Ransac
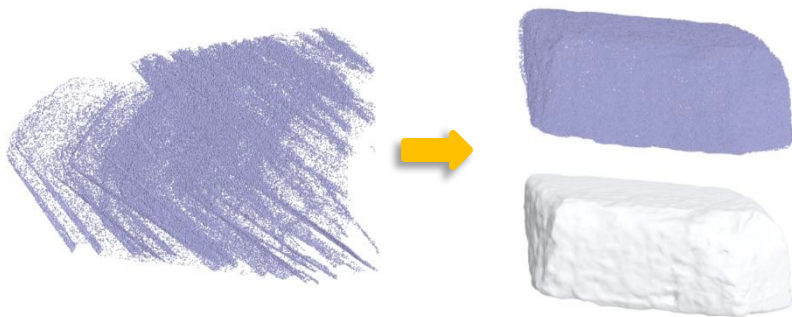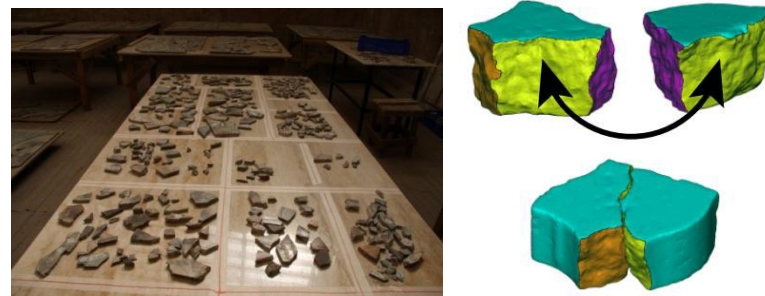
Paolo Cignoni

3D GEOMETRIC MODELING & PROCESSING
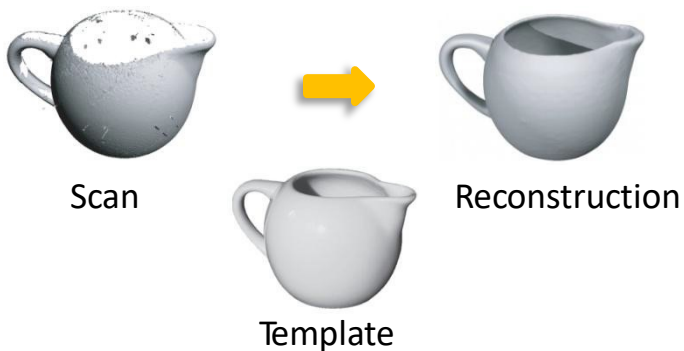
Applications

