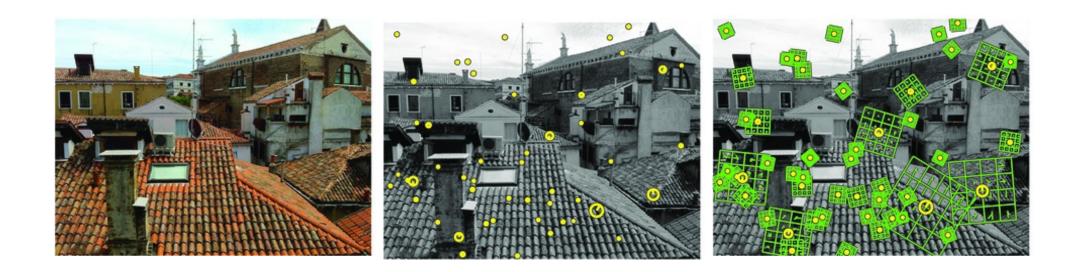


#### THE UNIVERSITY OF BRITISH COLUMBIA

# **CPSC 425: Computer Vision**



#### **Lecture 14:** Planar Geometry and RANSAC

## Menu for Today

### **Topics:**

- **Planar** Geometry
- Image Alignment, Object Recognition

### **Readings:**

- Today's Lecture: Szeliski 2.1, 8.1, Forsyth & Ponce 10.4.2

### **Reminders:**

- Assignment 3: due tonight
- Photos at the end of the class today



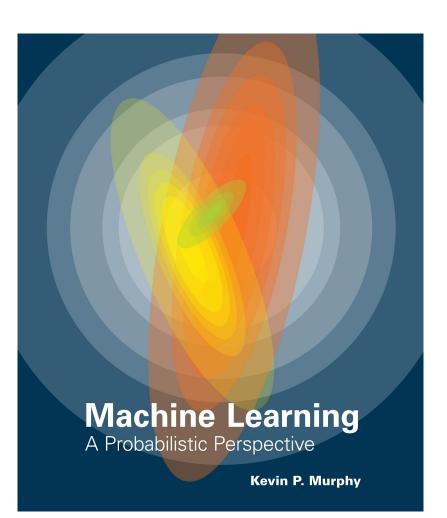
# Assignment 4: RANSAC and Panorama Stitching — available tonight



### ICCV 2015 paper by Kevin Murphy

(UBC's former faculty)





Coincidently Kevin is also author of one of the most prominent ML books

| <i>Step1:</i><br>Image Acquisition       | Top View                                 | Side View                            |
|--|--|--------------------------------------|
| <i>Step2:</i><br>Object Detection        |  |                                      |
| <i>Step3:</i><br>Image Segmenta-<br>tion |  |                                      |
| Step4:<br>Volume Estimation              | apple:<br>V=311.6 <i>cm</i> <sup>3</sup> | qiwi:<br>V=135.7 <i>cm</i> ³         |
| <i>Step5:</i><br>Calorie Estimation      |  | apple: 126.857Kc<br>qiwi: 80.297Kcal |

Figure 1: Calorie Estimation Flowchart



#### Im2Calories: towards an automated mobile vision food diary

Austin Myers, Nick Johnston, Vivek Rathod, Anoop Korattikara, Alex Gorban Nathan Silberman, Sergio Guadarrama, George Papandreou, Jonathan Huang, Kevin Murphy amyers@umd.edu, (nickj, rathodv, kbanoop, gorban)@google.com (nsilberman, sguada, gpapan, jonathanhuang, kpmurphy)@google.com

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### Fun **on-line demo**: <u>http://www.caloriemama.ai/api</u>

Keypoint is an image location at which a descriptor is computed

- Locally distinct points
- Easily localizable and identifiable

#### Locally distinct



Locally non-distinct

**Keypoint** is an image location at which a descriptor is computed

- Locally distinct points
- Easily localizable and identifiable

The feature **descriptor** summarizes the local structure around the key point

- Allows us to (hopefully) unique matching of keypoints in presence of object pose variations, image and photometric deformations

#### Locally distinct



Locally non-distinct

**Keypoint** is an image location at which a descriptor is computed

- Locally distinct points
- Easily localizable and identifiable
- The feature **descriptor** summarizes the local structure around the key point
- Allows us to (hopefully) unique matching of keypoints in presence of object pose variations, image and photometric deformations

Note, for repetitive structure this would still not give us unique matches.

#### Locally distinct



- We motivated SIFT for identifying locally distinct keypoints in an image (detection)

robust to 3D pose and illumination

2. Keypoint localization

3. Orientation assignment

4. Keypoint descriptor

- SIFT features (**description**) are invariant to translation, rotation, and scale;

- 1. Multi-scale extrema detection

## Lecture 13: Re-Cap Four steps to SIFT feature generation:

### 1. Scale-space representation and local extrema detection

- Use DoG pyramid Output: (x, y, s) for each keypoint
- 3 scales/octave, down-sample by factor of 2 each octave



## Lecture 13: Re-Cap Four steps to SIFT feature generation:

1. Scale-space representation and local extrema detection

- Use DoG pyramid Output: (x, y, s) for each keypoint
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- 2. Keypoint localization
  - principal curvatures)

### - select stable keypoints (threshold on magnitude of extremum, ratio of

Output: Remove some (weak) keypoints



# Lecture 13: Re-Cap Four steps to SIFT feature generation:

- 1. Scale-space representation and local extrema detection
  - Use DoG pyramid Output: (x, y, s) for each keypoint
  - 3 scales/octave, down-sample by factor of 2 each octave
- 2. Keypoint localization
  - principal curvatures)
- 3. Keypoint orientation assignment based on histogram of local image gradient directions

### - select stable keypoints (threshold on magnitude of extremum, ratio of

Output: Remove some (weak) keypoints

**Output:** Orientation for each keypoint



# Lecture 13: Re-Cap Four steps to SIFT feature generation: 1. Scale-space representation and local extrema detection

- Use DoG pyramid Output: (x, y, s) for each keypoint
- 3 scales/octave, down-sample by factor of 2 each octave
- 2. Keypoint localization
  - principal curvatures) Output: Remove some (weak) keypoints
- 3. Keypoint orientation assignment
  - based on histogram of local image gradient directions
- 4. Keypoint descriptor

  - vector normalized (to unit length)

### - select stable keypoints (threshold on magnitude of extremum, ratio of

Output: Orientation for each keypoint

### — histogram of local gradient directions — vector with $8 \times (4 \times 4) = 128$ dim

**Output:** 128D normalized vector characterizing the keypoint region



## **Lecture 13**: Histogram of Oriented Gradients (HOG)

#### 1 cell step size

### Pedestrian detection

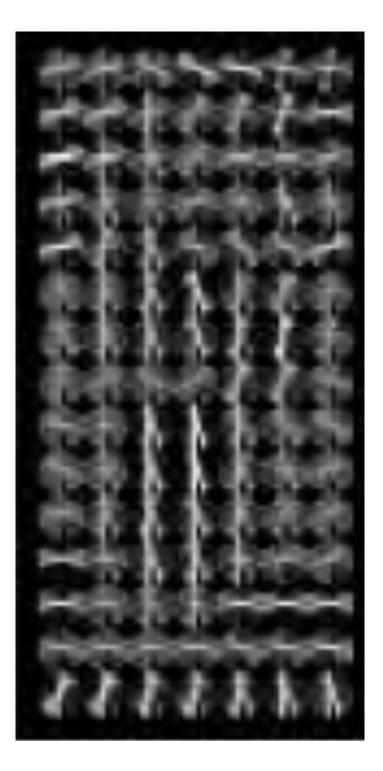
128 pixels 16 cells 15 blocks



64 pixels 8 cells 7 blocks

Redundant representation due to overlapping blocks

#### visualization



 $15 \times 7 \times 4 \times 9 =$ 3780



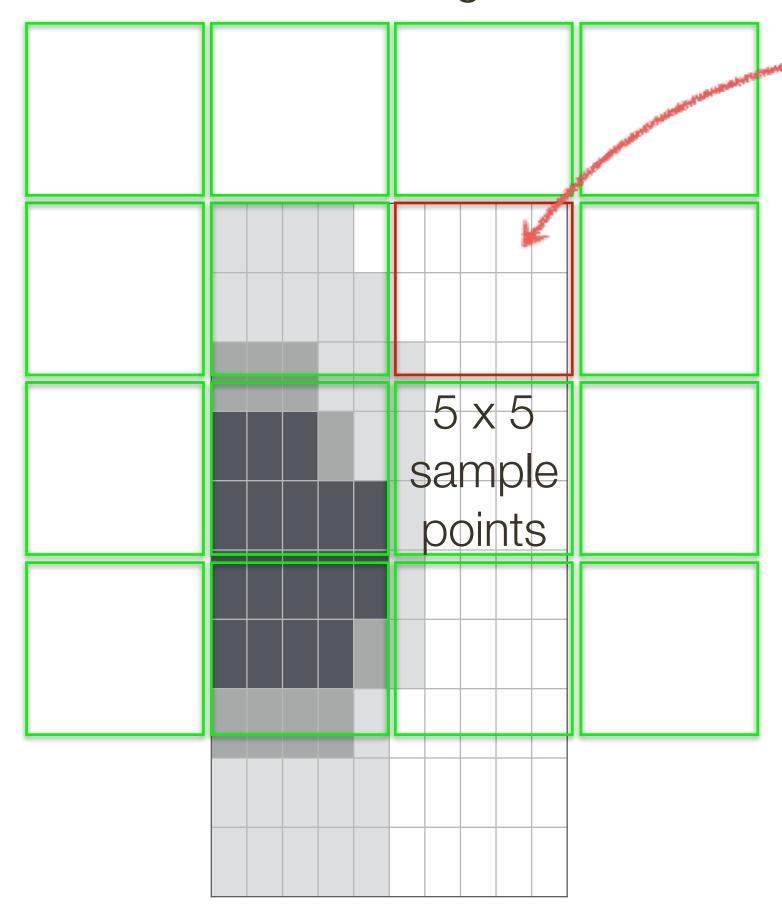
**Slide Credit**: Ioannis (Yannis) Gkioulekas (CMU)





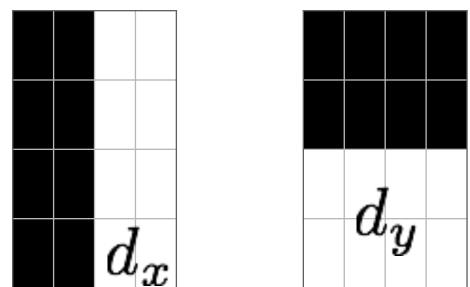
## Lecture 13: 'Speeded' Up Robust Features

4 x 4 cell grid



### Each cell is represented by 4 values: $\left[\sum d_x, \sum d_y, \sum |d_x|, \sum |d_y|\right]$

Haar wavelets filters (Gaussian weighted from center)



### How big is the SURF descriptor? 64 dimensions

**Slide Credit**: Ioannis (Yannis) Gkioulekas (CMU)



## Lecture 13: Summary

| Keypoint Detection<br>Algorithms | Representation | Keypoint Description<br>Algorithms | Representation |
|----------------------------------|----------------|------------------------------------|----------------|
| Harris Corners                   | (x,y,s)        | SIFT                               | 128D           |
| LoG / Blobs                      | (x,y,s)        | Histogram of Oriented<br>Gradients | 3780D          |
| SIFT                             | (x,y,s,theta)  | SURF                               | 64D            |



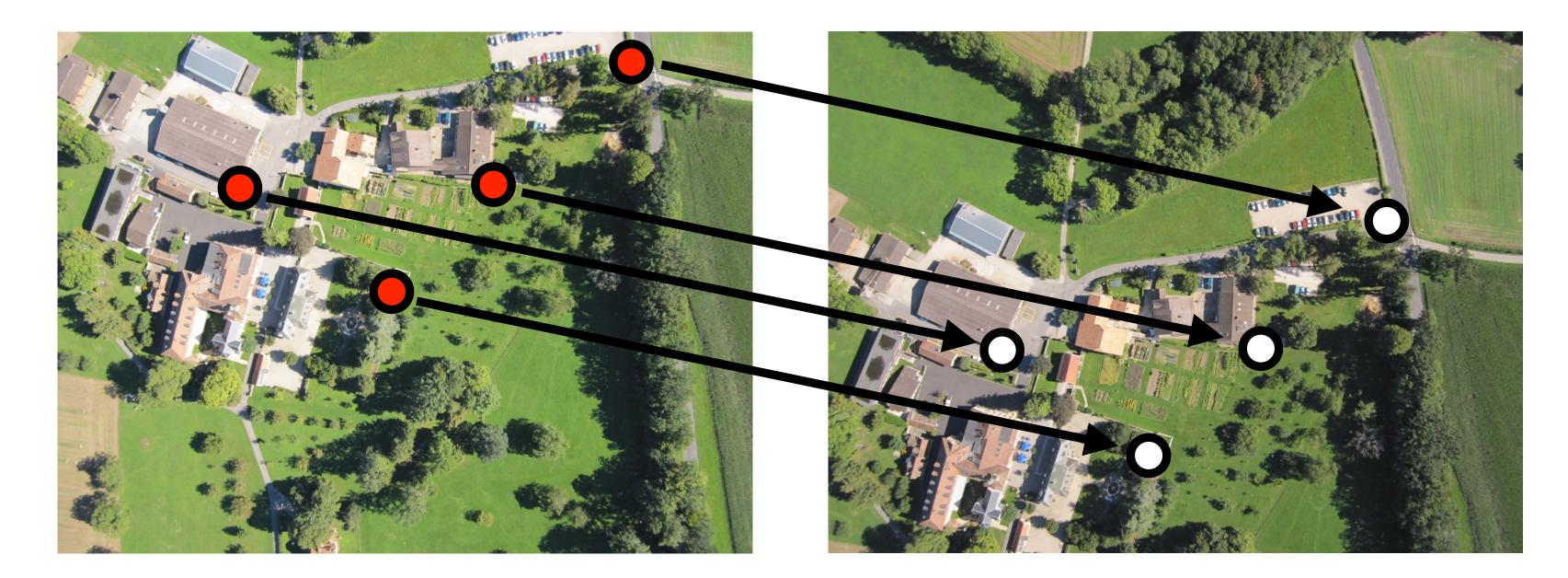
### Aim: Warp one image to align with another



