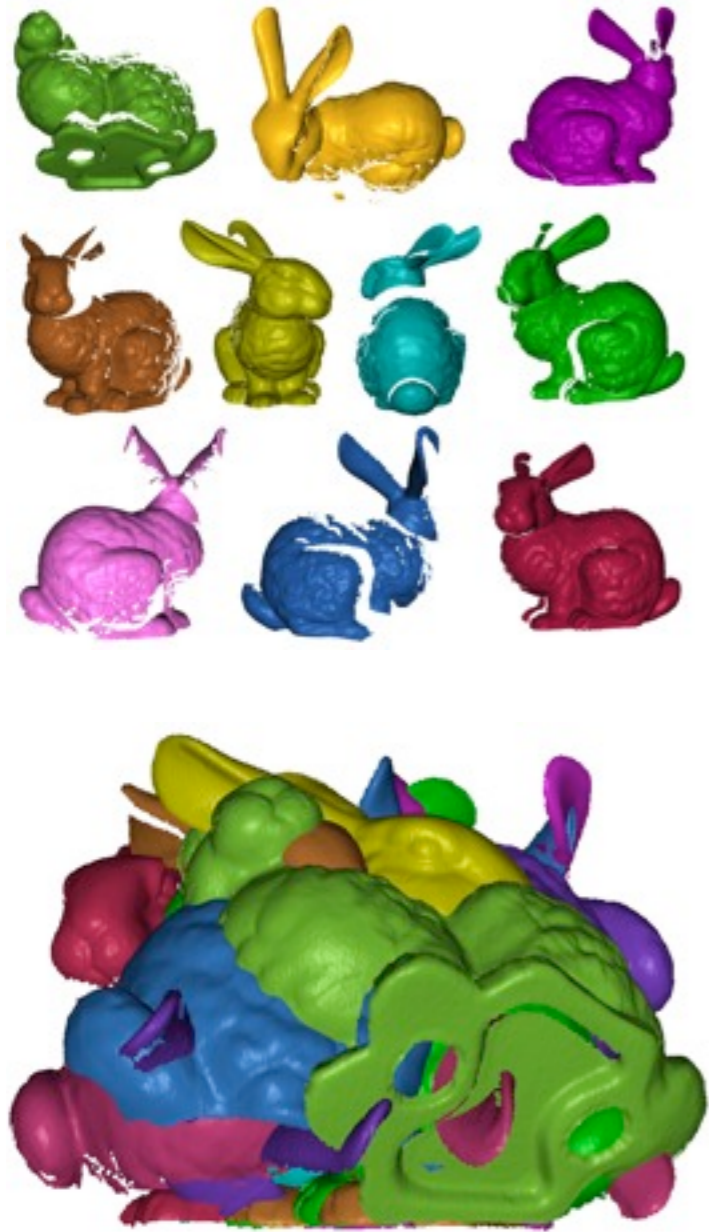
global alignment



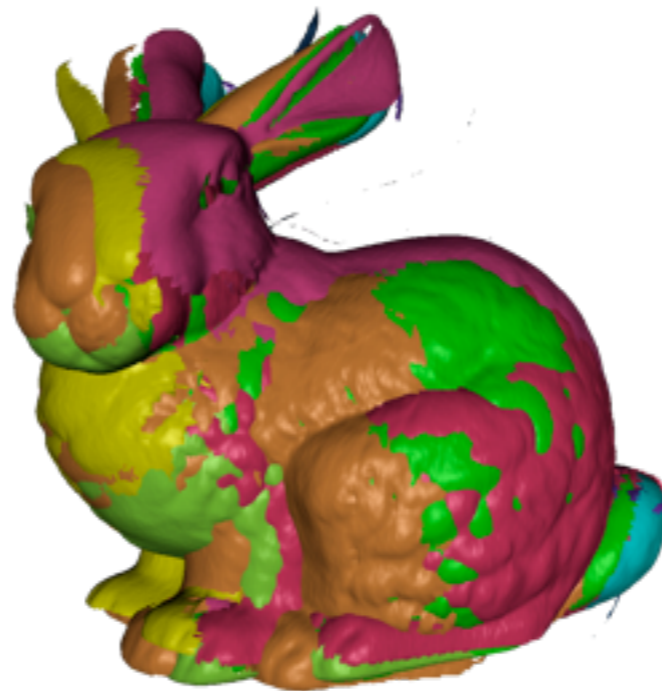
refined by ICP



Alignment Results



input: 10 scans



global alignment

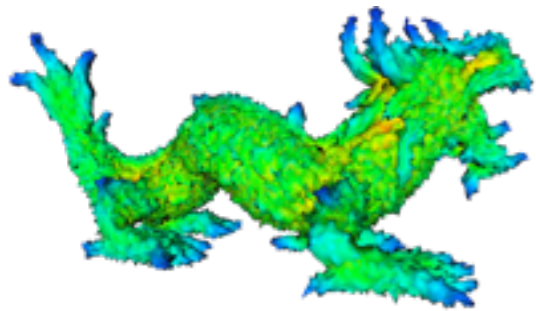


refined by ICP

References



Robust Global Registration,
Natasha Gelfand, Niloy J. Mitra, Leonidas Guibas, Helmut Pottmann,
SGP 2005.



Principal Curvatures from the Integral Invariant Viewpoint,
Helmut Pottmann, Johannes Waller, Yong-Liang Yang, Yu-Kun Lai, Shi-Min Hu
CAGD 2007.