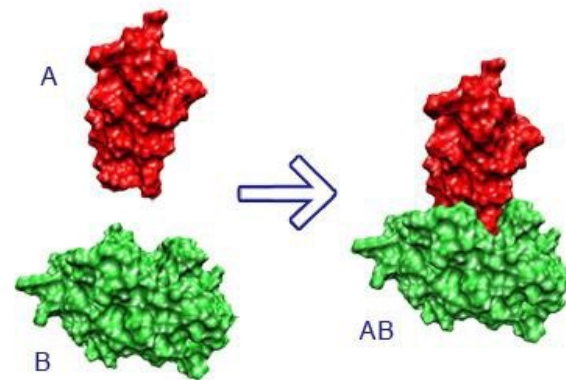Surface reconstruction

Fragment assembly
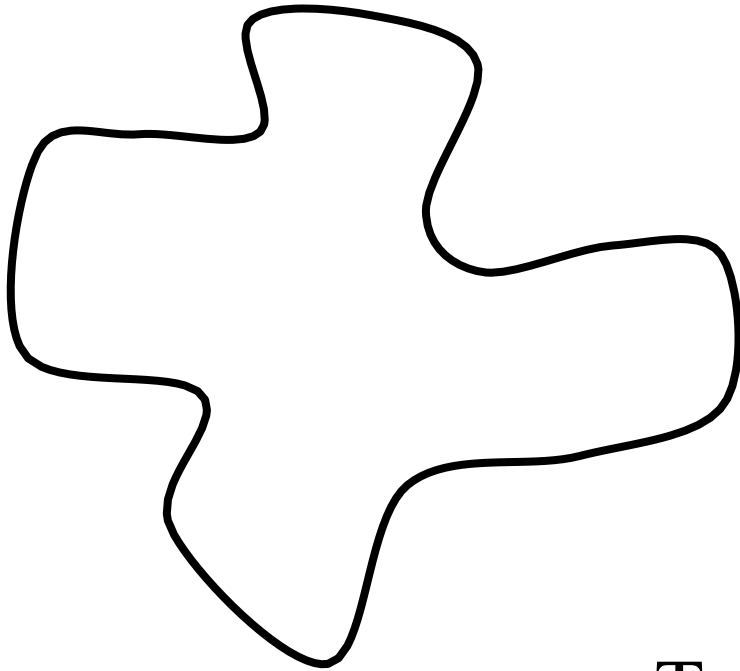

Scan   Reconstruction

Template

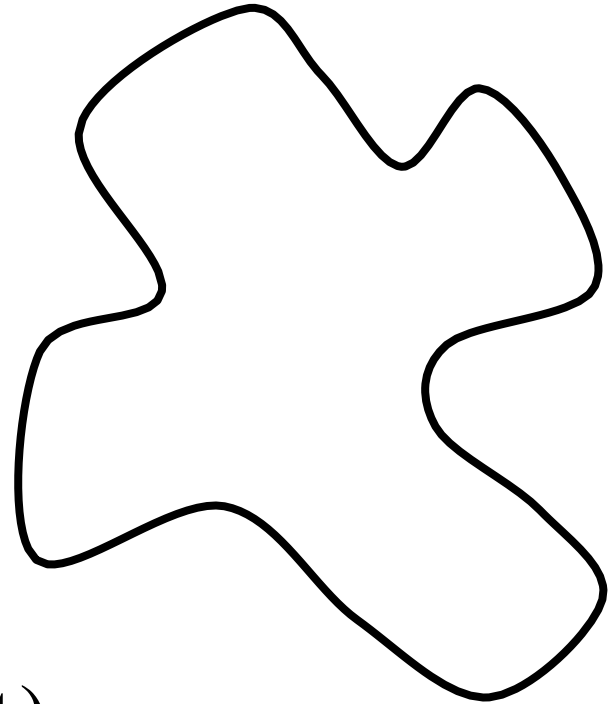Object completion

Protein docking

Rigid Matching

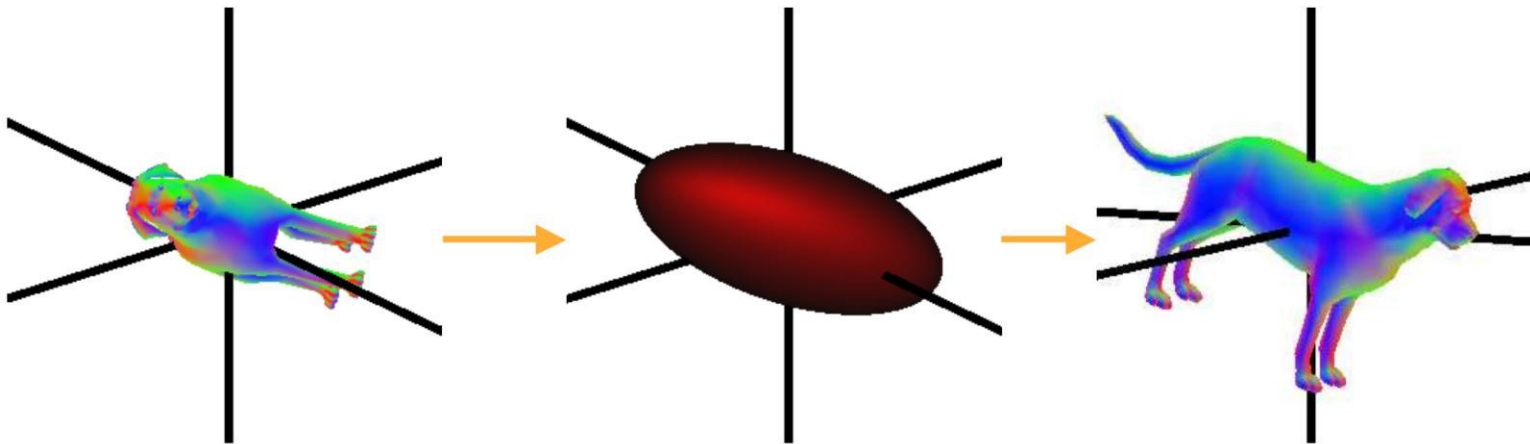

$$T = (R; t)$$

S_1

Rotation and translation

Approach --- PCA

- Use PCA to place models into a canonical coordinate frame

Covariance
matrix computation

Principal Axis
alignment

Principal Axis Computation

