

ECE 1390/2390

Image Processing and Computer Vision – Fall 2021

RANSAC

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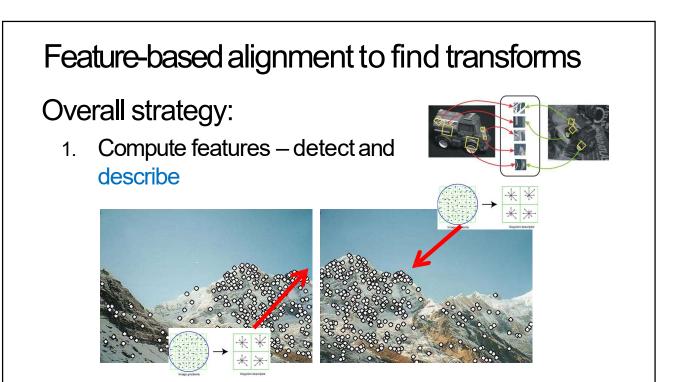
Feature-based alignment to find transforms

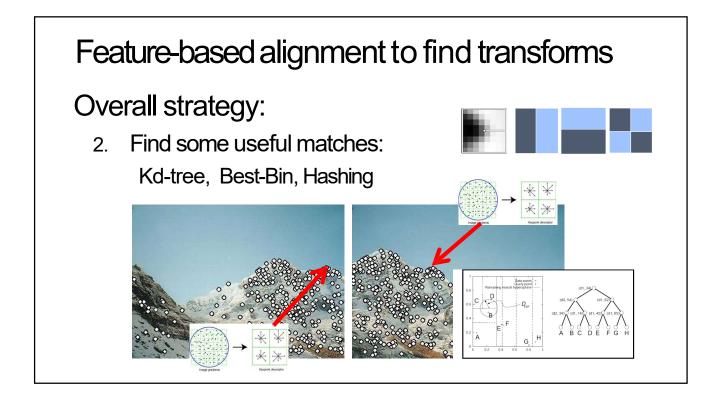
Overall strategy:

Compute features – detect and describe

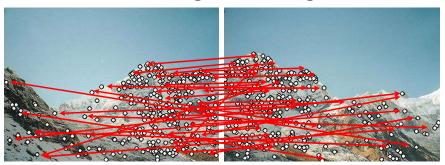








Feature-based alignment algorithm



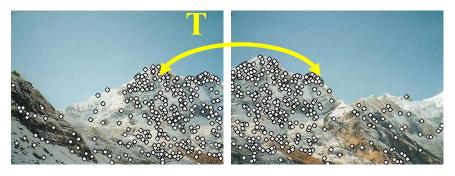
2. Compute *putative matches* - e.g. "closest descriptor"

Kd-tree, best bin, etc...

Feature-based alignment to find transforms

Overall strategy:

3. Compute and apply the best transformation: e.g. affine, translation, or homography



Feature-based alignment to find transforms

Overall strategy:

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How to get "putative" matches?

Feature matching

- Exhaustive search one against another
- Hashing
- Nearest neighbor techniques

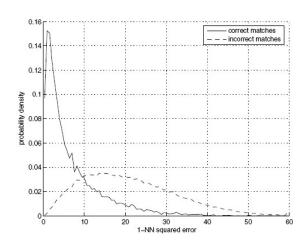
....but these give the best match. How do we know it's a good one?

Feature-space outlier rejection

- Let's not match all features, but only these that have "similar enough" matches?
- How can we do it?
 - SSD(patch1,patch2) < threshold
 - How to set threshold?

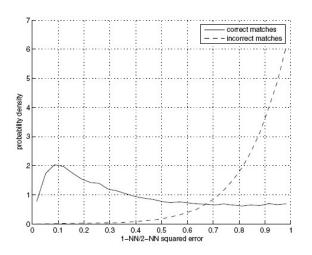
Feature-space outlier rejection

• How to setthreshold?



Abetter way [Lowe, 1999]:

- 1-NN: SSD of the closest match
- 2-NN: SSD of the secondclosest match
- Look at how much better 1-NN is than 2-NN, e.g. $\frac{1-NN SSD}{2-NN SSD}$
 - That is, is our best match much better than the next?



