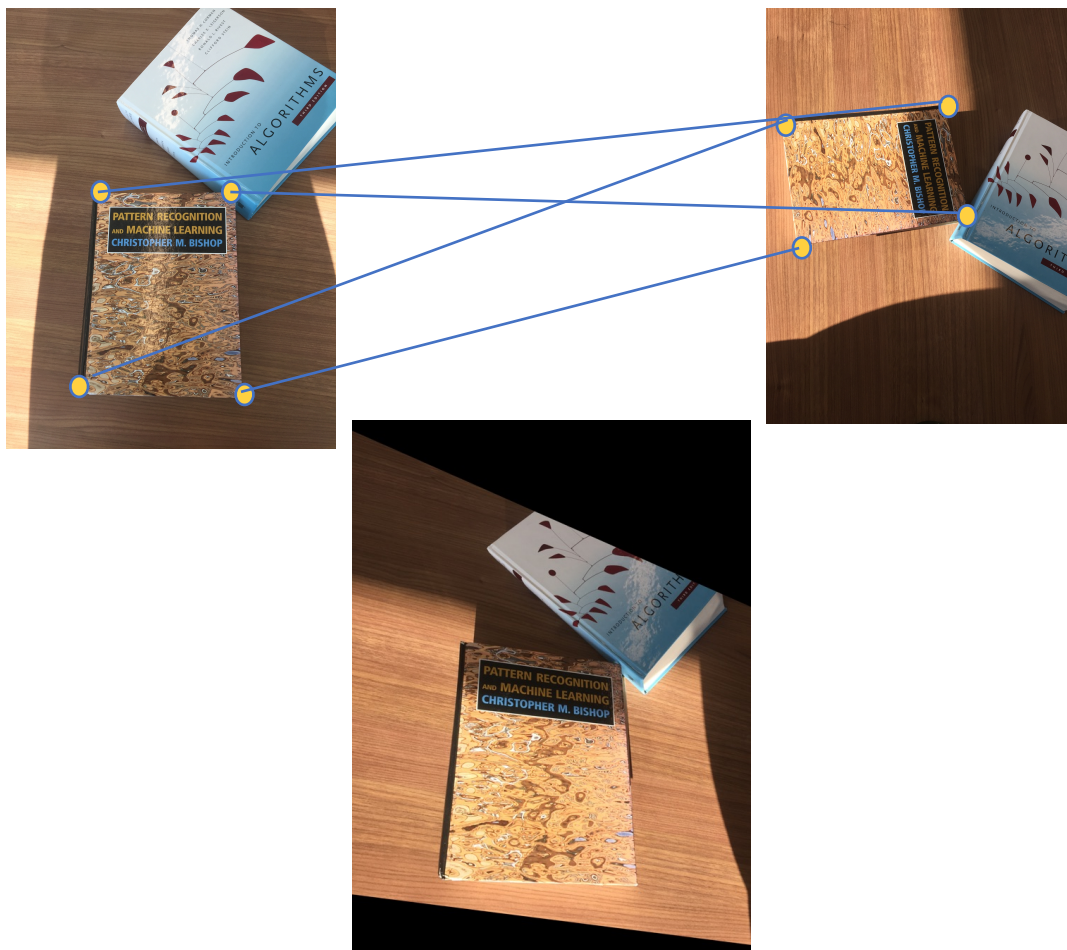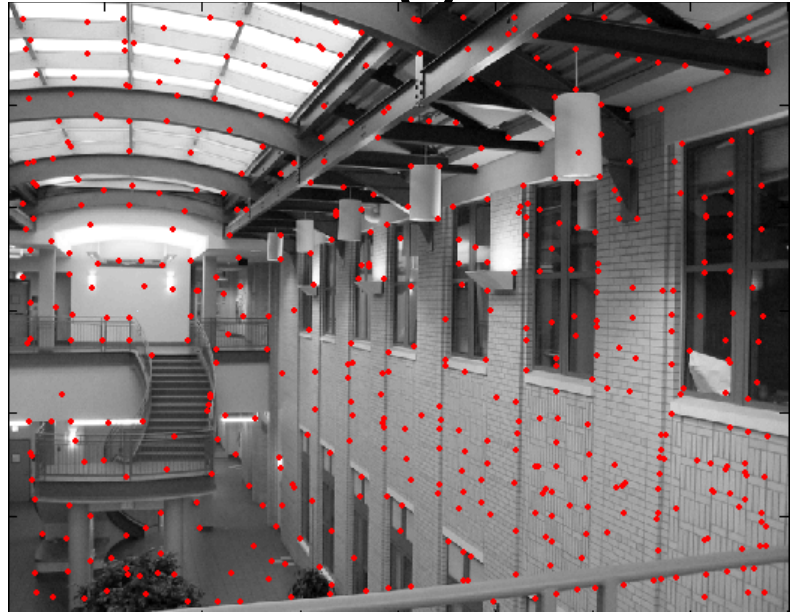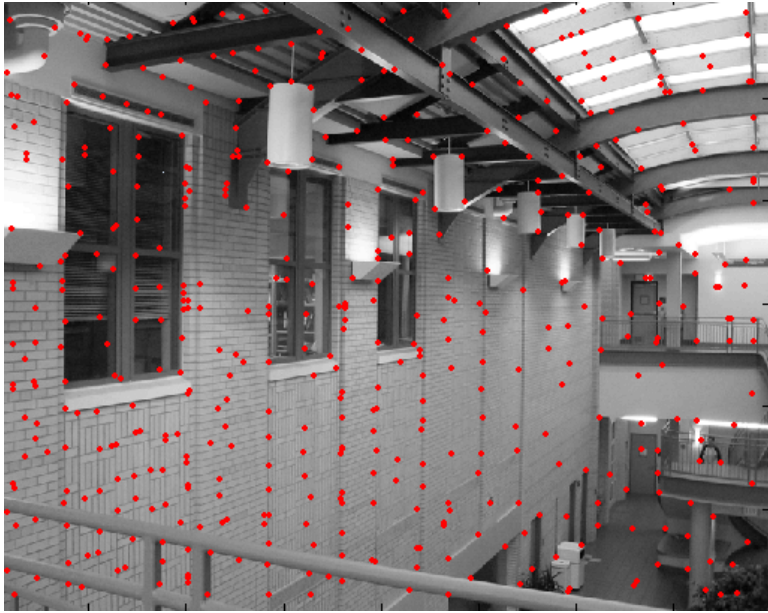