Digital Geometry - Shape Matching

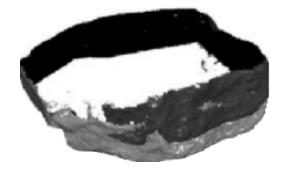
Junjie Cao @ DLUT Spring 2018

http://jjcao.github.io/DigitalGeometry/

Last Time

- Surface Registration
 - Pairwise ICP & Variants
 - Point-to-point/plane metric
 - BSP closes point search
 - Stability Analysis
 - Global Registration

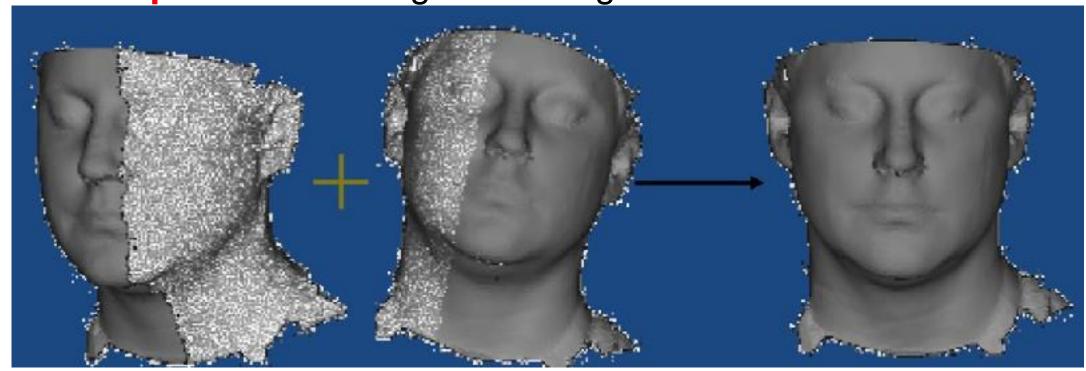






Shape Matching for Model Alignment

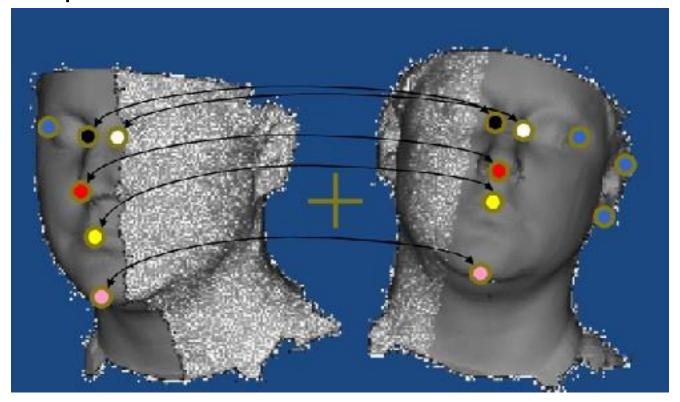
- Goal
- Given two partially overlapping scans, compute transformation that aligns the two.
- No assumption about rough initial alignment



Shape Matching for Model Alignment

Approach

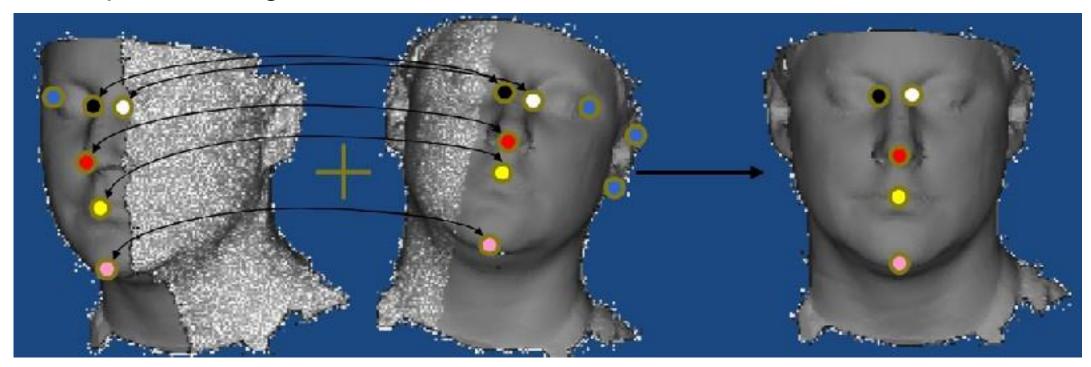
- Find feature points on the two scans
- Establish correspondences



Shape Matching for Model Alignment

Approach

- 1. Find feature points on the two scans
- 2. Establish correspondences
- 3. Compute the alignment



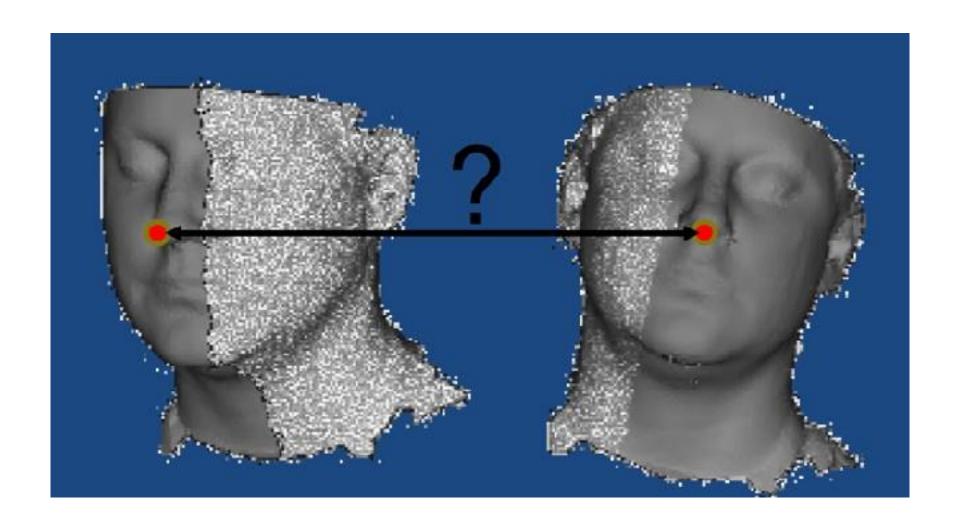
Partially Overlapping Scans

Outline

- Global Shape Correspondence
 - Shape Descriptors
 - Alignment
- Partial Shape Correspondence
 - From Global to Local
 - Pose Normalization
 - Partial Shape Descriptors
- Registration
 - Closed Form Solutions
 - Branch & Bound
 - Random Sample Consensus (RANSAC)

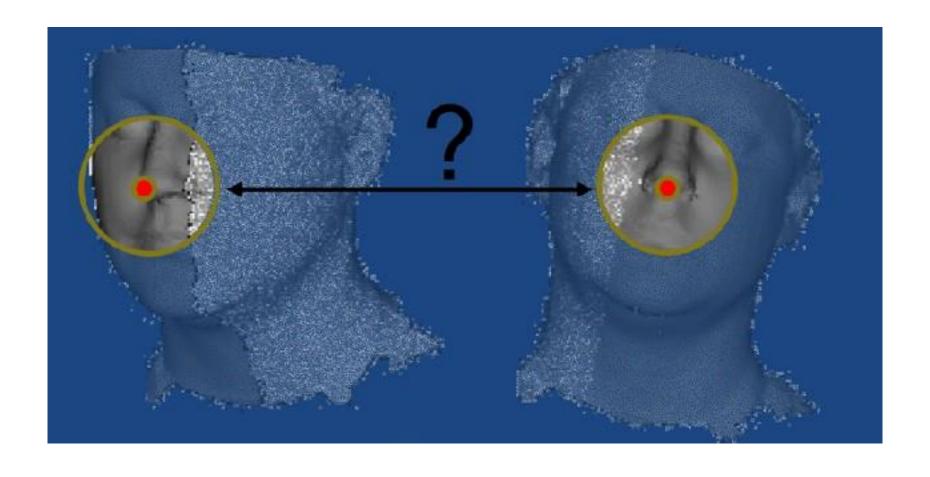
Correspondence

- Goal
 - Identify when two points on different scans represent the same feature



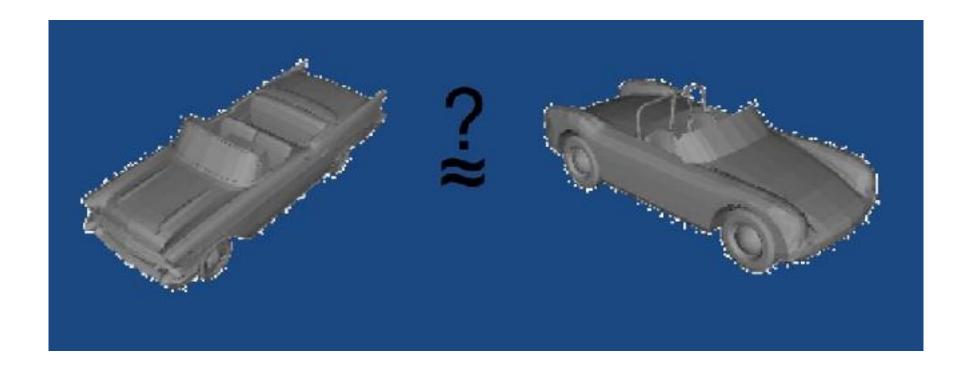
Local Correspondence

- Goal
 - Identify when two points on different scans represent the same feature
 - Are the surrounding regions similar?