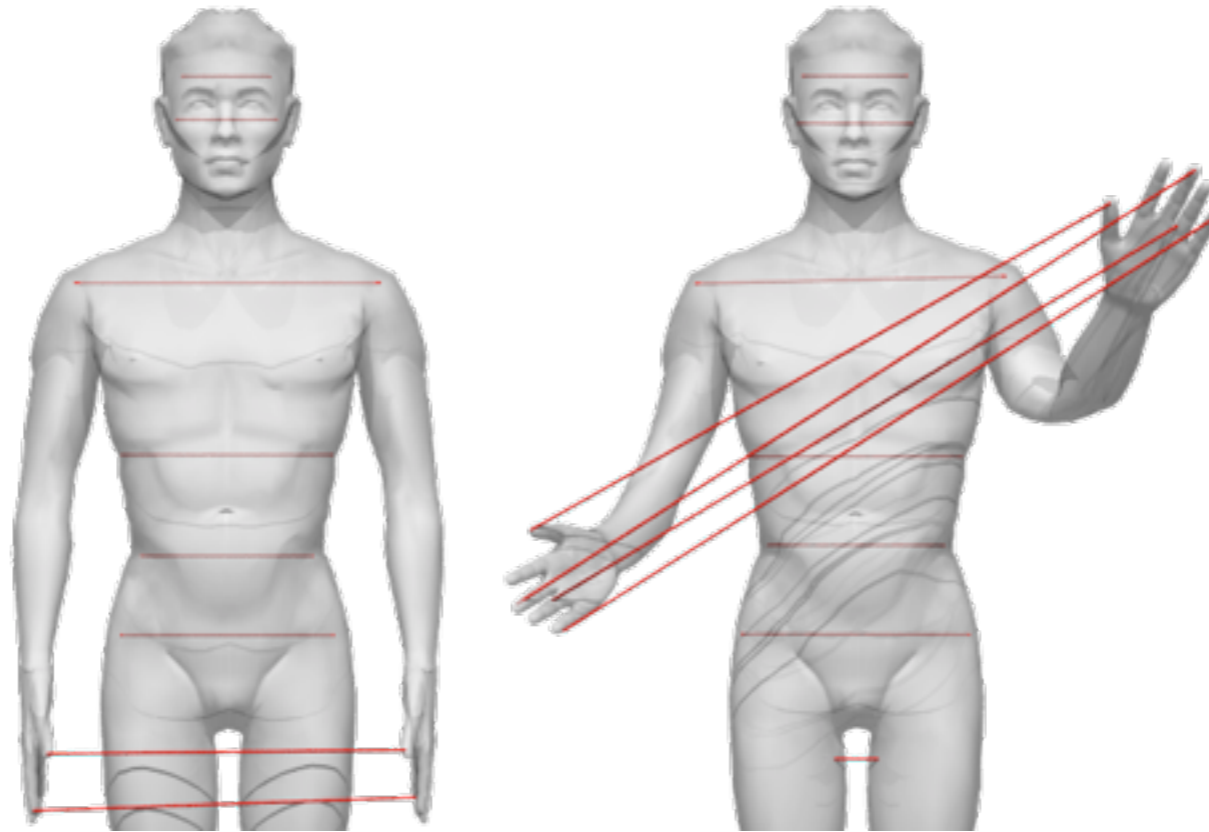
Robust Global Registration

Intrinsic Descriptors



(Modified) Goal

Intrinsic Comparison of Points



Isometry invariant symmetries

$$T : M \rightarrow M, \text{ s.t. } d_M(x, y) = d_M(T(x), T(y)) \forall x, y$$

Goal

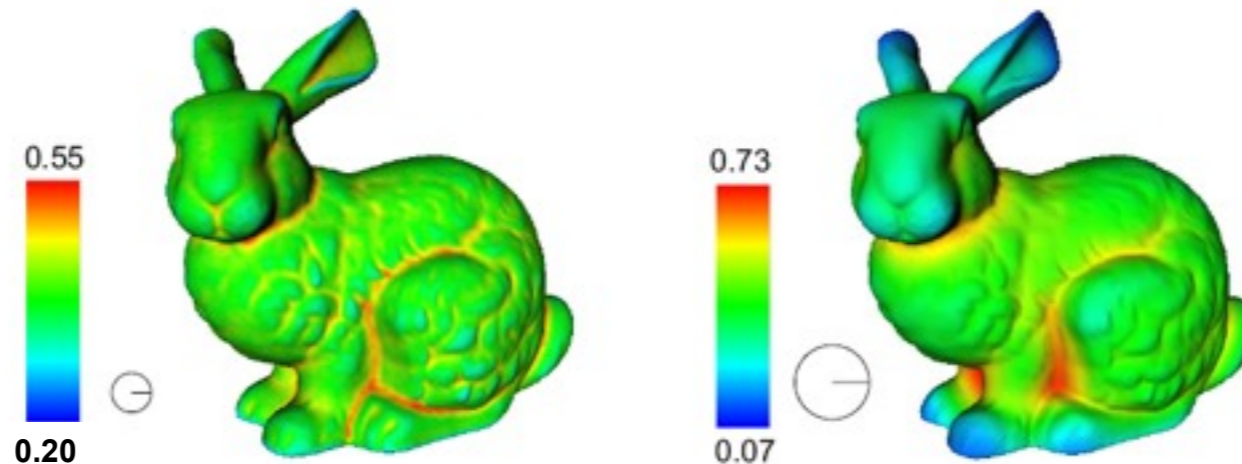
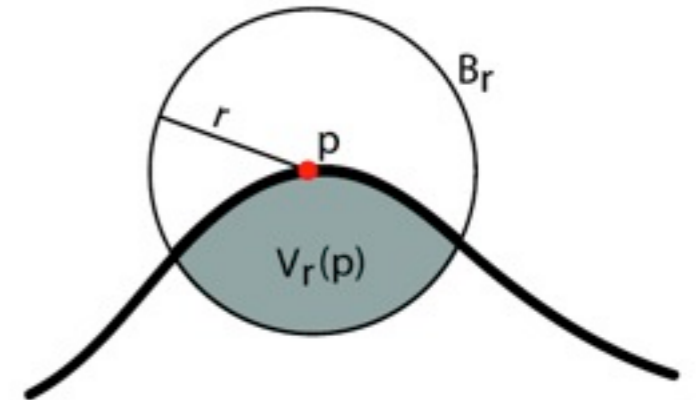
Multi-Scale Intrinsic Comparison of Points