Feature matching

- Exhaustive search
- Hashing
- Nearest neighbor techniques
- But...remember the distinctive vs invariant competition? Implies:
- Problem: Even when pick best match, still lots (and lots) of wrong matches - "outliers". What should we do?

Another way to remove mistakes

- •Why are we doing matching?
 - To compute a model of the relation between entities

"Find consistent matches"???

- Some points (many points) are static in the world
- Some are not
- Need to find the right ones so can compute pose.
- Well tried approach:
 - Random Sample Consensus (RANSAC)

RANSAC		

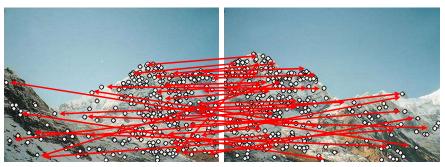
Feature-based alignment algorithm





1. Extract features

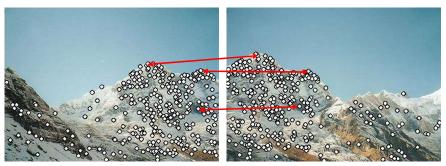
Feature-based alignment algorithm



Compute putative matches - e.g. "closest descriptor"

Kd-tree, best bin, etc...

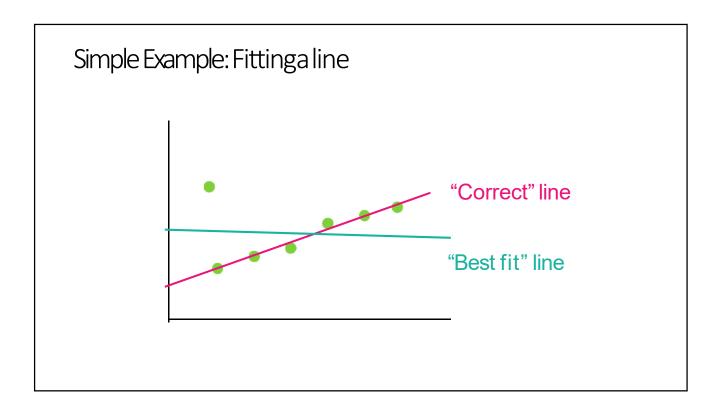
Feature-based alignment algorithm



- Loop until happy:
 - Hypothesize transformation T from some matches
 - Verify transformation (search for other matches consistent with T) – mark best

"Find consistent matches"?

- Some "best" matches are correct
- Some are not. And the "not" are not part of any other consistent match...
- Need to find the right ones so can compute the pose/transform/fundamental... the model.
- Today: Random Sample Consensus (RANSAC)



RANSAC: Main idea

- Fitting a line (model) is easy if we know which points belong and which do not. (duh...)
- If we had a proposed line (model), we could probably guess which points belong to that line (model): *inliers*.
- RANdom SAmple Consensus: randomly pick some points to define your line (model). Repeat enough times until you find a good line (model) – on with many inliers.
- Fischler & Bolles 1981 Copes with a large proportion of outliers

RANSAC for general model

Agiven model type has a *minimal set* – the smallest number of samples from which the model can be computed.

Line: 2 points

RANSAC for general model

Image transformations are models. Minimal set of *s* of point pairs/matches:

- Translation: pick one pair of matched points
- Homography (for plane) pick 4 point pairs
- Fundamental matrix pick 8 point pairs (really 7 but lets not gothere)

RANSAC for general model

General RANSAC algorithm

- Randomly select s points (or point pairs) to form a sample
- Instantiate the model
- Get consensus set C_i: The points within error bounds (distance threshold) of the model
- If $|C_i| > T$, terminate and return model, or
- Repeat for N trials, return model with $\max |C_i|$

RANSAC algorithm

- 1. Sample (randomly) the number of points required to fit the model
- 2. Solve for model parameters using sample
- **3. Score** by the fraction of *inliers* within a preset threshold of the model
- **4. Repeat** 1-3 until the best model is found with high confidence

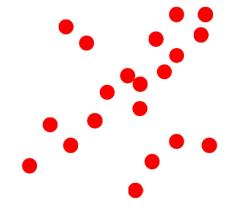
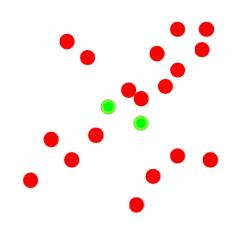


