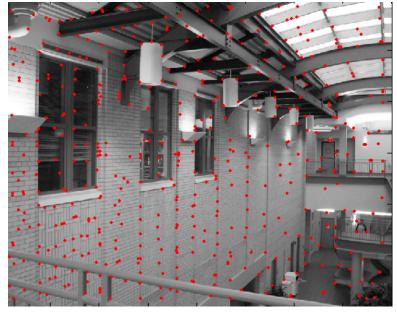
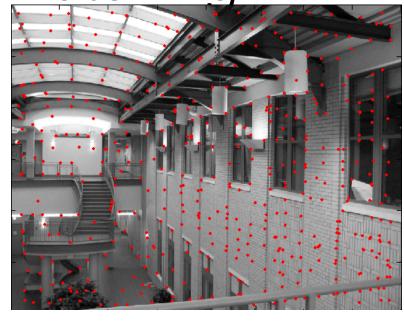
# RANSAC

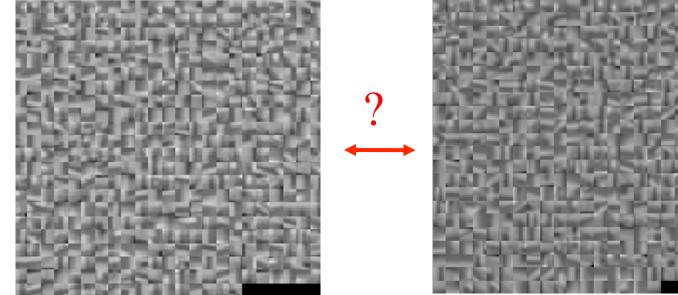
Feature matching





descriptors for left image feature points

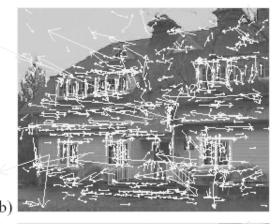
descriptors for right image feature points



### 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

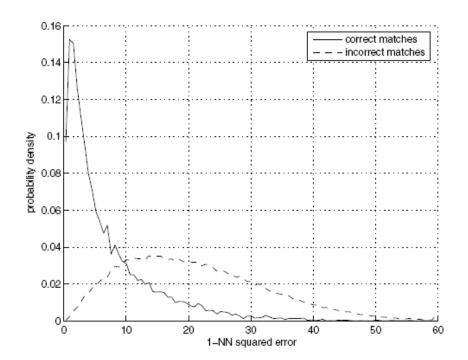
- (a) Working with individual features: For each feature point, find most similar point in other image (SIFT distance)

  Reject ambiguous matches where there are too many similar points
- (b) Working with all the features: Given some good feature matches, look for possible homographies relating the two images

Reject homographies that don't have many feature matches.

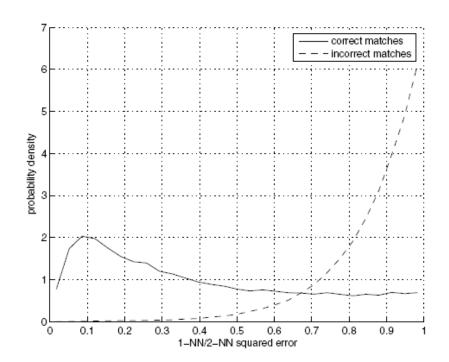
## (a) Feature-space outlier rejection

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

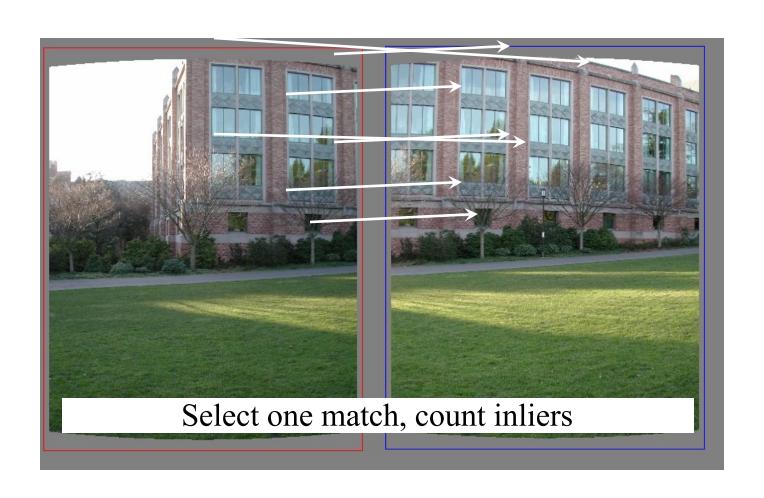


## Feature-space outlier rejection

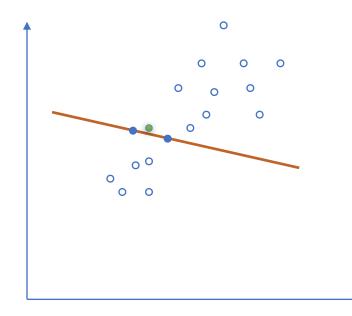
- A better way [Lowe, 1999]:
  - 1-NN: SSD of the closest match
  - 2-NN: SSD of the second-closest match
  - Look at how much better 1-NN is than 2-NN, e.g. 1-NN/2-NN
  - That is, is our best match so much better than the rest?