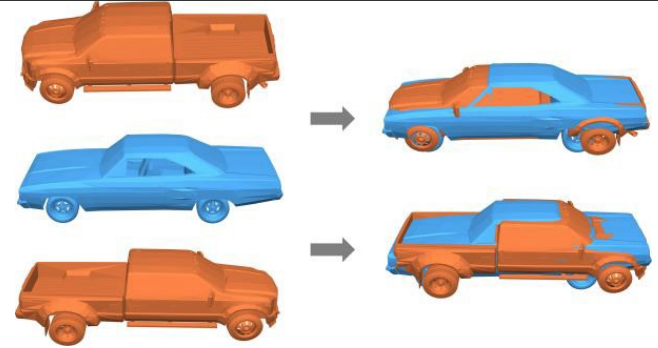- Given a collection of points {$\mathbf{p_i}$}, form the co-variance matrix:

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

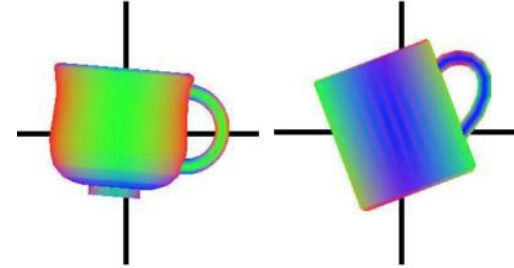$$C = \frac{1}{N} \sum_{i=1}^{N} \mathbf{p}_i \mathbf{p}_i^T - \mathbf{c}\mathbf{c}^T$$

- Compute eigenvectors of matrix C

Issues with PCA

- Principal axes are not oriented

- Axes are unstable when principal values are similar

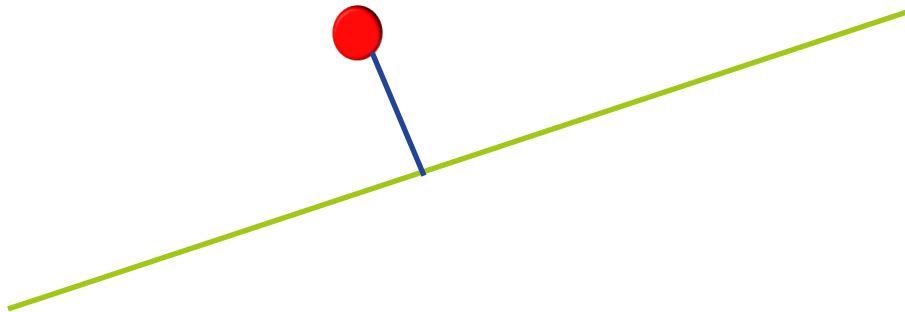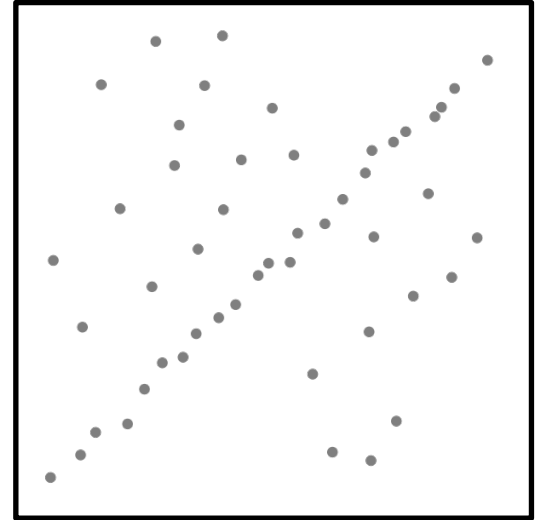- Partial similarity