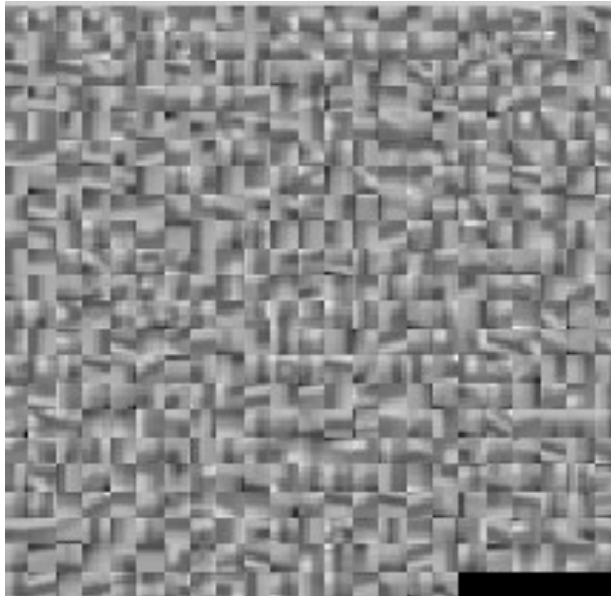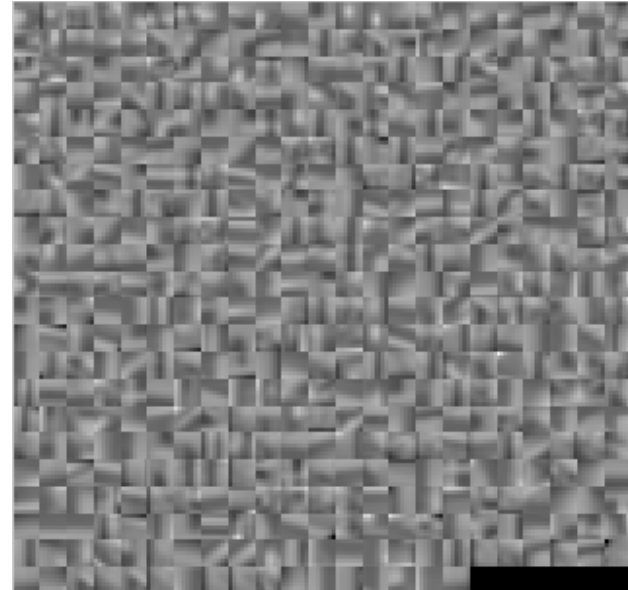# Homography