Aim: Warp one image to align with another <u>using a 2D transformation</u>



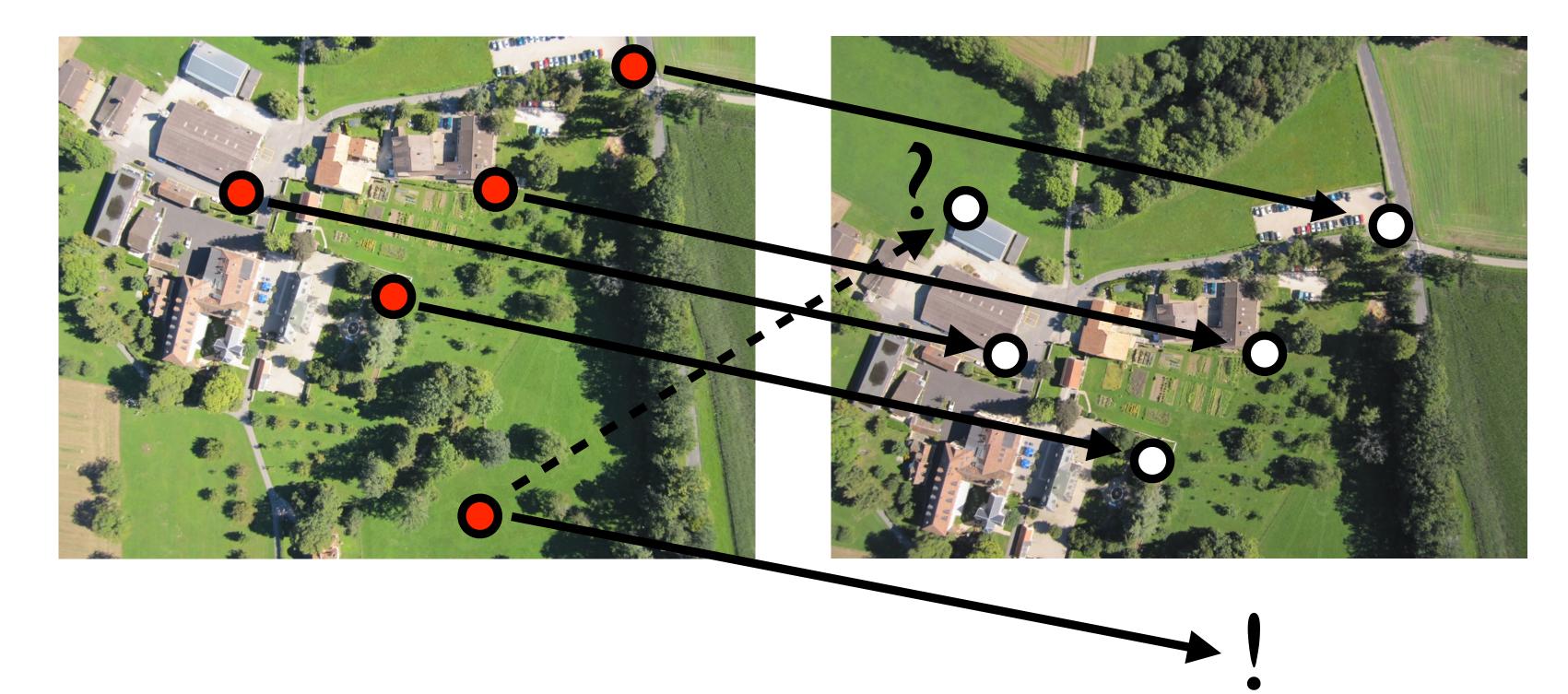
### Step 1: Find correspondences (matching points) across two images



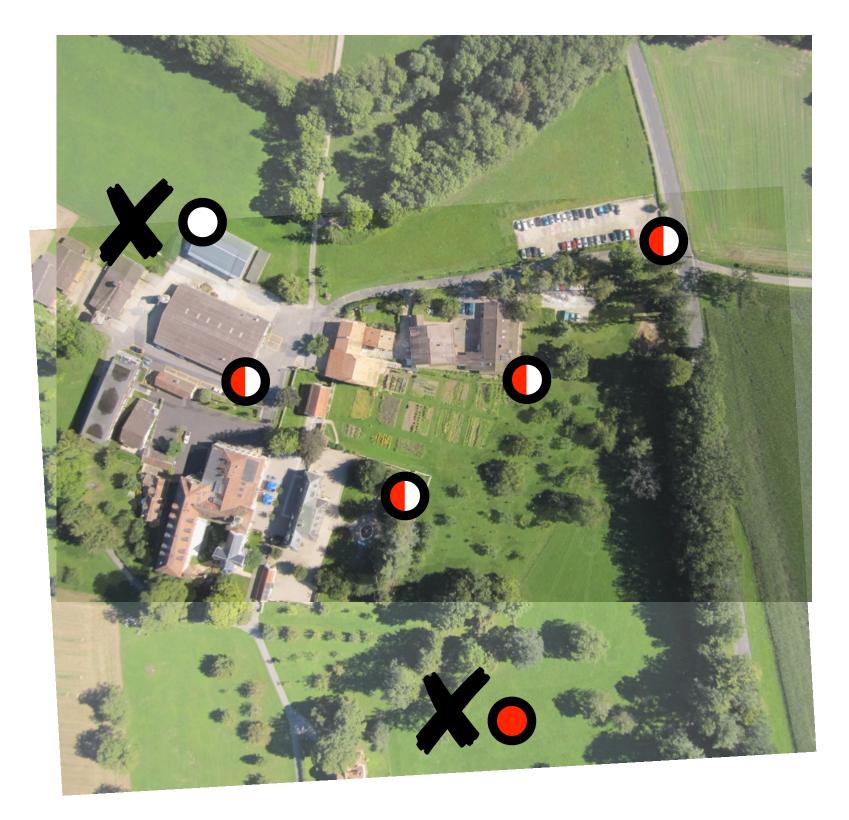
Step 2: Compute the transformation to align the two images



### Not all points will match across two images, we can also reject outliers



Not all points will match across two images, we can also reject outliers



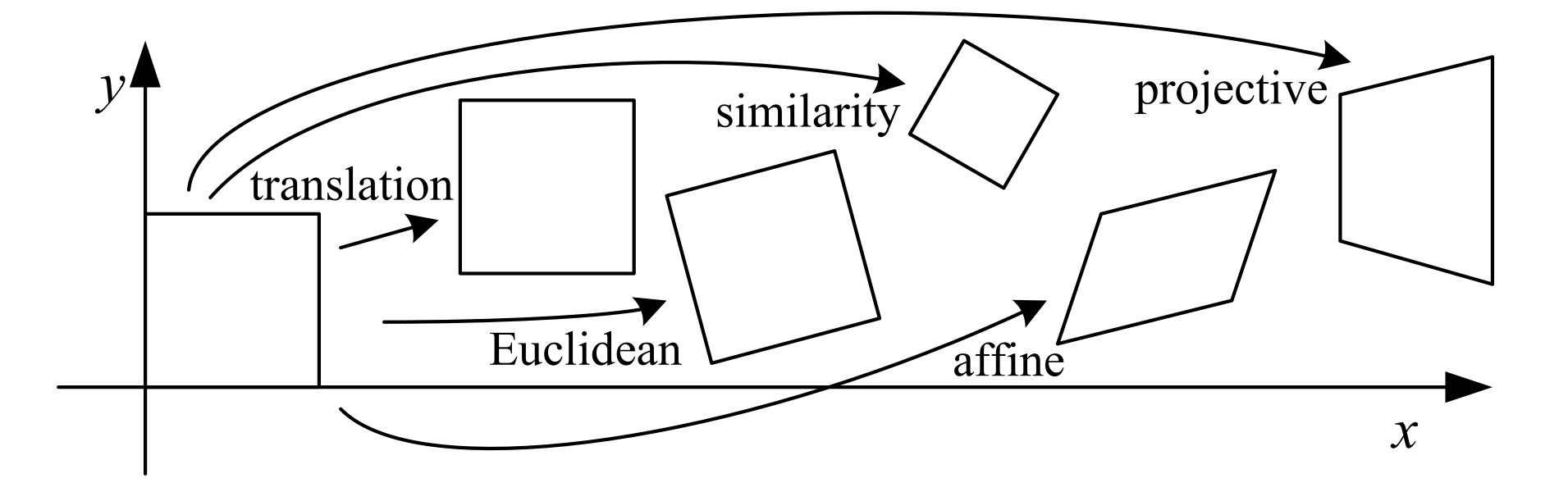
## **Planar** Geometry

- 2D Linear + **Projective** transformations Euclidean, Similarity, Affine, Homography

### Robust Estimation and RANSAC Estimating 2D transforms with noisy correspondences

## 2D Transformations

— We will look at a family that can be represented by 3x3 matrices



This group represents perspective projections of planar surfaces

## **Affine** Transformation

- Transformed points are a linear function of the input points

$$\begin{bmatrix} x' \\ y' \end{bmatrix} = \begin{bmatrix} a_{11} \\ a_{21} \end{bmatrix}$$

$$\begin{array}{c} a_{12} \\ a_{22} \end{array} \begin{bmatrix} x \\ y \end{bmatrix} + \begin{bmatrix} a_{13} \\ a_{23} \end{bmatrix}$$

## Affine Transformation

### - Transformed points are a linear function of the input points

$$\begin{bmatrix} x' \\ y' \end{bmatrix} = \begin{bmatrix} a_{11} \\ a_{21} \end{bmatrix}$$

# This can be written as a single matrix multiplication using homogeneous coordinates

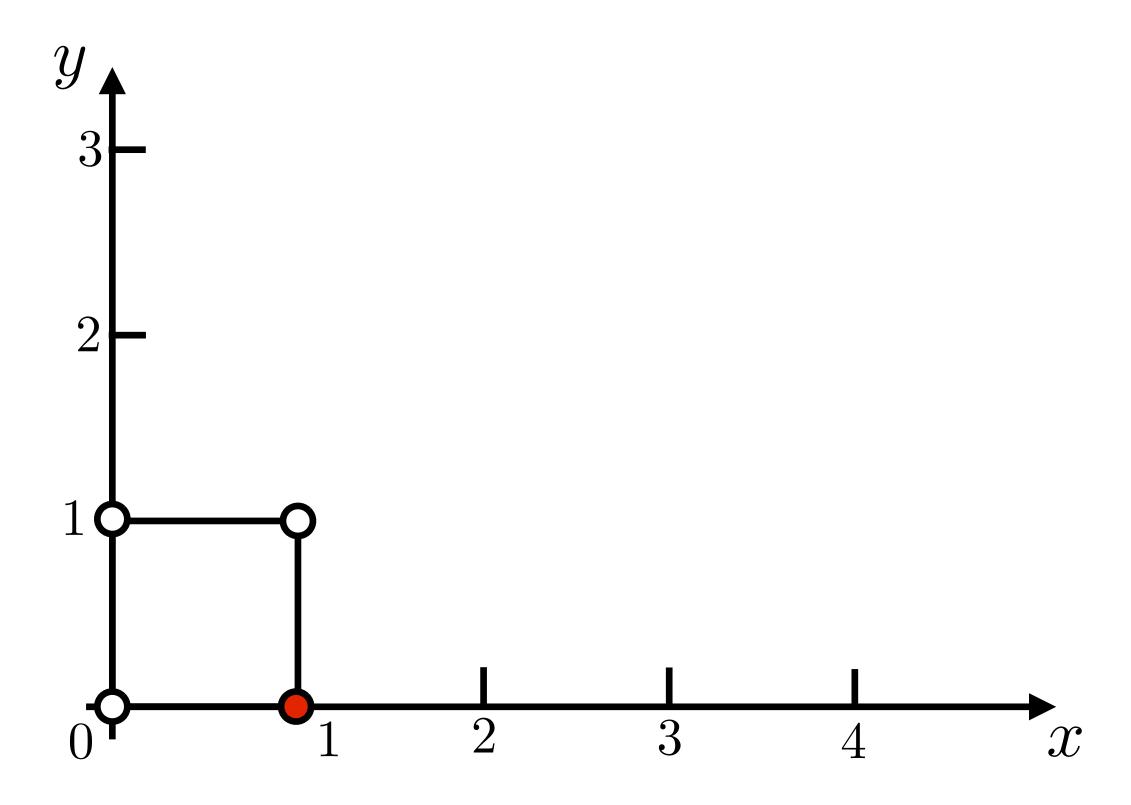
$$\begin{bmatrix} x'_1 \\ y'_1 \\ 1 \end{bmatrix} = \begin{bmatrix} a_{11} \\ a_{21} \\ 0 \end{bmatrix}$$

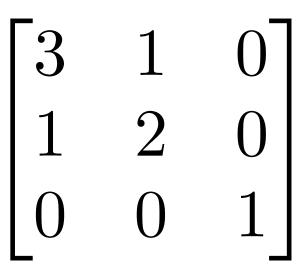
$$\begin{array}{c} a_{12} \\ a_{22} \end{array} \begin{bmatrix} x \\ y \end{bmatrix} + \begin{bmatrix} a_{13} \\ a_{23} \end{bmatrix}$$

$$\begin{array}{ccc} a_{12} & a_{13} \\ a_{22} & a_{23} \\ 0 & 1 \end{array} \begin{bmatrix} x_1 \\ y_1 \\ 1 \end{bmatrix}$$

## **Linear** Transformation

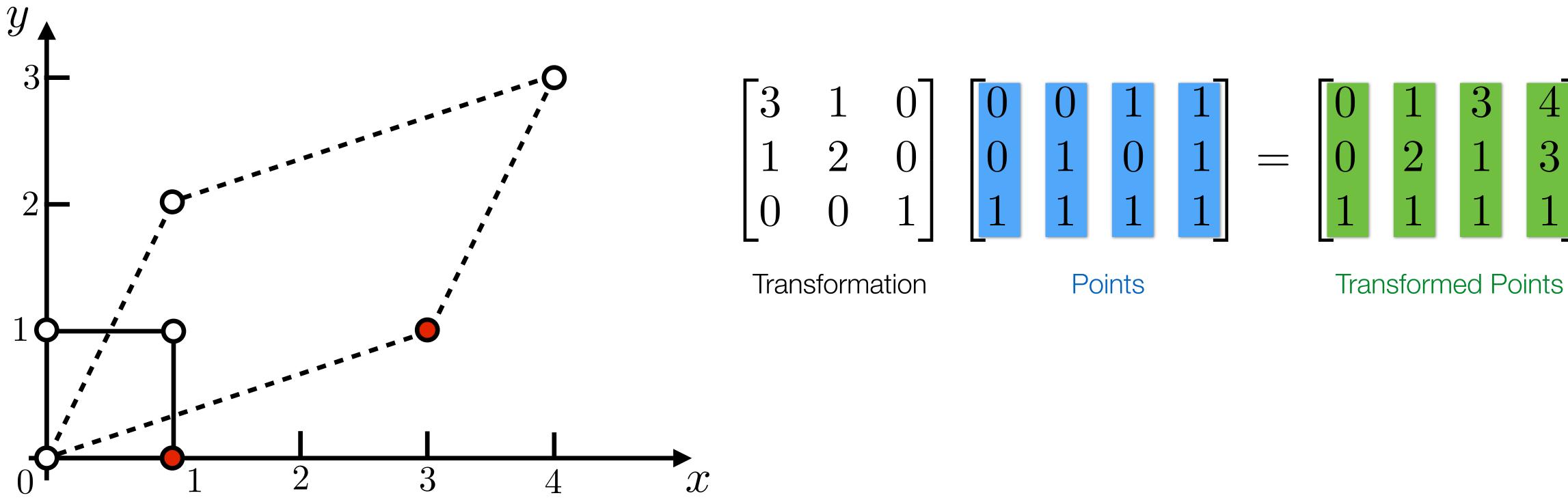
- Consider the action of the unit square under, sample transform  $\begin{bmatrix} 3 & 1 & 0 \\ 1 & 2 & 0 \\ 0 & 0 & 1 \end{bmatrix}$ 