Ransac: Basis

- **Ran**dom **Sa**mple **C**onsensus
  - Hypothesize and test.

- Used for Parametric Matching
  - Want to match two things.
  - Hypothesized match can be described by parameters (eg., translation, affine.)

- Match enough features to determine a hypothesis.
  - See if it is good.
  - Repeat.

Ransac Example

- Grouping Points into Lines

- Basic Info on lines

Ransac

- Select a random subset of the original data. Call this subset the hypothetical inliers.

- A model is fitted to the set of hypothetical inliers.

- All other data are then tested against the fitted model.

- The estimated model is reasonably good if sufficiently many points have been classified as part of the consensus set.

- Afterwards, the model may be improved by re-estimating it using all members of the consensus set.
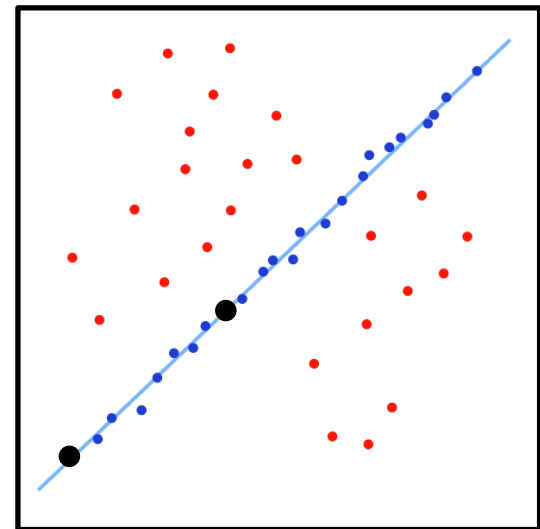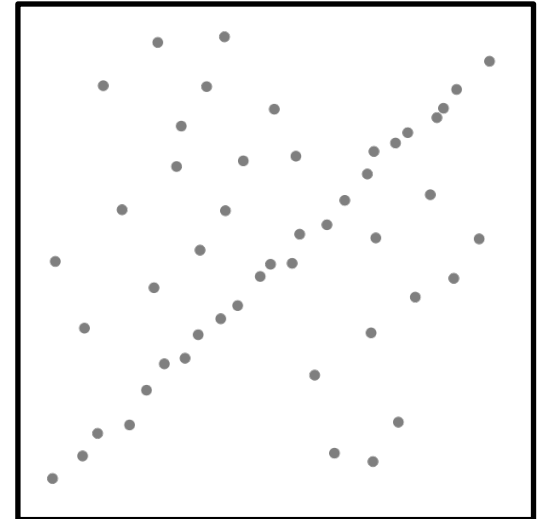
Ransac

- Complexity?

- How many samples?
  - **p** is fraction of points on the line.
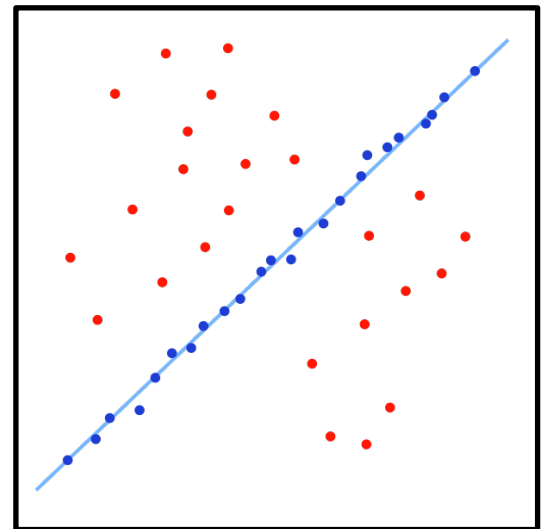   - Fraction of inlayer/total
  - **n** points needed to define hypothesis (2 for lines)
  - **k** number of trials.