$$T : M \rightarrow M, \text{ s.t. } d_M(x, y) = d_M(T(x), T(y)) \\ \forall y \in \mathcal{N}(x)$$

Integral Volume Descriptor

$$V_r(p) = \int_{B_r(p) \cap S} dx$$



Relation to mean curvature

$$V_r(p) = \frac{2\pi}{3} r^3 - \frac{\pi H(p)}{4} r^4 + o(r^5)$$

Desirable Properties

Find “similar” points at multiple scales.

robust

not sensitive to perturbations of the shape

intrinsic

invariant to isometric deformations

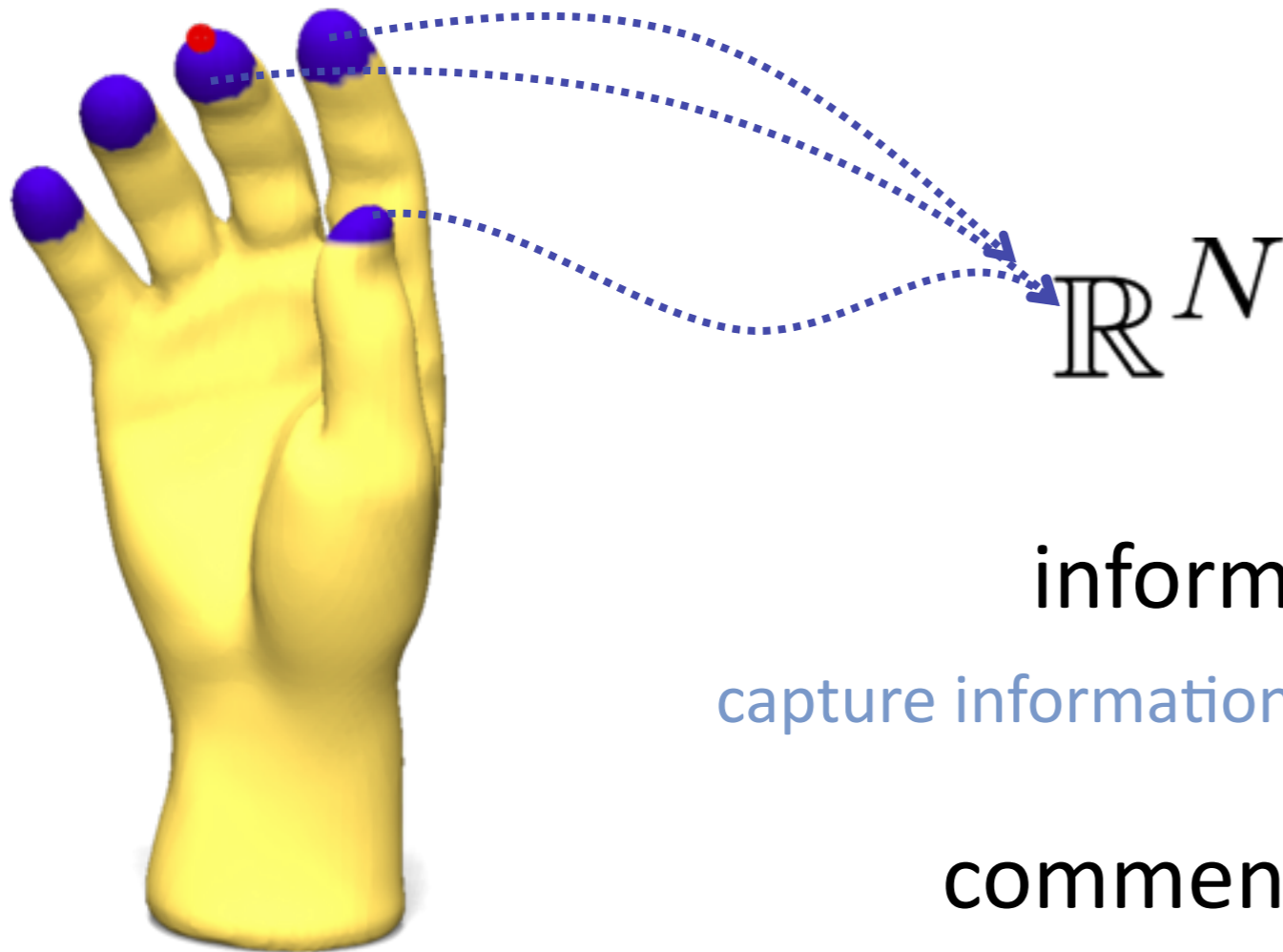
efficient

easily computable across many scales



Old Idea

Define a multiscale signature for every point
Compare points by comparing their signatures



