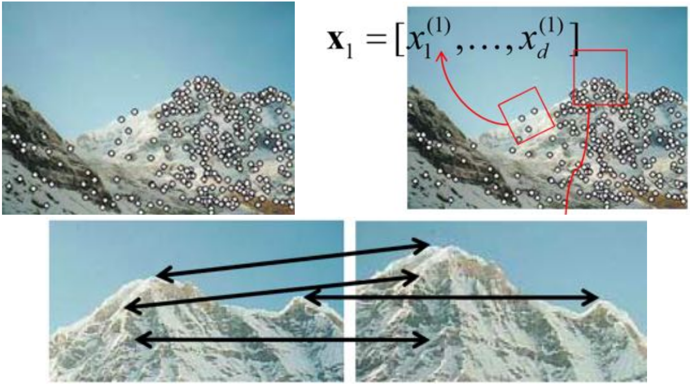
Image Features:

Local Descriptors

Local Features

- **Detection**: Identify the interest points.
- **Description**: Extract a feature descriptor around each interest point.
- **Matching**: Determine correspondence between descriptors in two views.



[Source: K. Grauman]

The Ideal Feature Descriptor

- **Repeatable**: Invariant to rotation, scale, photometric variations
- **Distinctive**: We will need to match it to lots of images/objects!
- **Compact**: Should capture rich information yet not be too high-dimensional (otherwise matching will be slow)
- **Efficient**: We would like to compute it (close-to) real-time

Invariances

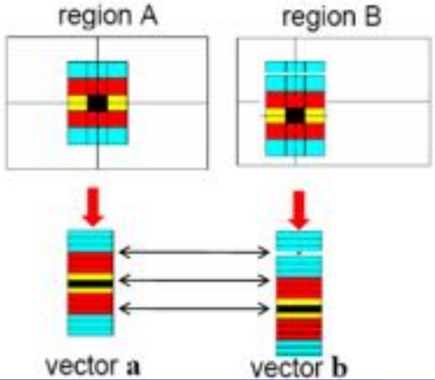
[Source: T. Tuytelaars]

Invariances

[Source: T. Tuytelaars]

What If We Just Took Pixels?

- The simplest way is to write down the list of intensities to form a feature vector, and normalize them (i.e., mean 0, variance 1).
- Why normalization?
- But this is very sensitive to even small shifts, rotations and any affine transformation.



Tones Of Better Options

- SIFT
- PCA-SIFT
- GLOH
- HOG
- SURF
- DAISY
- LBP
- Shape Contexts
- Color Histograms

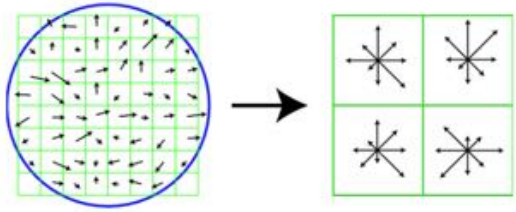
Tones Of Better Options

- **SIFT** **TODAY**
- PCA-SIFT
- GLOH
- HOG
- SURF
- DAISY
- LBP
- Shape Contexts
- Color Histograms

SIFT Descriptor [Lowe 2004]

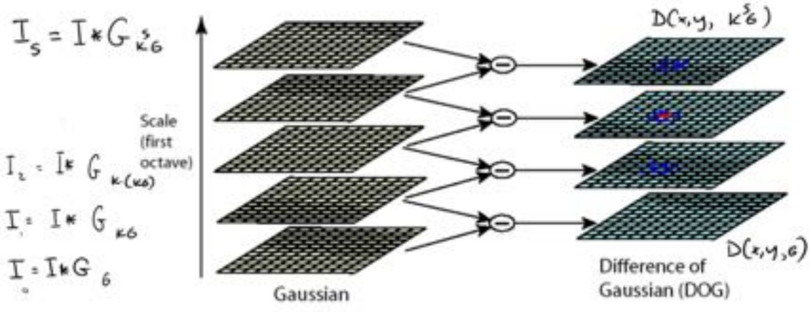
- SIFT stands for Scale Invariant Feature Transform
- Invented by David Lowe, who also did DoG scale invariant interest points
- Actually in the same paper, which you should read:

David G. Lowe
Distinctive image features from scale-invariant keypoints
International Journal of Computer Vision, 2004
Paper: `http://www.cs.ubc.ca/~lowe/papers/ijcv04.pdf`



SIFT Descriptor

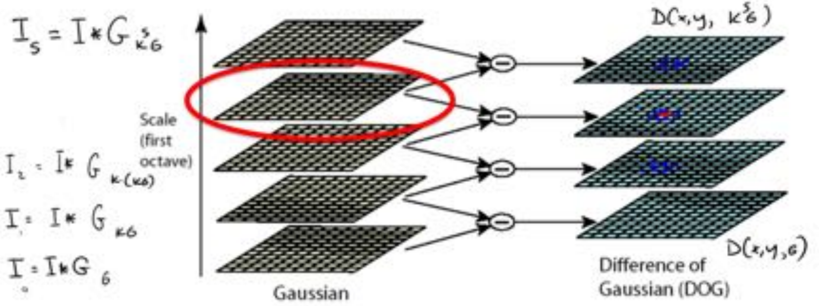
1. Our scale invariant interest point detector gives scale ρ for each keypoint



[Adopted from: F. Flores-Mangas]

SIFT Descriptor

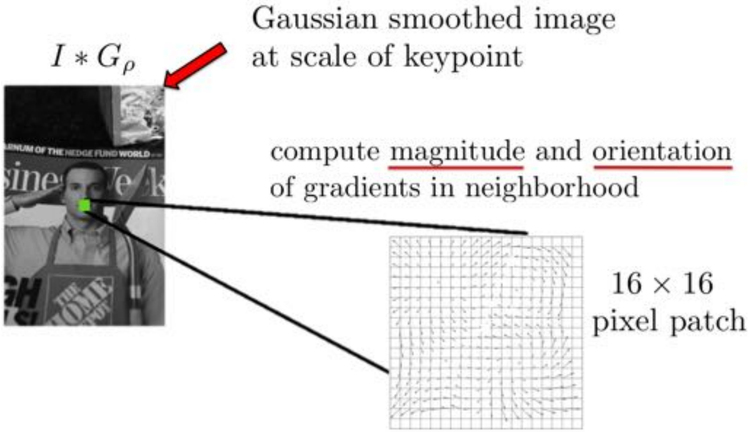
2. For each keypoint, we take the Gaussian-blurred image at corresponding scale ρ



[Adopted from: F. Flores-Mangas]

SIFT Descriptor

3. Compute the gradient magnitude and orientation in neighborhood of each keypoint



[Adopted from: F. Flores-Mangas]

SIFT Descriptor

3. Compute the gradient magnitude and orientation in neighborhood of each keypoint

magnitude of gradient:

$$|\nabla I(x,y)| = \sqrt{\left(\frac{\partial(I(x,y) * G_\rho)}{\partial x}\right)^2 + \left(\frac{\partial(I(x,y) * G_\rho)}{\partial y}\right)^2}$$

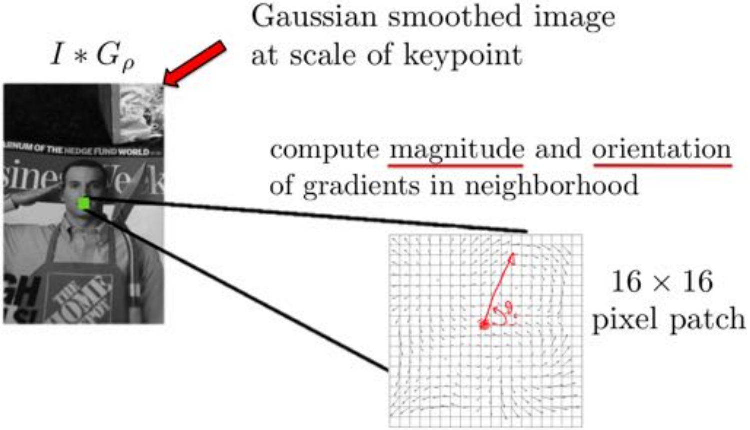
gradient orientation:

$$\theta(x,y) = \arctan\left(\frac{\partial I * G_\rho}{\partial y} / \frac{\partial I * G_\rho}{\partial x}\right)$$

(in case you forgot ;))

SIFT Descriptor

4. Compute dominant orientation of each keypoint. How?

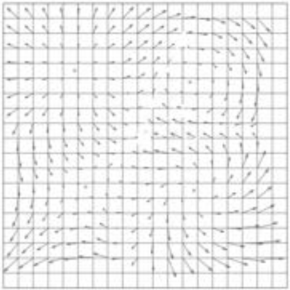


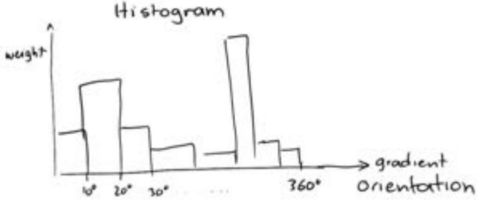
[Adopted from: F. Flores-Mangas]