- Probability that after **N** trials I've the correct solution is:

$$1-(1-p^n)^N$$
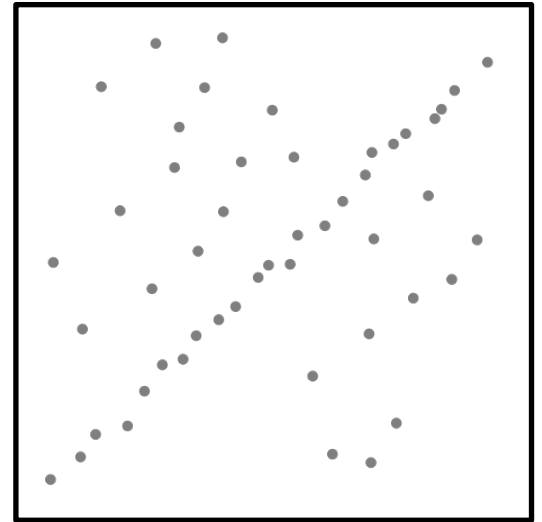
Ransac

- How many point-pairs specify a rigid transform?
  - In R2?
  - In R3?

- Additional constraints?
  - Distance preserving
  - Stability?
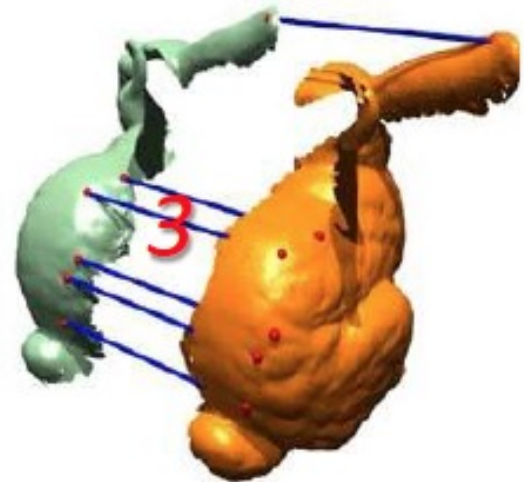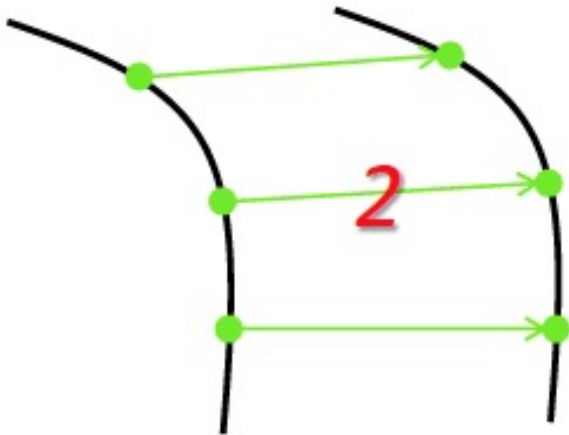
Ransac

- Preprocessing: sample each object

- Iterate
  - Step I: Sample three (two) pairs, check distance constraints
  - Step II: Fit a rigid transform
  - Step III: Check how many point pairs agree. If above threshold, terminates; otherwise goes to Step I