informative

capture information around the point

commensurable

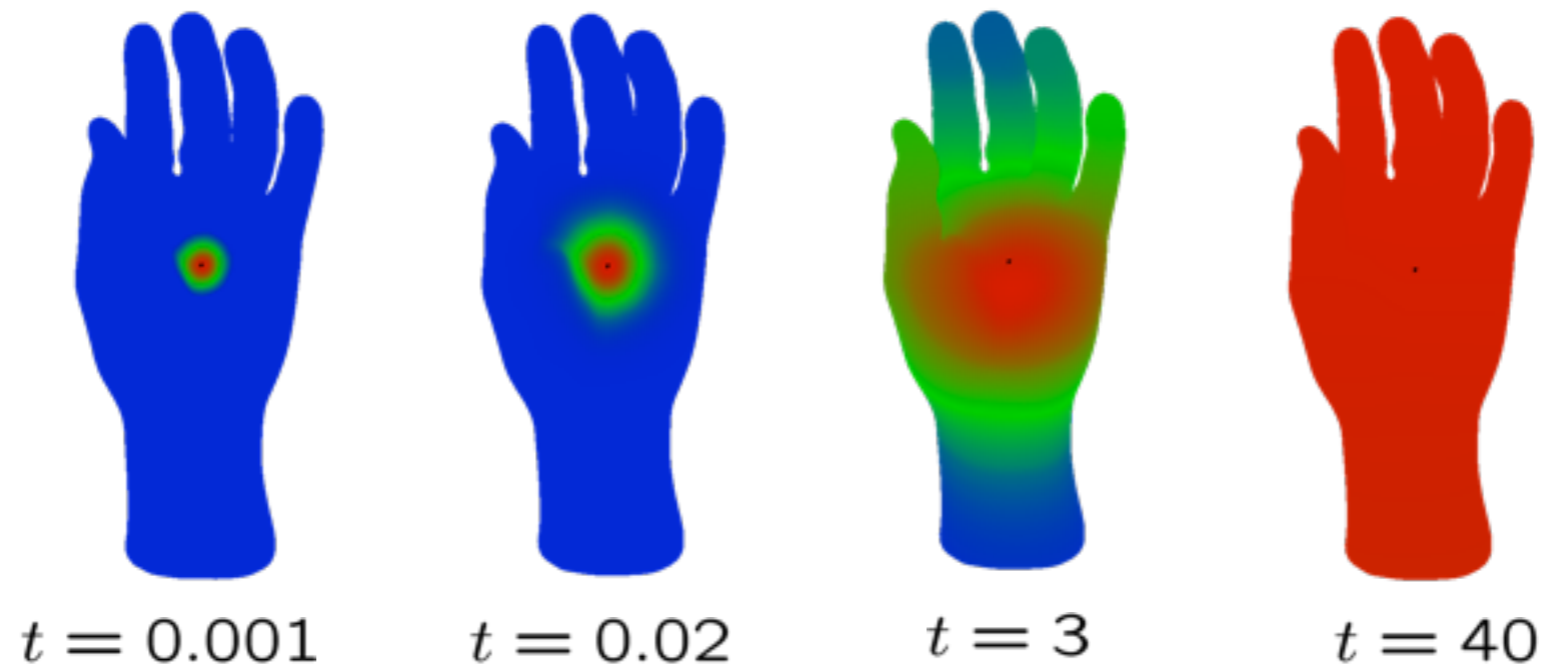
easy to compare across points

Heat Equation on a Manifold

Heat kernel $k_t(x, y) : \mathbb{R}^+ \times \mathcal{M} \times \mathcal{M} \rightarrow \mathbb{R}$

$$f(x, t) = \int_{\mathcal{M}} k_t(x, y) f(y, 0) dy$$

$k_t(x, y)$: amount of heat transferred from x to y in time t .



Heat Kernel Properties

- Invariant under isometric deformations

If $T : X \rightarrow Y$ is an isometry then:

$$k_t(x, y) = k_t(T(x), T(y))$$

- Robust: $k_t(x, \cdot)$ is the probability density function of Brownian motion on X . Average of all possible paths.

- Multi-Scale:

For a fixed x , as t increases, heat diffuses to larger and larger neighborhoods.