- Compute a histogram of gradient orientations, each bin covers 10°

compute histograms of orientations
by orientation increments of 10°

16×16

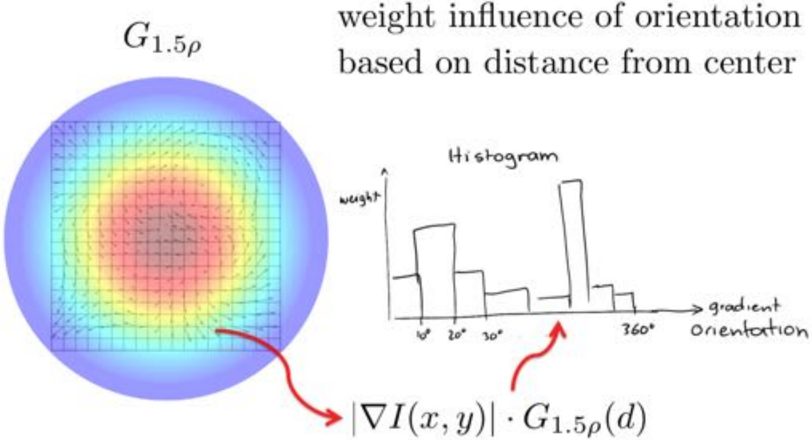




[Adopted from: F. Flores-Mangas]

SIFT Descriptor: Computing Dominant Orientation

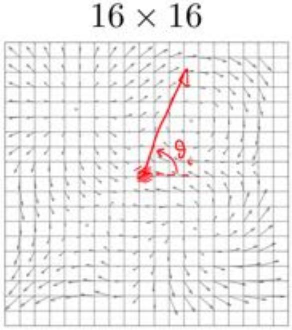
- Compute a histogram of gradient orientations, each bin covers 10°
- Orientations closer to the keypoint center should contribute more

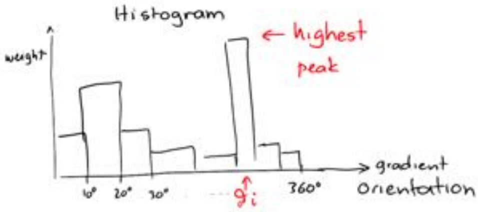


[Adopted from: F. Flores-Mangas]

SIFT Descriptor: Computing Dominant Orientation

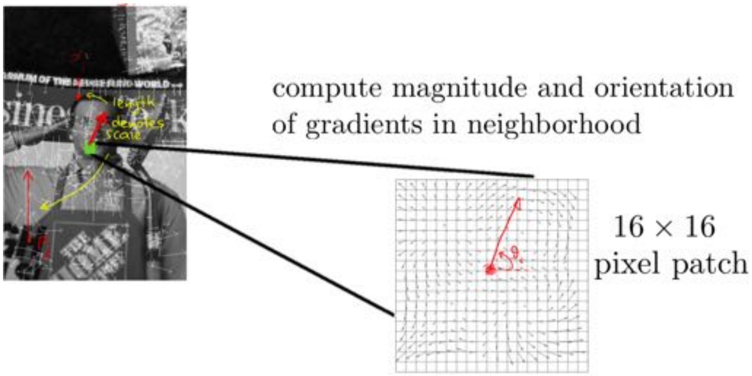
- Compute a histogram of gradient orientations, each bin covers 10°
- Orientations closer to the keypoint center should contribute more
- Orientation giving the peak in the histogram is the keypoint's orientation





SIFT Descriptor

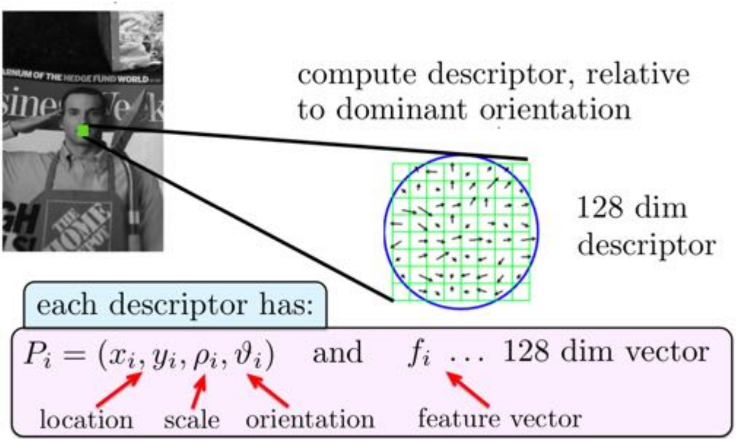
4. Compute dominant orientation



[Adopted from: F. Flores-Mangas]

SIFT Descriptor

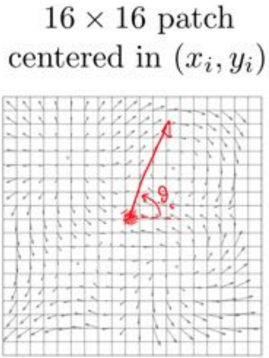
5. Compute a 128 dimensional descriptor: 4×4 grid, each cell is a histogram of 8 orientation bins relative to dominant orientation

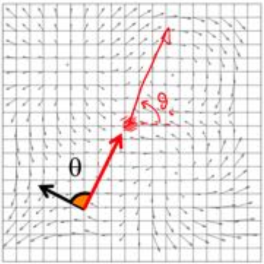


[Adopted from: F. Flores-Mangas]

SIFT Descriptor: Computing the Feature Vector

- Compute the orientations **relative** to the **dominant orientation**

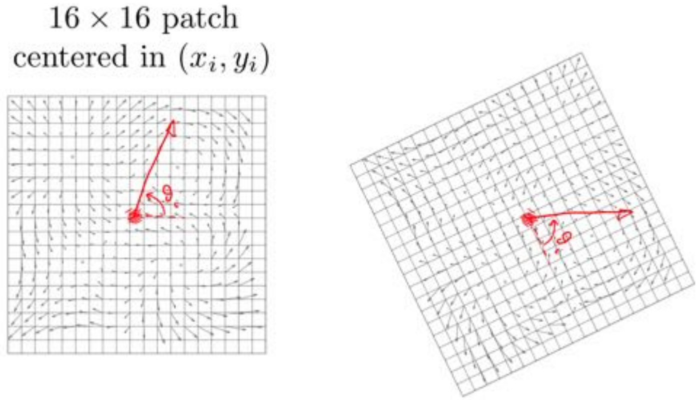




[Adopted from: F. Flores-Mangas]

SIFT Descriptor: Computing the Feature Vector

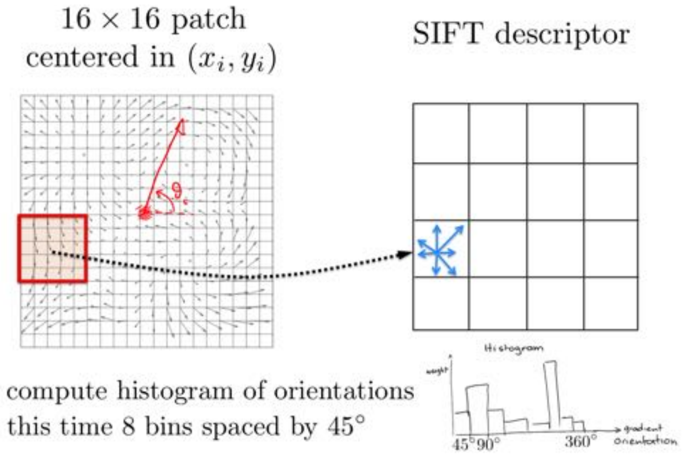
- Compute the orientations **relative** to the **dominant orientation**



[Adopted from: F. Flores-Mangas]

SIFT Descriptor: Computing the Feature Vector

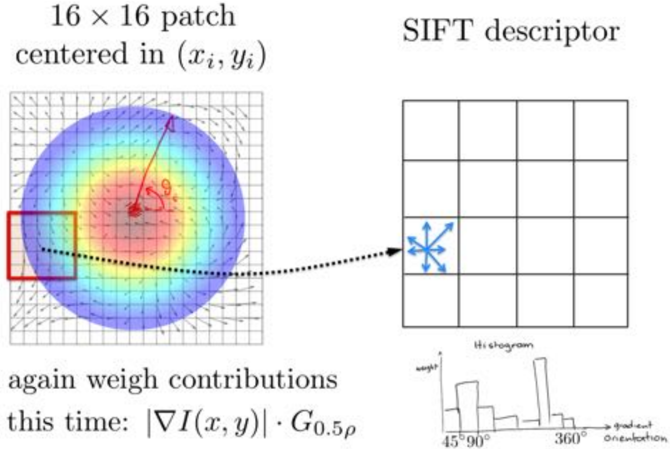
- Compute the orientations **relative** to the **dominant orientation**
- Form a 4×4 grid. For each grid cell compute a histogram of orientations for 8 orientation bins spaced apart by $45°$



[Adopted from: F. Flores-Mangas]