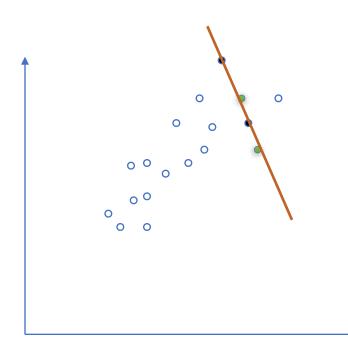
## RAndom SAmple Consensus



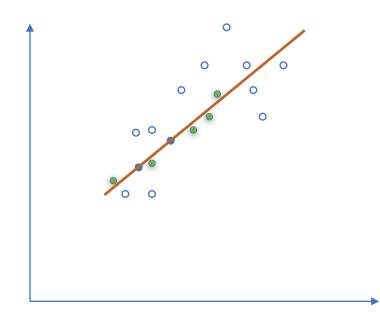
- Pick 2 points
- Fit line
- Count inliers (3 inliers)



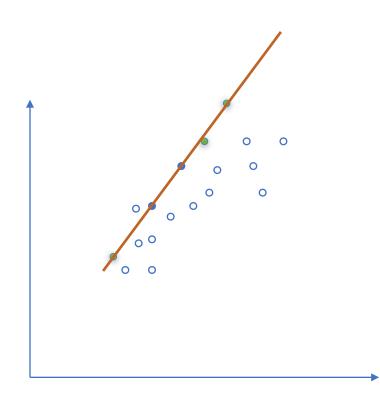
- Pick 2 points
- Fit line
- Count inliers (4 inliers)



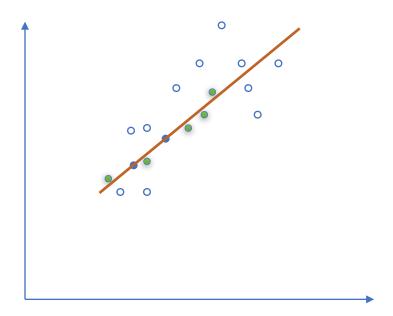
- Pick 2 points
- Fit line
- Count inliers (7 inliers)



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



- Use biggest set of inliers
- Least squares fit



# RANSAC for estimating homography

```
Determine:
    n—the smallest number of points required (e.g., for lines, n=2,
      for circles, n = 3) n=8 for homography
    k—the number of iterations required
    t—the threshold used to identify a point that fits well
    d—the number of nearby points required Size of Inlier set
      to assert a model fits well
Until k iterations have occurred
    Draw a sample of n points from the data
      uniformly and at random
    Fit to that set of n points
                                    Compute homography, H
    For each data point outside the sample
                                                             Decision Threshold: |p' - Hp| < t
      Test the distance from the point to the structure
         against t; if the distance from the point to the structure
        is less than t, the point is close
    end
    If there are d or more points close to the structure
      then there is a good fit. Refit the structure using all
      these points. Add the result to a collection of good fits.
end
Use the best fit from this collection, using the
 fitting error as a criterion
```

Algorithm 10.4: RANSAC: Fitting Structures Using Random Sample Consensus.

#### Forsyth & Ponce

# RANSAC for estimating homography

RANSAC loop:

Select four feature pairs (at random)

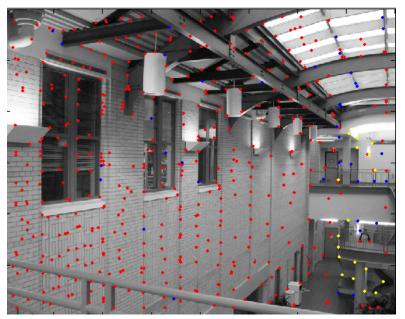
Compute homography H (exact)

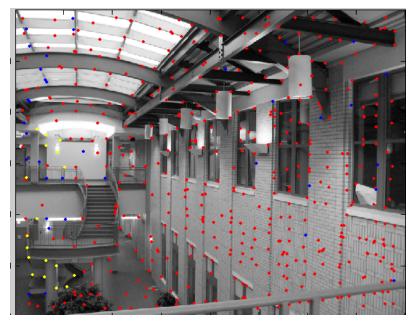
Compute inliers where ||p'-Hp|| < t

Keep largest set of inliers

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

## RANSAC





red:

rejected by 2nd nearest neighbor criterion

blue:

Ransac outliers

yellow:

inliers



### Robustness

- Proportion of inliers in our pairs is g (for "good")
- Our model needs n pairs
  - -n = 4 for homography
- Probability that we pick n inliers?  $g^n$
- Probability that after k RANSAC iterations we have not picked a set of inliers?

$$- (1 - g^n)^k$$

## Robustness: example

- Proportion of inliers g=0.5
- Probability that we pick n=4 inlier pairs?