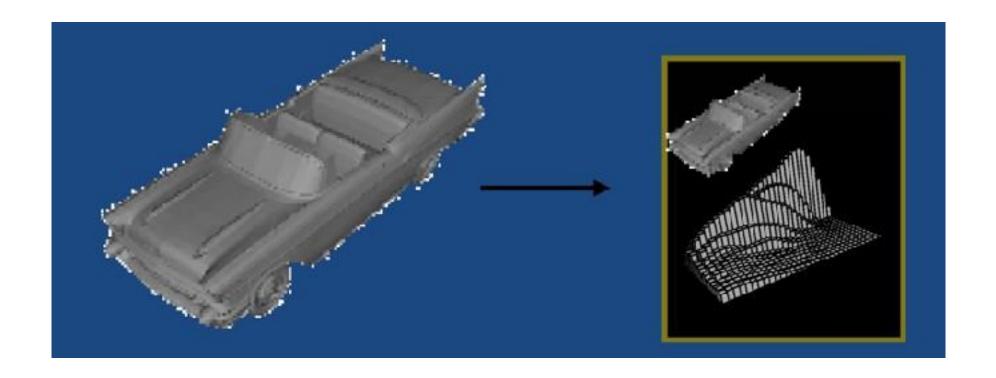
Global Correspondence

- More Generally:
 - Given two models, determine if they represent the same/similar shapes
 - models can have different representations, tesselations, topologies, etc.



Global Correspondence

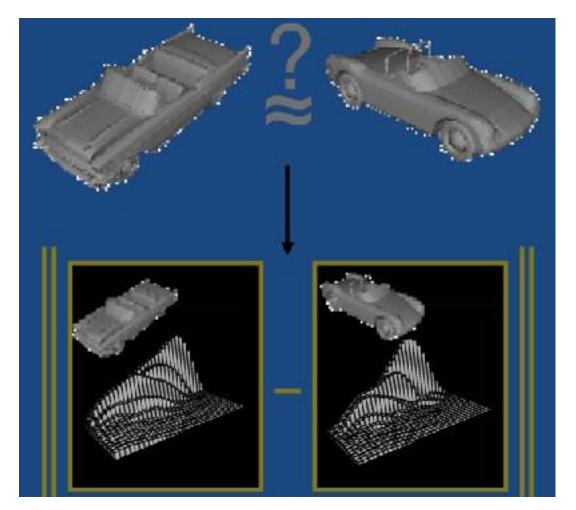
- Approach:
- Represent each model by a shape descriptor:
 - A **structured** abstraction of a 3D model
 - that captures **salient** shape information



Global Correspondence

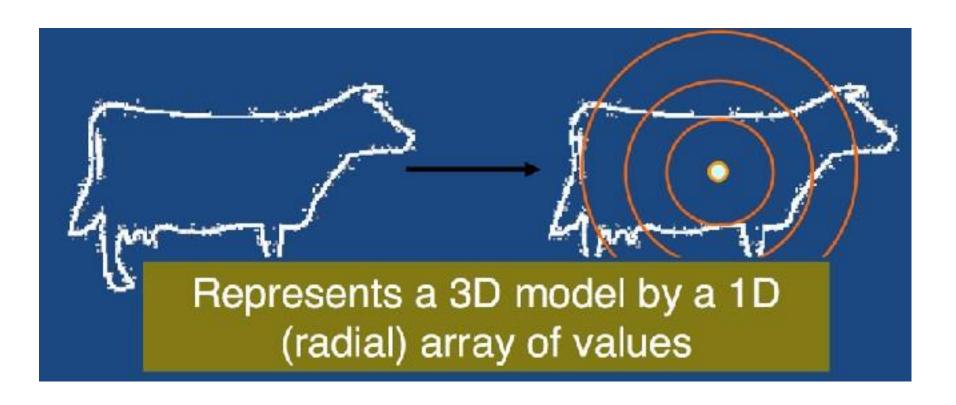
Approach:

- Represent each model by a shape descriptor
- Compare shapes by comparing their shape descriptors



Shape Descriptors: Examples

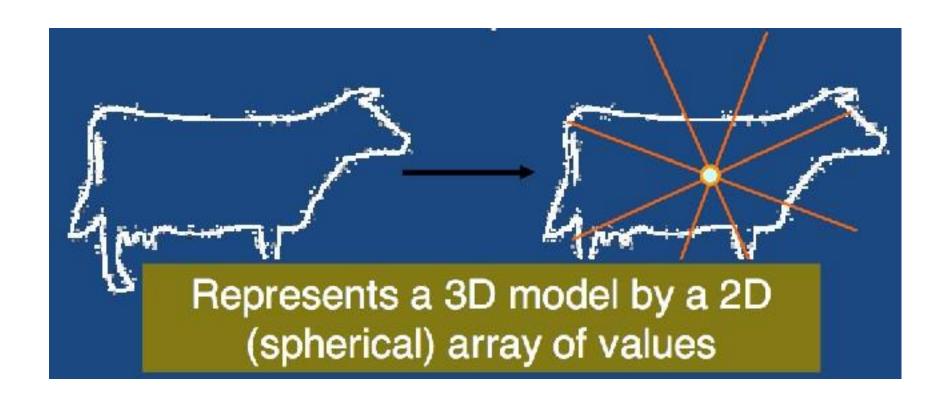
 Shape descriptor stores a histogram of how much surface area resides within different concentric shells in space



[Ankerst et al. 1999]

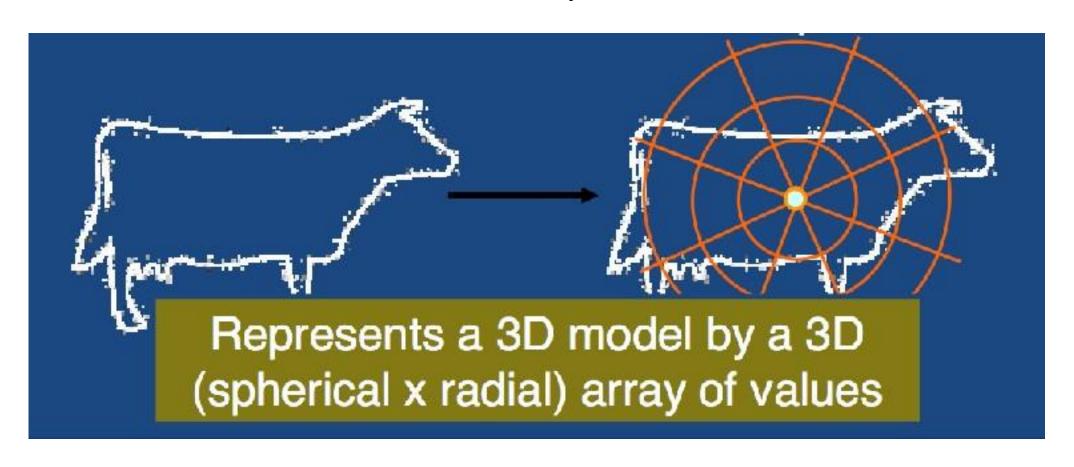
Shape Descriptors: Examples

• Shape descriptor stores a histogram of how much surface **area** resides within different **sectors** in space