SIFT Descriptor: Computing the Feature Vector

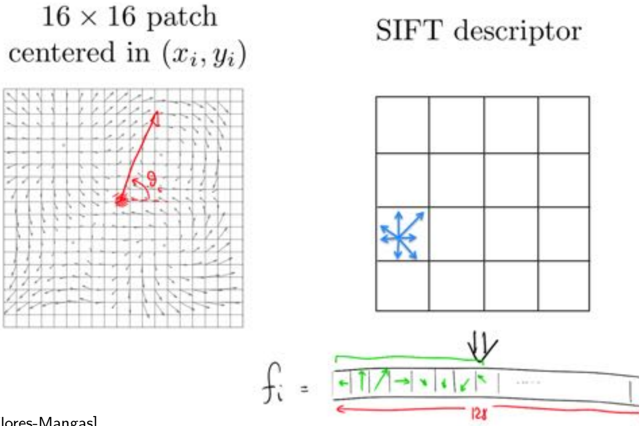
- Compute the orientations **relative** to the **dominant orientation**
- Form a 4×4 grid. For each grid cell compute a histogram of orientations for 8 orientation bins spaced apart by 45°



[Adopted from: F. Flores-Mangas]

SIFT Descriptor: Computing the Feature Vector

- Compute the orientations **relative** to the **dominant orientation**
- Form a 4×4 grid. For each grid cell compute a histogram of orientations for 8 orientation bins spaced apart by 45°
- Form the 128 dimensional feature vector



[Adopted from: F. Flores-Mangas]

SIFT Descriptor: Post-processing

- The resulting 128 non-negative values form a **raw version** of the SIFT descriptor vector.
- To reduce the **effects of contrast or gain** (additive variations are already removed by the gradient), the 128-D vector is normalized to unit length: $f_i = f_i / ||f_i||$

SIFT Descriptor: Post-processing

- The resulting 128 non-negative values form a **raw version** of the SIFT descriptor vector.
- To reduce the **effects of contrast or gain** (additive variations are already removed by the gradient), the 128-D vector is normalized to unit length: $f_i = f_i / ||f_i||$
- To further make the descriptor robust to other **photometric variations**, values are clipped to 0.2 and the resulting vector is once again renormalized to unit length.

SIFT Descriptor: Post-processing

- The resulting 128 non-negative values form a **raw version** of the SIFT descriptor vector.
- To reduce the **effects of contrast or gain** (additive variations are already removed by the gradient), the 128-D vector is normalized to unit length: $f_i = f_i / ||f_i||$
- To further make the descriptor robust to other **photometric variations**, values are clipped to 0.2 and the resulting vector is once again renormalized to unit length.
- Great engineering effort!

SIFT Descriptor: Post-processing

- The resulting 128 non-negative values form a **raw version** of the SIFT descriptor vector.
- To reduce the **effects of contrast or gain** (additive variations are already removed by the gradient), the 128-D vector is normalized to unit length: $f_i = f_i / ||f_i||$
- To further make the descriptor robust to other **photometric variations**, values are clipped to 0.2 and the resulting vector is once again renormalized to unit length.
- Great engineering effort!
- What is SIFT invariant to?

SIFT Descriptor: Post-processing

- The resulting 128 non-negative values form a **raw version** of the SIFT descriptor vector.
- To reduce the **effects of contrast or gain** (additive variations are already removed by the gradient), the 128-D vector is normalized to unit length: $f_i = f_i / ||f_i||$
- To further make the descriptor robust to other **photometric variations**, values are clipped to 0.2 and the resulting vector is once again renormalized to unit length.
- Great engineering effort!
- What is SIFT invariant to?

Properties of SIFT

Invariant to:

- Scale
- Rotation

Partially invariant to:

- Illumination changes (sometimes even day vs. night)
- Camera viewpoint (up to about 60 degrees of out-of-plane rotation)
- Occlusion, clutter (why?)

Also important:

- Fast and efficient – can run in real time
- Lots of code available

Examples

Figure: Matching in day / night under viewpoint change

[Source: S. Seitz]

Example

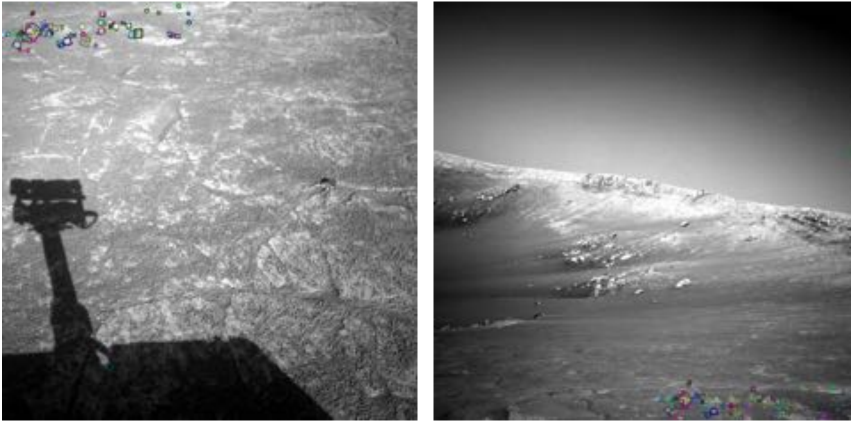


Figure: NASA Mars Rover images with SIFT feature matches

[Source: N. Snavely]

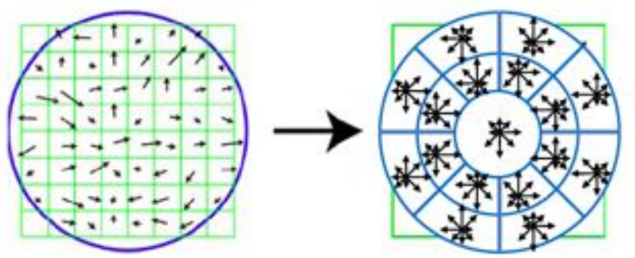
PCA-SIFT

- The dimensionality of SIFT is pretty high, i.e., 128D for each keypoint
- Reduce the dimensionality using linear dimensionality reduction
- In this case, principal component analysis (PCA)
- Use 10D or so descriptor

[Source: R. Urtasun]

Gradient location-orientation histogram (GLOH)

- Developed by Mikolajczyk and Schmid (2005): variant of SIFT that uses a log-polar binning structure instead of the four quadrants.
- The spatial bins are 11, and 15, with eight angular bins (except for the central region), for a total of 17 spatial bins and 16 orientation bins.
- The 272D histogram is then projected onto a 128D descriptor using PCA trained on a large database.



(a) image gradients (b) keypoint descriptor

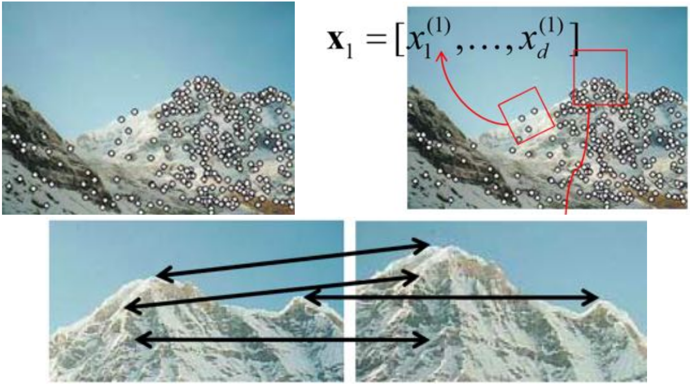
[Source: R. Szeliski]

Other Descriptors

- SURF
- DAISY
- LBP
- HOG
- Shape Contexts
- Color Histograms

Local Features

- **Detection**: Identify the interest points.
- **Description**: Extract feature descriptor around each interest point.
- **Matching**: Determine correspondence between descriptors in two views.



[Source: K. Grauman]

Image Features:

Matching the Local Descriptors

Matching the Local Descriptors

Once we have extracted keypoints and their descriptors, we want to match the features between pairs of images.

- Ideally a match is a correspondence between a local part of the object on one image to the same local part of the object in another image
- How should we compute a match?

Figure: Images from K. Grauman

Matching the Local Descriptors

Once we have extracted keypoints and their descriptors, we want to match the features between pairs of images.

- Ideally a match is a correspondence between a local part of the object on one image to the same local part of the object in another image
- How should we compute a match?