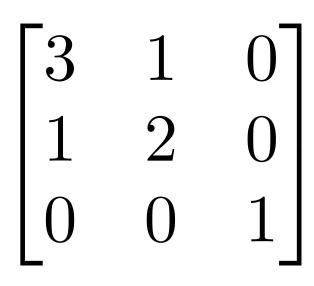




## Linear Transformation

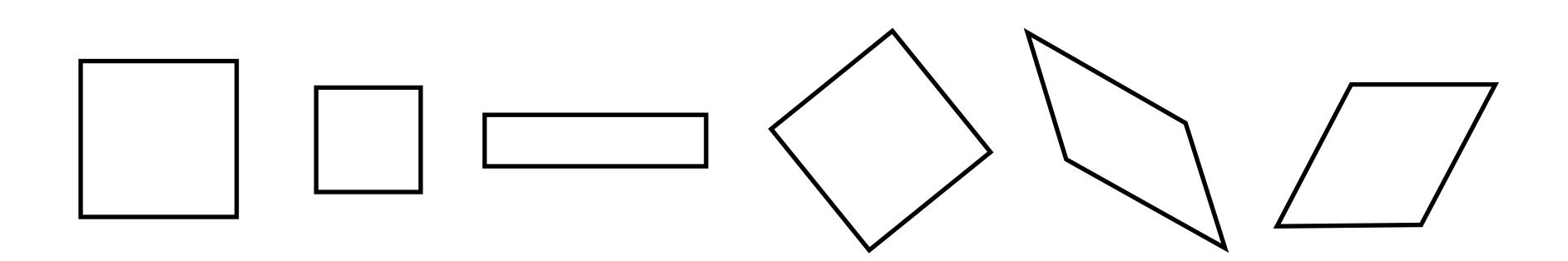
Consider the action of the unit square under, sample transform



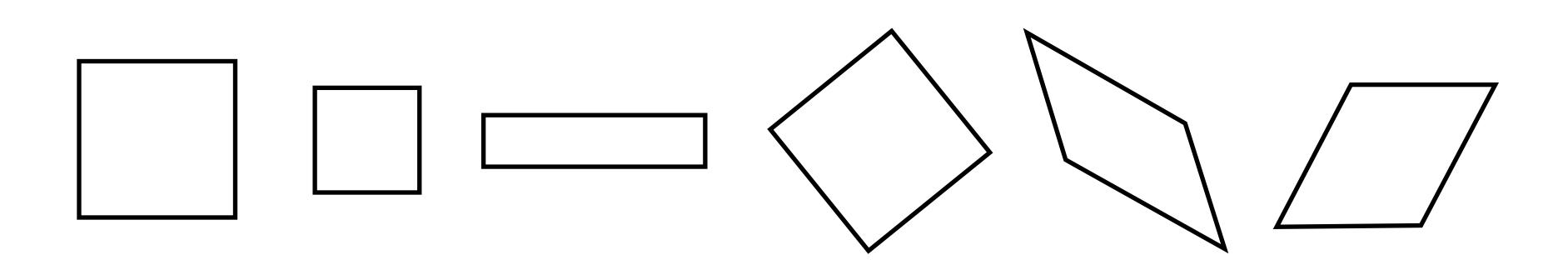


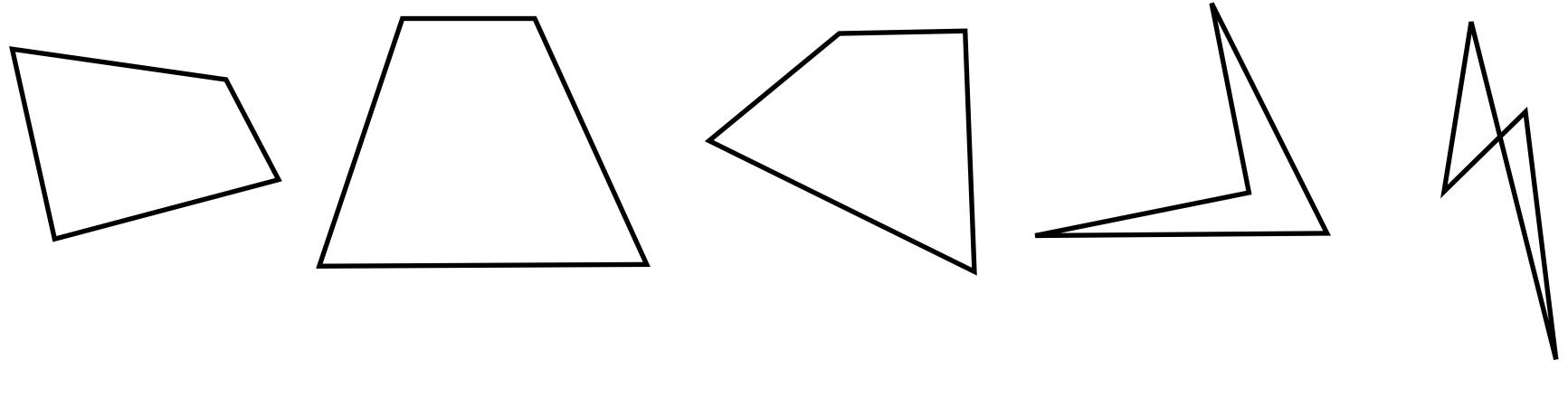






Translation, rotation, scale, shear (parallel lines preserved)



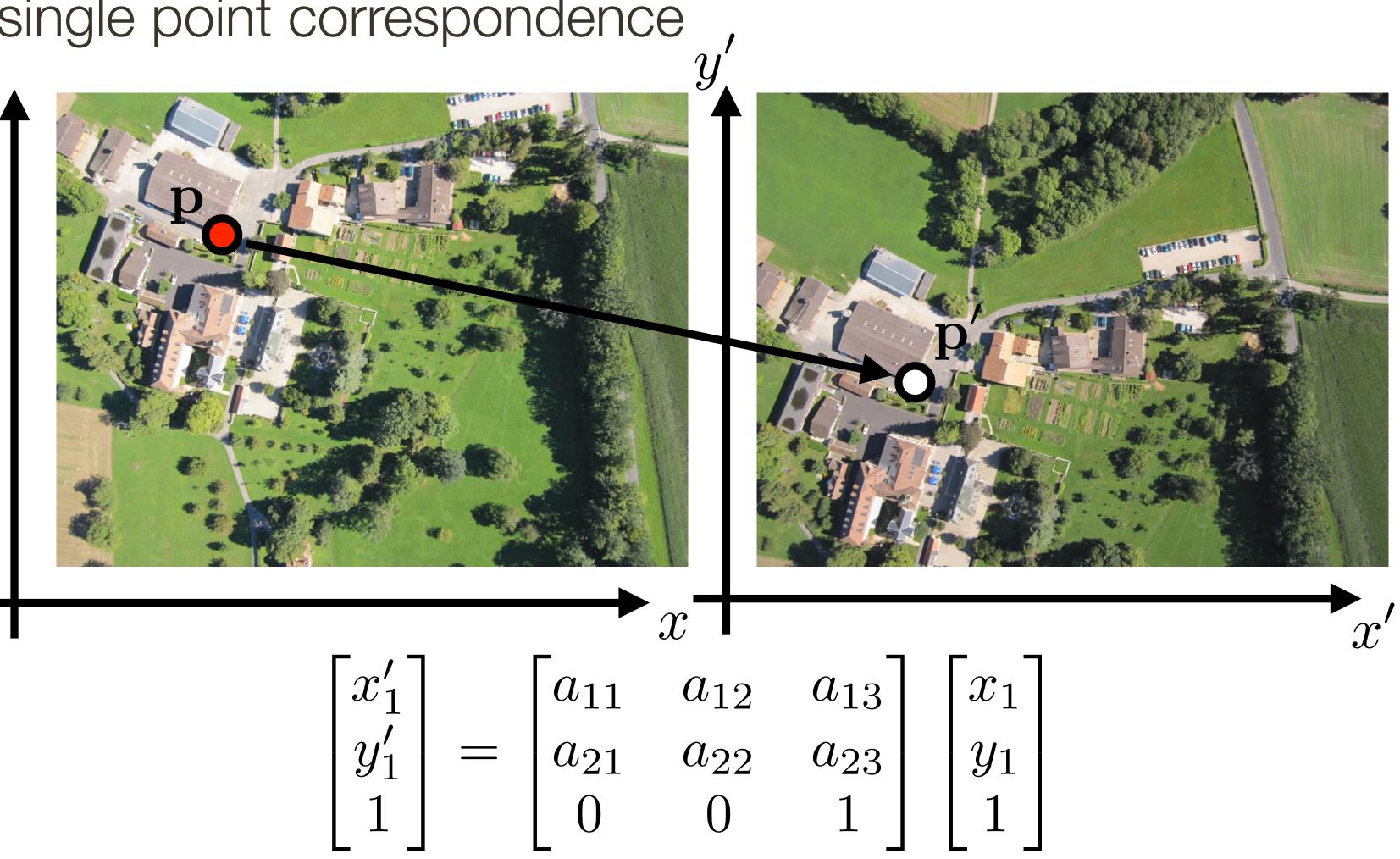


Translation, rotation, scale, shear (parallel lines preserved)

These transforms are not affine (parallel lines not preserved)

### Consider a single point correspondence

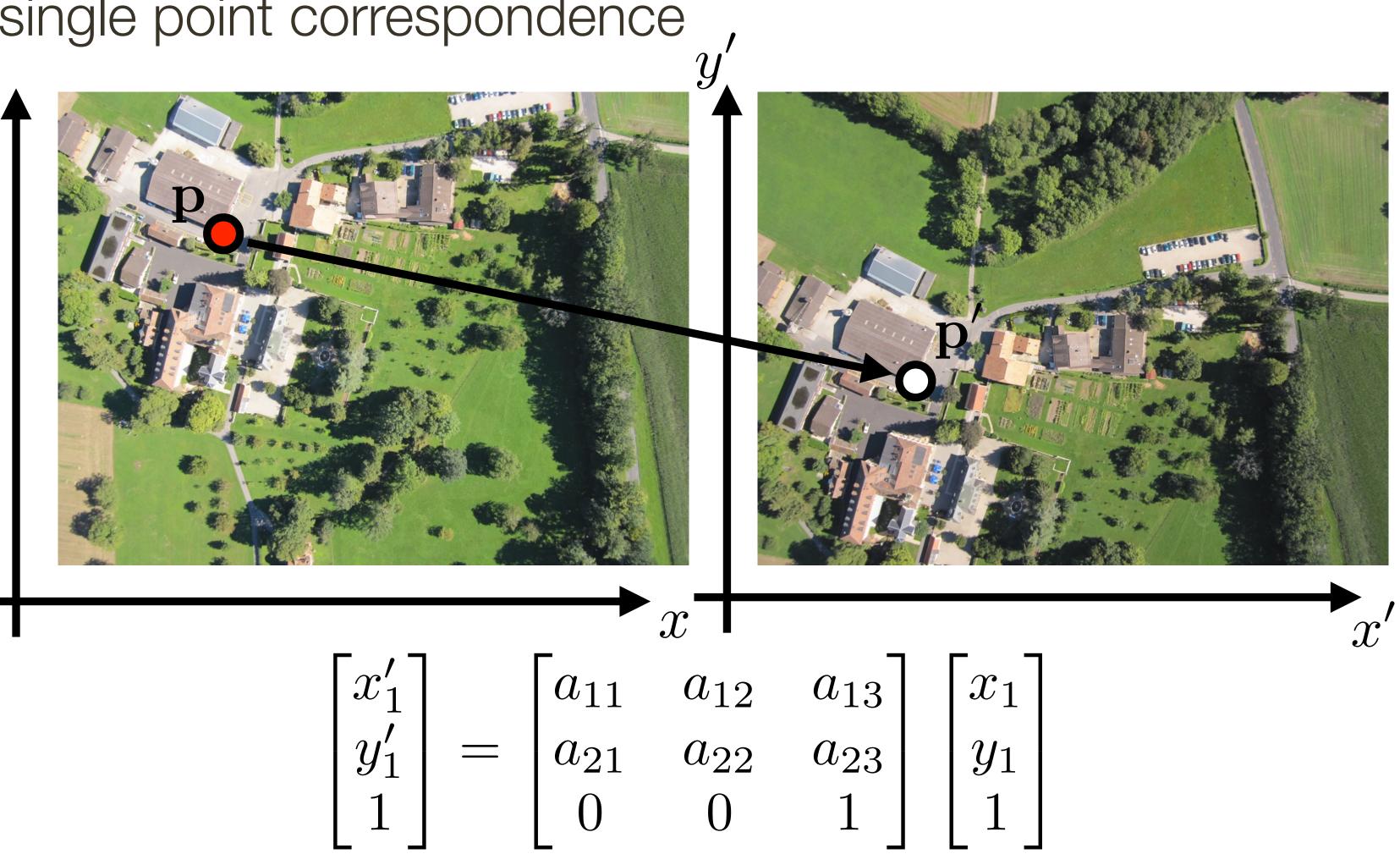
Y



$$\begin{bmatrix} x_1' \\ y_1' \\ 1 \end{bmatrix} = \begin{bmatrix} a_{12} \\ a_{22} \\ 0 \end{bmatrix}$$

### Consider a single point correspondence

Y



$$\begin{bmatrix} x_1' \\ y_1' \\ 1 \end{bmatrix} = \begin{bmatrix} a_{11} \\ a_{21} \\ 0 \end{bmatrix}$$

How many points are needed to solve for **a**?