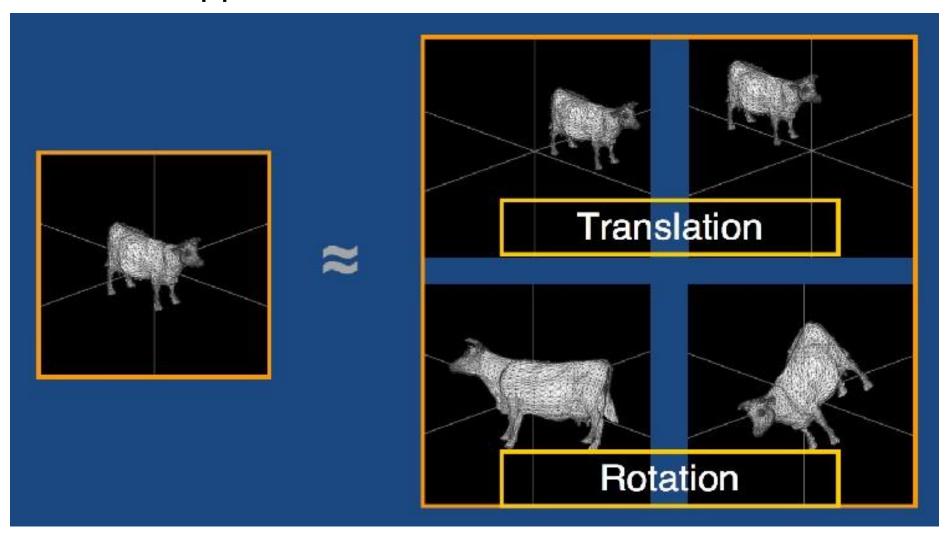
Shape Descriptors: Examples

 Shape descriptor stores a histogram of how much surface area resides within different shells and sectors in space



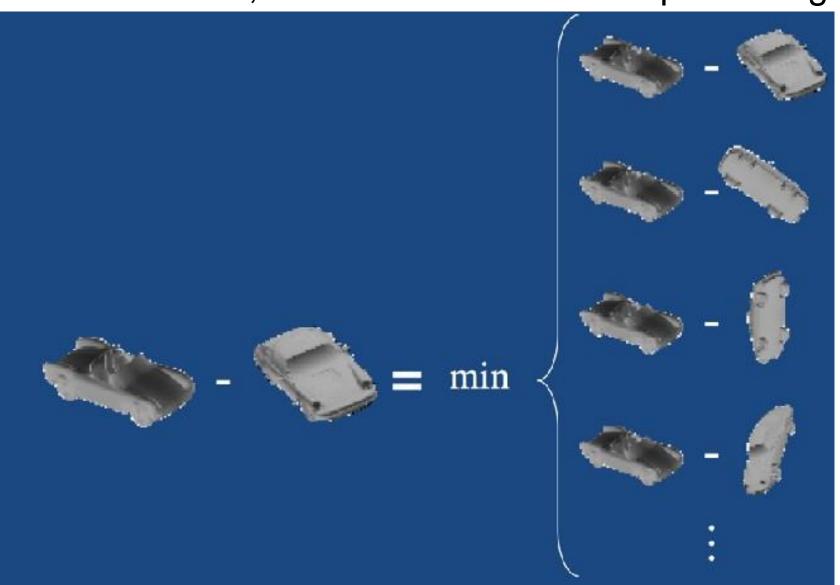
Shape Descriptors: Challenge

 The shape of a model does not change when a rigid body transformation is applied to the model



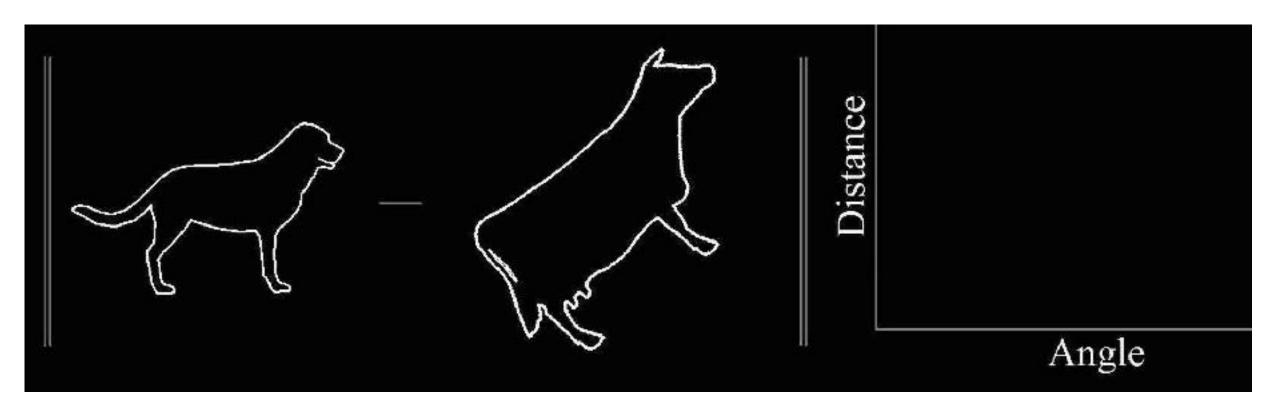
Shape Descriptors: Challenge

• To compare two models, we need them at their optimal alignment



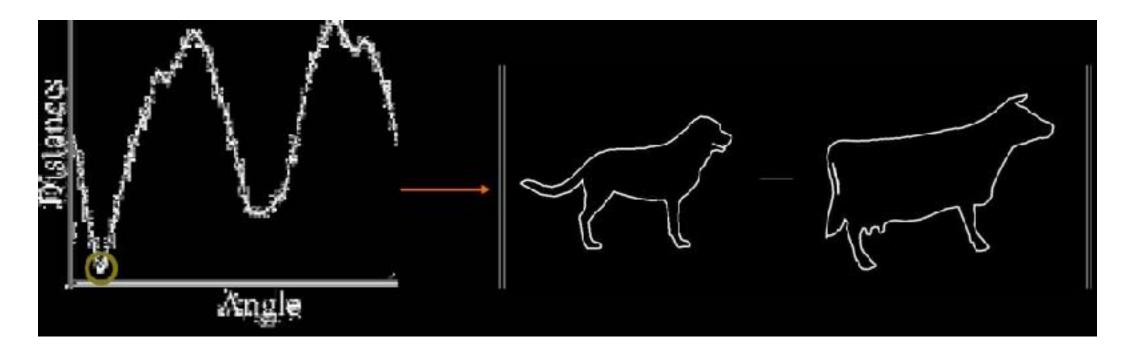
- Three general methods:
 - Exhaustive Search
 - Normalization
 - Invariance

- Exhaustive Search:
 - Compare at all alignments



Exhaustive search for optimal rotation

- Exhaustive Search:
 - Compare at all alignments
 - Correspondence is determined by the alignment at which the models are closest



Exhaustive search for optimal rotation

Exhaustive Search:

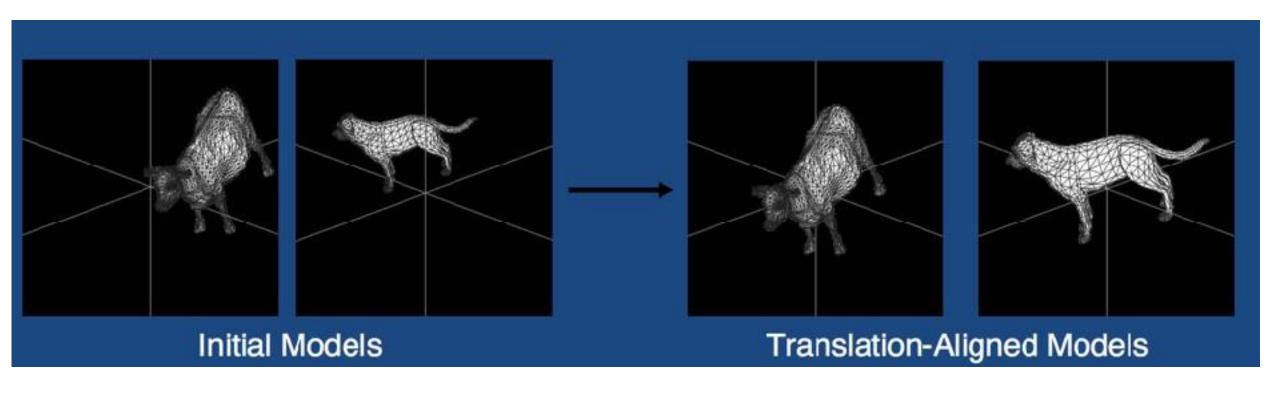
- Compare at all alignments
- Correspondence is determined by the alignment at which the models are closest

Properties:

- Gives the correct answer (w.r.t. the metric)
- While slow on a single processor, it can be parallelized (Clusters? Multi-Threading? GPU?)