Illustration by Savarese

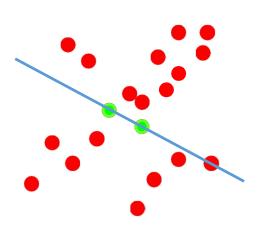
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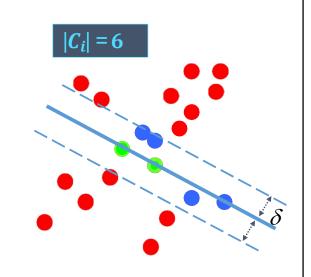
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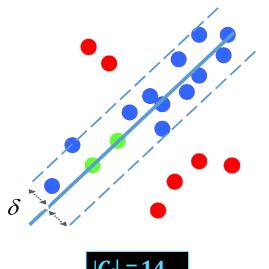
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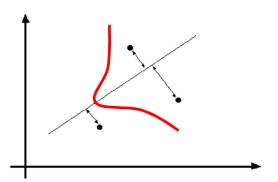
Choosing the parameters

- 1. Initial number of points in the minimal set s
 - Typically minimum number needed to fit the model
- 2. Distance threshold δ (sometimes called t)
 You need a noise model

Distance Threshold

- Let's assume location noise is Gaussian with σ^2
- Then the distance d has Chi distribution with k degrees of freedoms where k is the dimension of the Gaussian.
- If one dimension, e.g.distance off a line, then 1 DOF

$$f(d) = \frac{2e^{-(\frac{d^2}{2\sigma^2})}}{\pi\sigma}, d \ge 0$$



Distance Threshold

For 95% cumulative threshold t when Gaussian with σ^2 : $t^2 = 3.84\sigma^2$

That is: if $t^2 = 3.84\sigma^2$ then 95% probability that d < t when point is inlier

Choosing the parameters

Initial number of points s

Typically minimum number needed to fit the model

Distance threshold t

- Choose t so probability for inlier is high (e.g. 0.95)
- Zero-mean Gaussian noise with std. dev. σ : t^2 = 3.84 σ^2

Number of samples N

- Choose N so that, with probability p, at least one random sample set is free from outliers (e.g. p=0.99)
- Need to set N based upon the outlier ratio e

Calculate N

- 1. s-number of points to compute solution
- 2. p probability of success
- 3. e- proportion outliers, so % inliers = (1 e)
- 4. $P(sample set with all inliers)=(1-e)^s$
- 5. $P(sample set will have at least one outlier) = (1 (1 e)^s)$
- 6. $P(all\ N\ samples\ have\ outlier)=(1-(1-e)^s)^N$
- 7. We want $P(all \ N \ samples \ have \ outlier) < (1 p)$
- 8. So $(1 (1 e^{s}))^N < (1 p)$

Calculate N

$$N > \log(1 - p) / \log(1 - (1 - e)^{s})$$

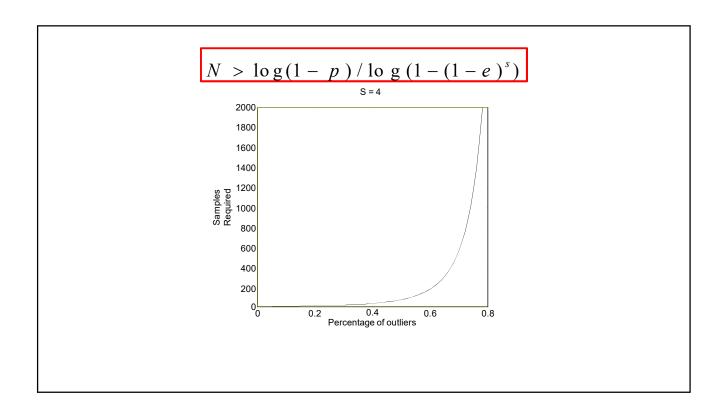
$$N > \log (1 - p) / \log (1 - (1 - e)^{s})$$

Set p=0.99 – chance of getting good sample

s=2, e=5% => N=2 s=2, e=50% => N=17 s=4, e=5% => N=3 s=4, e=50% => N=72 s=8, e=5% => N=5 s=8, e=50% => N=1177

	proportion of outliers e								
	<u>5%</u>	<u>10%</u>	<u>20%</u>	<u>25%</u>	<u>30%</u>	<u>40%</u>	<u>50%</u>		
S									
							. –		
2	2	3	5	6	7	11	17		
3	3	4	7	9	11	19	35		
4	3	5	9	13	17	34	72		
5	4	6	12	17	26	57	146		
6	4	7	16	24	37	97	293		
7	4	8	20	33	54	163	588		
8	5	9	26	44	78	272	1177		