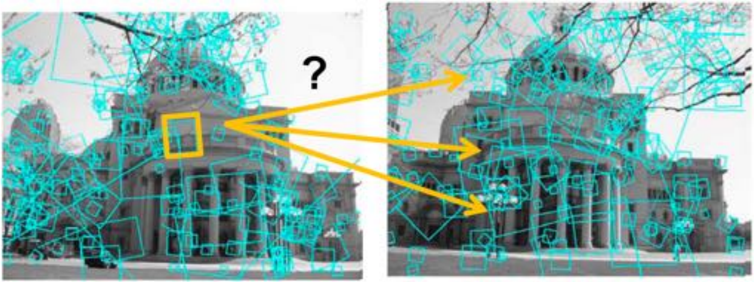
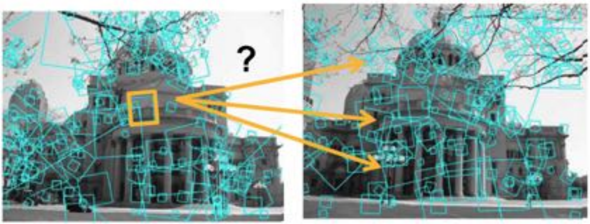
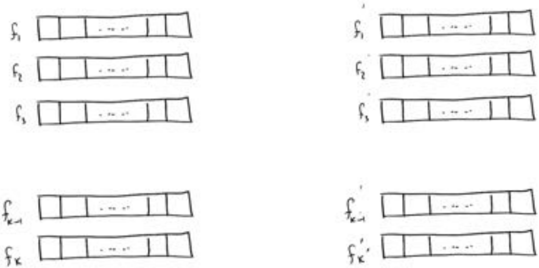


Figure: Images from K. Grauman

Matching the Local Descriptors

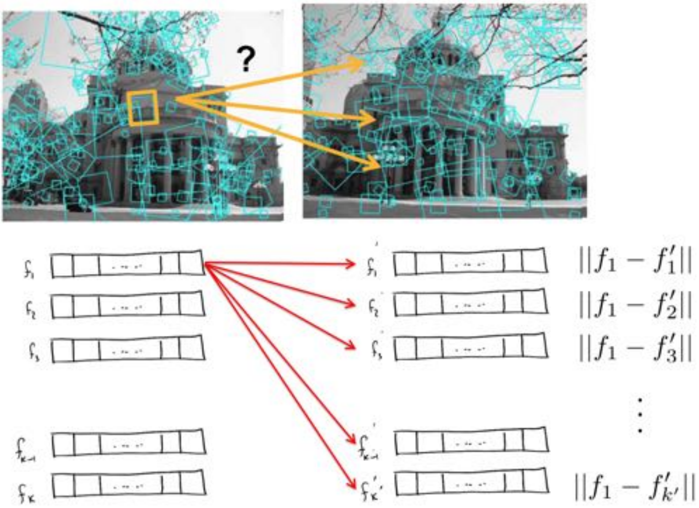
- Simple: **Compare them all**, compute Euclidean distance





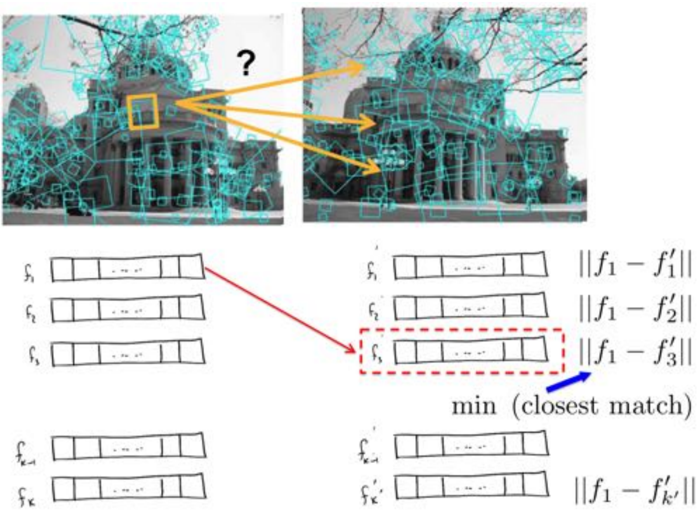
Matching the Local Descriptors

- Simple: **Compare them all**, compute Euclidean distance



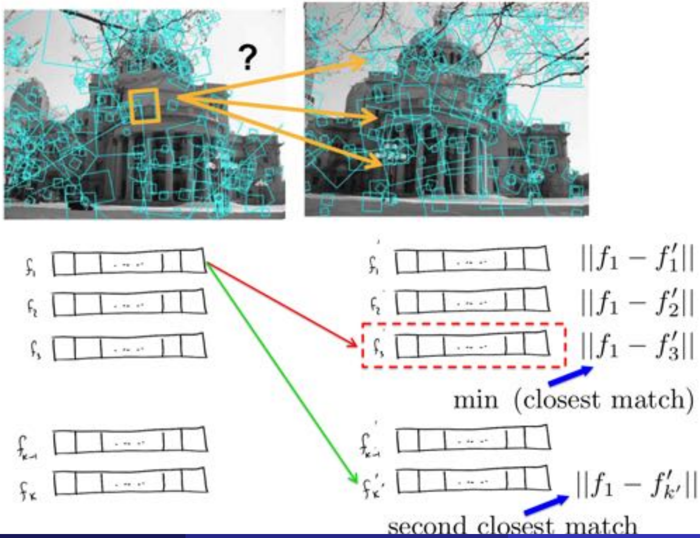
Matching the Local Descriptors

- Find closest match (min distance). How do we know if match is **reliable**?



Matching the Local Descriptors

- Find also the second closest match. Match reliable if first distance "much" smaller than second distance

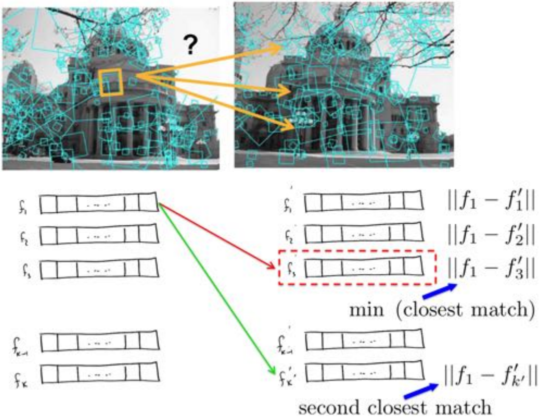


Matching the Local Descriptors

- Compute the ratio:

$$\phi_i = \frac{||f_i - f'^{*}_i||}{||f_i - f'^{**}_i||}$$

where f'^{*}_i is the closest and f'^{**}_i second closest match to f_i.



Which Threshold to Use?

- Setting the threshold too high results in too many false positives, i.e., incorrect matches being returned.
- Setting the threshold too low results in too many false negatives, i.e., too many correct matches being missed

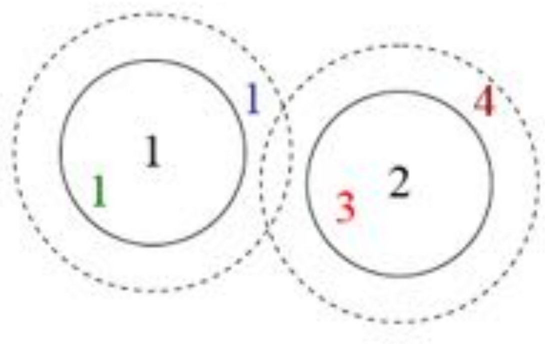


Figure: Images from R. Szeliski

Which Threshold to Use?

- Threshold ratio of nearest to 2nd nearest descriptor
- Typically: $\phi_i < 0.8$

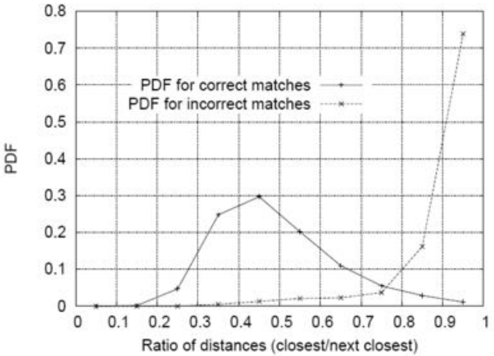


Figure: Images from D. Lowe

[Source: K. Grauman]

Applications of Local Invariant Features

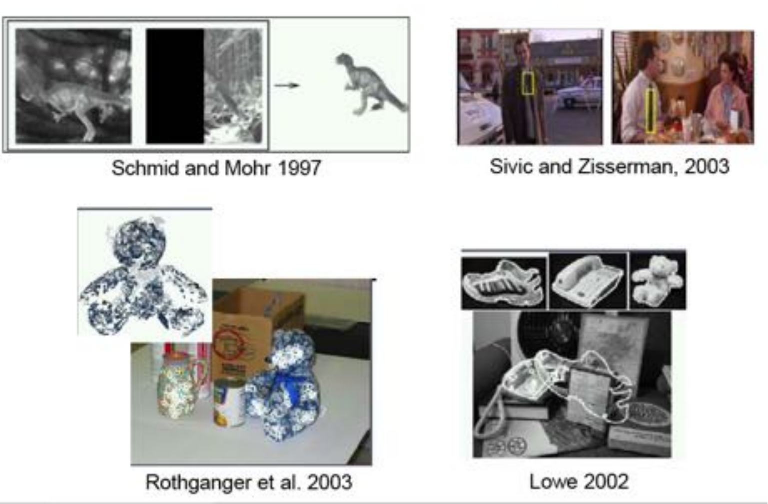
- Wide baseline stereo
- Motion tracking
- Panorama stitching
- Mobile robot navigation
- 3D reconstruction
- Recognition
- Retrieval

[Source: K. Grauman]

Wide Baseline Stereo

[Source: T. Tuytelaars]

Recognizing the Same Object



[Source: K. Grauman]

Motion Tracking

Figure: Images from J. Pilet

Now What

- Now we know how to extract scale and rotation invariant features
- We even know how to match features across images
- Can we use this to find Waldo in an even more sneaky scenario?

Now What

- Now we know how to extract scale and rotation invariant features
- We even know how to match features across images
- Can we use this to find Waldo in an even more sneaky scenario?

Waldo on the road

template

Now What

- Now we know how to extract scale and rotation invariant features
- We even know how to match features across images
- Can we use this to find Waldo in an even more sneaky scenario?

template

He comes closer... We know how to solve this

Now What

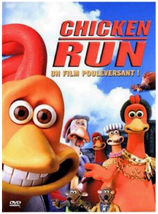
- Now we know how to extract scale and rotation invariant features
- We even know how to match features across images
- Can we use this to find Waldo in an even more sneaky scenario?