Homography

Homography

Feature matching
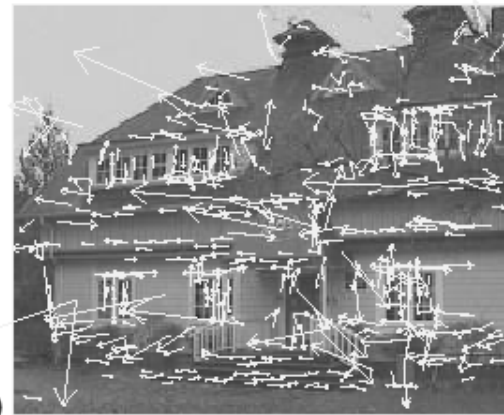

descriptors for left image feature points

descriptors for right image feature points

?

SIFT features

- Example

(a) 233x189 image
(b) 832 DOG extrema
(c) 729 left after peak value threshold
(d) 536 left after testing ratio of principle curvatures

Strategies to match images robustly

(a)<u>Working with individual features:</u>   For each feature point, find most similar point in other image (SIFT distance)

Reject ambiguous matches where there are too many similar points

(b)<u>Working with all the features:</u>   Given some good feature matches, look for possible homographies relating the two images

Reject homographies that d o n ' t have many feature matches.

# (a) 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?
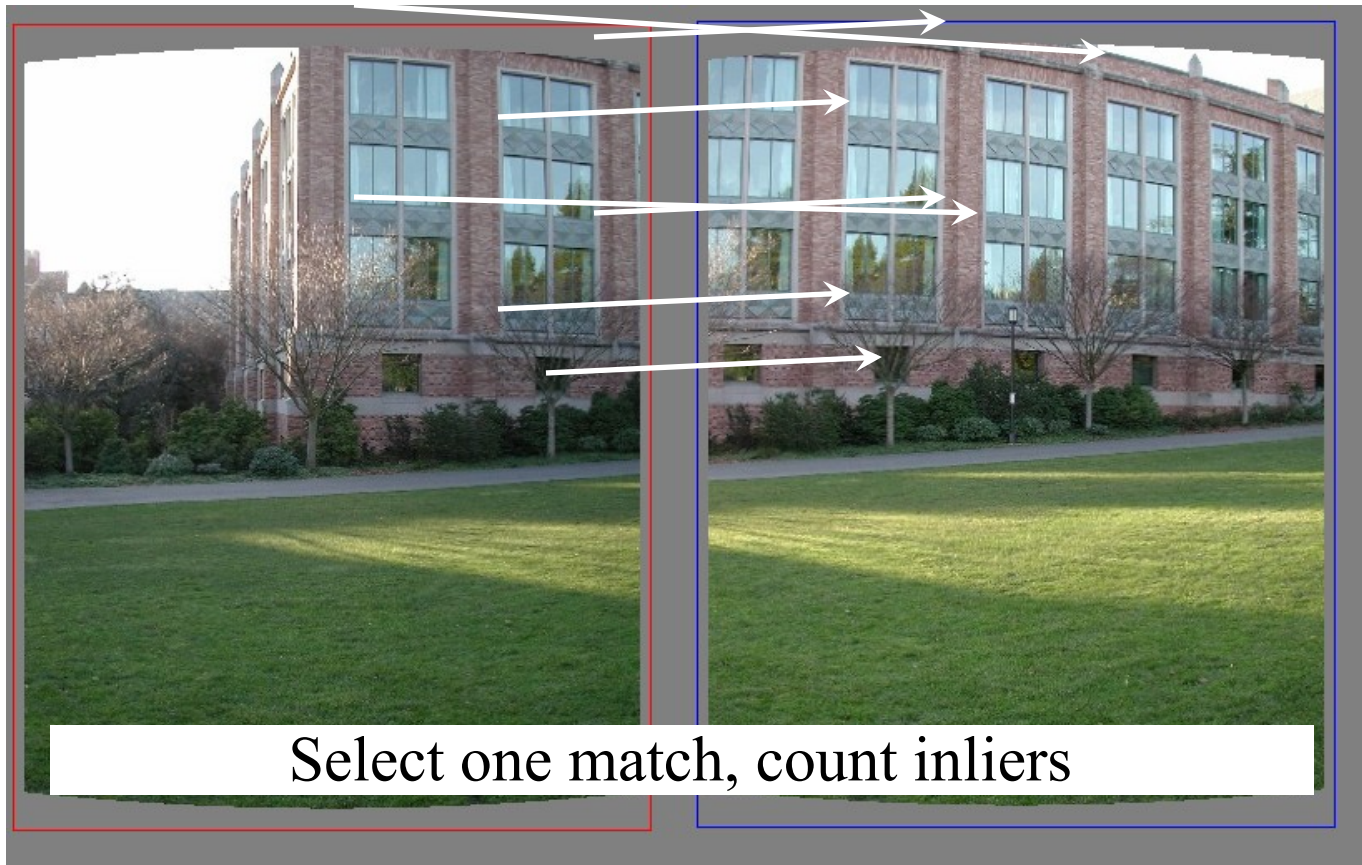   Not so easy.
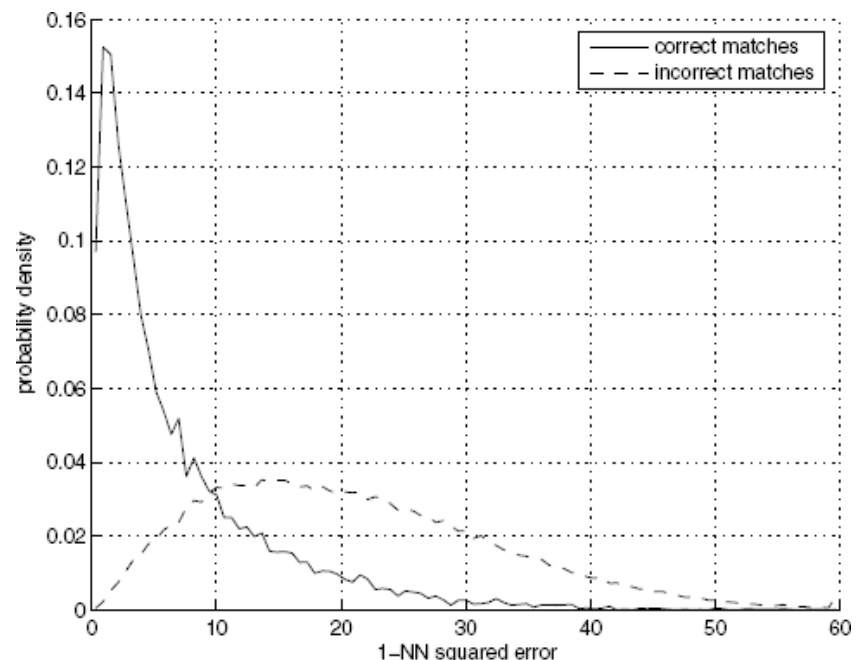
Feature-space outlier   rejection