Normalization:

- Put each model into a canonical frame:
 - Translation: Center of Mass
 - Rotation

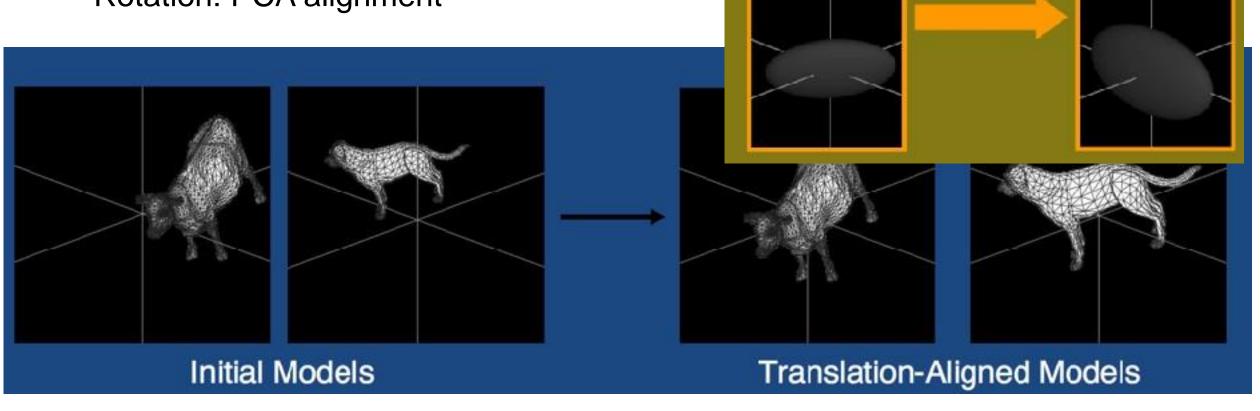


Normalization:

• Put each model into a canonical frame:

Translation: Center of Mass

Rotation: PCA alignment

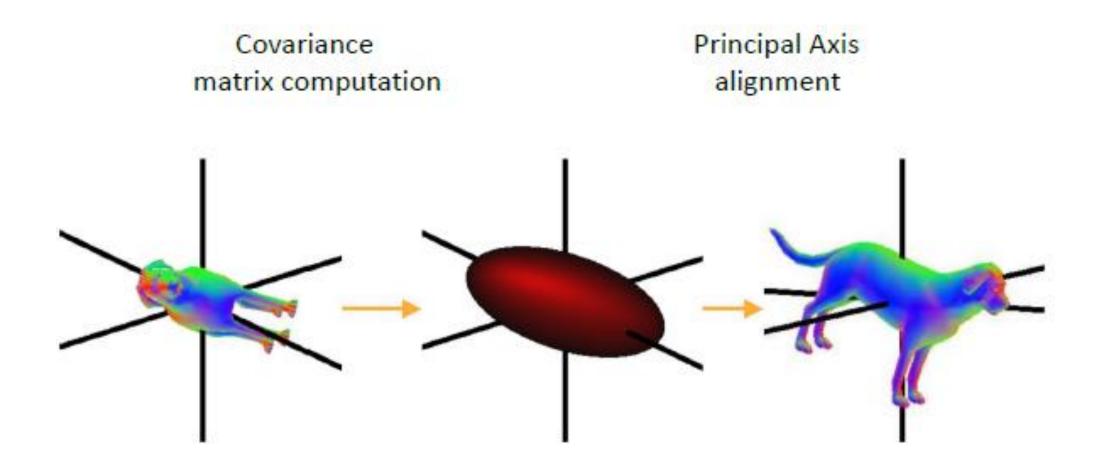


PCA

Alignment

Coarse alignment – PCA

Use PCA to place models into a canonical coordinate frame



2018/2/28

Principal axis computation

Given a collection of points {pi}, form the co-variance matrix:

$$\mathbf{c} = \frac{1}{N} \sum_{i=1}^{N} \mathbf{p}_i$$

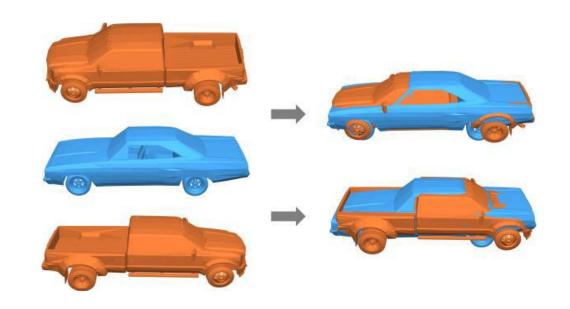
$$C = \frac{1}{N} \sum_{i=1}^{N} \mathbf{p}_i \mathbf{p}_i^T - \mathbf{c} \mathbf{c}^T$$

Compute eigenvectors of matrix C

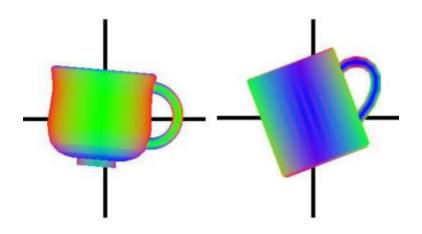
2018/2/28

Issues with PCA

Principal axes are not oriented



Axes are unstable when principal values are similar



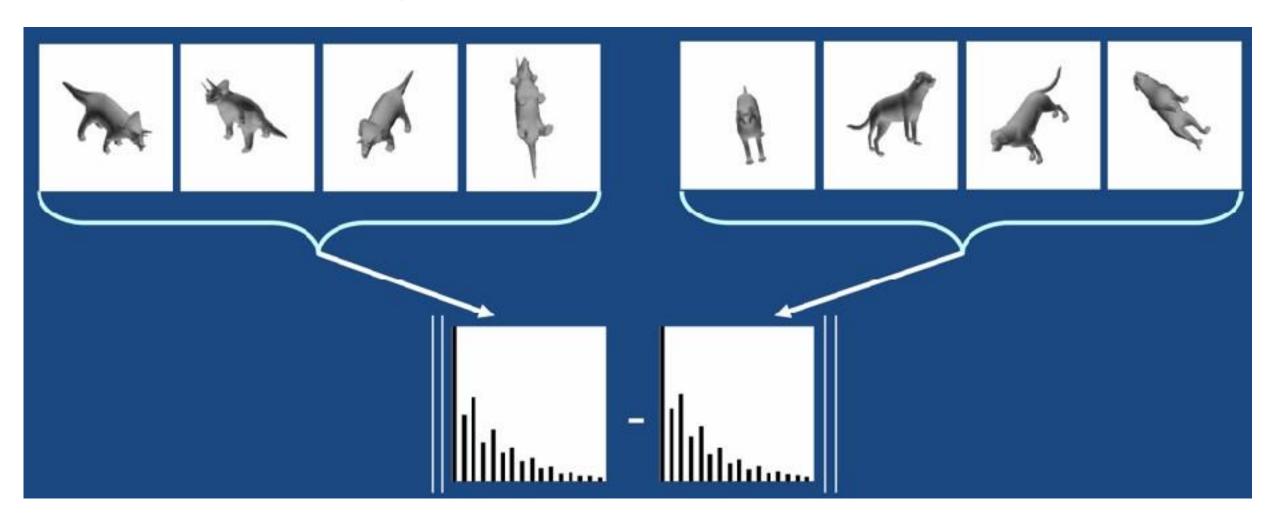
2018/2/28

Normalization:

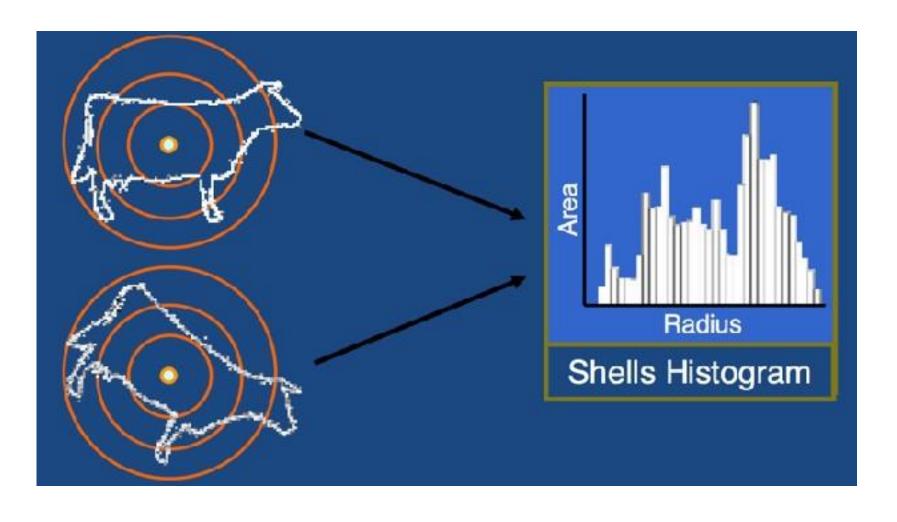
- Put each model into a canonical frame:
 - Translation: Center of Mass
 - Rotation: PCA alignment
- Properties:
 - Efficient
 - Not always robust
 - Not suitable for local feature matching

• Invariance:

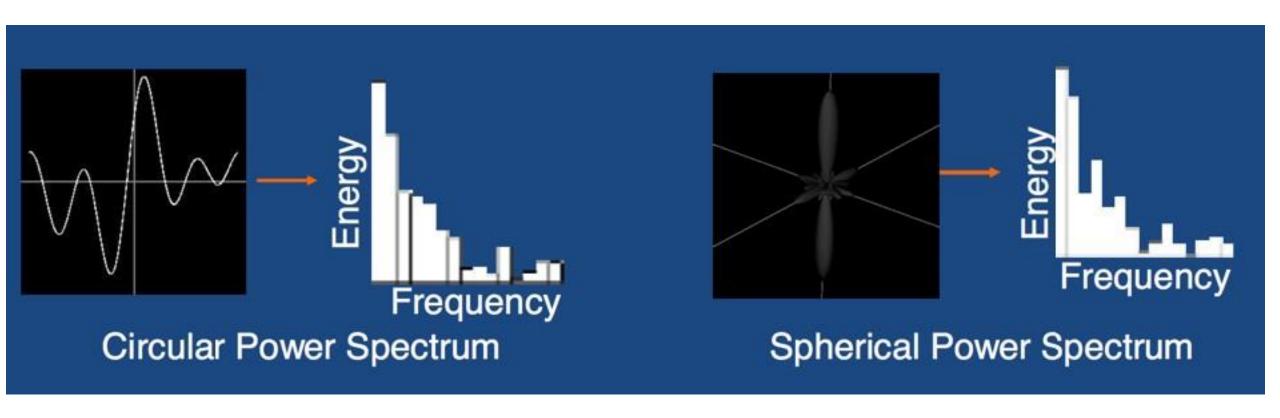
Represent a model by a shape descriptor that is independent of the pose.



- Example: Ankerst's Shells
 - A histogram of the radial distribution of surface area



- Invariance
 - Power spectrum representation
 - Fourier transform for translations
 - Spherical harmonic transform for rotations



storing only the amplitudes of the different frequency components, discarding phase.

Invariance:

Represent a model by a shape descriptor that is independent of the pose

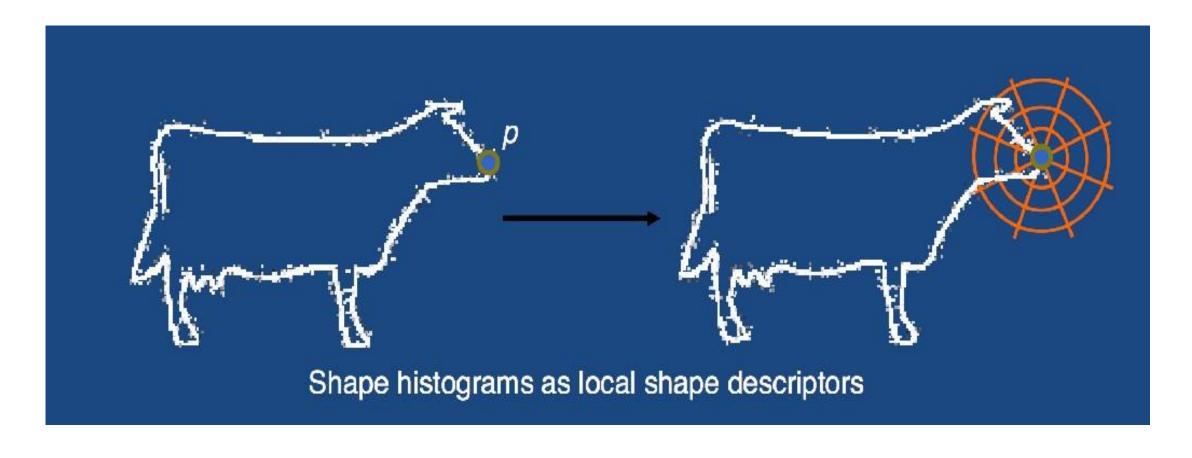
Properties:

- Compact representation
- Not always discriminating

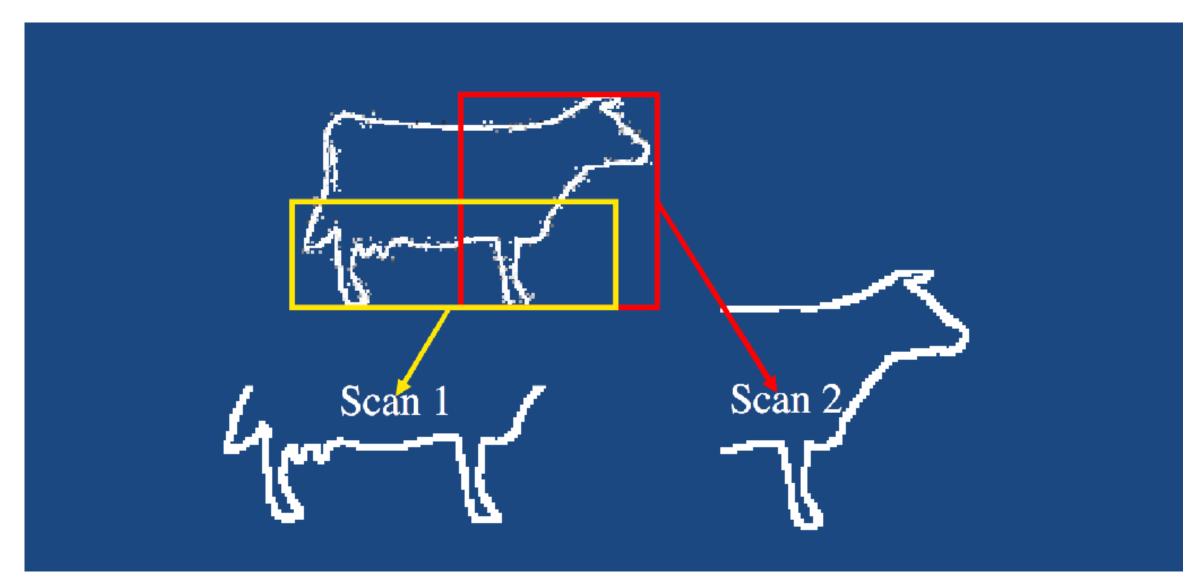
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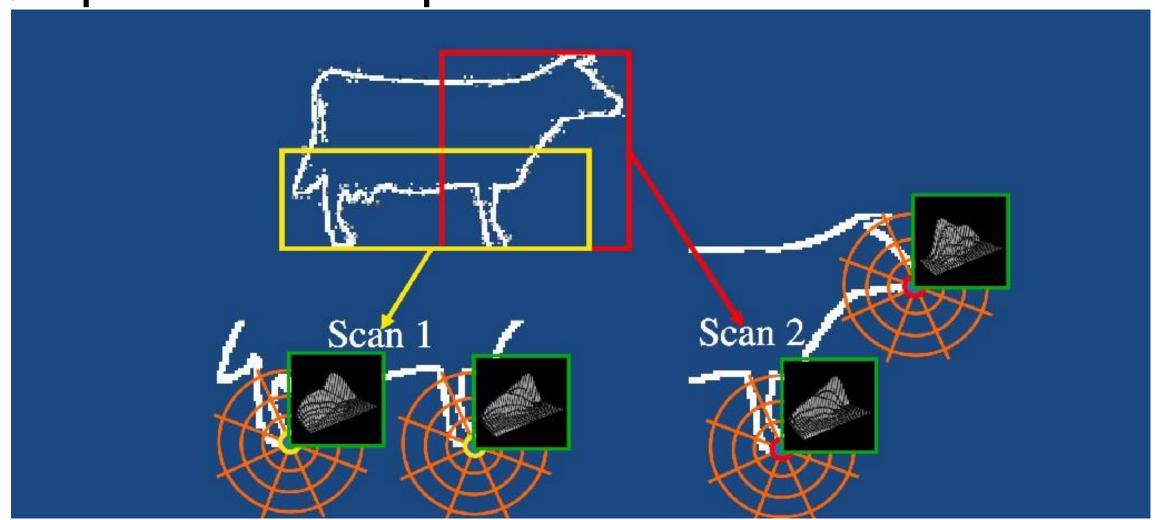
- To characterize the surface about a point p, take global descriptor and:
 - center it about p (instead of center of mass), and
 - restrict the extent to a small region about p