Ransac

- Sampling
  - Feature point detection
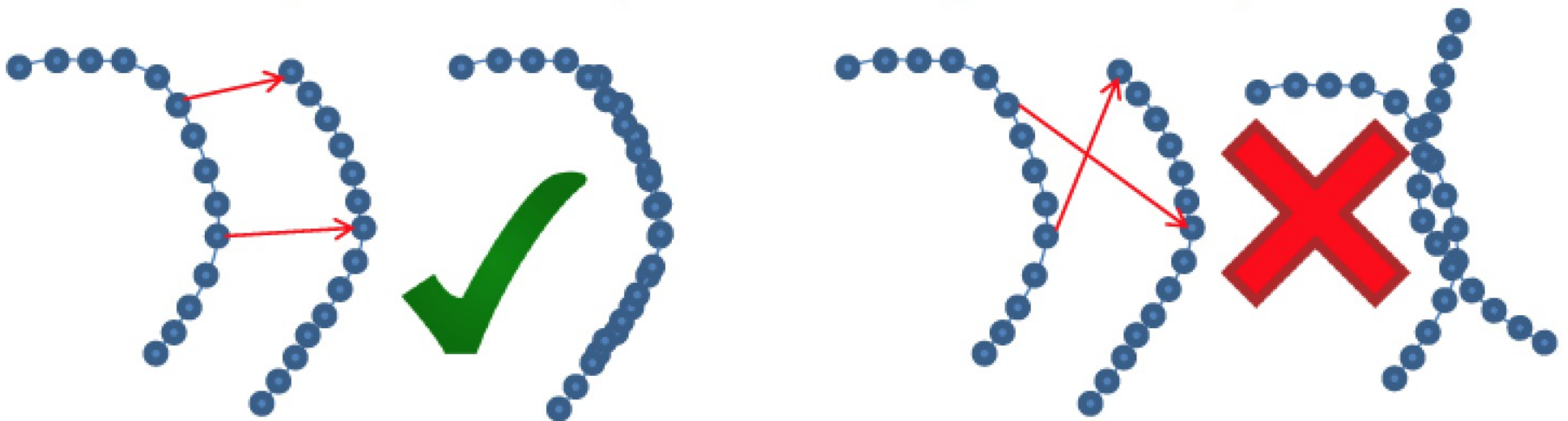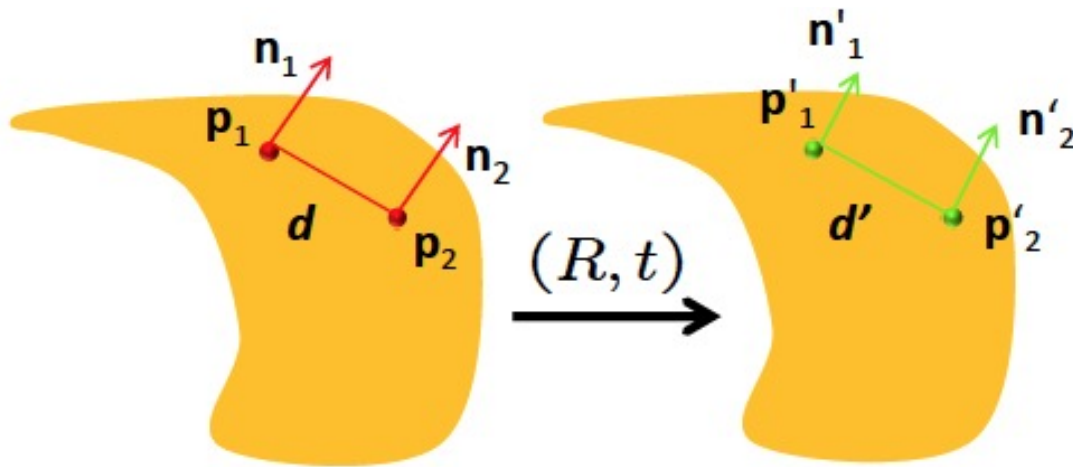
- Correspondences
  - Use feature descriptors
  - Denote a larger success rate p
  - Probability a descriptor identifies the correct match
  - Try only candidated made by pair of samplese with similar descriptor.

- Basic analysis
  - The probability of having a valid triplet p^3
  - The probability of having a valid triplet in N trials is $1-(1-p^3)^N$

Ransac +

- How many surfel (position + normal) correspondences specify a rigid transform?