- A better way [Lowe, 1999]:
    - 1-NN: SSD of the closest match
    - 2-NN: SSD of the <u>second-closest</u> match
    - Look at how much better 1-NN is than 2-NN, e.g. 1-NN/2-NN
    - That is, is our best match so much better than the rest?
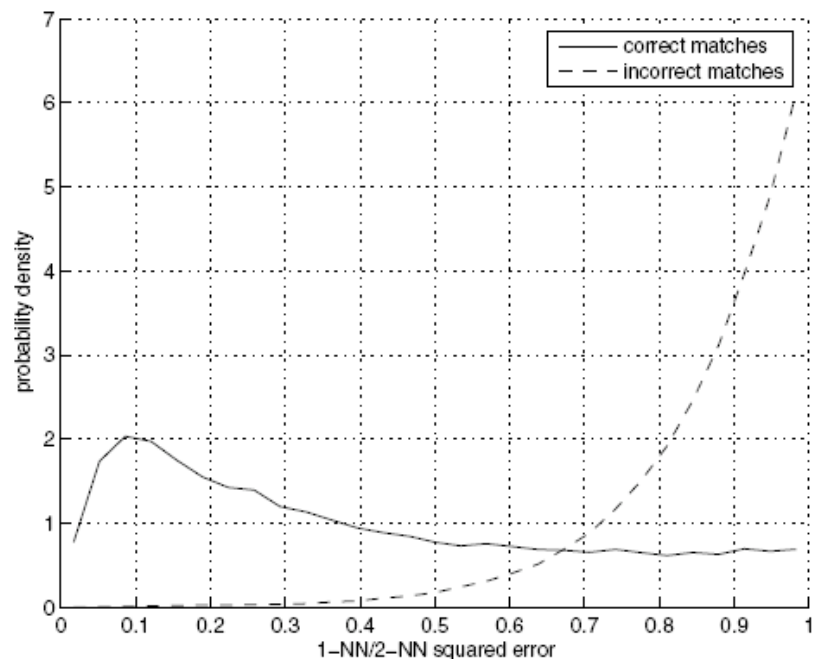
RAndom SAmple Consensus

Select one match, count inliers

RANSAC for estimating homography

RANSAC loop:

Select four feature pairs (at random)
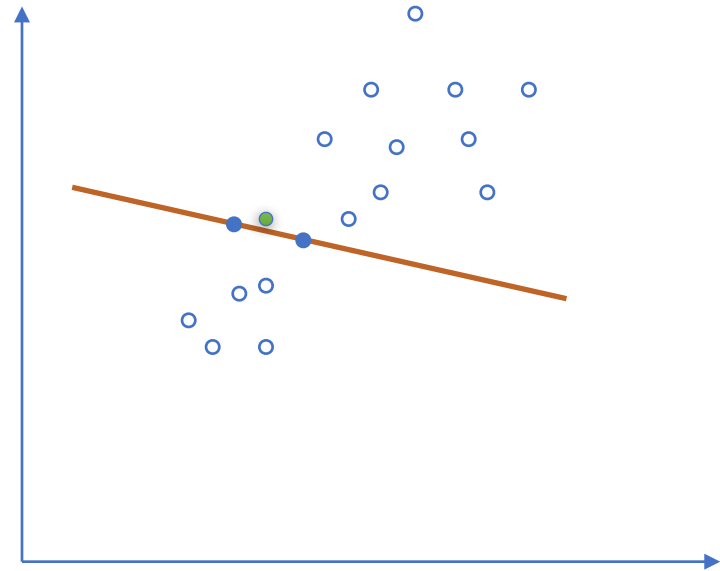
Compute homography H (exact)

Compute inliers where $||p_i', H p_i|| < \varepsilon$

Keep largest set of inliers

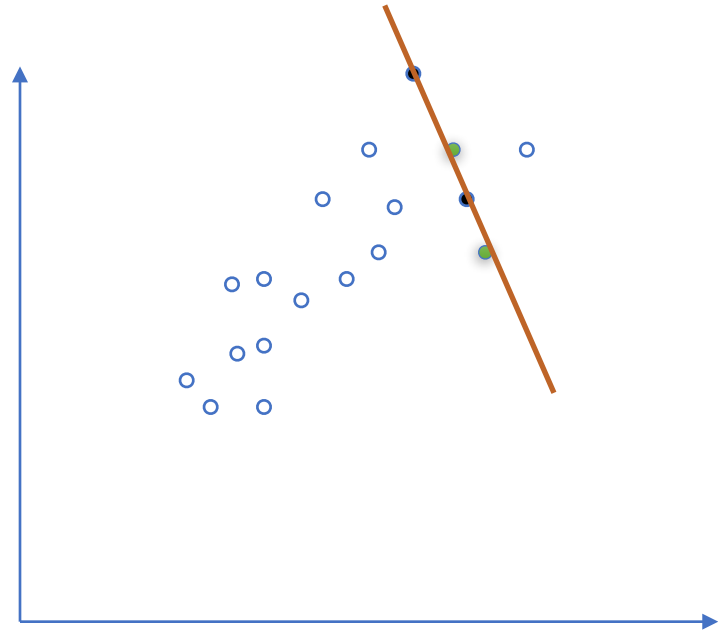Re-compute least-squares H estimate using all of the inliers