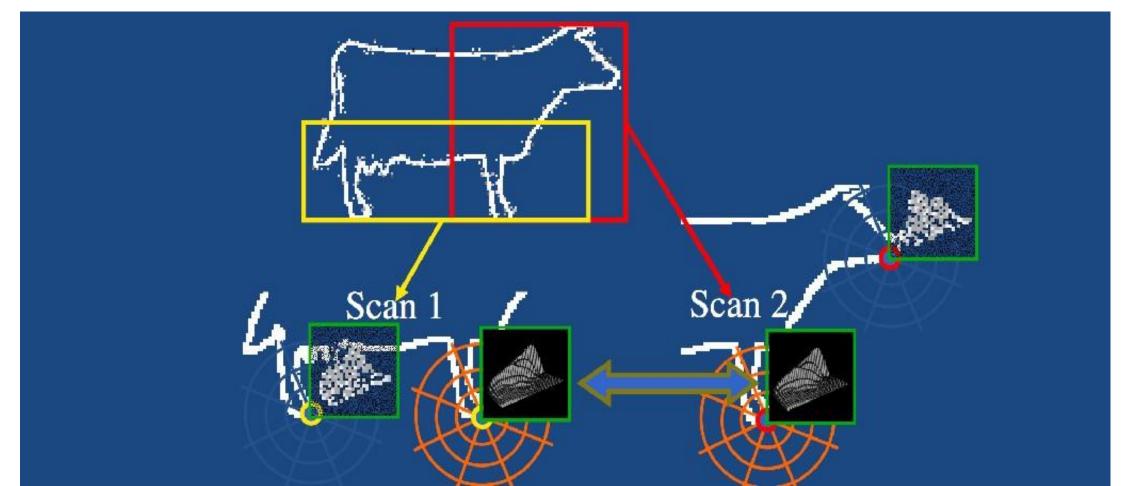
Given scans of a model:



- Identify the features
- Computer a local descriptor for each feature



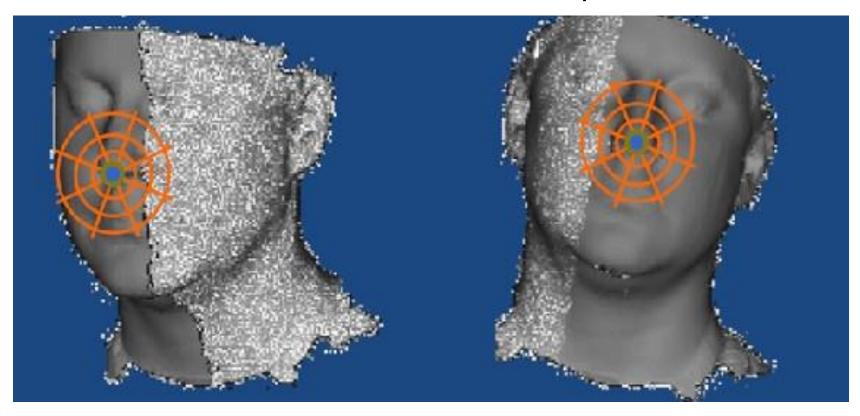
- Identify the features
- Computer a local descriptor for each feature
- Feature correspond → descriptors are similar



Pose Normalization

Optimal Transportation is better

- Translation: Accounted for by centering the descriptor at the point of interest.
- Rotation: We still need to be able to match descriptors across different rotations.



Pose Normalization

Challenge

Since only parts of the models are given, we cannot use global normalization to

Alignment

align the local descriptors

Solutions

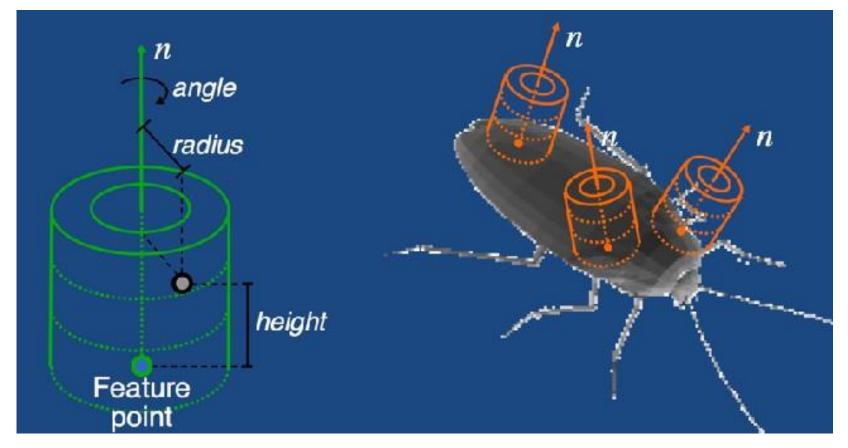
Normalize using local information?

Local Descriptors: Examples

Variations of Shape Histograms

• For each feature, represent its local geometry in cylindrical coordinates about

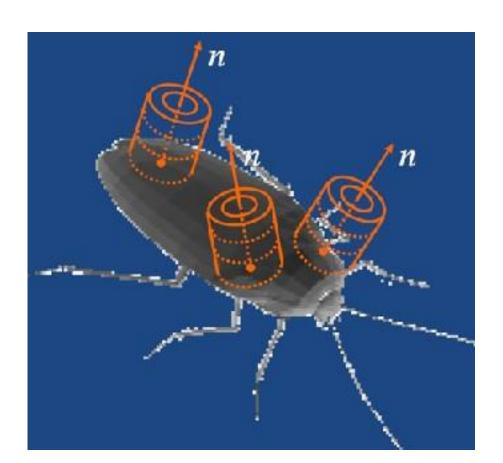
the normal



Since the surface normal is consistent across corresponding feature points, the height and radius are in normalized coordinates. However, there is no normalization for the angle about the normal,

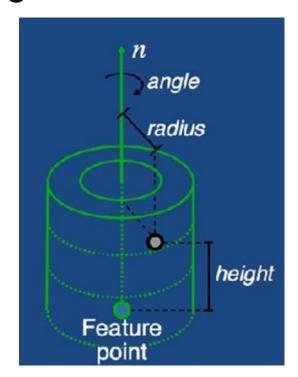
Local Descriptors: Examples

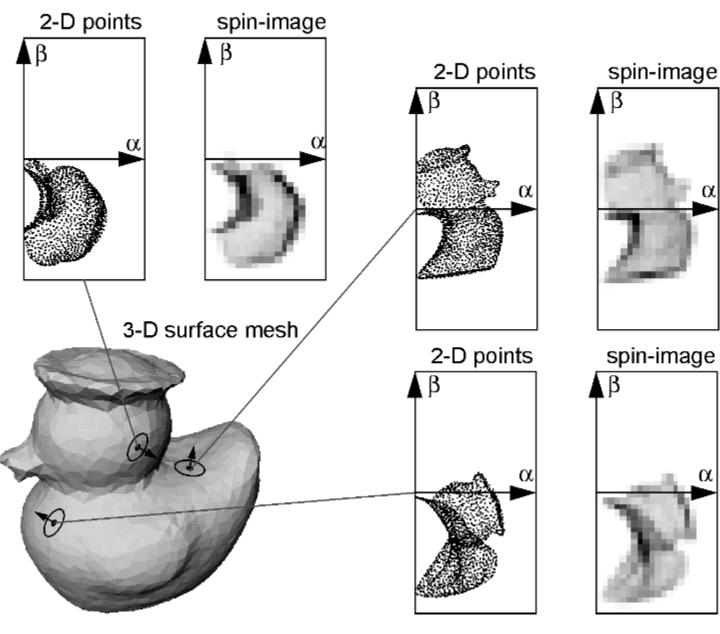
- Variations of Shape Histograms
 - For each feature, represent its local geometry in cylindrical coordinates about the normal
- Spin Images (1997): Store energy in each normal ring