## **Computing** Affine Transform

Lets compute an affine transform from correspondences:

$$\begin{bmatrix} x_1' \\ y_1' \\ 1 \end{bmatrix} = \begin{bmatrix} a_{11} \\ a_{21} \\ 0 \end{bmatrix}$$

Re-arrange unknowns into a vector

$$\begin{bmatrix} x_1' \\ y_1' \end{bmatrix} = \begin{bmatrix} a_{11} & a_{12} & a_{13} & a_{21} & a_{22} & a_{23} \end{bmatrix} \begin{bmatrix} 0 & x_1 \\ 0 & y_1 \\ 0 & 1 \\ x_2 & 0 \\ y_2 & 0 \\ 1 & 0 \end{bmatrix}$$

$$\begin{array}{ccc} a_{12} & a_{13} \\ a_{22} & a_{23} \\ 0 & 1 \end{array} \begin{bmatrix} x_1 \\ y_1 \\ 1 \end{bmatrix}$$

## **Computing** Affine Transform

Linear system in the unknown parameters **a** 

| $x_1$ | $y_1$ | 1 | 0     |
|-------|-------|---|-------|
| 0     | 0     | 0 | $x_1$ |
| $x_2$ | $y_2$ | 1 | 0     |
| 0     | 0     | 0 | $x_2$ |
| $x_3$ | $y_3$ | 1 | 0     |
| 0     | 0     | 0 | $x_3$ |

### Of the form

## Ma = y

## **Computing** Affine Transform

Linear system in the unknown parameters **a** 

| $x_1$ | $y_1$ | 1 | 0     |
|-------|-------|---|-------|
| 0     | 0     | 0 | $x_1$ |
| $x_2$ | $y_2$ | 1 | 0     |
| 0     | 0     | 0 | $x_2$ |
| $x_3$ | $y_3$ | 1 | 0     |
| 0     | 0     | 0 | $x_3$ |

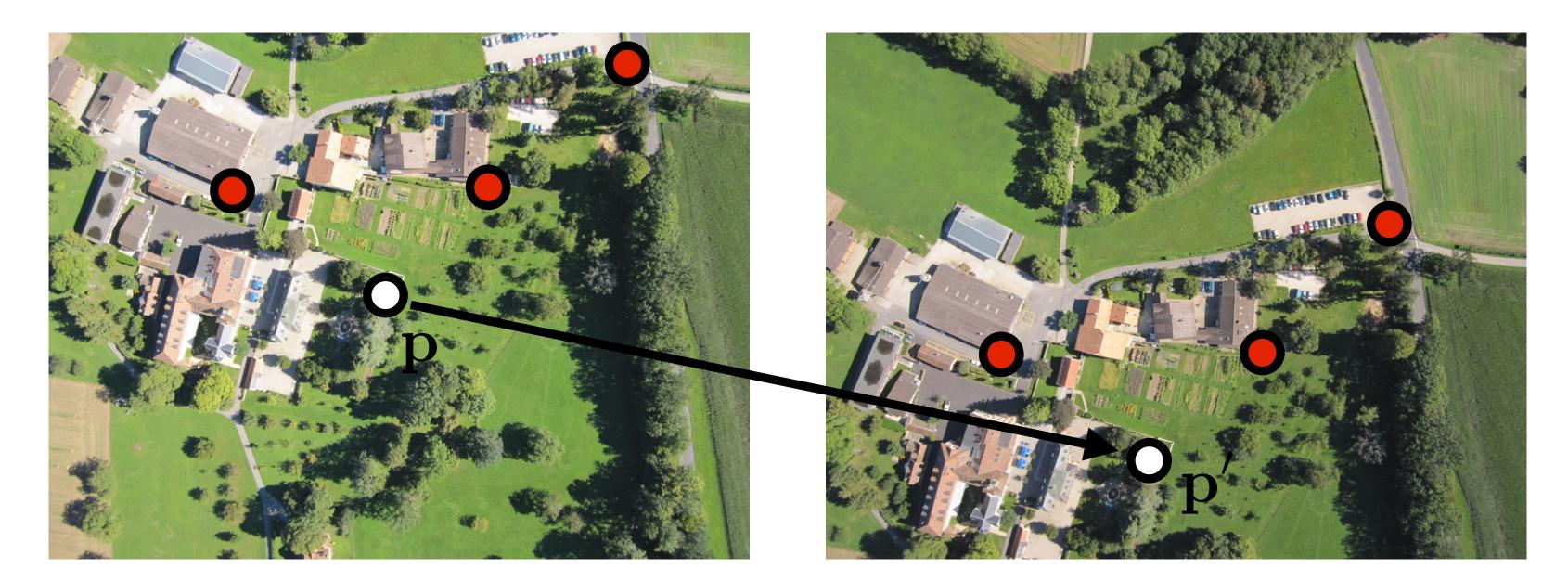
### Of the form

## Ma = y

### Solve for a using Gaussian Elimination

# **Computing** Affine Transform

Once we solve for a transform, we can now map any <u>other points</u> between the two images ... or resample one image in the coordinate system of the other



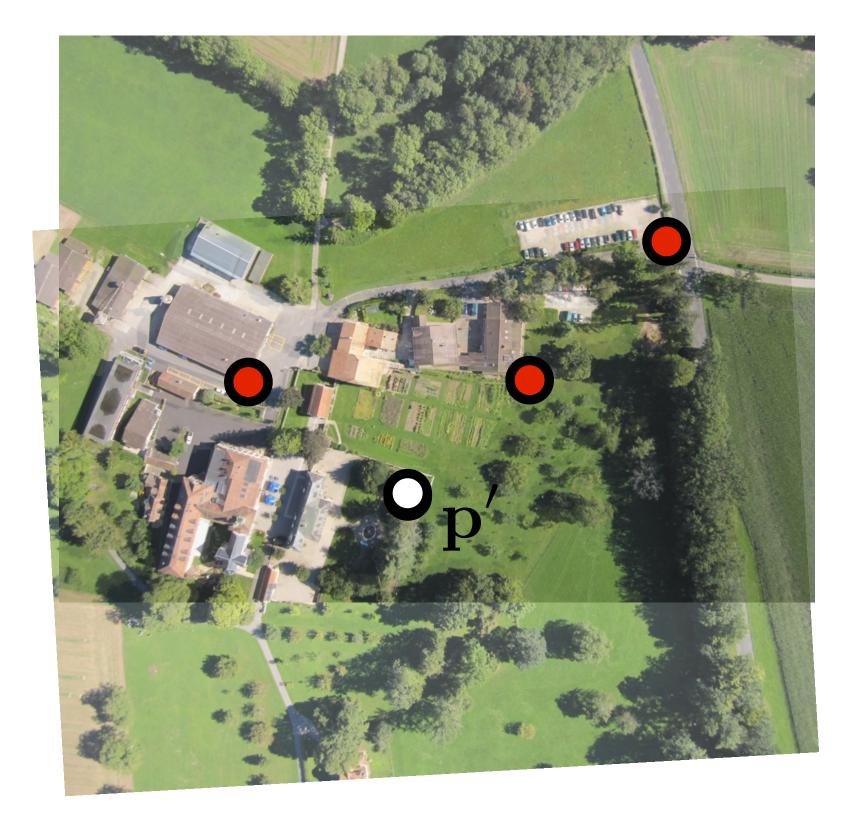
$$\begin{bmatrix} x_1' \\ y_1' \\ 1 \end{bmatrix} = \begin{bmatrix} a_{11} & a_{21} \\ a_{21} & a_{21} \\ 0 \end{bmatrix}$$

$$\begin{array}{ccc} a_{12} & a_{13} \\ a_{22} & a_{23} \\ 0 & 1 \end{array} \begin{bmatrix} x_1 \\ y_1 \\ 1 \end{bmatrix}$$

# **Computing** Affine Transform

This allows us to "stitch" the two images

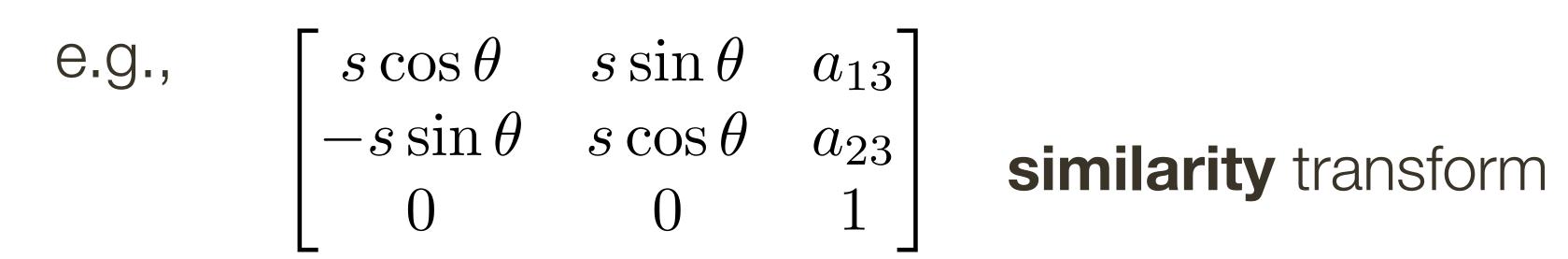
# Once we solve for a transform, we can now map any other points between the two images ... or resample one image in the coordinate system of the other



Other linear transforms are special cases of **affine** transform:

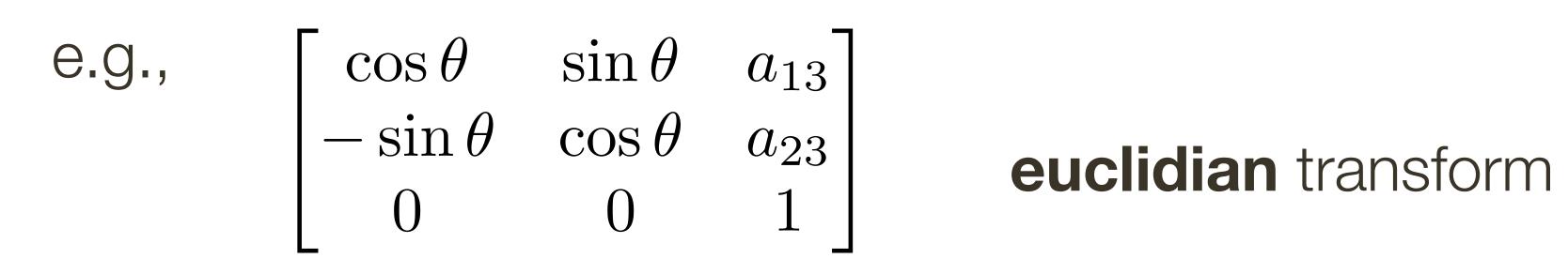
 $\begin{bmatrix} a_{11} & a_{12} & a_{13} \\ a_{21} & a_{22} & a_{23} \\ 0 & 0 & 1 \end{bmatrix}$ 

Other linear transforms are special cases of **affine** transform:



 $\begin{bmatrix} a_{11} & a_{12} & a_{13} \\ a_{21} & a_{22} & a_{23} \\ 0 & 0 & 1 \end{bmatrix}$ 

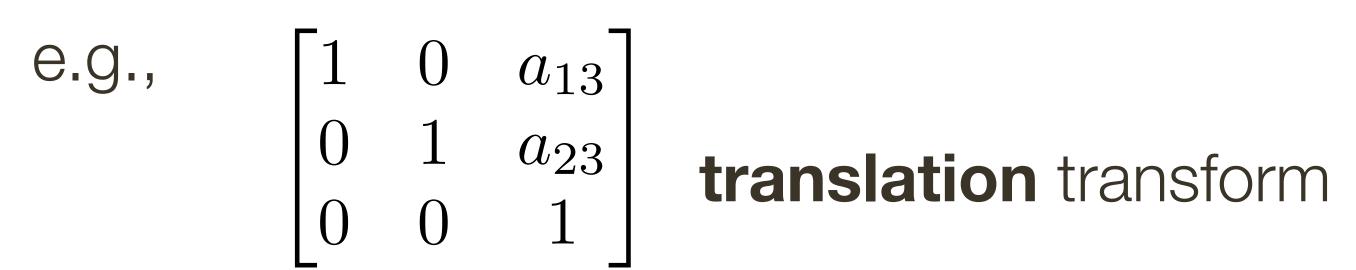
Other linear transforms are special cases of **affine** transform:



 $\begin{bmatrix} a_{11} & a_{12} & a_{13} \\ a_{21} & a_{22} & a_{23} \\ 0 & 0 & 1 \end{bmatrix}$ 

Other linear transforms are special cases of **affine** transform:

 $\begin{vmatrix} a_{11} \\ a_{21} \\ 0 \end{vmatrix}$ 

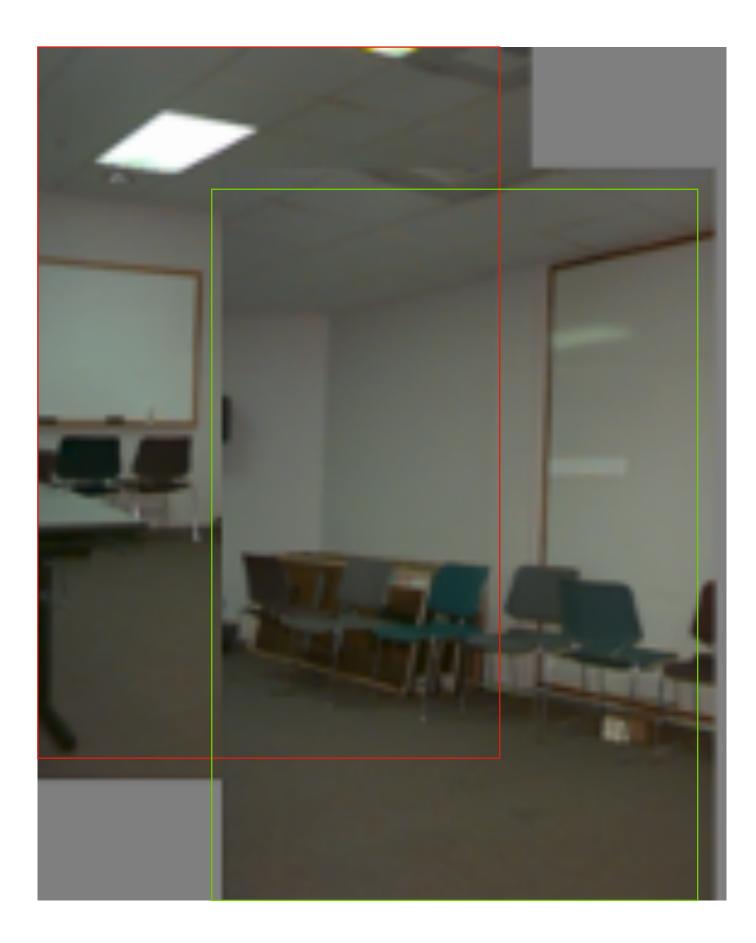


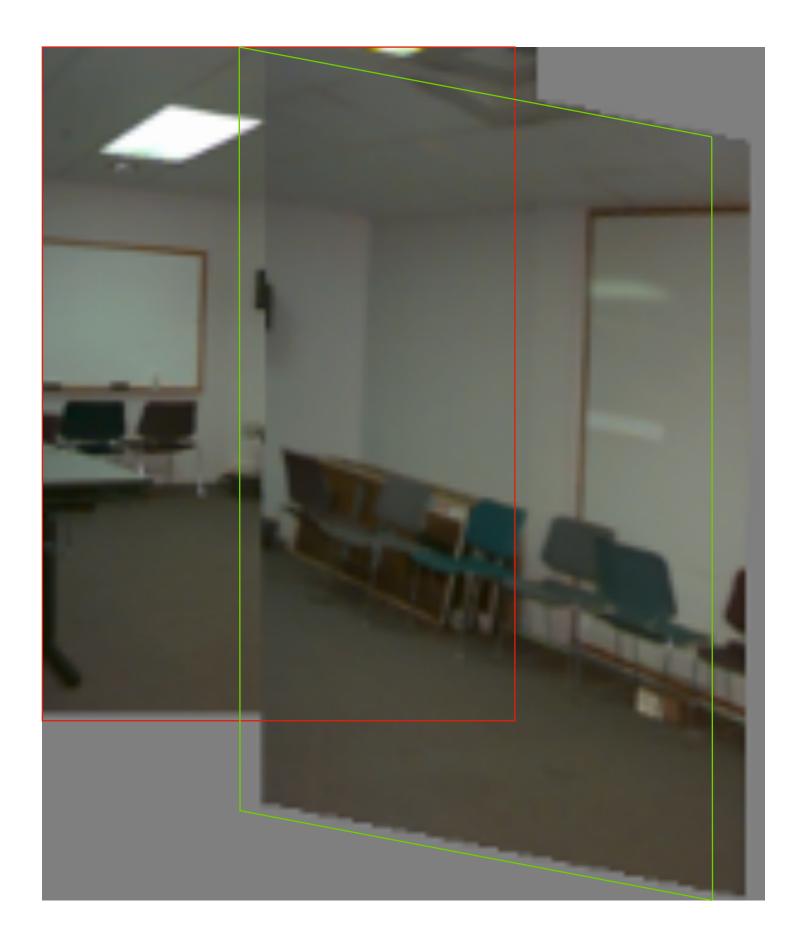
$$\begin{array}{ccc} a_{12} & a_{13} \\ a_{22} & a_{23} \\ 0 & 1 \end{array}$$