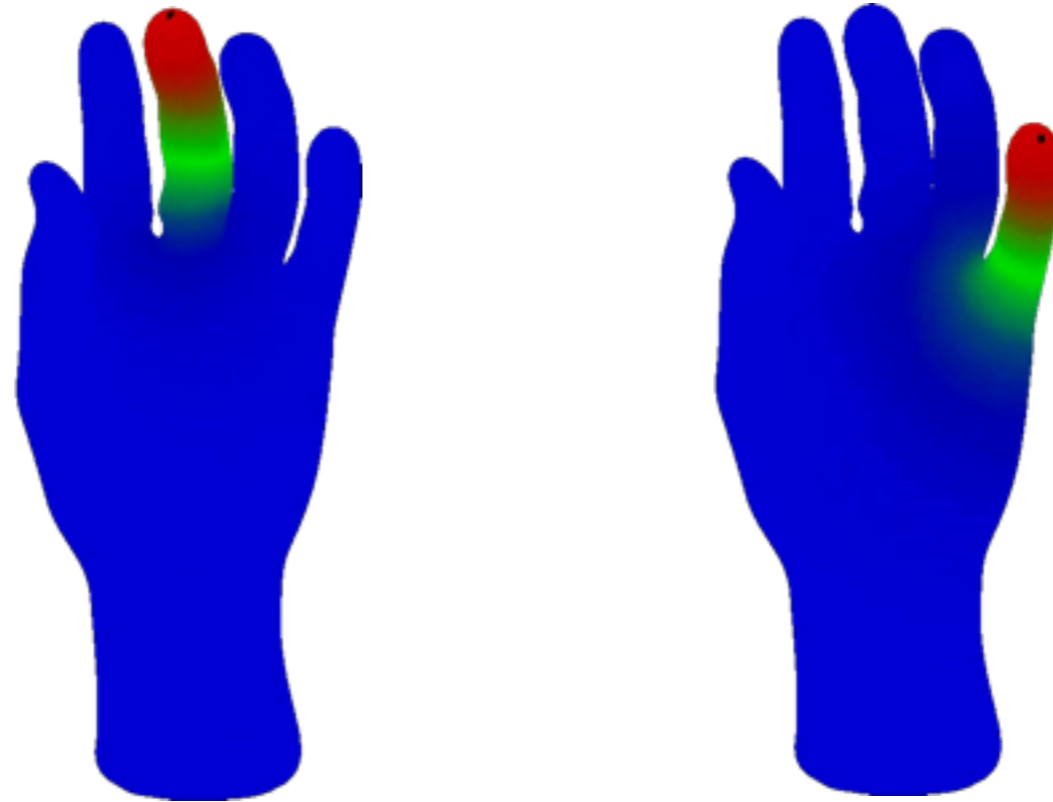


Defining a Signature

Let $k_t(x, \cdot)$ be the signature of x at scale t .

Has all the properties we want.

Except easy comparison!



$k_t(x, \cdot)$ is a function on the entire manifold!

Heat Kernel Signature (HKS)

Define:

$HKS(x, t) = k_t(x, x)$ signature of x at scale t .

Now HKSs of two points can be easily compared since they are defined on a common domain (time)

HKS is a restriction of the heat kernel, and thus:

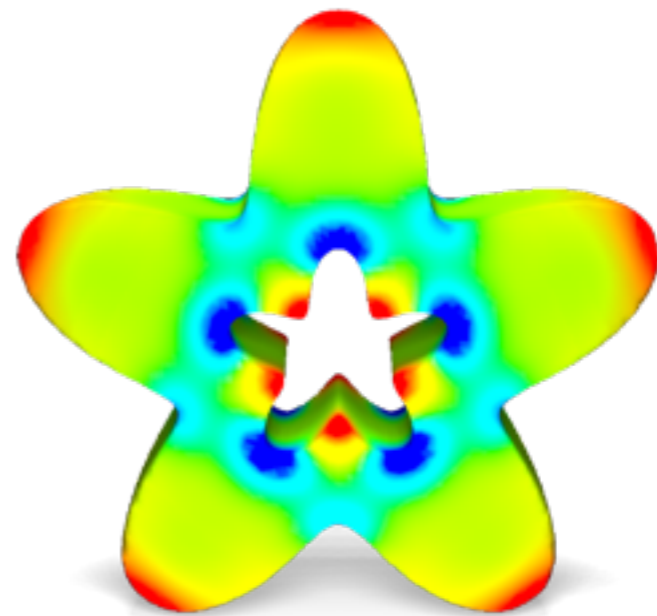
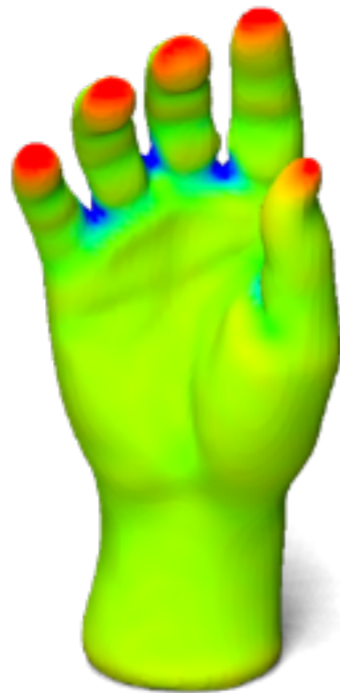
- isometry-invariant
- multi-scale
- robust

Question: How informative is it?

Heat Kernel Signature (HKS)

Relation to scalar curvature for small t :

$$k_t(x, x) = \frac{1}{4\pi t} \sum_{i=0}^{\infty} a_i t^i \quad a_0 = 1, a_1 = \frac{1}{6}K$$



Informative Theorem

The set of all HKS on the shape almost always defines it up to isometry!