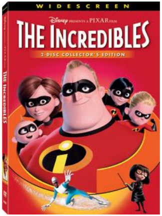
Someone takes a (weird) picture of him!

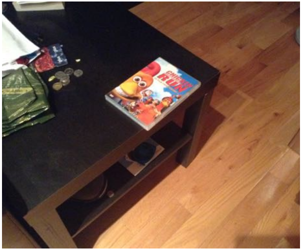
template

Find My DVD!

- More interesting: If we have DVD covers (e.g., from Amazon), can we match them to DVDs in real scenes?

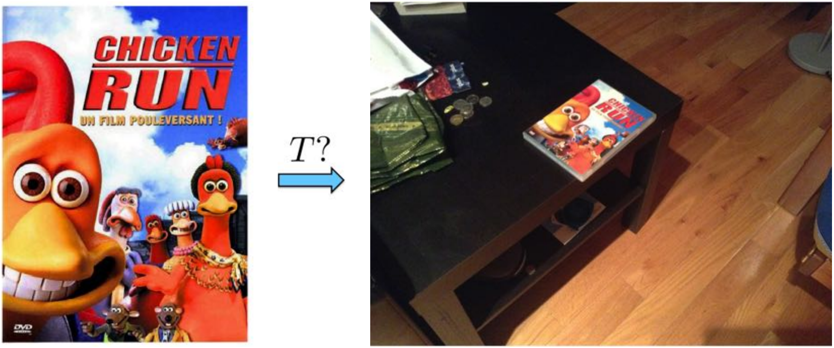




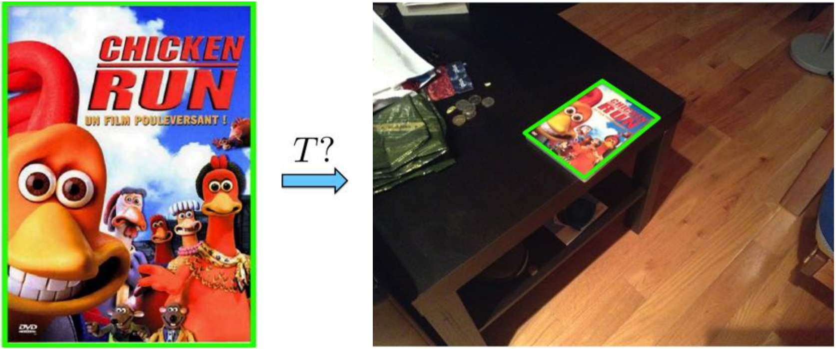

Matching Planar Objects In New Viewpoints

What Kind of Transformation Happened To My DVD?



What Kind of Transformation Happened To My DVD?

- Rectangle goes to a parallelogram (almost but not really, but let's believe that for now)



All 2D Linear Transformations

Linear transformations are combinations of

- Scale,
- Rotation
- Shear
- Mirror

$$\begin{bmatrix} x' \\ y' \end{bmatrix} = \begin{bmatrix} a & b \\ c & d \end{bmatrix} \begin{bmatrix} x \\ y \end{bmatrix}$$

[Source: N. Snavely]

All 2D Linear Transformations

Properties of linear transformations:

- Origin maps to origin
- Lines map to lines

All 2D Linear Transformations

Properties of linear transformations:

- Origin maps to origin
- Lines map to lines
- Parallel lines remain parallel

All 2D Linear Transformations

Properties of linear transformations:

- Origin maps to origin
- Lines map to lines
- Parallel lines remain parallel
- Ratios are preserved

All 2D Linear Transformations

Properties of linear transformations:

- Origin maps to origin
- Lines map to lines
- Parallel lines remain parallel
- Ratios are preserved
- Closed under composition

All 2D Linear Transformations

Properties of linear transformations:

- Origin maps to origin
- Lines map to lines
- Parallel lines remain parallel
- Ratios are preserved
- Closed under composition

$$\begin{bmatrix} x' \\ y' \end{bmatrix} = \begin{bmatrix} a & b \\ c & d \end{bmatrix} \begin{bmatrix} e & f \\ g & h \end{bmatrix} \begin{bmatrix} i & j \\ k & l \end{bmatrix} \begin{bmatrix} x \\ y \end{bmatrix}$$

All 2D Linear Transformations

Properties of linear transformations:

- Origin maps to origin
- Lines map to lines
- Parallel lines remain parallel
- Ratios are preserved
- Closed under composition

$$\begin{bmatrix} x' \\ y' \end{bmatrix} = \begin{bmatrix} a & b \\ c & d \end{bmatrix} \begin{bmatrix} e & f \\ g & h \end{bmatrix} \begin{bmatrix} i & j \\ k & l \end{bmatrix} \begin{bmatrix} x \\ y \end{bmatrix}$$

What about the translation?

[Source: N. Snavely]

All 2D Linear Transformations

Properties of linear transformations:

- Origin maps to origin
- Lines map to lines
- Parallel lines remain parallel
- Ratios are preserved
- Closed under composition

$$\begin{bmatrix} x' \\ y' \end{bmatrix} = \begin{bmatrix} a & b \\ c & d \end{bmatrix} \begin{bmatrix} e & f \\ g & h \end{bmatrix} \begin{bmatrix} i & j \\ k & l \end{bmatrix} \begin{bmatrix} x \\ y \end{bmatrix}$$

What about the translation?

[Source: N. Snavely]

Affine Transformations

Affine transformations are combinations of

- Linear transformations, and
- Translations

$$\begin{bmatrix} x' \\ y' \end{bmatrix} = \begin{bmatrix} a & b \\ c & d \end{bmatrix} \begin{bmatrix} x \\ y \end{bmatrix} + \begin{bmatrix} e \\ f \end{bmatrix}$$

same as:

$$\begin{bmatrix} x' \\ y' \end{bmatrix} = \begin{bmatrix} a & b & e \\ c & d & f \end{bmatrix} \begin{bmatrix} x \\ y \\ 1 \end{bmatrix}$$

Affine Transformations

Affine transformations are combinations of

- Linear transformations, and
- Translations

$$\begin{bmatrix} x' \\ y' \end{bmatrix} = \begin{bmatrix} a & b \\ c & d \end{bmatrix} \begin{bmatrix} x \\ y \end{bmatrix} + \begin{bmatrix} e \\ f \end{bmatrix}$$

same as:

$$\begin{bmatrix} x' \\ y' \end{bmatrix} = \begin{bmatrix} a & b & e \\ c & d & f \end{bmatrix} \begin{bmatrix} x \\ y \\ 1 \end{bmatrix}$$

Affine Transformations

Affine transformations are combinations of

- Linear transformations, and
- Translations

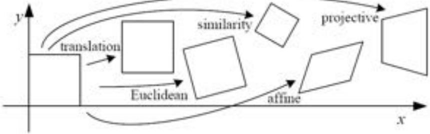
$$\begin{bmatrix} x' \\ y' \end{bmatrix} = \begin{bmatrix} a & b & e \\ c & d & f \end{bmatrix} \begin{bmatrix} x \\ y \\ 1 \end{bmatrix}$$

Properties of affine transformations:

- Origin does not necessarily map to origin
- Lines map to lines
- Parallel lines remain parallel
- Ratios are preserved
- Closed under composition
- Rectangles go to parallelograms

[Source: N. Snavely]

2D Image Tranformations

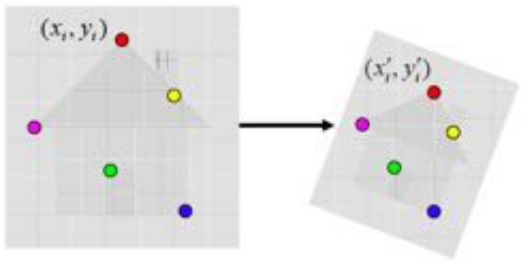


Transformation	Matrix	# DoF	Preserves	Icon
translation	$\begin{bmatrix} I \mid t \end{bmatrix}_{2\times 3}$	2	orientation	
rigid (Euclidean)	$\begin{bmatrix} R \mid t \end{bmatrix}_{2\times 3}$	3	lengths	
similarity	$\begin{bmatrix} sR \mid t \end{bmatrix}_{2\times 3}$	4	angles	
affine	$\begin{bmatrix} A \end{bmatrix}_{2\times 3}$	6	parallelism	
projective	$\begin{bmatrix} \tilde{H} \end{bmatrix}_{3\times 3}$	8	straight lines	

- These transformations are a nested set of groups
- Closed under composition and inverse is a member

What Transformation Happened to My DVD?

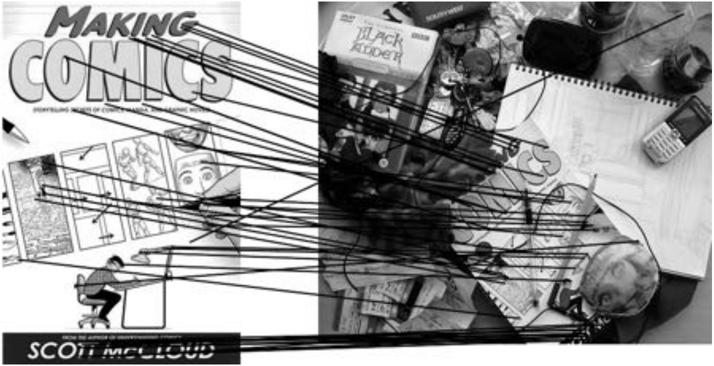
- Affine transformation approximates viewpoint changes for roughly **planar objects** and roughly **orthographic cameras** (more about these later in class)
- DVD went affine!