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

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

```
k = 100 iterations  (1 - 0.5^4)^{100} = 0.00157(1 \text{ chance in } 600)   k = 1000 \text{ iterations}   (1 - 0.5^4)^{100} = 0.00157(1 \text{ chance in } 10^{28})
```

## Robustness: example

• Proportion of inliers g=0.3





- Probability that we pick n=4 inlier pairs?
  - $-0.3^4 = 0.0081 (0.8\% \text{ chance})$
- Probability that we have not picked a set of inliers?
  - -k=100 iterations:  $(1-0.3^4)^{100} = 0.44(1 \text{ chance in 2})$
  - $-k=1000 iterations: (1-0.3^4)^{1000} \rightarrow (1 chance in 3400)$

## Robustness: example

• Proportion of inliers g=0.1





- Probability that we pick n=4 inlier pairs?
  - $-0.1^4 = 0.0001(0.01\% \text{ chances}, 1 \text{ in} 10,000)$
- Probability that we have not picked a set of inliers?
  - -k=100 iterations:  $(1-0.14)^{100}=0.99$
  - -k=1000 iterations: 90%
  - -k=10,000:36%
  - -k=100,000: 1 in 22,000

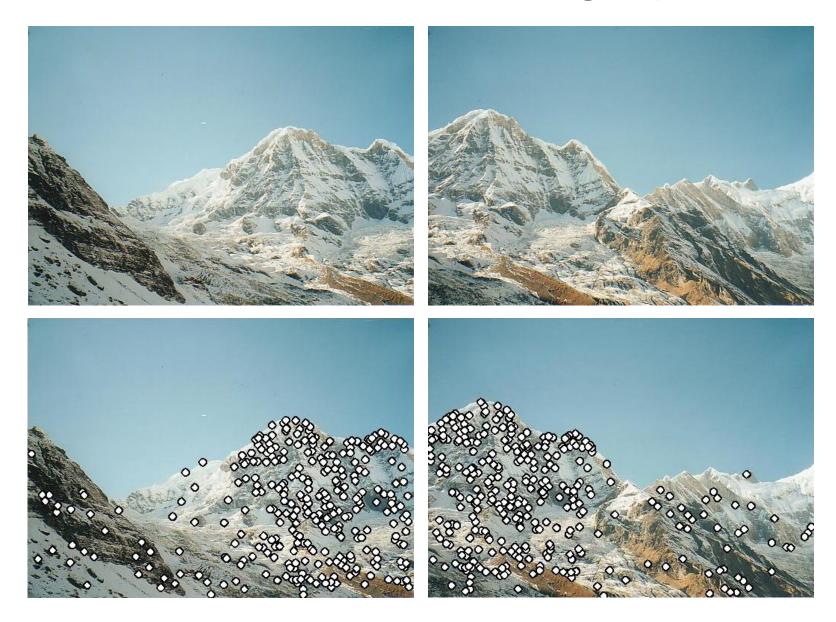
### Robustness: conclusions

- 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

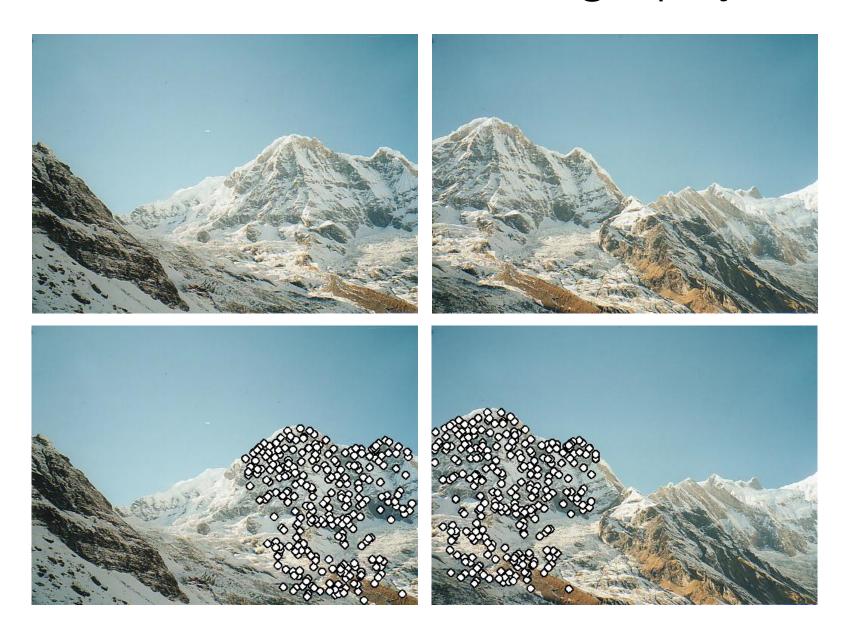
## RANSAC recap

- For fitting a model with low number n of parameters (4 pairs for homographies)
- Loop
  - Select n 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