Theorem: If X and Y are two compact manifolds, such that Δ_X and Δ_Y have only non-repeating eigenvalues. Then a homeomorphism $T : X \rightarrow Y$ is an isometry **if and only if**

$$\text{HKS}(x) = \text{HKS}(T(x)) \quad \forall x$$

Computing HKS

On a compact manifold:

$$k_t(x, y) = \sum_{i=0}^N e^{-t\lambda_i} \phi_i(x) \phi_i(y)$$

λ_i, ϕ_i : i^{th} eigen value/function of Laplace-Beltrami operator.

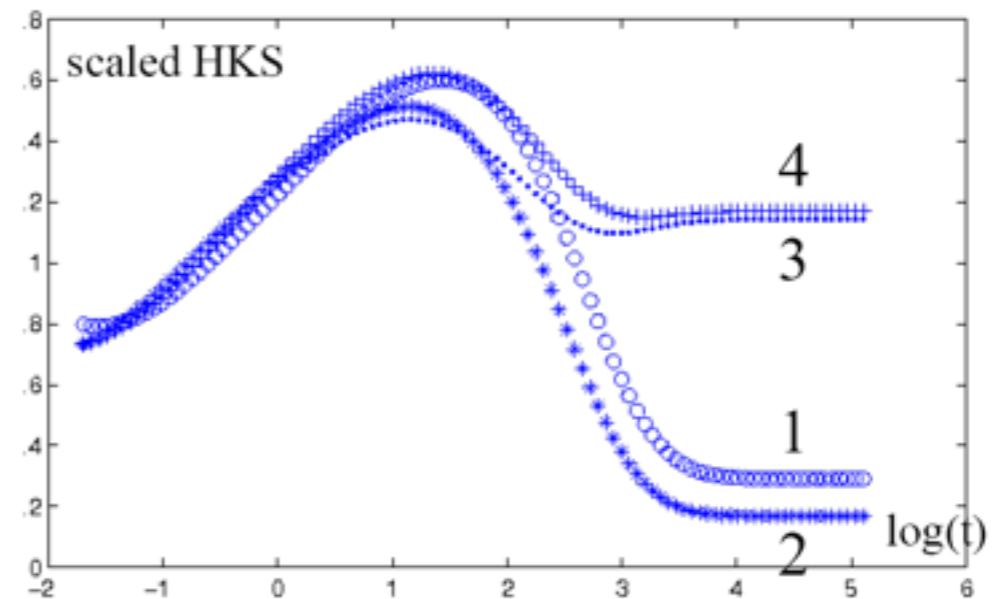
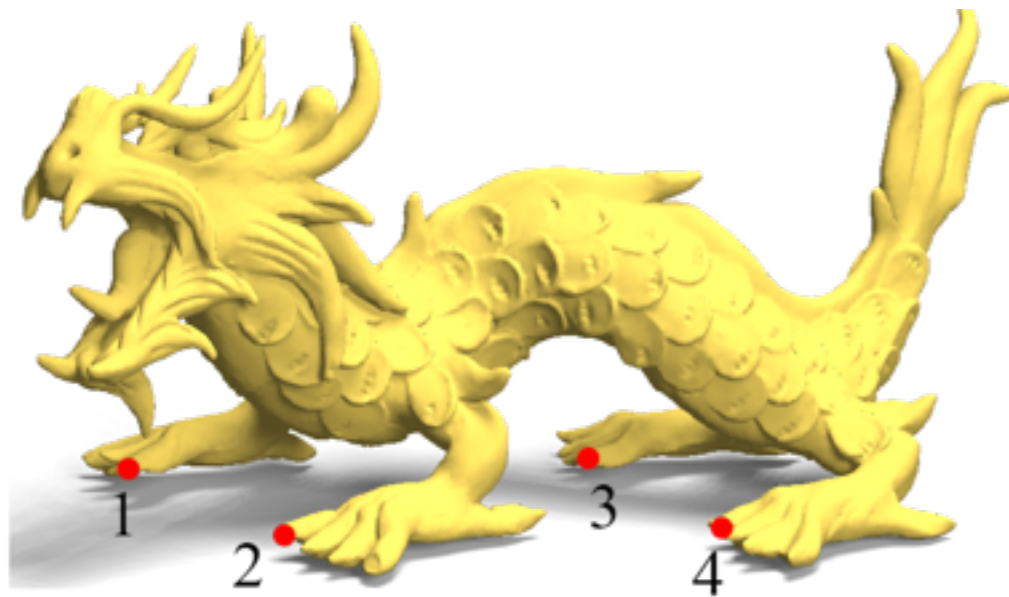
Laplace operator on a mesh is a matrix. Use eigenvalues & eigenvectors of that matrix.

Once the eigen-decomposition is computed can obtain
HKS at any scale.