Computing the (Affine) Transformation

Given a set of matches between images I and J

- How can we compute the affine transformation A from I to J?
- Find transform A that best agrees with the matches

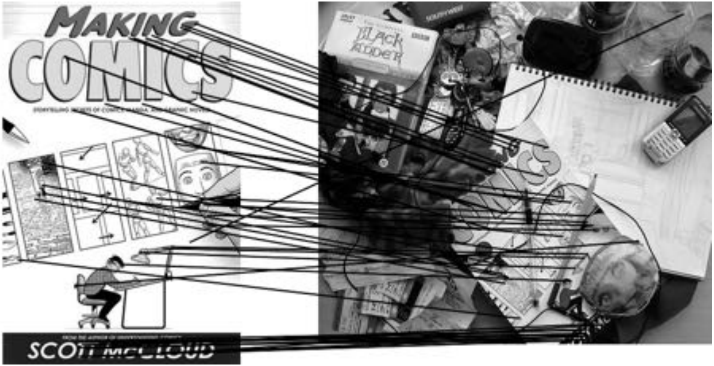


[Source: N. Snavely]

Computing the (Affine) Transformation

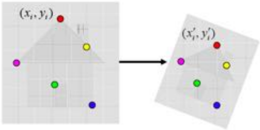
Given a set of matches between images I and J

- How can we compute the affine transformation A from I to J?
- Find transform A that best agrees with the matches



[Source: N. Snavely]

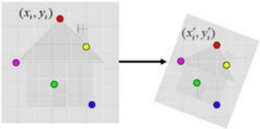
Computing the Affine Transformation



- Let (x_i, y_i) be a point on the reference (model) image, and (x_i', y_i') its match in the test image
- An affine transformation A maps (x_i, y_i) to (x_i', y_i'):

$$\begin{bmatrix} x_i' \\ y_i' \end{bmatrix} = \begin{bmatrix} a & b & e \\ c & d & f \end{bmatrix} \begin{bmatrix} x_i \\ y_i \\ 1 \end{bmatrix}$$

Computing the Affine Transformation



- Let (x_i, y_i) be a point on the reference (model) image, and (x_i', y_i') its match in the test image
- An affine transformation A maps (x_i, y_i) to (x_i', y_i'):

$$\begin{bmatrix} x_i' \\ y_i' \end{bmatrix} = \begin{bmatrix} a & b & e \\ c & d & f \end{bmatrix} \begin{bmatrix} x_i \\ y_i \\ 1 \end{bmatrix}$$

- We can rewrite this into a simple linear system:

$$\begin{bmatrix} x_i & y_i & 0 & 0 & 1 & 0 \\ 0 & 0 & x_i & y_i & 0 & 1 \end{bmatrix} \begin{bmatrix} a \\ b \\ c \\ d \\ e \\ f \end{bmatrix} = \begin{bmatrix} x_i' \\ y_i' \end{bmatrix}$$

Computing the Affine Transformation

- But we have many matches:

$$\underbrace{\begin{bmatrix} & & \vdots & & & \\ x_i & y_i & 0 & 0 & 1 & 0 \\ 0 & 0 & x_i & y_i & 0 & 1 \\ & & \vdots & & & \end{bmatrix}}_{\mathbf{P}} \underbrace{\begin{bmatrix} a \\ b \\ c \\ d \\ e \\ f \end{bmatrix}}_{\mathbf{a}} = \underbrace{\begin{bmatrix} \vdots \\ x'_i \\ y'_i \\ \vdots \end{bmatrix}}_{\mathbf{P'}}$$

- For each match we have two more equations

Computing the Affine Transformation

- But we have many matches:

$$\underbrace{\begin{bmatrix} & & \vdots & & & \\ x_i & y_i & 0 & 0 & 1 & 0 \\ 0 & 0 & x_i & y_i & 0 & 1 \\ & & \vdots & & & \end{bmatrix}}_{\mathbf{P}} \underbrace{\begin{bmatrix} a \\ b \\ c \\ d \\ e \\ f \end{bmatrix}}_{\mathbf{a}} = \underbrace{\begin{bmatrix} \vdots \\ x'_i \\ y'_i \\ \vdots \end{bmatrix}}_{\mathbf{P}'}$$

- For each match we have two more equations
- How many matches do we need to compute A?

Computing the Affine Transformation

- But we have many matches:

$$\underbrace{\begin{bmatrix} & & \vdots & & & \\ x_i & y_i & 0 & 0 & 1 & 0 \\ 0 & 0 & x_i & y_i & 0 & 1 \\ & & \vdots & & & \end{bmatrix}}_{\mathbf{P}} \underbrace{\begin{bmatrix} a \\ b \\ c \\ d \\ e \\ f \end{bmatrix}}_{\mathbf{a}} = \underbrace{\begin{bmatrix} \vdots \\ x'_i \\ y'_i \\ \vdots \end{bmatrix}}_{\mathbf{P}'}$$

- For each match we have two more equations
- How many matches do we need to compute A?

Computing the Affine Transformation

- But we have many matches:

$$\underbrace{\begin{bmatrix} & & \vdots & & & \\ x_i & y_i & 0 & 0 & 1 & 0 \\ 0 & 0 & x_i & y_i & 0 & 1 \\ & & \vdots & & & \end{bmatrix}}_{\mathbf{P}} \underbrace{\begin{bmatrix} a \\ b \\ c \\ d \\ e \\ f \end{bmatrix}}_{\mathbf{a}} = \underbrace{\begin{bmatrix} \vdots \\ x_i' \\ y_i' \\ \vdots \end{bmatrix}}_{\mathbf{P}'}$$

- For each match we have two more equations
- How many matches do we need to compute A?
- 6 parameters $\rightarrow$ 3 matches
- But the more, the better (more reliable)
- How do we compute A?

Computing the Affine Transformation

$$\underbrace{\begin{bmatrix} & & \vdots & & & \\ x_i & y_i & 0 & 0 & 1 & 0 \\ 0 & 0 & x_i & y_i & 0 & 1 \\ & & \vdots & & & \end{bmatrix}}_{\mathbf{P}} \underbrace{\begin{bmatrix} a \\ b \\ c \\ d \\ e \\ f \end{bmatrix}}_{\mathbf{a}} = \underbrace{\begin{bmatrix} \vdots \\ x_i' \\ y_i' \\ \vdots \end{bmatrix}}_{\mathbf{P}'}$$

- If we have 3 matches, then computing A is really easy:

$$\mathbf{a} = \mathbf{P}^{-1}\mathbf{P}'$$

Computing the Affine Transformation

$$\underbrace{\begin{bmatrix} & & \vdots & & & \\ x_i & y_i & 0 & 0 & 1 & 0 \\ 0 & 0 & x_i & y_i & 0 & 1 \\ & & \vdots & & & \end{bmatrix}}_{\mathbf{P}} \underbrace{\begin{bmatrix} a \\ b \\ c \\ d \\ e \\ f \end{bmatrix}}_{\mathbf{a}} = \underbrace{\begin{bmatrix} \vdots \\ x_i' \\ y_i' \\ \vdots \end{bmatrix}}_{\mathbf{P}'}$$

- If we have 3 matches, then computing A is really easy:

$$\mathbf{a} = \mathbf{P}^{-1}\mathbf{P}'$$

- If we have more than 3, then we do **least-squares estimation**:

$$\min_{a,b,\cdots,f} ||\mathbf{Pa} - \mathbf{P}'||_2^2$$

Computing the Affine Transformation

$$\underbrace{\begin{bmatrix} & & \vdots & & & \\ x_i & y_i & 0 & 0 & 1 & 0 \\ 0 & 0 & x_i & y_i & 0 & 1 \\ & & \vdots & & & \end{bmatrix}}_{\mathbf{P}} \underbrace{\begin{bmatrix} a \\ b \\ c \\ d \\ e \\ f \end{bmatrix}}_{\mathbf{a}} = \underbrace{\begin{bmatrix} \vdots \\ x'_i \\ y'_i \\ \vdots \end{bmatrix}}_{\mathbf{P}'}$$

- If we have 3 matches, then computing A is really easy:

$$\mathbf{a} = \mathbf{P}^{-1}\mathbf{P}'$$

- If we have more than 3, then we do **least-squares estimation**:

$$\min_{a,b,\cdots,f} ||\mathbf{Pa} - \mathbf{P}'||_2^2$$

- Which has a closed form solution:

$$\mathbf{a} = (\mathbf{P}^T\mathbf{P})^{-1}\mathbf{P}^T\mathbf{P}'$$

Image Alignment Algorithm: Affine Case

Given images I and J

1. Compute image features for I and J
2. Match features between I and J
3. Compute affine transformation A between I and J using least squares on the set of matches

Image Alignment Algorithm: Affine Case

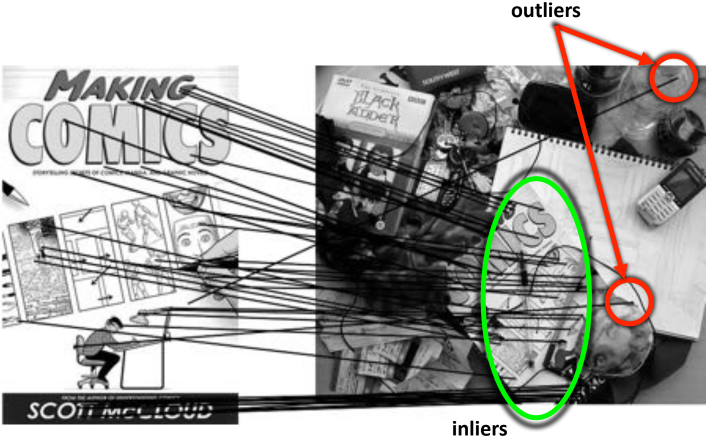
Given images I and J

1. Compute image features for I and J
2. Match features between I and J
3. Compute affine transformation A between I and J using least squares on the set of matches

Is there a problem with this?