Spin images

 average of some geometry info, such as surface area, number of vertex, by intersecting the local geometry with rings => 2D histogram



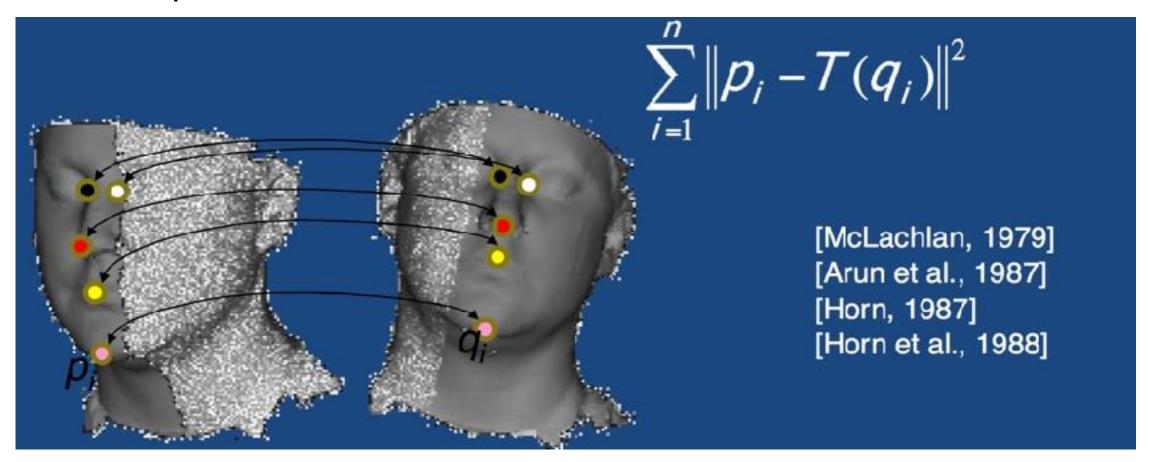


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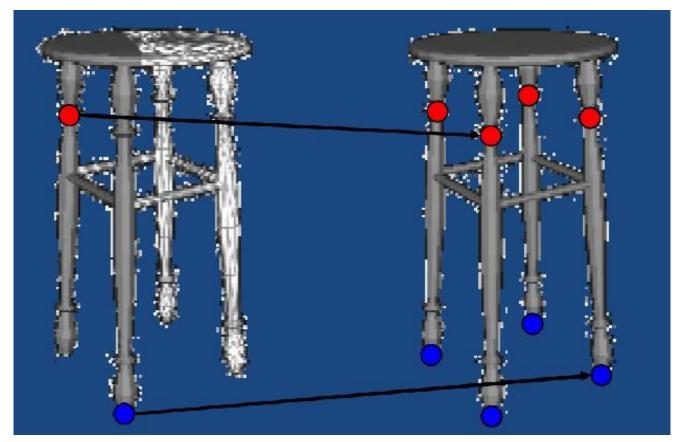
Registration - Ideal Case

- Every feature point on one scan has a single corresponding feature on the other.
- Solve for optimal transformation T



Registration - Challenge

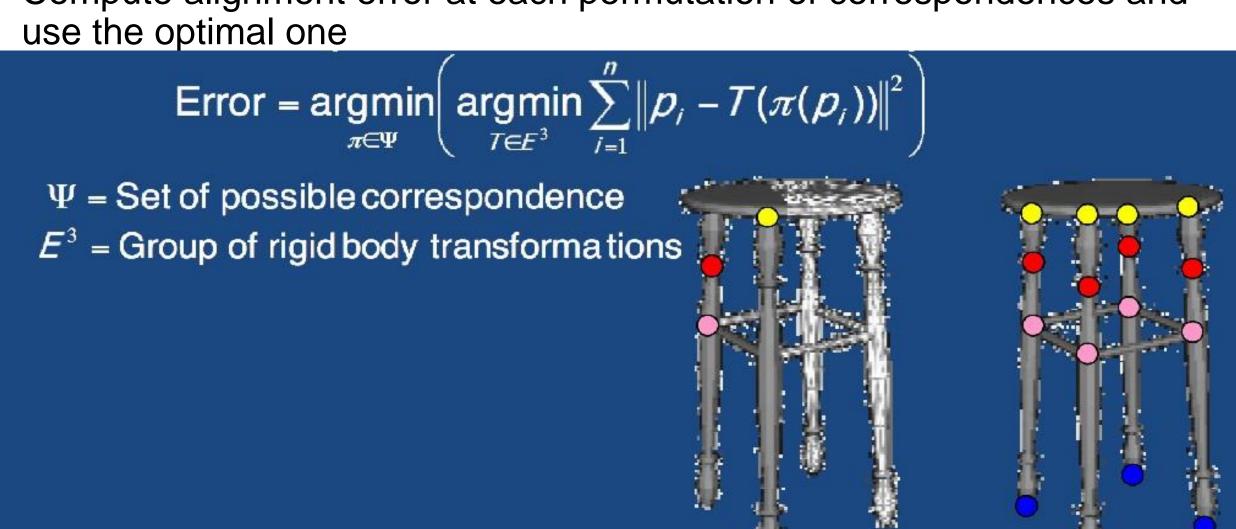
• Even with good descriptors, **symmetries** in the model and the **locality** of descriptors can result in multiple and incorrect correspondences



we can no longer treat the correspondences independently!

Registration - Exhaustive Search

 Compute alignment error at each permutation of correspondences and use the optimal one



Registration - Exhaustive Search

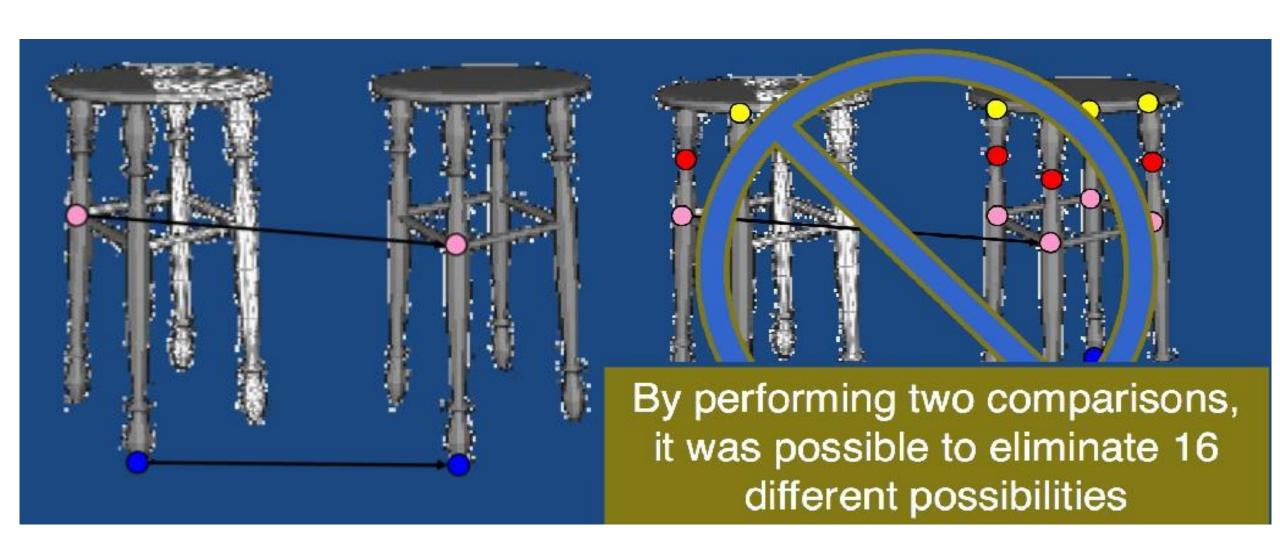
 Compute alignment error at each permutation of correspondences and use the optimal one