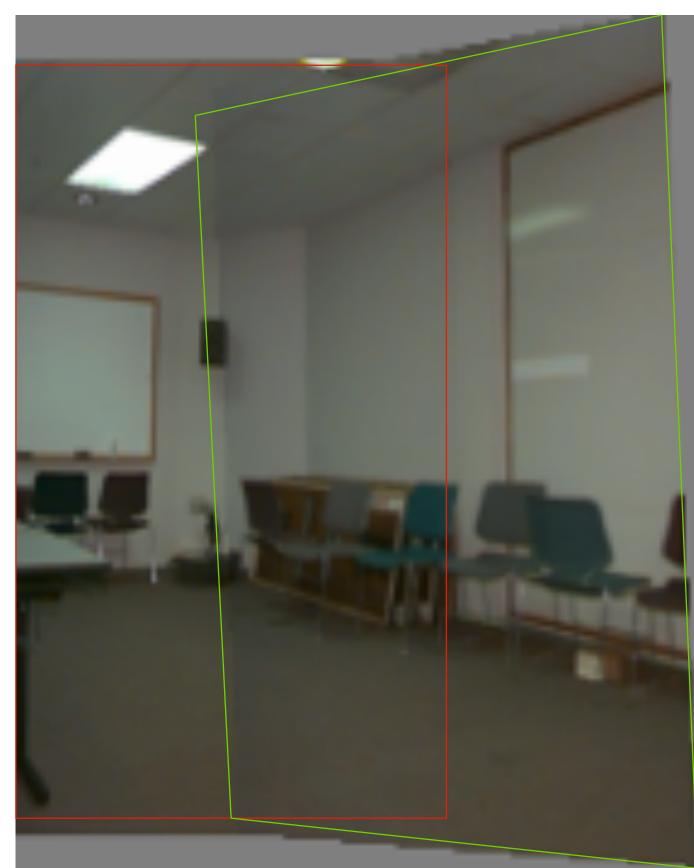
# 2D Transformations

| Transformation    | Matrix   | # DoF | Preserves      | Icon |
|-------------------|--|-------|----------------|------|
| translation       | $\left[ egin{array}{c c} oldsymbol{I} & t \end{array}  ight]_{2	imes 3}$   | 2     | orientation    |      |
| rigid (Euclidean) | $\left[ egin{array}{c c} m{R} & t \end{array}  ight]_{2 	imes 3}$  | 3     | lengths        |      |
| similarity        | $\left[ \begin{array}{c c} s oldsymbol{R} & t \end{array}  ight]_{2 	imes 3}$  | 4     | angles         |      |
| affine            | $\left[ egin{array}{c} egin{arr$ | 6     | parallelism    |      |
| projective        | $\left[ \begin{array}{c} 	ilde{m{H}} \end{array}  ight]_{3	imes 3}$  | 8     | straight lines |      |

## **Example:** Warping with Different Transformations Projective Translation Affine (homography)







**Slide Credit**: Ioannis (Yannis) Gkioulekas (CMU)

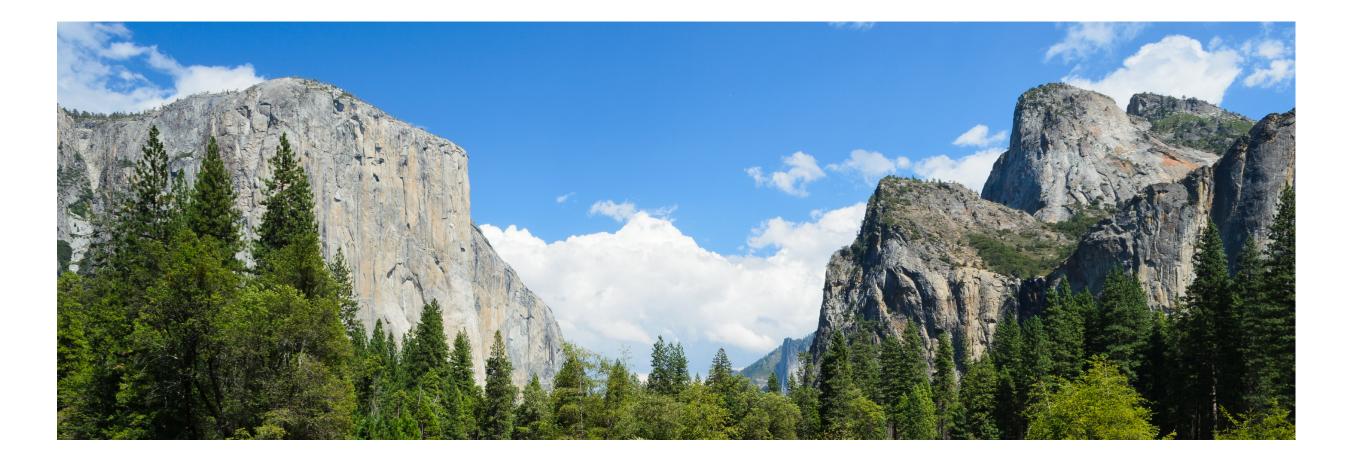




# **Aside:** We can use homographies when ...

1.... the scene is planar; or

2.... the scene is very far or has small (relative) depth variation → scene is approximately planar





**Slide Credit**: Ioannis (Yannis) Gkioulekas (CMU)

# **Aside:** We can use homographies when ...

# 3.... the scene is captured under camera rotation only (no translation) or pose change)



Slide Credit: Ioannis (Yannis) Gkioulekas (CMU)

# **Projective** Transformation

General 3x3 matrix transformation

$$\begin{bmatrix} x_1' \\ y_1' \\ 1 \end{bmatrix} = \begin{bmatrix} a_1 \\ a_2 \\ a_3 \end{bmatrix}$$

## 

# **Projective** Transformation

General 3x3 matrix transformation

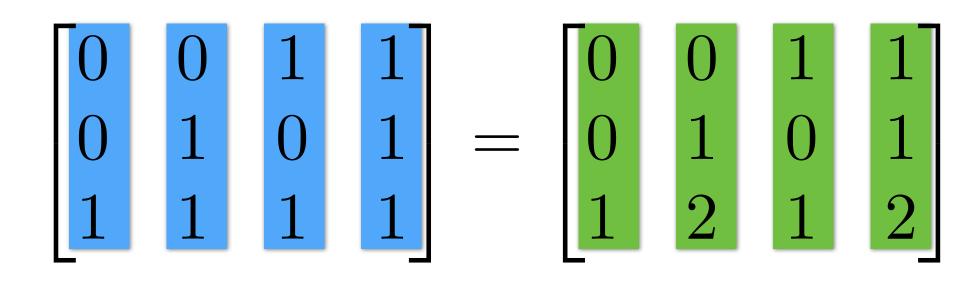
$$\begin{bmatrix} x_1' \\ y_1' \\ 1 \end{bmatrix} = \begin{bmatrix} a_1 \\ a_2 \\ a_3 \end{bmatrix}$$

Lets try an example:

$$\begin{bmatrix} x' \\ y' \\ 1 \end{bmatrix} = \mathbf{H} \begin{bmatrix} x \\ y \\ 1 \end{bmatrix} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 1 & 1 \end{bmatrix}$$

Transformation

# $= \begin{bmatrix} a_{11} & a_{12} & a_{13} \\ a_{21} & a_{22} & a_{23} \\ a_{31} & a_{32} & a_{33} \end{bmatrix} \begin{bmatrix} x_1 \\ y_1 \\ 1 \end{bmatrix}$



Points

**Transformed Points** 

# **Projective** Transformation

General 3x3 matrix transformation

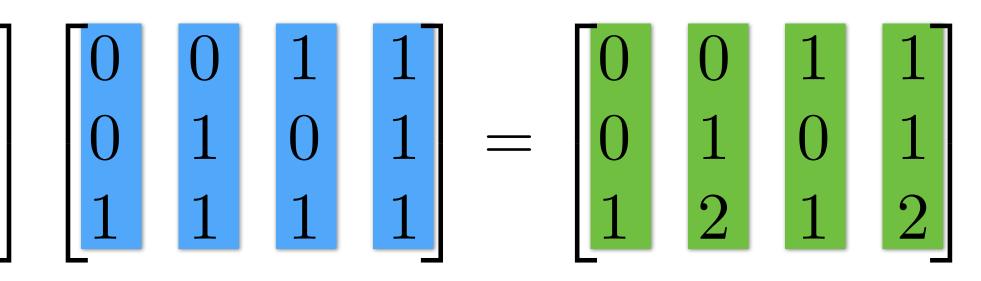
$$\begin{bmatrix} x_1' \\ y_1' \\ 1 \end{bmatrix} = \begin{bmatrix} a_1 \\ a_2 \\ a_3 \end{bmatrix}$$

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Transformation

# $= \begin{bmatrix} a_{11} & a_{12} & a_{13} \\ a_{21} & a_{22} & a_{23} \\ a_{31} & a_{32} & a_{33} \end{bmatrix} \begin{bmatrix} x_1 \\ y_1 \\ 1 \end{bmatrix}$



Points

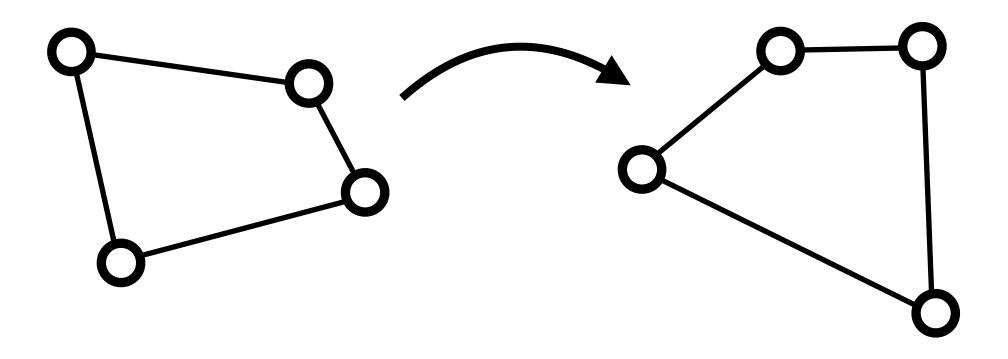
**Transformed Points** 

Divide by the last row: $\begin{bmatrix} 0 & 0 & 1 & 0.5 \\ 0 & 0.5 & 0 & 0.5 \\ 1 & 1 & 1 & 1 \end{bmatrix}$ 

# Compute H from Correspondences

Each match gives 2 equations to solve for 8 parameters

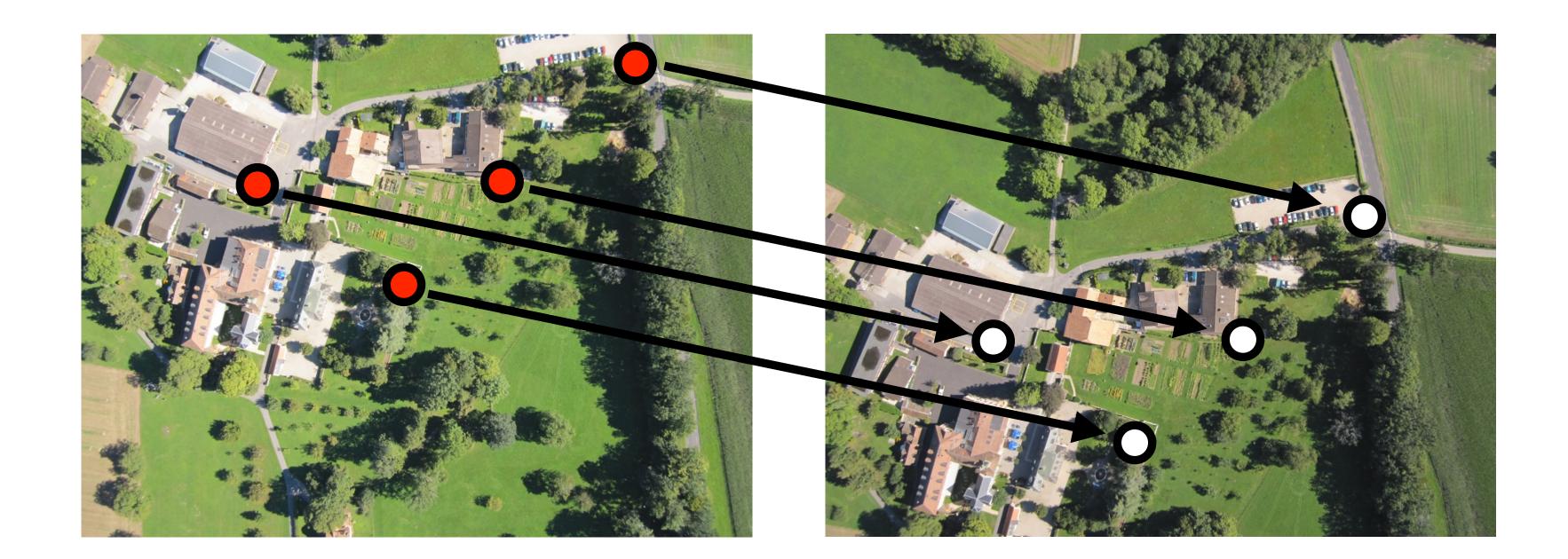
$$\begin{bmatrix} x_1' \\ y_1' \\ 1 \end{bmatrix} = \begin{bmatrix} a_1 \\ a_2 \\ a_3 \end{bmatrix}$$



 $\rightarrow$  4 correspondences to solve for **H** matrix Solution uses **Singular Value Decomposition** (SVD) In Assignment 4 you can compute this using cv2.findHomography

|   | $a_{11}$ | $a_{12}$ | $a_{13}$ | $\begin{bmatrix} x_1 \end{bmatrix}$ |
|---|----------|----------|----------|-------------------------------------|
| — | $a_{21}$ | $a_{22}$ | $a_{23}$ | $y_1$                               |
|   | $a_{31}$ | $a_{32}$ | $a_{33}$ | 1                                   |