Fit a line

- Pick 2 points
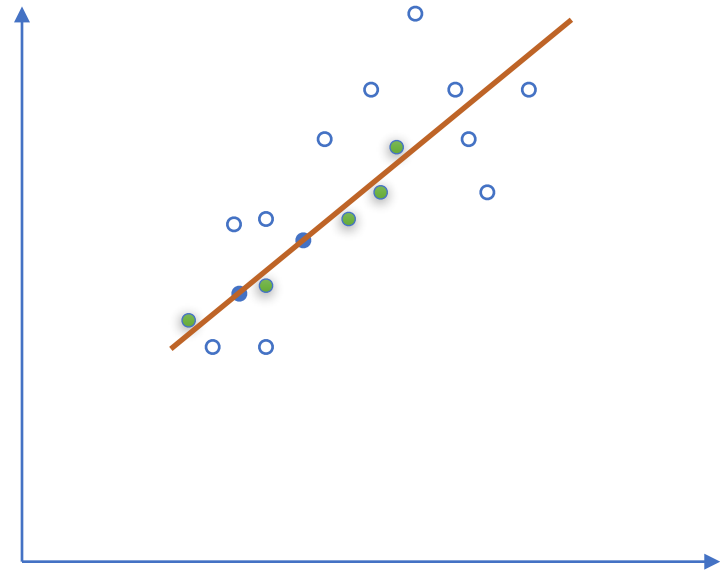- Fit line
- Count inliers (3 inliers)

Fit a line

- Pick 2 points
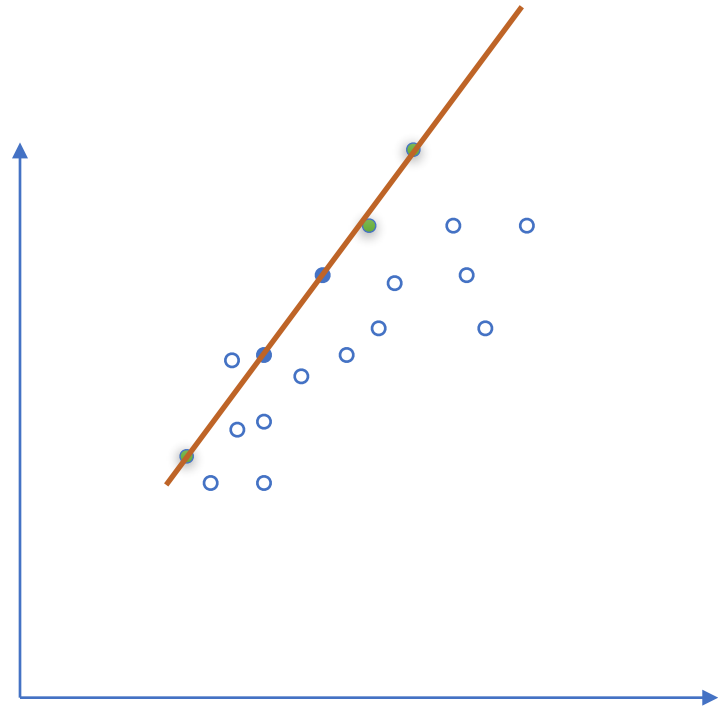- Fit line
- Count inliers (4 inliers)

Fit a line

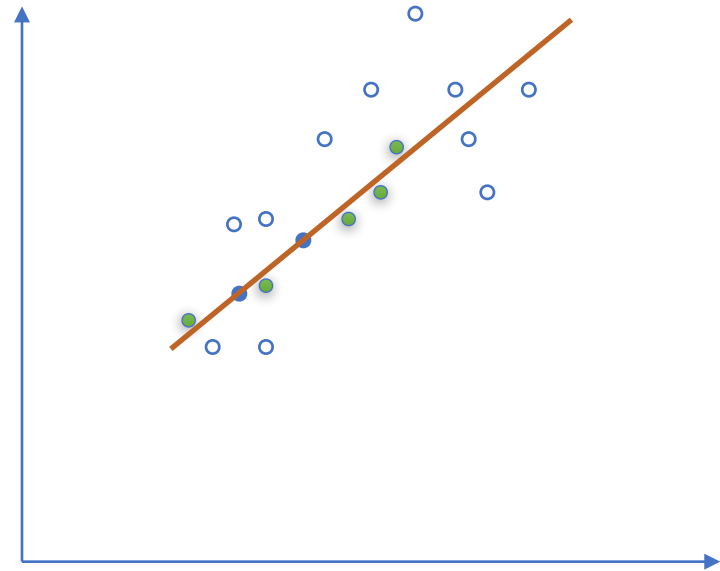- Pick 2 points
- Fit line
- Count inliers (7 inliers)