Error =
$$\underset{\pi \in \Psi}{\operatorname{argmin}} \left[\underset{f \in E^3}{\operatorname{argmin}} \sum_{i=1}^n \| p_i - T(\pi(p_i)) \|^2 \right]$$
 $\Psi = \operatorname{Set} \text{ of possible correspondence } E^3 = \operatorname{Group of rigid body transformations}$

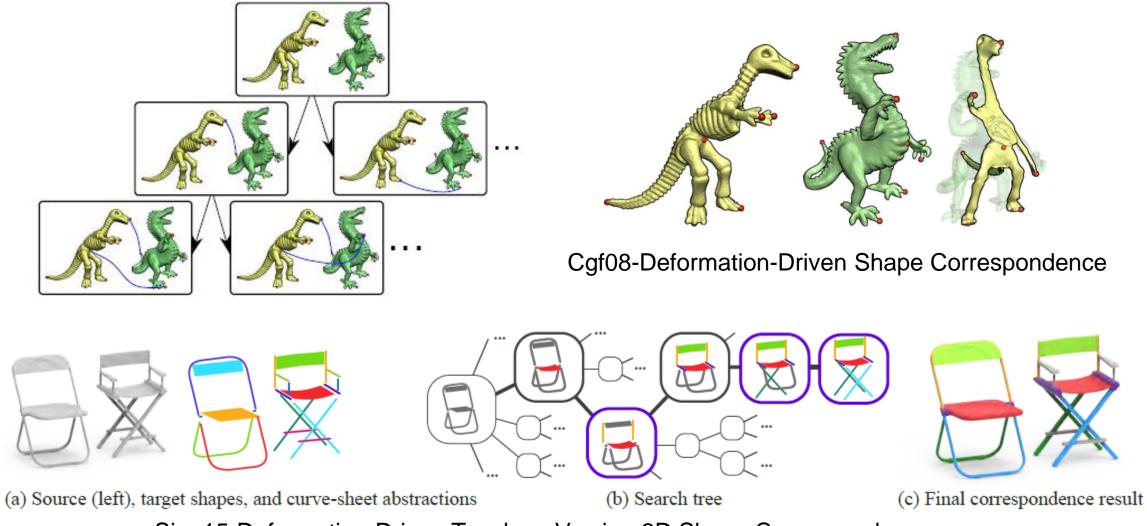
Given points $\{p_1, \dots, p_n\}$ on the query, if p_i matches m_i different target points:
$$|\Psi| = \prod_{i=1}^n m_i$$
 $|\Psi| = 4^4 = 256 \text{ possible permutations}$

Registration - Branch & Bound (Decision tree)

 Try all permutations but terminate early if the alignment can be predicted to be bad



Tree-based search Branch & Bound



Siga15-Deformation-Driven Topology-Varying 3D Shape Correspondence

There are more papers using this in CG

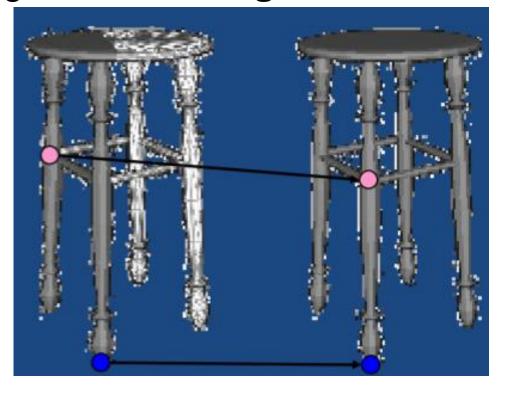
Tree-based search Branch & Bound



Registration - Goal

Need to be able to determine if the alignment will be good without

knowing all of the correspondences



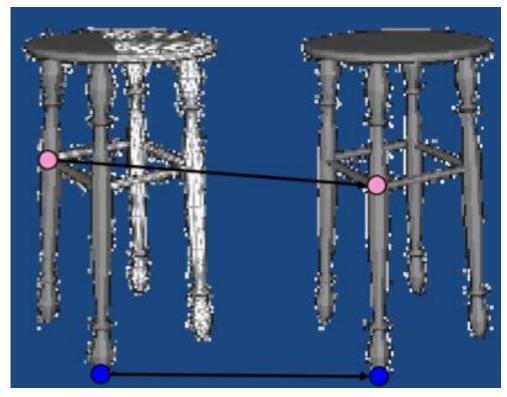
How to evaluate the alignment by using no more correspondences, i.e. just the two?

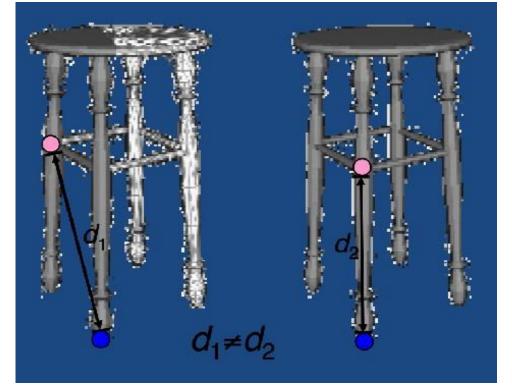
Registration - Goal

 Need to be able to determine if the alignment will be good without knowing all of the correspondences

Observation

Alignment needs to preserve the lengths between points in a single scan





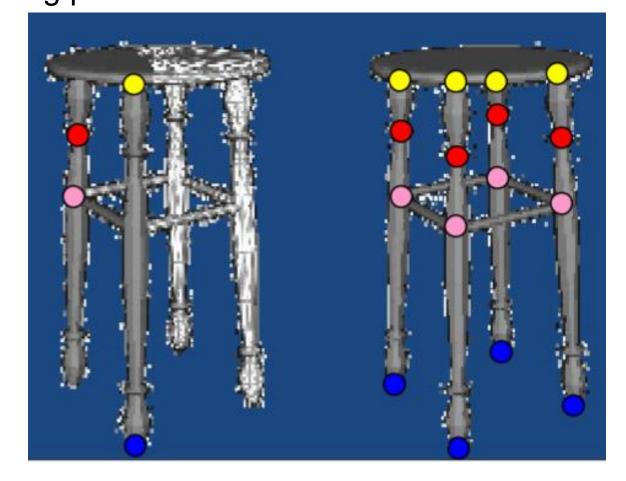
These distances depend only on the correspondences and not on the alignment

An alternative approach - RANdom SAmple Consensus

Observation:

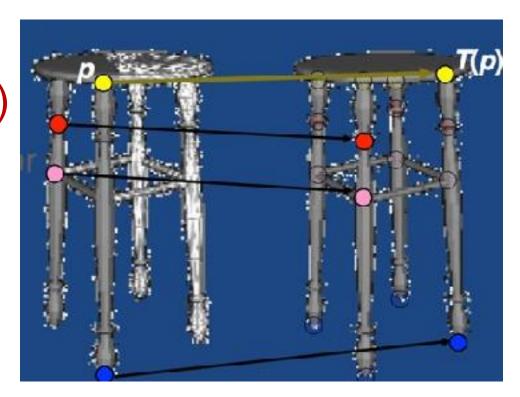
In 3D only three pairs of corresponding points are needed to define a

transformation.



RANdom SAmple Consensus

- Algorithm (iterate 100 times)
- Randomly choose 3 points on source
- For all possible correspondences on target:
 - Compute T
 - For every other source p:
 - find closest correspondence T(p)
 - Compute alignment error



Summary

Global Shape Correspondences

- Shape Descriptors
 - Shells (1D)
 - Sectors (2D)
 - Sectors & Shells (3D)
- Alignment
 - Exhaustive Search
 - Normalization
 - Invariance

Summary

Partial-Shape/Point Correspondences

- From Global to Local
 - Center at feature
 - Restrict extent
- Pose Normalization
 - Normal-based alignment
- Partial Shape Descriptors
 - Normalization/invariance
 - Normalization/exhaustive-search

Summary

Registration

- Closed Form Solutions
 - Global symmetry
 - Local self similarity
- Branch & Bound
 - Inter-feature distances for early termination
- RANdom SAmple Consensus
 - Efficient transformation computation

Thanks