# Find corresponding (matching) points between the image

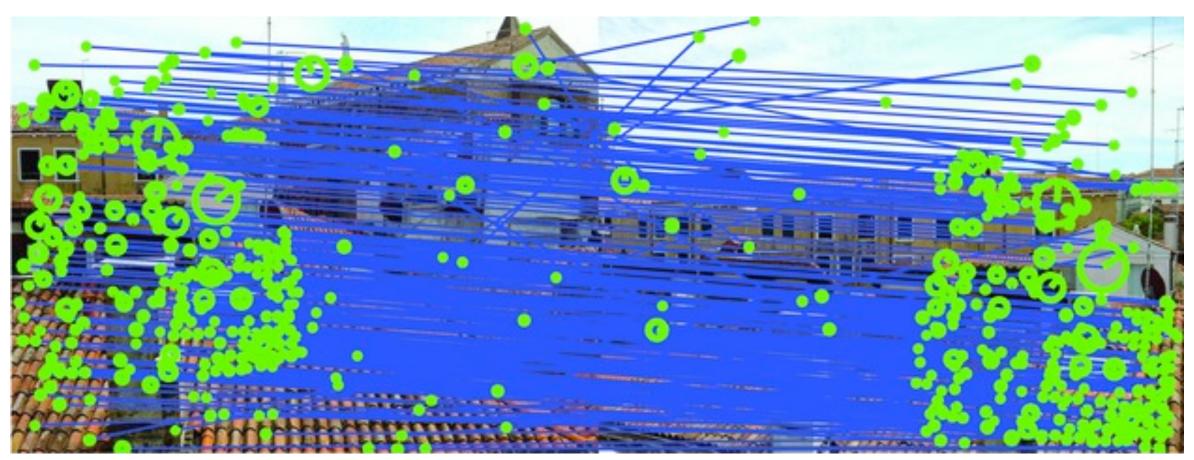


# $\mathbf{u} = \mathbf{H}\mathbf{x}$

2 points for Similarity3 for Affine4 for Homography

# In practice we have many noisy correspondences + outliers



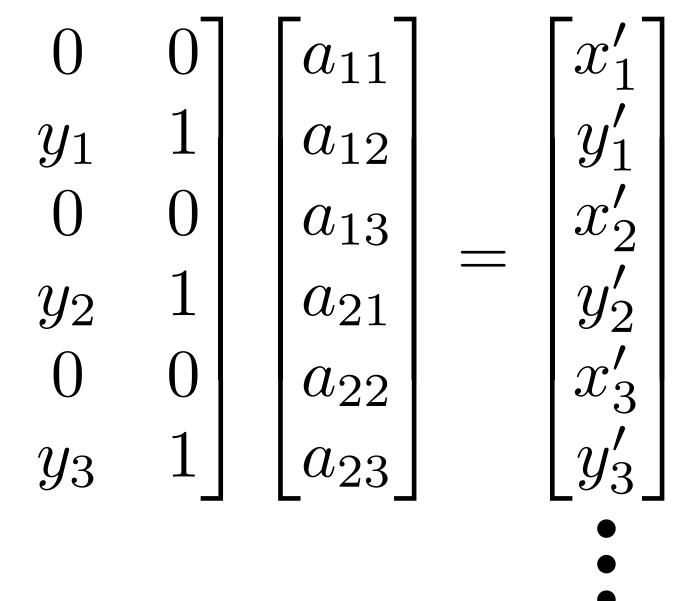


In practice we have many noisy correspondences + outliers

e.g., for an affine transform we have a linear system in the parameters a:

| $\int x_1$ | $y_1$ | 1 | 0     |
|------------|-------|---|-------|
| 0          | 0     | 0 | $x_1$ |
| $x_2$      | $y_2$ | 1 | 0     |
| 0          | 0     | 0 | $x_2$ |
| $x_3$      | $y_3$ | 1 | 0     |
| 0          | 0     | 0 | $x_3$ |
|            |       |   |       |
|            |       |   |       |

It is overconstrained (more equations than unknowns) and subject to outliers (some rows are completely wrong)



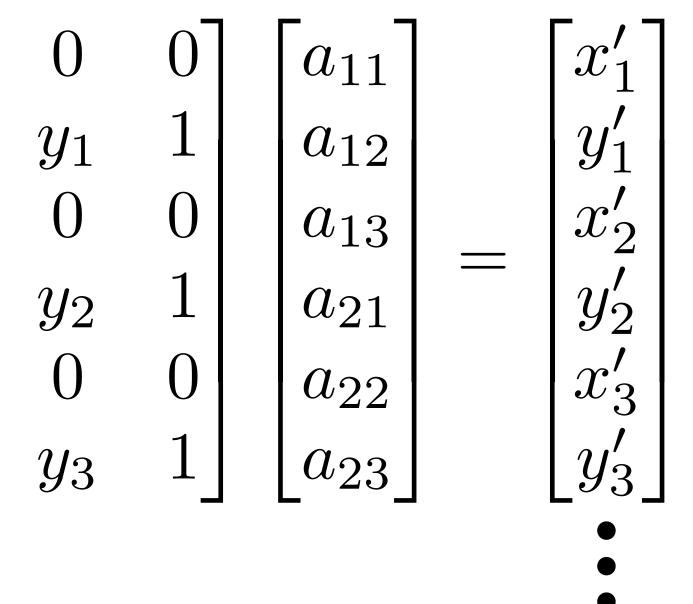
In practice we have many noisy correspondences + outliers

e.g., for an affine transform we have a linear system in the parameters a:

| $\lceil x_1 \rceil$ | $y_1$ | 1 | 0     |
|---------------------|-------|---|-------|
| 0                   | 0     | 0 | $x_1$ |
| $x_2$               | $y_2$ | 1 | 0     |
| 0                   | 0     | 0 | $x_2$ |
| $x_3$               | $y_3$ | 1 | 0     |
|                     | 0     | 0 | $x_3$ |
| —                   |       |   | •     |
|                     |       |   |       |

It is overconstrained (more equations than unknowns) and subject to outliers (some rows are completely wrong)

Let's deal with these problems in a simpler context ...



# Fitting a Model to Noisy Data

We can fit a line using two points

# Suppose we are **fitting a line** to a dataset that consists of 50% outliers

# If we draw pairs of points uniformly at random, what fraction of pairs will consist entirely of 'good' data points (inliers)?

# Fitting a Model to Noisy Data Suppose we are **fitting a line** to a dataset that consists of 50% outliers We can fit a line using two points

will consist entirely of 'good' data points (inliers)

points lie close to the line fitted to the pair

that lie close to the line

- If we draw pairs of points uniformly at random, then about 1/4 of these pairs
- We can identify these good pairs by noticing that a large collection of other
- A better estimate of the line can be obtained by refitting the line to the points

# **RANSAC** (**RAN**dom **SA**mple **C**onsensus)

- sample)
- Size of consensus set is model's **support**
- 3. Repeat for N samples; model with biggest support is most robust fit
  - Points within distance t of best model are inliers
  - Fit final model to all inliers

1. Randomly choose minimal subset of data points necessary to fit model (a

2. Points within some distance threshold, t, of model are a **consensus set**.

Slide Credit: Christopher Rasmussen

# **RANSAC** (**RAN**dom **SA**mple **C**onsensus)

- sample)
- Size of consensus set is model's **support**
- 3. Repeat for N samples; model with biggest support is most robust fit
  - Points within distance t of best model are inliers
  - Fit final model to all inliers

# RANSAC is very useful for variety of applications

1. Randomly choose minimal subset of data points necessary to fit model (a

2. Points within some distance threshold, t, of model are a **consensus set**.

Slide Credit: Christopher Rasmussen

# **RANSAC** (**RAN**dom **SA**mple **C**onsensus)

# sample) Fitting a Line: 2 points

2. Points within some distance threshold, t, of model are a **consensus set**. Size of consensus set is model's support

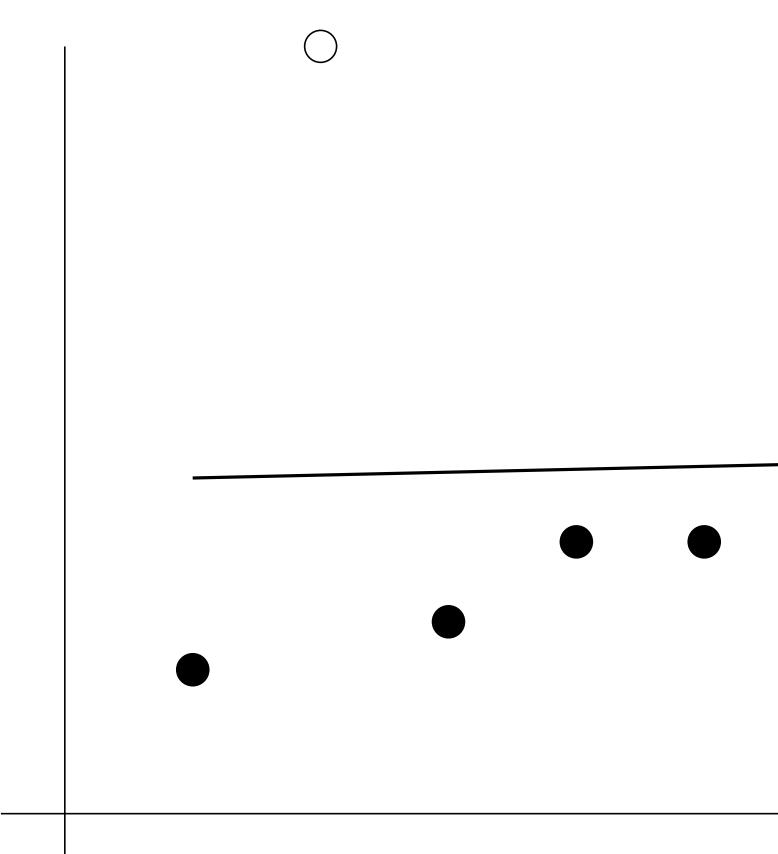
3. Repeat for N samples; model with biggest support is most robust fit Points within distance t of best model are inliers

- Fit final model to all inliers

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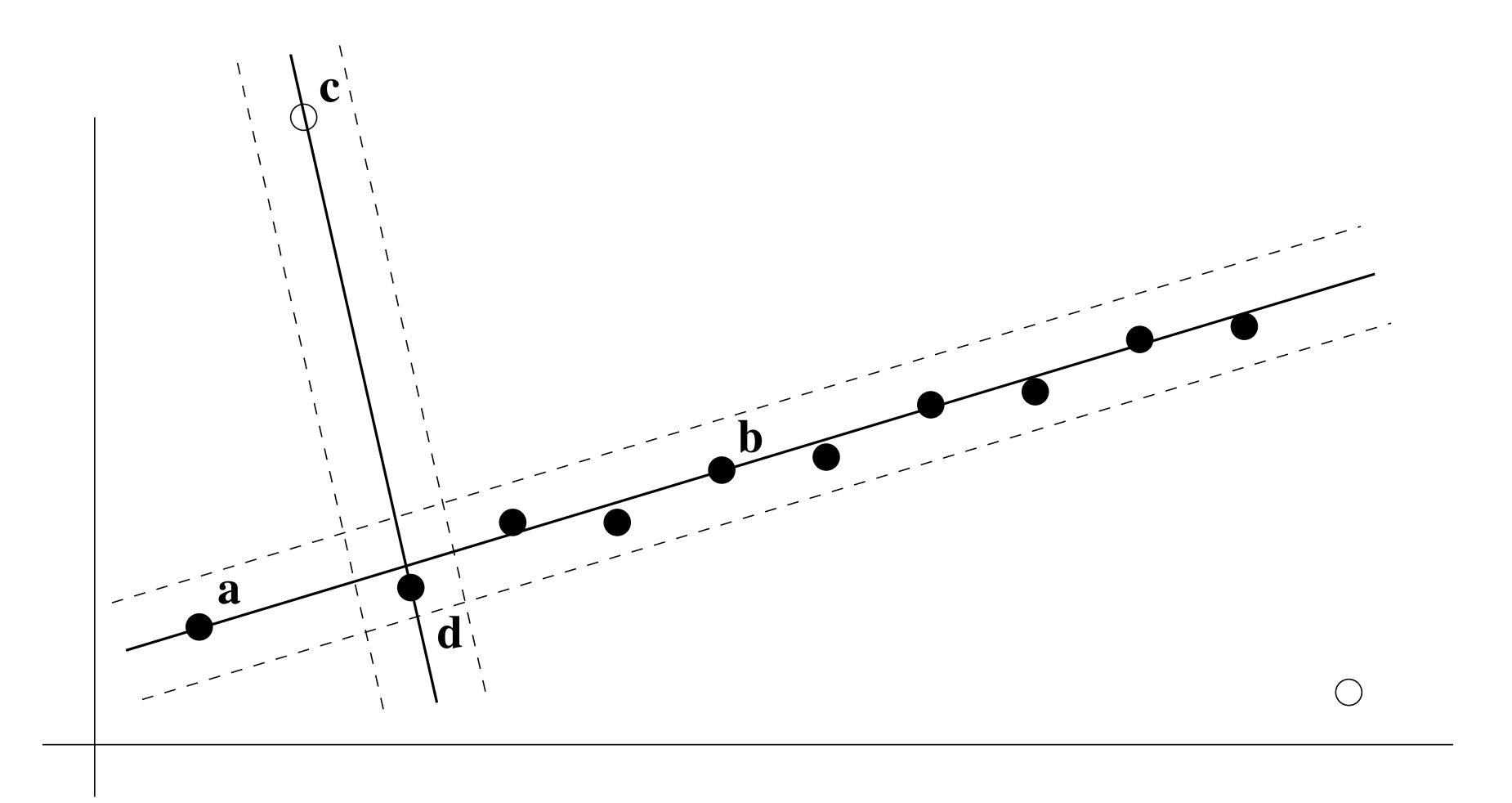
Slide Credit: Christopher Rasmussen