Fit a line

- Pick 2 points
- Fit line
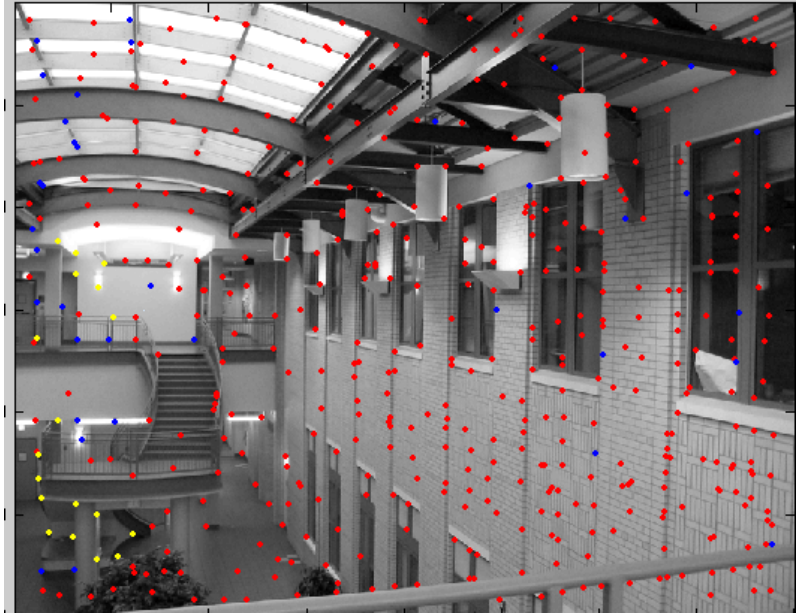- Count inliers (5 inliers)

Fit a line

- Use biggest set of inliers
- Least squares fit

RANSAC
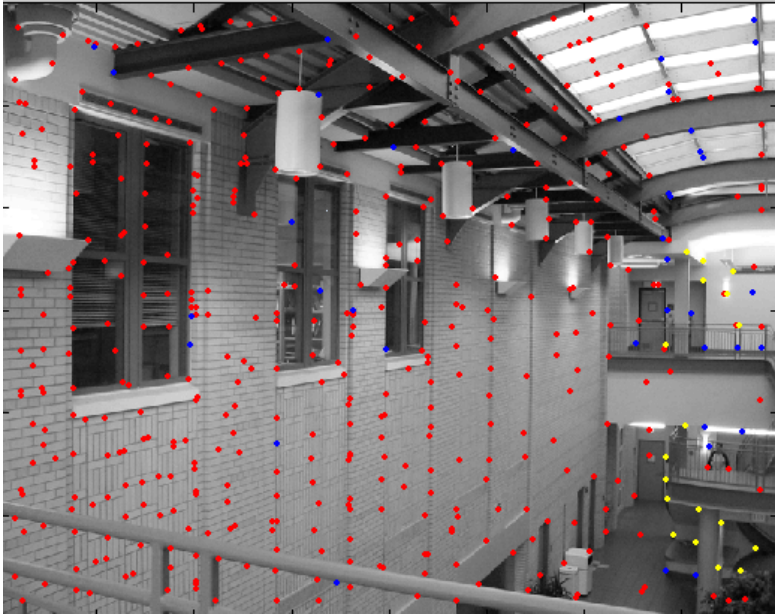
red:
rejected by 2nd nearest
neighbor criterion
blue:
Ransac outliers
yellow:
inliers

RANSAC parameters

Decision Threshold: $|X' - HX| < \epsilon$

Number of trials: N

Size of the inlier set: M

Robustness

- Proportion of inliers in our pairs is g (for "g o o d")

- Our model needs P pairs
  - P=4 for homography

- Probability that we pick P inliers?

$$g^p$$

- Probability that after N RANSAC iterations we have not picked a set of inliers?
  - $(1 - g^p)^N$

Robustness: example

- Proportion of inliers G=0.5
- Probability that we pick P=4 inliers?

$$-\,0.5^4 = 0.0625(6\,\%\ chance)$$

- Probability that we have not picked a set of inliers?