Constraints:

1. $\|\mathbf{p}_1 - \mathbf{p}_2\| \approx \|\mathbf{p}'_1 - \mathbf{p}'_2\|$
2. $\angle(\mathbf{n}_1, \mathbf{d}) = \angle(\mathbf{n}'_1, \mathbf{d}')$
3. $\angle(\mathbf{n}_2, \mathbf{d}) = \angle(\mathbf{n}'_2, \mathbf{d}')$
4. $\angle(\mathbf{n}_1, \mathbf{n}_2) = \angle(\mathbf{n}'_1, \mathbf{n}'_2)$

- Reduce the number of trials from **O(m³)** to **O(m²)**

- Success rate: $1-(1-p^2)^N$

$$\mathbf{t} = \frac{\mathbf{p}'_1 + \mathbf{p}'_2}{2} - \frac{\mathbf{p}_1 + \mathbf{p}_2}{2}$$

$$[\mathbf{n}_1, \mathbf{n}_2, d] \xrightarrow{R} [\mathbf{n}'_1, \mathbf{n}'_2, d']$$

Ransac ++

- How many frame correspondences specify a rigid transform?
  - Principal curvatures
  - Local PCA
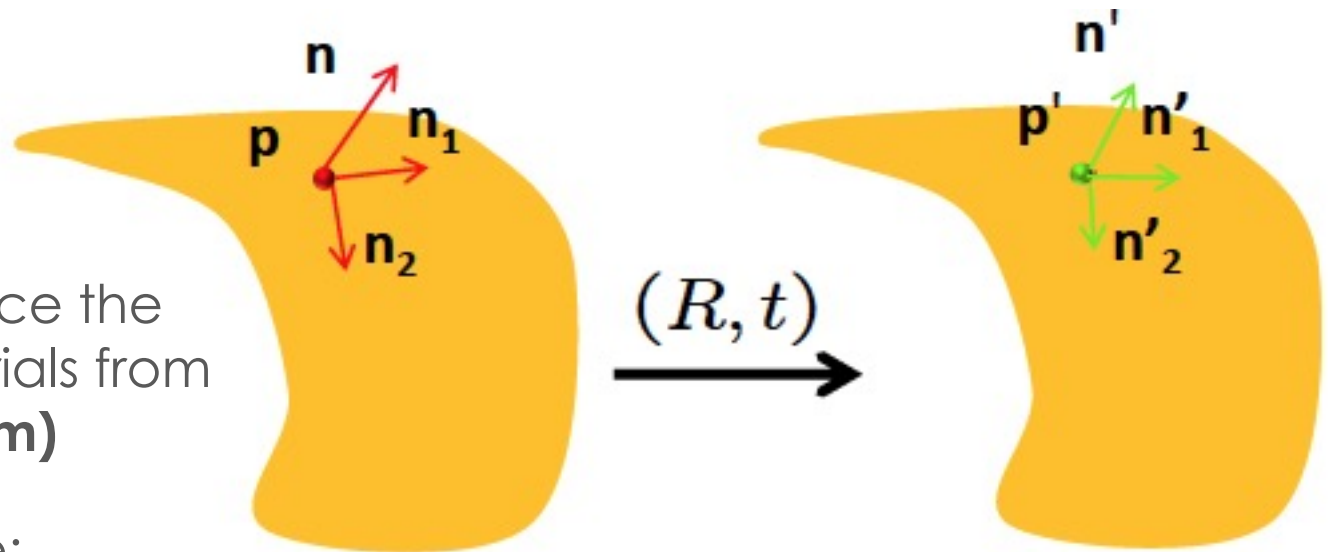
- Further reduce the number of trials from **O(m²)** to **O(m)**

- Success rate: **1-(1-p)ᴺ**

$$t = p' - p$$
$$R(n, n_1, n_2) \approx (n', n'_1, n'_2)$$

Post Processing

- Refine the match via ICP

Input   After matching   After registration