# **Example 1**: Fitting a Line

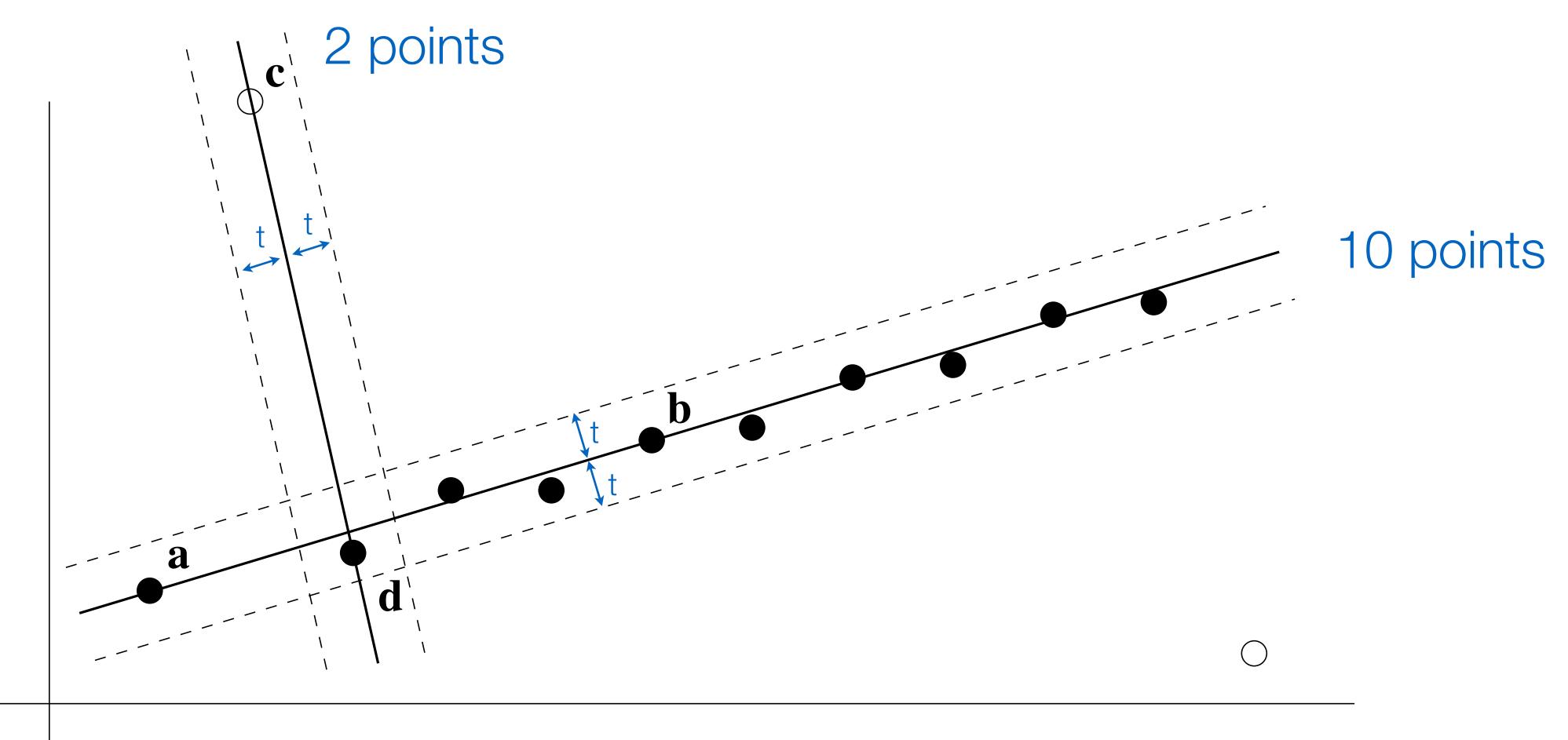


# $\bigcirc$

# **Example 1**: Fitting a Line



# **Example 1**: Fitting a Line



# Algorithm 10.4

This was Algorithm 15.4 in Forsyth & Ponce (1st ed.)

## Algorithm 15.4: RANSAC: fitting lines using random sample consensus

Determine:

n — the smallest number of points required k — the number of iterations required t — the threshold used to identify a point that fits well d — the number of nearby points required 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 For each data point outside the sample Test the distance from the point to the line against t; if the distance from the point to the line is less than t, the point is close end If there are d or more points close to the line then there is a good fit. Refit the line using all these points. end Use the best fit from this collection, using the

fitting error as a criterion

# RANSAC: Fitting Lines Using Random Sample Consensus

# **RANSAC:** How many samples?

Let  $\omega$  be the fraction of inliers (i.e., points on line)

- Let n be the number of points needed to define hypothesis (n = 2 for a line in the plane)
- Suppose k samples are chosen
- The probability that a single sample of n points is correct (all inliers) is

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$$\omega^n$$

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- Let n be the number of points needed to define hypothesis (n = 2 for a line in the plane)
- Suppose k samples are chosen
- The probability that a single sample of n points is correct (all inliers) is

The probability that all k samples fail is ] Choose k large enough (to keep this below a target failure rate)

$$\omega^n$$

$$(-\omega^n)^k$$

# **RANSAC**: *k* Samples Chosen (p = 0.99)

| Sample<br>size | Proportion of outliers |     |          |     |     |     |      |
|----------------|------------------------|-----|----------|-----|-----|-----|------|
| n              | 5%                     | 10% | 20%      | 25% | 30% | 40% | 50%  |
| 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   | 12<br>16 |     | 37  | 97  | 293  |
| 7              | 4                      | 8   | 20<br>26 | 33  | 54  | 163 | 588  |
| 8              | 5                      | 9   | 26       | 44  | 78  | 272 | 1177 |

# After RANSAC

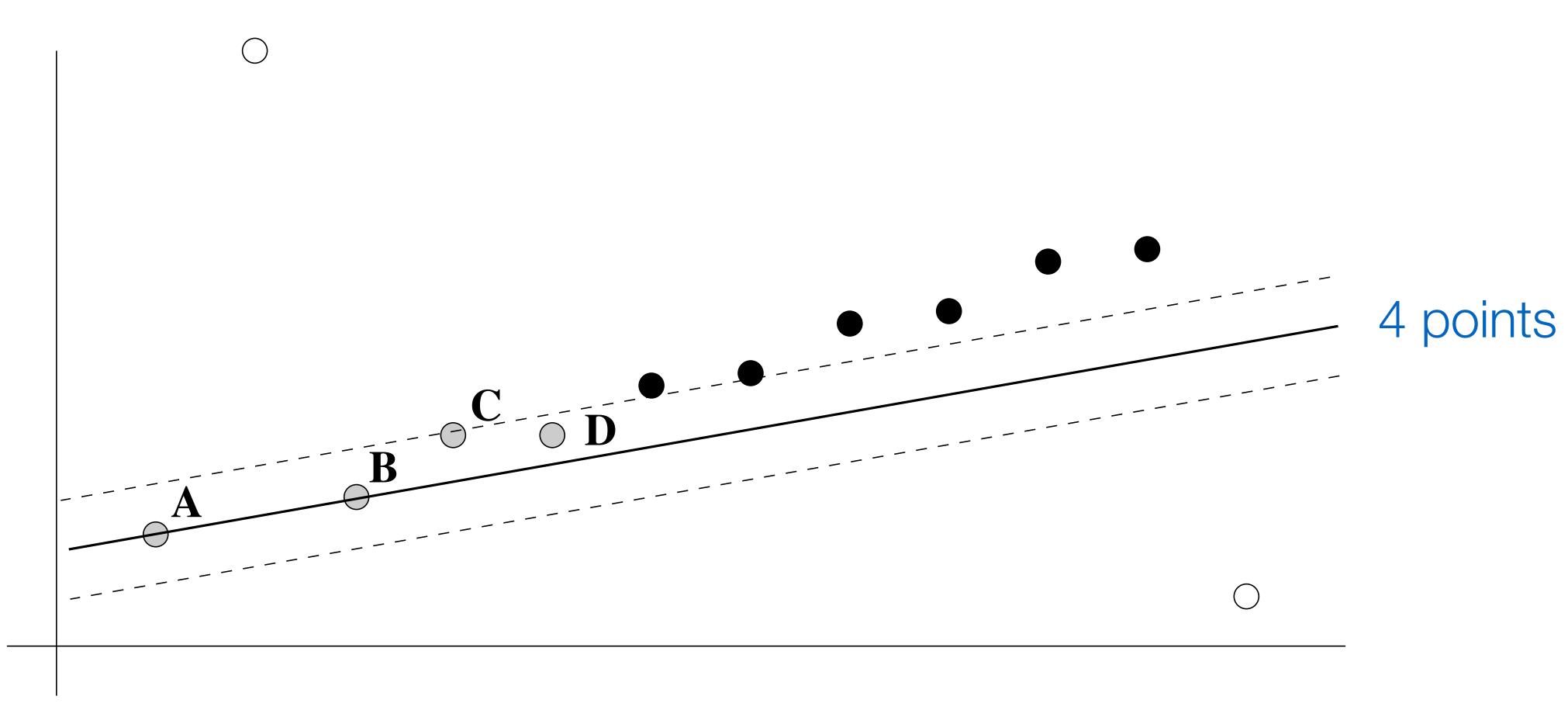
from minimal set of inliers

Improve this initial estimate with estimation over all inliers (e.g., with standard least-squares minimization)

But this may change inliers, so alternate fitting with re-classification as inlier/ outlier