[Source: N. Snavely]

Robustness

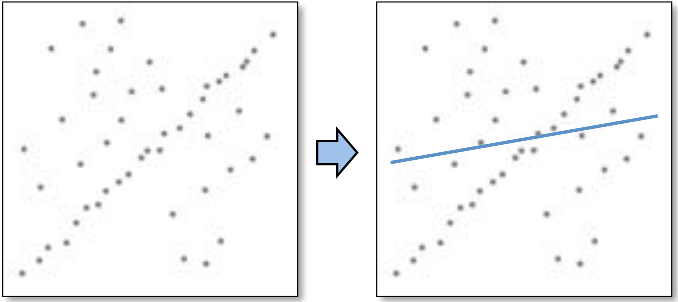


[Source: N. Snavely]

Simple Case

(This example is unrelated to the object matching example, but it nicely shows how to robustify estimation)

- Lets consider a simpler example ... Fit a line to the points below!



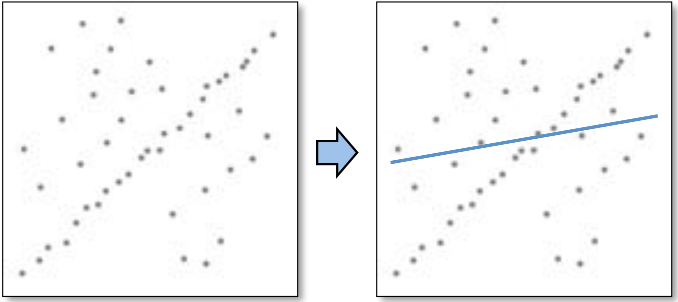
Problem: Fit a line to these datapoints

Least squares fit

Simple Case

(This example is unrelated to the object matching example, but it nicely shows how to robustify estimation)

- Lets consider a simpler example ... Fit a line to the points below!



Problem: Fit a line to these datapoints

Least squares fit

- How can we fix this?

[Source: N. Snavely]

Simple Idea: RANSAC

- Take the minimal number of points to compute what we want. In the line example, two points (in our affine example, three matches)

Simple Idea: RANSAC

- Take the minimal number of points to compute what we want. In the line example, two points (in our affine example, three matches)
- By "take" we mean choose at random from all points

Simple Idea: RANSAC

- Take the minimal number of points to compute what we want. In the line example, two points (in our affine example, three matches)
- By "take" we mean choose at random from all points
- Fit a line to the selected pair of points

Simple Idea: RANSAC

- Take the minimal number of points to compute what we want. In the line example, two points (in our affine example, three matches)
- By "take" we mean choose at random from all points
- Fit a line to the selected pair of points
- Count the number of all points that "agree" with the line: We call the agreeing points **inliers**

Simple Idea: RANSAC

- Take the minimal number of points to compute what we want. In the line example, two points (in our affine example, three matches)
- By "take" we mean choose at random from all points
- Fit a line to the selected pair of points
- Count the number of all points that "agree" with the line: We call the agreeing points **inliers**
- "Agree" = within a small distance of the line

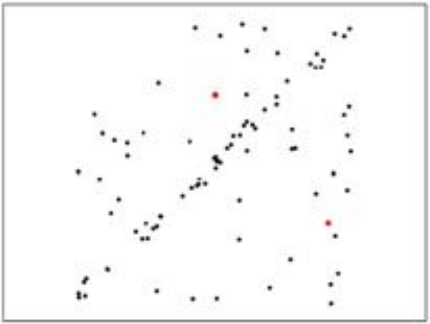
Simple Idea: RANSAC

- Take the minimal number of points to compute what we want. In the line example, two points (in our affine example, three matches)
- By "take" we mean choose at random from all points
- Fit a line to the selected pair of points
- Count the number of all points that "agree" with the line: We call the agreeing points **inliers**
- "Agree" = within a small distance of the line
- Repeat this many times, remember the number of inliers for each trial
- Among several trials, select the one with the largest number of inliers

This procedure is called **RA**ndom **SA**mple **C**onsensus

RANSAC for Line Fitting Example

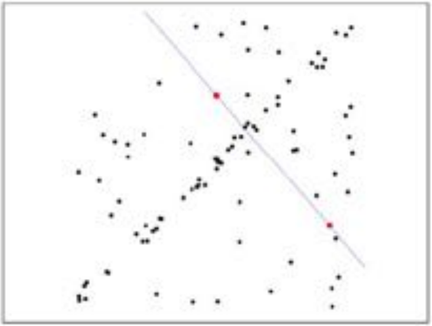
1. Randomly select minimal subset of points



[Source: R. Raguram]

RANSAC for Line Fitting Example

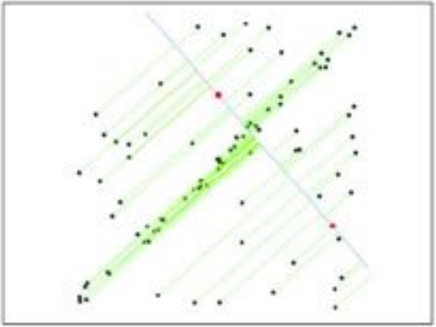
1. Randomly select minimal subset of points
2. Hypothesize a model



[Source: R. Raguram]

RANSAC for Line Fitting Example

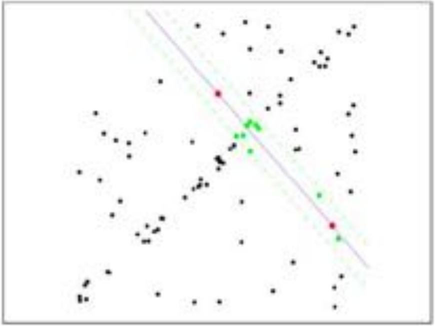
1. Randomly select minimal subset of points
2. Hypothesize a model
3. Compute error function



[Source: R. Raguram]

RANSAC for Line Fitting Example

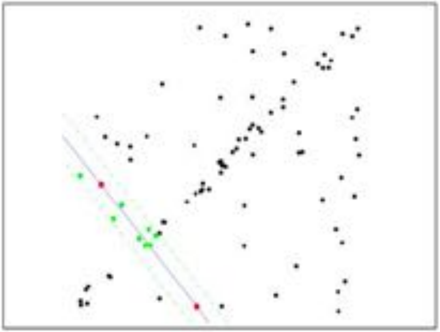
1. Randomly select minimal subset of points
2. Hypothesize a model
3. Compute error function
4. Select points consistent with model



[Source: R. Raguram]

RANSAC for Line Fitting Example

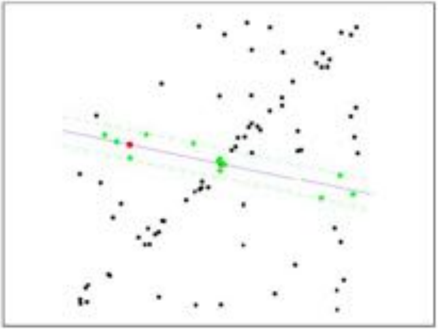
1. Randomly select minimal subset of points
2. Hypothesize a model
3. Compute error function
4. Select points consistent with model
5. Repeat hypothesize and verify loop



[Source: R. Raguram]

RANSAC for Line Fitting Example

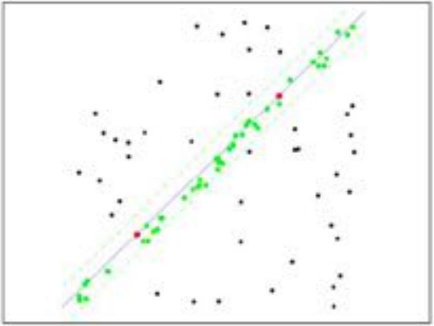
1. Randomly select minimal subset of points
2. Hypothesize a model
3. Compute error function
4. Select points consistent with model
5. Repeat hypothesize and verify loop



[Source: R. Raguram]