N increases steeply with s

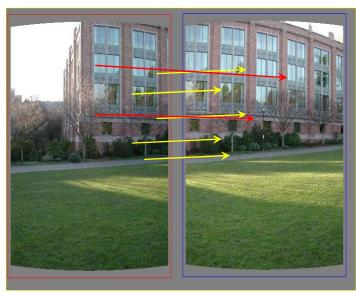


How big does N need to be?

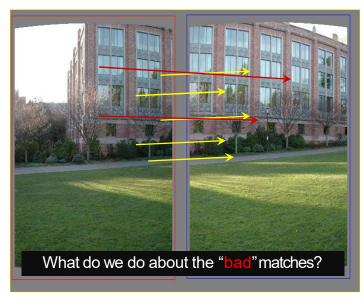
$$N > \log (1 - p) / \log (1 - (1 - e)^{s})$$

N = f(e,s,p), but not the number of points/features!

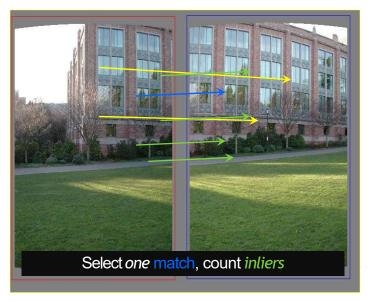
Matching features



Matching features - Example

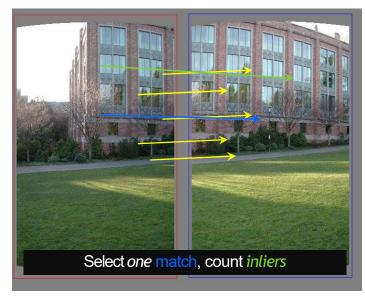


RAndom SAmple Consensus (1)



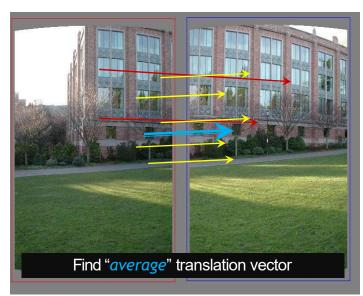
5 total inliers (including selected)

RAndom SAmple Consensus (2)



2 total inliers

Least squares fit



Note: We use the first set of matches as it had stronger consensus (5 inliers)

2D transformation models 2matches: Similarity (translation, scale, rotation) 3matches: Affine 4matches: Projective (homography)

RANSAC for estimating homography

RANSAC loop:

- 1. Select four feature pairs (at random)
- 2. Compute homography *H* (exact)
- 3. Compute *inliers* where $SSD(p_i', H p_i) < \varepsilon$
- 4. Keep largest set of inliers
- 5. Re-compute least-squares *H* estimate on all of the inliers

Adaptively determining the number of samples

- Inlier ratio e is often unknown apriori
- Pick worst case, e.g. 50% (e = 0.5) and adapt if more inliers are found

e.g. 80% inliers would yield e=0.2

Source: M. Pollefeys

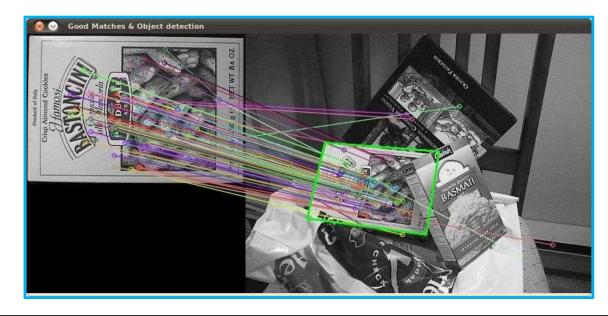
Adaptive procedure

- N= ∞ , sample_count = 0, e = 1.0
- While N > sample_count
 - Choose a sample and count the number of inliers
 - Set $e_0 = 1 \frac{number\ of\ inliers}{total\ number\ of\ points}$
 - If $e_0 < e$ Set $e = e_0$ and recompute N from e:

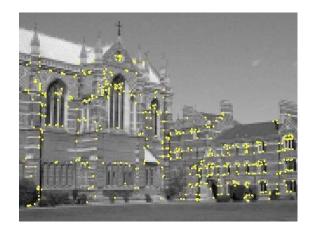
$$N = \log(1 - p) / \log(1 - (1 - e)^s)$$

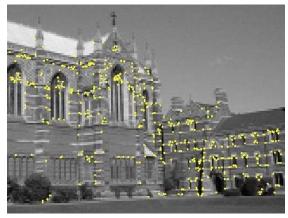
Increment the sample_count by 1

RANSAC for recognition

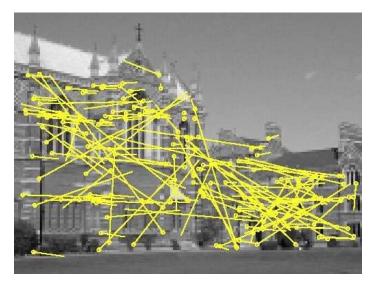


RANSAC for finding fundamental matrix





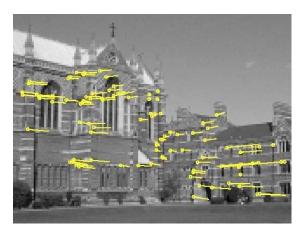
Putative matches (motion) by cross-correlation



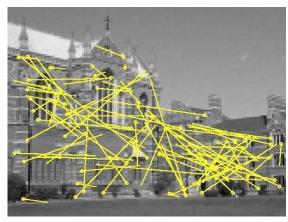
188 matches

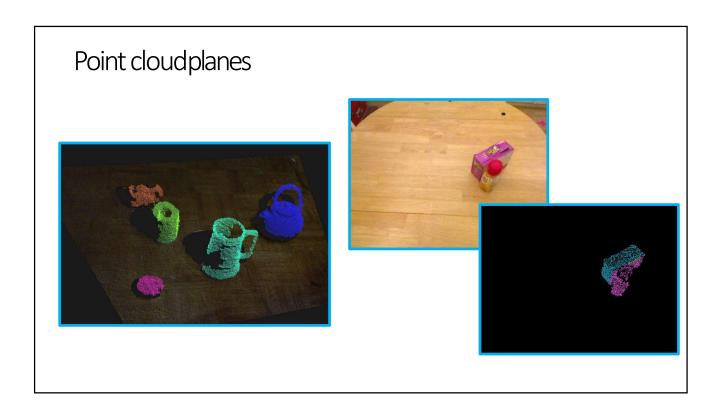
RANSACfor fundamental matrix

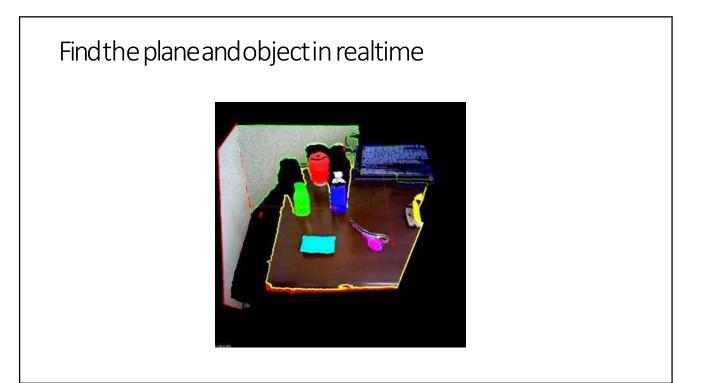
Inliers (99)



Outliers (89)







RANSAC: Conclusions

The good...

- Simple and general
- Applicable to many different problems, often works well in practice
- Robust to large numbers of outliers
- Applicable for larger number of parameters than Hough transform
- Parameters are easier to choose than Hough transform

RANSAC: Conclusions

The not-so-good...

- Computational time grows quickly with the number of model parameters
- Not as good for getting multiple fits
- Really not good for approximate models

RANSAC: Conclusions

Common applications

- Computing a homography (e.g., image stitching) or other imagetransform
- Estimating fundamental matrix (relating two views)
- Pretty much every problem in robot vision