$N = 100$ iterations
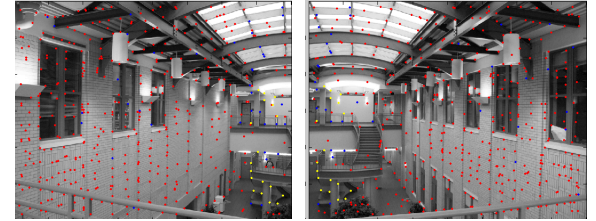
$$(1 - 0.5^4)^{100} = 0.00157(1 \text{ chance in } 600)$$

$N = 1000$ iterations

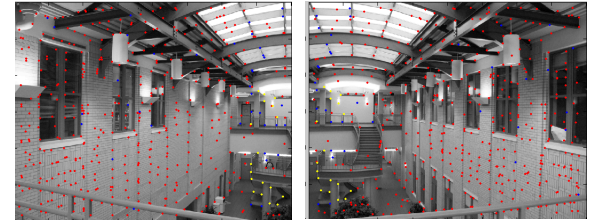$$(1 - 0.5^4)^{100} = 0.00157(1 \text{ chance in } 10^{28})$$

1 chance in 1e28

Robustness: example

- Proportion of inliers G=0.3
- Probability that we pick P=4 inliers?
  - 0.3^4=0.0081 (0.8% chance)
- Probability that we have not picked a set of inliers?
  - N=100 iterations:
    $(1-0.3^4)^{100}$=0.44 (1 chance in 2)
  - N=1000 iterations:

    1 chance in 3400

Robustness: example

- Proportion of inliers G=0.1
- Probability that we pick P=4 inliers?
  - 0.1^4=0.0001 (0.01% chances, 1 in 10,000)
- Probability that we have not picked a set of inliers?
  - N=100 iterations: $(1-0.1^4)^{100}$=0.99
  - N=1000 iterations: 90%
  - N=10,000: 36%
  - N=100,000: 1 in 22,000

Robustness: conclusions

- Effect of number of parameters of model/ number of necessary pairs
  - Bad exponential
- Effect of percentage of inliers
  - Base of the exponential
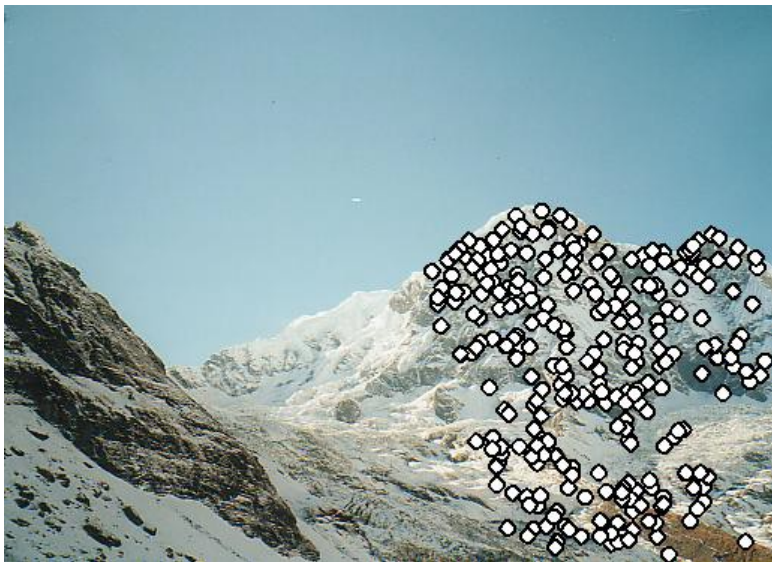- Effect of number of iterations
  - Good exponential

RANSAC recap

- For fitting a model with low number P of parameters (8 for homographies)
- Loop
  - Select P random data points
  - Fit model
  - Count inliers
    (other data points well fit by this model)
- Keep model with largest number of inliers

RANSAC for Homography

RANSAC for Homography

RANSAC for Homography