# **RANSAC** divides data into inliers and outliers and yields estimate computed

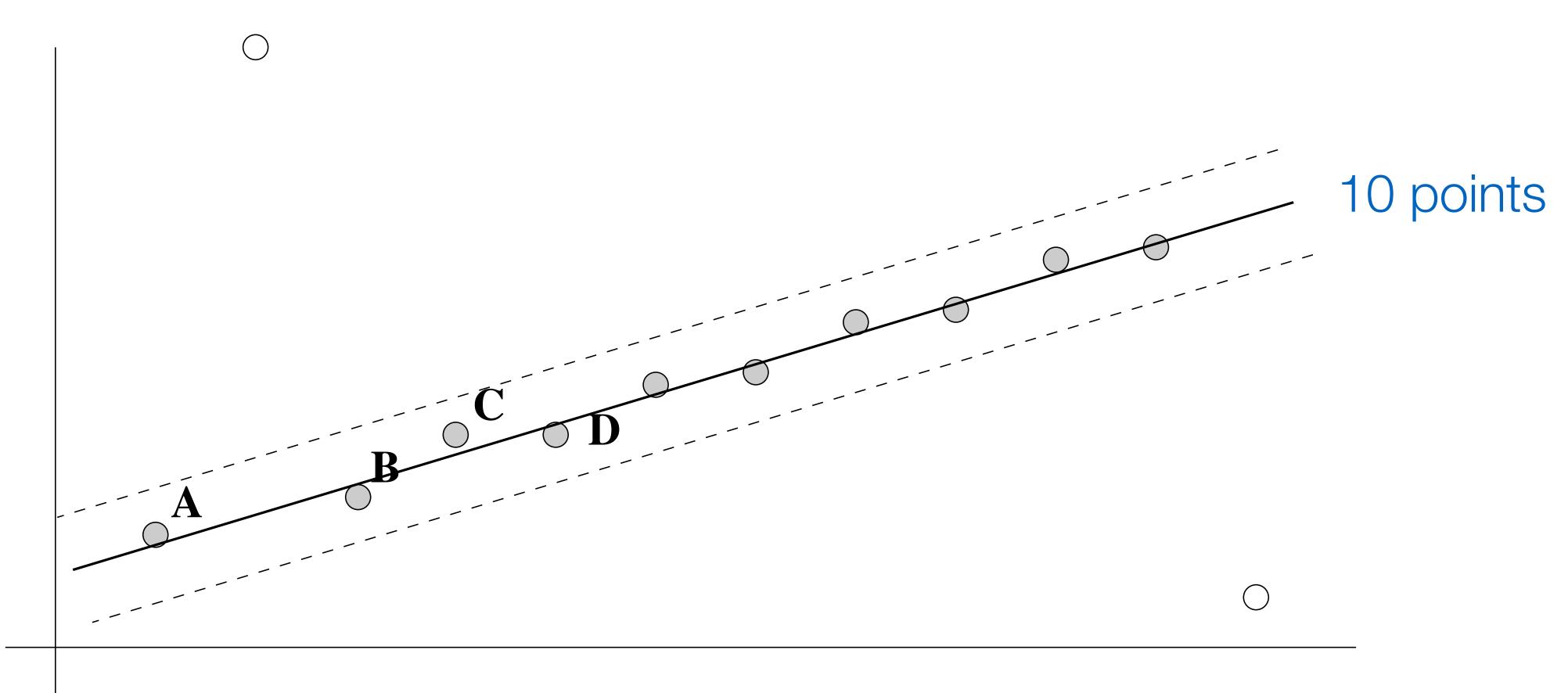
# Example 2: Fitting a Line







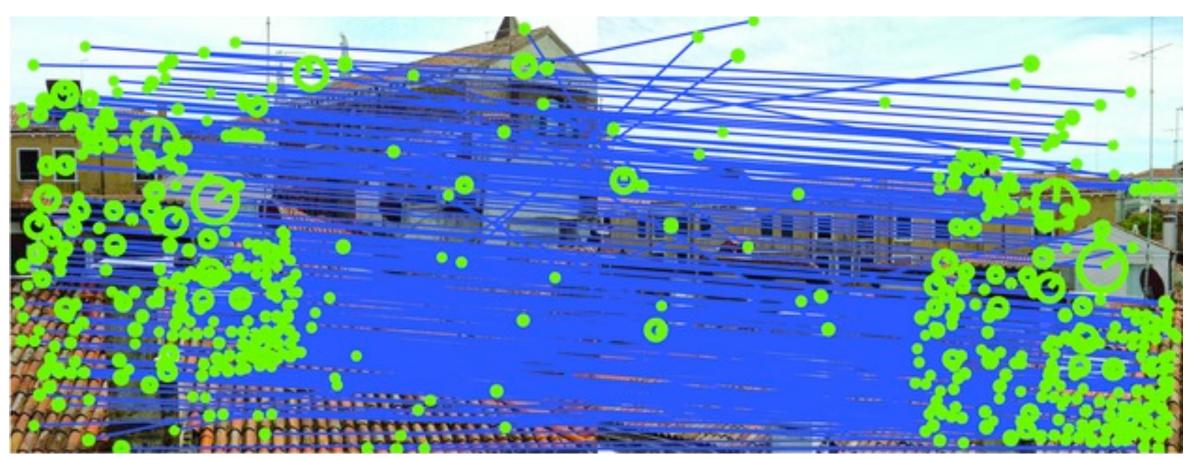
# **Example 2**: Fitting a Line



# Image Alignment + RANSAC

# In practice we have many noisy correspondences + outliers





# Image Alignment + RANSAC

# RANSAC solution for Similarity Transform (2 points)





## RANSAC solution for Similarity Transform (2 points)



#### 4 inliers (red, yellow, orange, brown),

## RANSAC solution for Similarity Transform (2 points)



#### 4 outliers (blue, light blue, purple, pink)

## RANSAC solution for Similarity Transform (2 points)



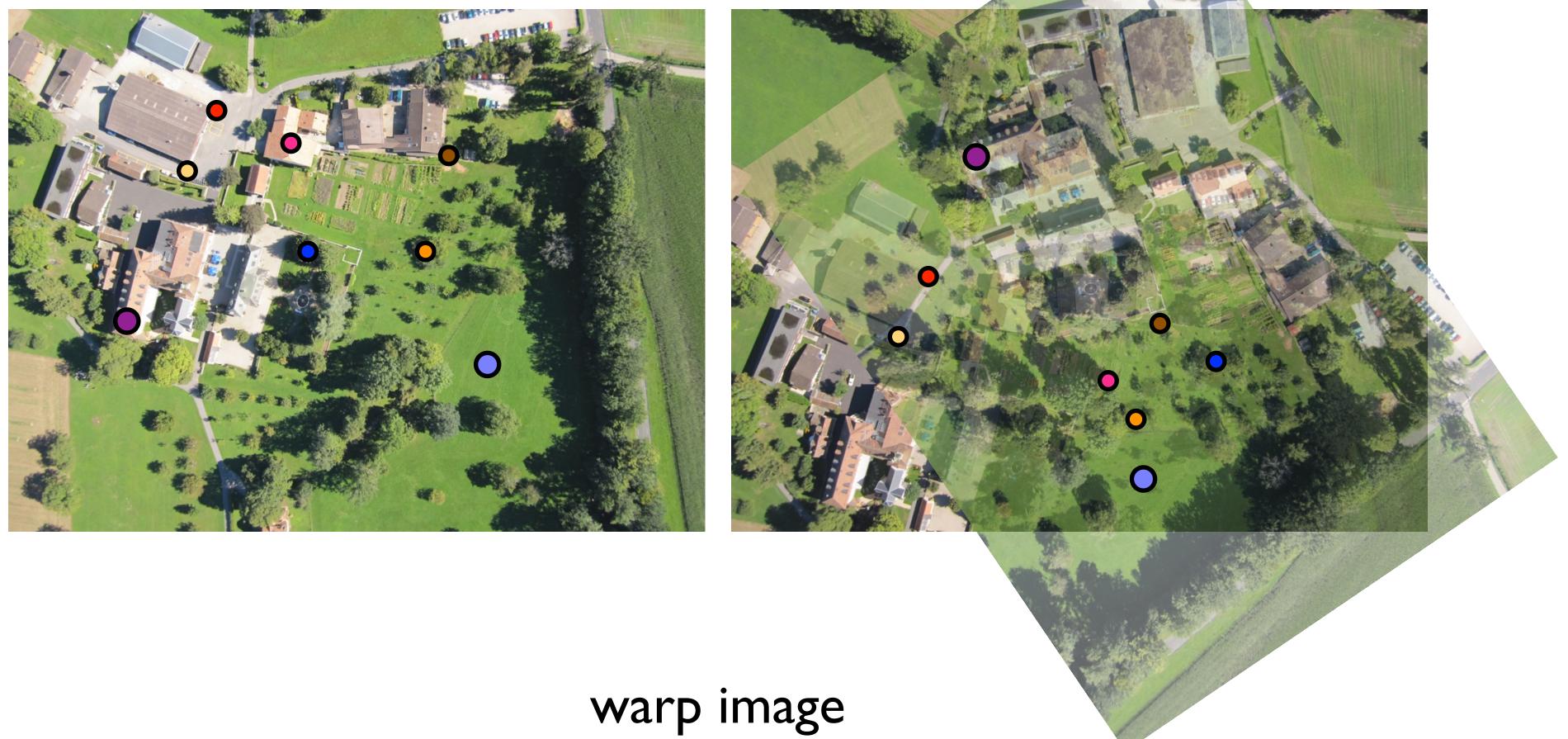
4 inliers (red, yellow, orange, brown), 4 outliers (blue, light blue, purple, pink)

## RANSAC solution for Similarity Transform (2 points)





#### choose light blue, purple



## RANSAC solution for Similarity Transform (2 points)



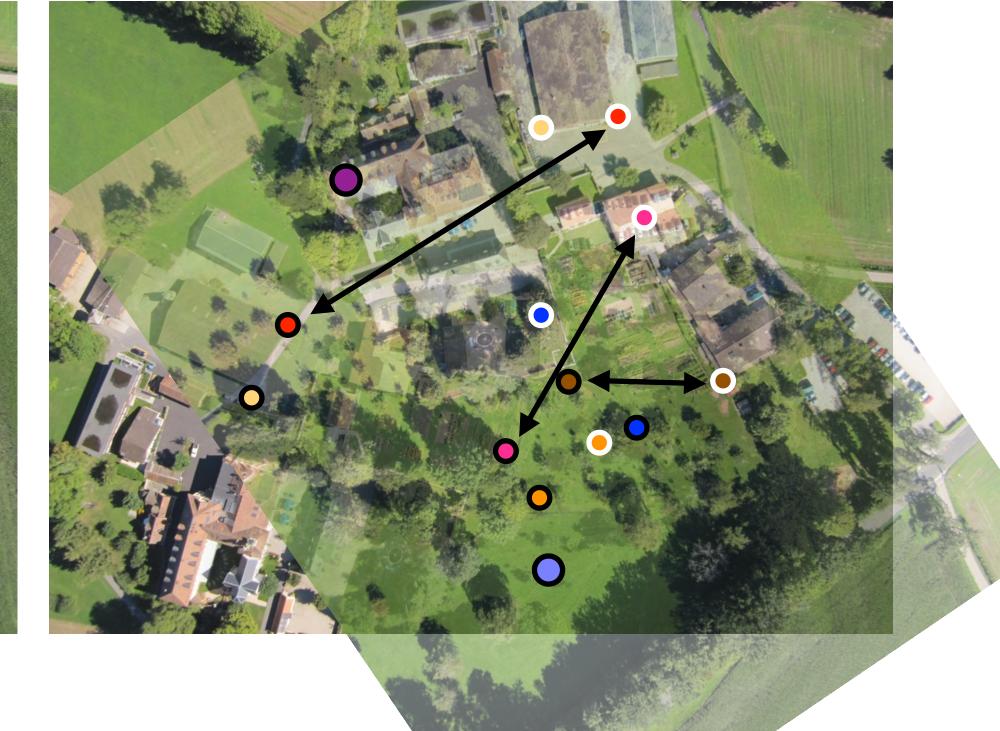
#### check match distances



## RANSAC solution for Similarity Transform (2 points)



#### check match distances



## RANSAC solution for Similarity Transform (2 points)





## check match distances #inliers = 2



## RANSAC solution for Similarity Transform (2 points)



#### choose pink, blue



warp image

## RANSAC solution for Similarity Transform (2 points)



#### check match distances

## RANSAC solution for Similarity Transform (2 points)



#### check match distances

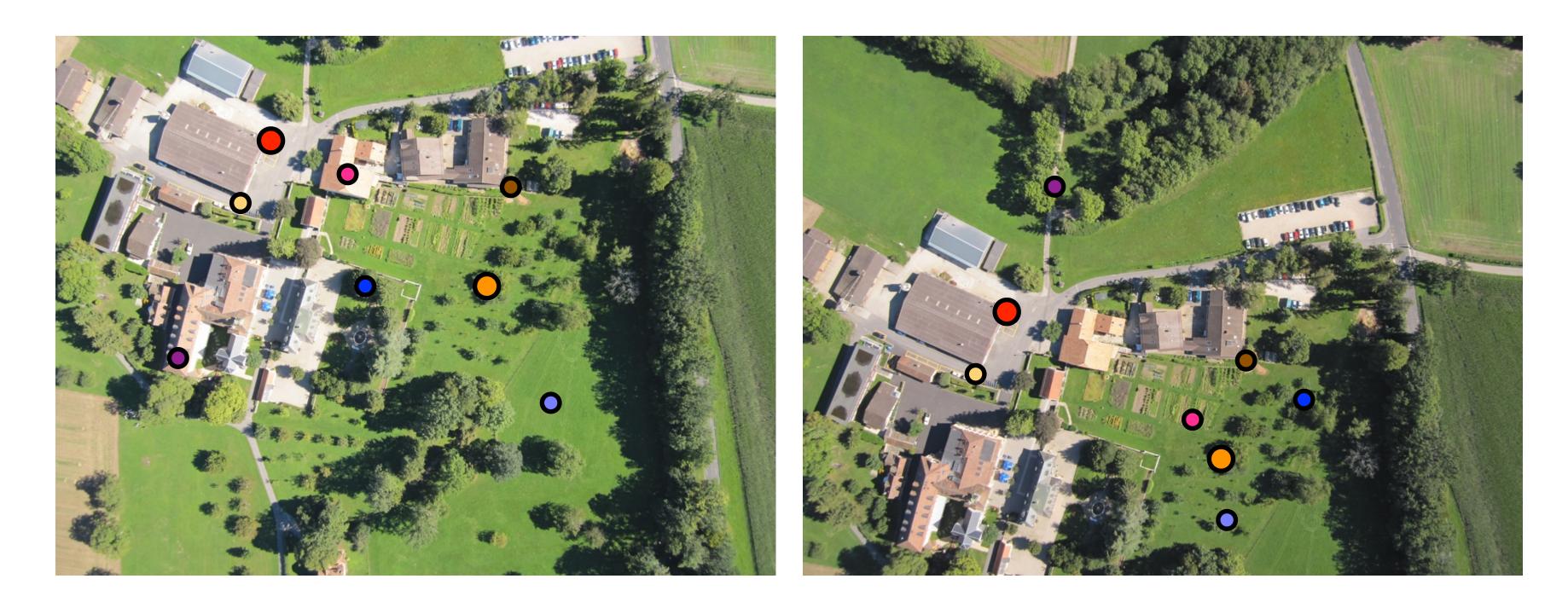
## RANSAC solution for Similarity Transform (2 points)



check match distances #inliers = 2



## RANSAC solution for Similarity Transform (2 points)





#### choose red, orange



## RANSAC solution for Similarity Transform (2 points)



check match distances

## RANSAC solution for Similarity Transform (2 points)



check match distances

## RANSAC solution for Similarity Transform (2 points)



check match distances

#inliers = 4



- **1.** Match feature points between 2 views
- **2.** Select minimal subset of matches<sup>\*</sup>
- **3.** Compute transformation T using minimal subset
- count #inliers with distance < threshold
- **5.** Repeat steps 2-4 to maximize #inliers

\* Similarity transform = 2 points, Affine = 3, Homography = 4



# Assignment 4

**4.** Check consistency of all points with T - compute projected position and



## **RANSAC**: *k* Samples Chosen (p = 0.99)

| Sample<br>size | Proportion of outliers |     |          |     |     |     |      |  |  |
|----------------|------------------------|-----|----------|-----|-----|-----|------|--|--|
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| 7              | 4                      | 8   | 20<br>26 | 33  | 54  | 163 | 588  |  |  |
| 8              | 5                      | 9   | 26       | 44  | 78  | 272 | 1177 |  |  |

Figure Credit: Hartley & Zisserman

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| 8              | 5                      | 9   | 26  | 44  | 78  | 272 | 1177 |  |  |

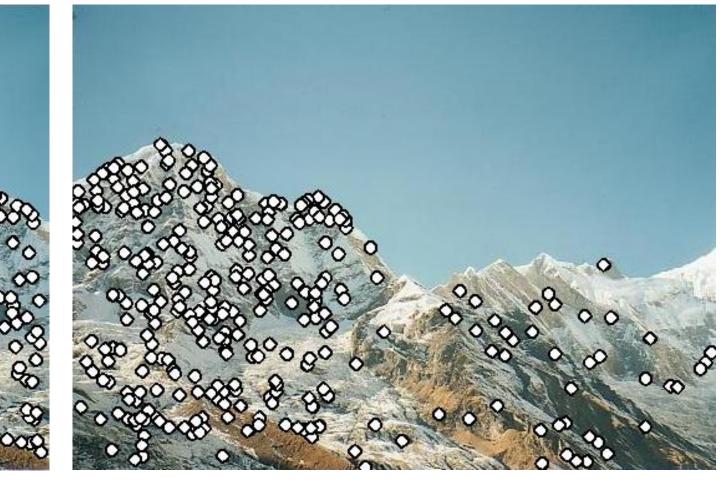
Figure Credit: Hartley & Zisserman

## 2-view Rotation Estimation

#### Find features + raw matches, use RANSAC to find Similarity





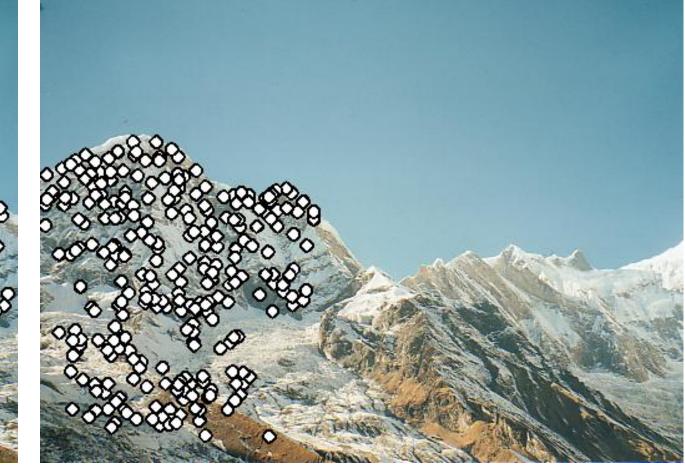


## 2-view Rotation Estimation

#### Remove outliers, can now solve for R using least squares







## 2-view Rotation Estimation

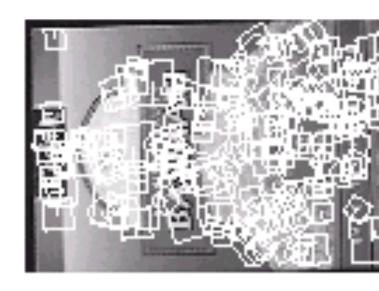
#### Final rotation estimation

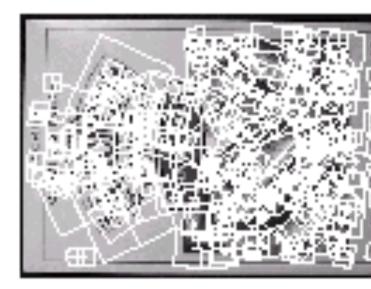


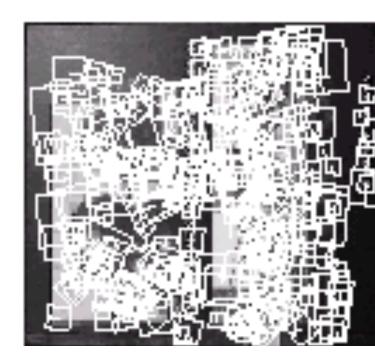


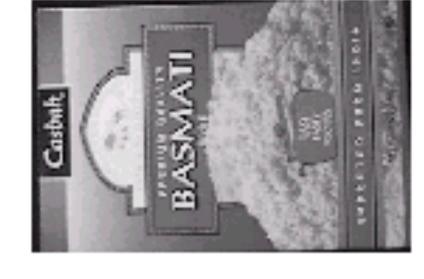
## Object Instance Recognition

#### Database of planar objects













#### Instance recognition





Slide Credit: Ioannis (Yannis) Gkioulekas (CMU)

# Object Instance Recognition with SIFT

- Match SIFT descriptors between query image and a database of known keypoints extracted from training examples
- use fast (approximate) nearest neighbour matching
- threshold based on ratio of distances between 1NN and 2NN
- Use **RANSAC** to find a **subset of matches** that all agree on an object and geometric transform (e.g., **affine transform**)
- Optionally **refine pose estimate** by recomputing the transformation using all the RANSAC inliers

## Re-cap RANSAC

**RANSAC** is a technique to fit data to a model

- divide data into inliers and outliers
- estimate model from minimal set of inliers
- improve model estimate using all inliers
- alternate fitting with re-classification as inlier/outlier

- easy to implement
- easy to estimate/control failure rate

**RANSAC** only handles a moderate percentage of outliers without cost blowing up

**RANSAC** is a general method suited for a wide range of model fitting problems