Multiscale Matching

Comparing points through their HKS signatures:

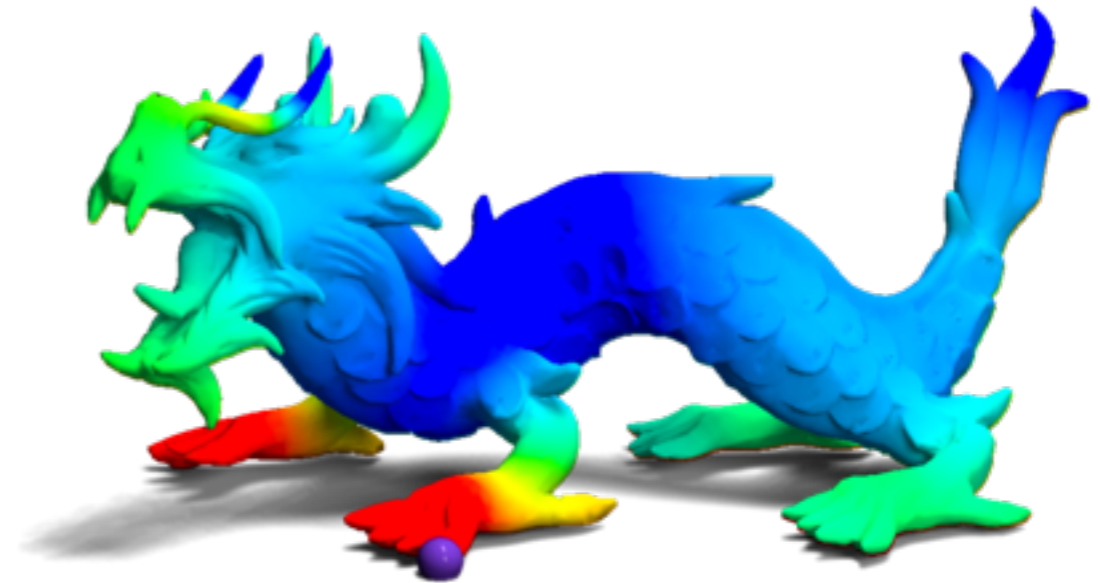


Multiscale Matching

Comparing points through their HKS signatures:



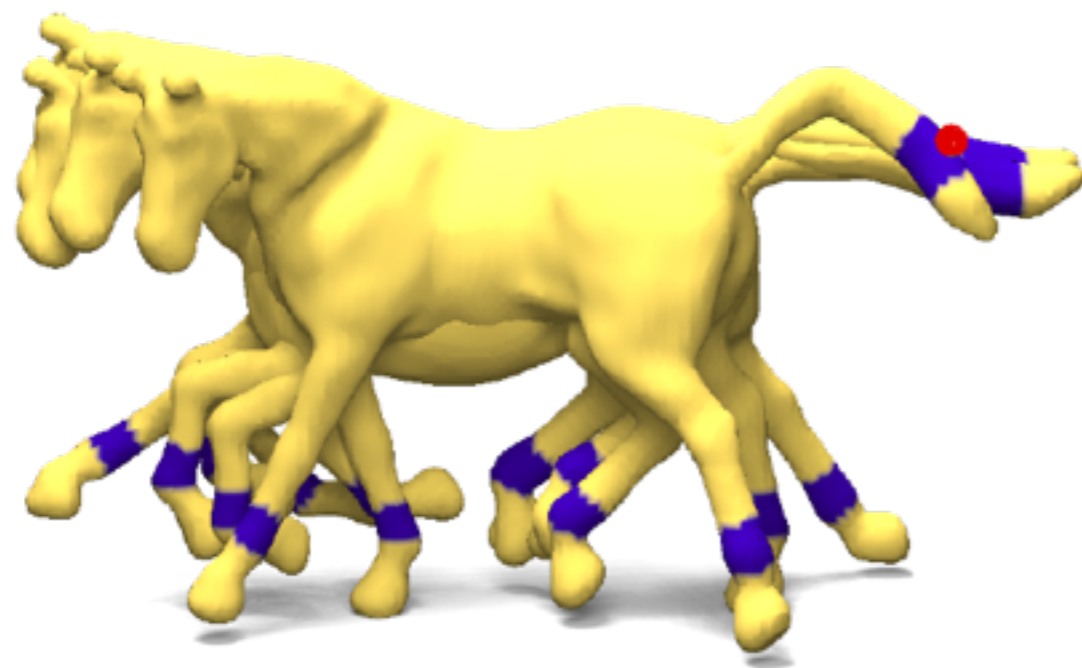
Medium scale



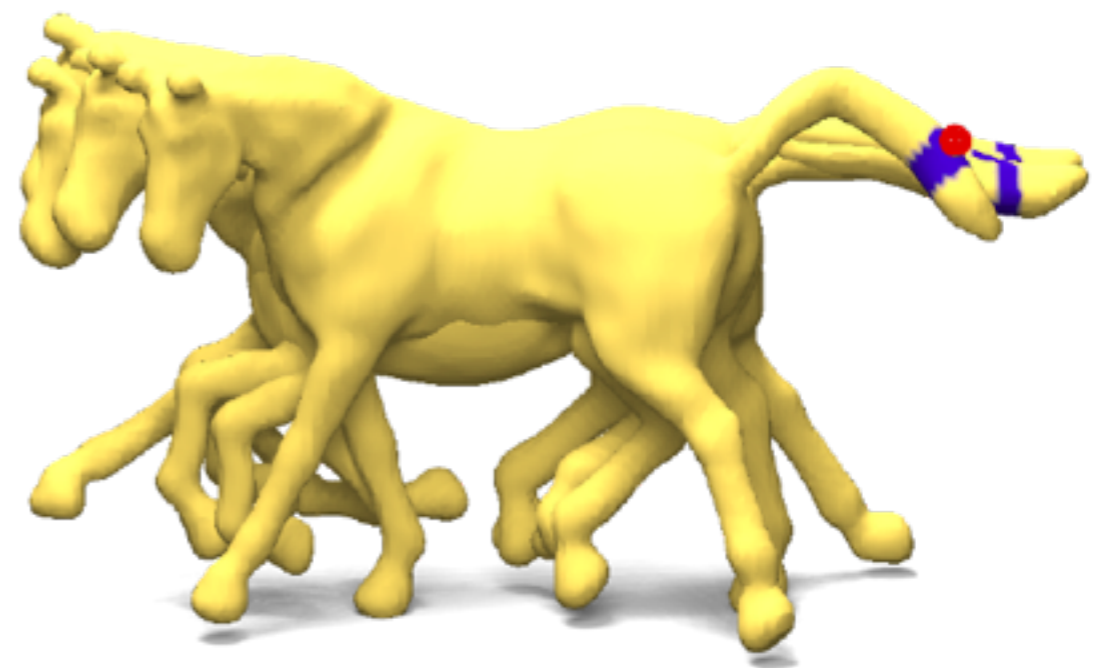
Full scale

Multiscale Matching

Finding similar points across multiple shapes:



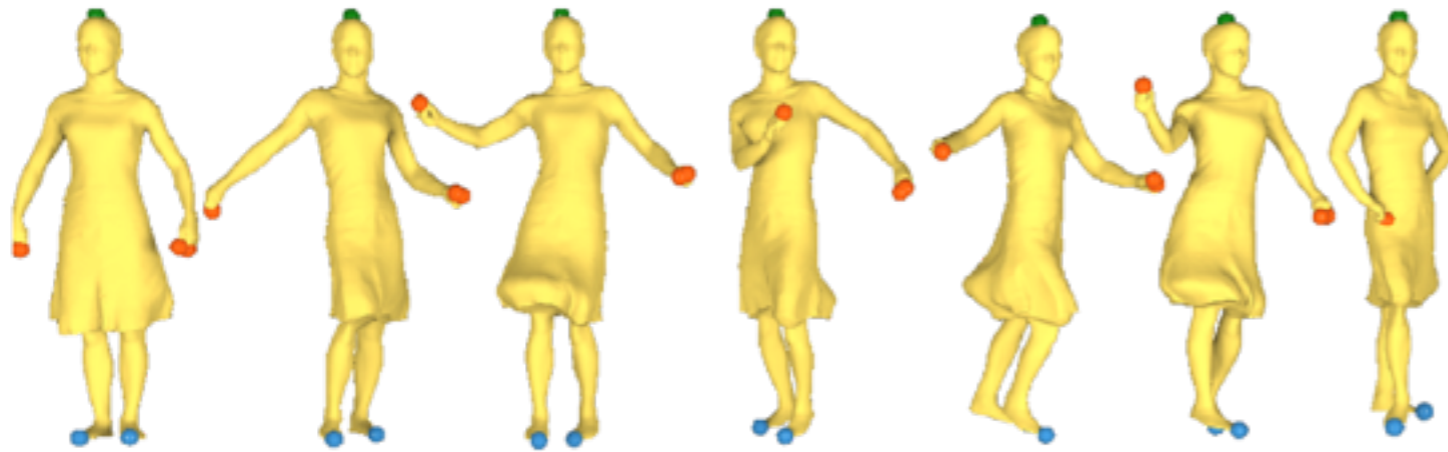
medium scale



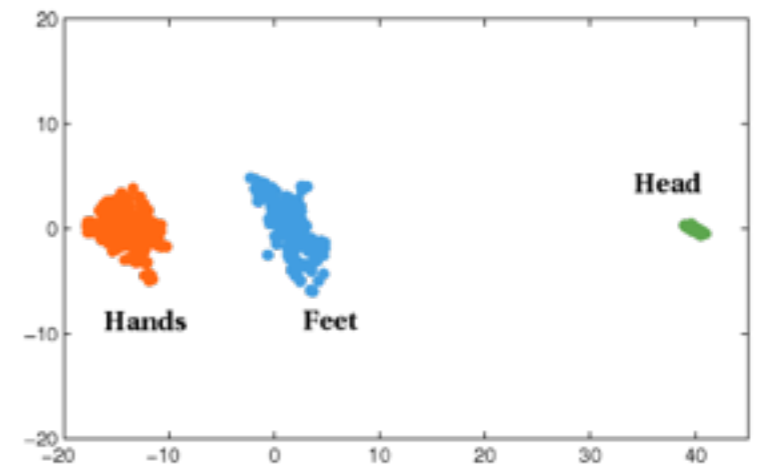
full scale

Shared Structure

2D MDS embedding of feature points on **175 shapes** according to distances of their HKS.

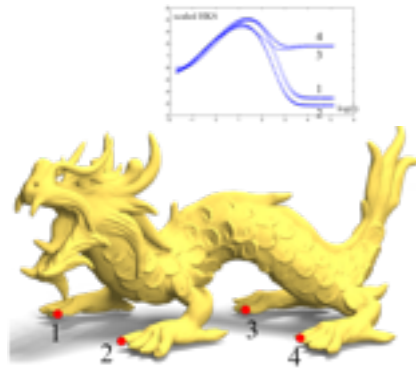


Feature points found on a few poses of the dancer model by Vlasic *et al.*



MDS of features from all 175 poses using a full range of scales

Reference



A Concise and Provably Informative Multi-scale Signature
Based on Heat Diffusion,
Jian Sun, Maks Ovsjanikov and Leonidas Guibas,
SGP 2009.