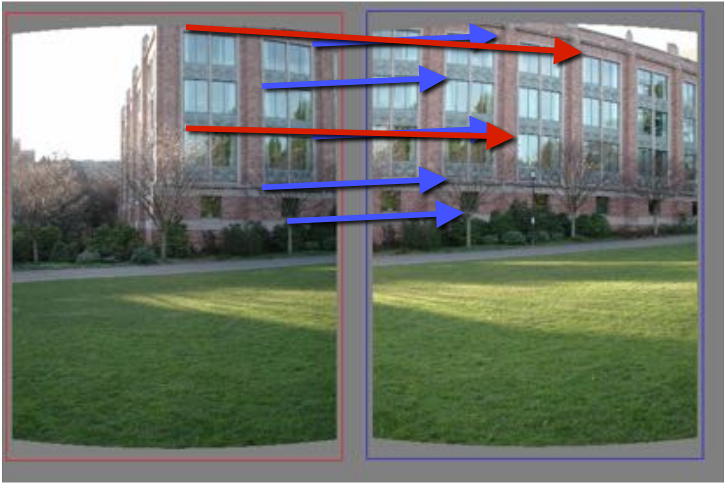
RANSAC for Line Fitting Example

1. Randomly select minimal subset of points
2. Hypothesize a model
3. Compute error function
4. Select points consistent with model
5. Repeat hypothesize and verify loop
6. Choose model with largest set of inliers



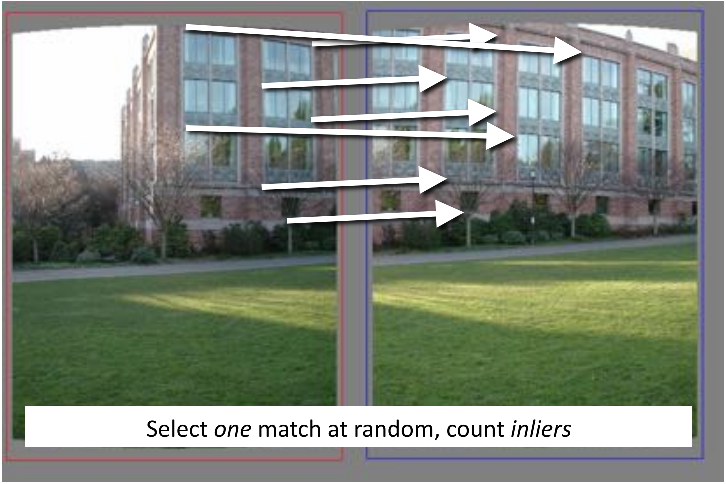
[Source: R. Raguram]

Translations



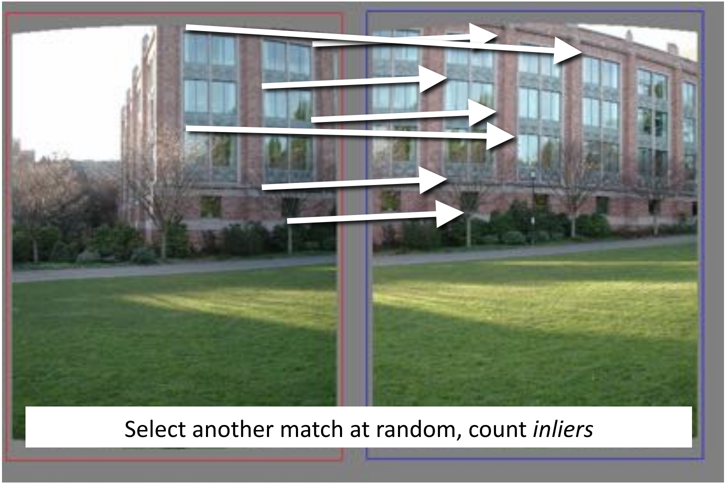
[Source: N. Snavely]

RAndom SAmple Consensus



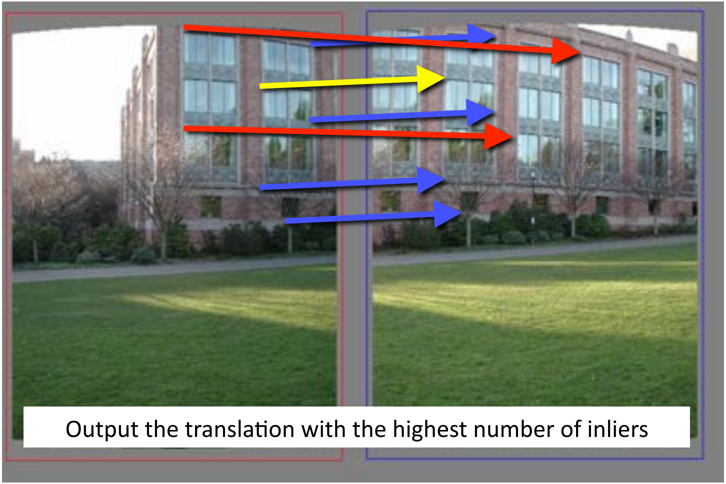
[Source: N. Snavely]

RAndom SAmple Consensus



[Source: N. Snavely]

RAndom SAmple Consensus



[Source: N. Snavely]

RANSAC

- All the inliers will agree with each other on the translation vector; the (hopefully small) number of outliers will (hopefully) disagree with each other

RANSAC

- All the inliers will agree with each other on the translation vector; the (hopefully small) number of outliers will (hopefully) disagree with each other
- RANSAC only has guarantees if there are $< 50\%$ outliers

RANSAC

- All the inliers will agree with each other on the translation vector; the (hopefully small) number of outliers will (hopefully) disagree with each other
- RANSAC only has guarantees if there are $< 50\%$ outliers
- "All good matches are alike; every bad match is bad in its own way." – [Tolstoy via Alyosha Efros]

[Source: N. Snavely]

Affine Transformation

How?

Affine Transformation

How?

- Find matches across images I and J. This gives us points X_I in image I and X_J in J, where we know that the point X_I^k is a match with X_J^k
- Iterate:
  - Choose 3 pairs of matches randomly
  - Compute the affine transformation
  - Project all matched points X_I from I to J via the computed transformation. This gives us $\hat{X}_I$
  - Find how many matches are inliers, i.e., $||\hat{X}_I^k - X_J^k|| < thresh$.
- Choose the transformation with the most inliers

RANSAC

- **Inlier threshold** related to the amount of noise we expect in inliers

RANSAC

- **Inlier threshold** related to the amount of noise we expect in inliers
- Often model noise as Gaussian with some standard deviation (e.g., 3 pixels)

RANSAC

- **Inlier threshold** related to the amount of noise we expect in inliers
- Often model noise as Gaussian with some standard deviation (e.g., 3 pixels)
- **Number of rounds** related to the percentage of outliers we expect, and the probability of success we'd like to guarantee

RANSAC

- **Inlier threshold** related to the amount of noise we expect in inliers
- Often model noise as Gaussian with some standard deviation (e.g., 3 pixels)
- **Number of rounds** related to the percentage of outliers we expect, and the probability of success we'd like to guarantee
- Suppose there are 20% outliers, and we want to find the correct answer with 99% probability

RANSAC

- **Inlier threshold** related to the amount of noise we expect in inliers
- Often model noise as Gaussian with some standard deviation (e.g., 3 pixels)
- **Number of rounds** related to the percentage of outliers we expect, and the probability of success we'd like to guarantee
- Suppose there are 20% outliers, and we want to find the correct answer with 99% probability
- How many rounds do we need?

[Source: R. Urtasun]

How many rounds?

- Sufficient number of trials S must be tried.

How many rounds?

- Sufficient number of trials S must be tried.
- Let p be the probability that any given correspondence is valid and P be the total probability of success after S trials.

How many rounds?

- Sufficient number of trials S must be tried.
- Let p be the probability that any given correspondence is valid and P be the total probability of success after S trials.
- The likelihood in one trial that all k random samples are inliers is p^k

How many rounds?

- Sufficient number of trials S must be tried.
- Let p be the probability that any given correspondence is valid and P be the total probability of success after S trials.
- The likelihood in one trial that all k random samples are inliers is p^k
- The likelihood that S such trials will all fail is

$$1 - P = (1 - p^k)^S$$

How many rounds?

- Sufficient number of trials S must be tried.
- Let p be the probability that any given correspondence is valid and P be the total probability of success after S trials.
- The likelihood in one trial that all k random samples are inliers is p^k
- The likelihood that S such trials will all fail is

$$1 - P = (1 - p^k)^S$$

- The required minimum number of trials is

$$S = \frac{\log(1 - P)}{\log(1 - p^k)}$$

How many rounds?

- Sufficient number of trials S must be tried.
- Let p be the probability that any given correspondence is valid and P be the total probability of success after S trials.
- The likelihood in one trial that all k random samples are inliers is p^k
- The likelihood that S such trials will all fail is

$$1 - P = (1 - p^k)^S$$

- The required minimum number of trials is

$$S = \frac{\log(1 - P)}{\log(1 - p^k)}$$

- The number of trials grows quickly with the number of sample points used.

How many rounds?

- Sufficient number of trials S must be tried.
- Let p be the probability that any given correspondence is valid and P be the total probability of success after S trials.
- The likelihood in one trial that all k random samples are inliers is p^k
- The likelihood that S such trials will all fail is

$$1 - P = (1 - p^k)^S$$

- The required minimum number of trials is

$$S = \frac{\log(1 - P)}{\log(1 - p^k)}$$

- The number of trials grows quickly with the number of sample points used.

[Source: R. Urtasun]

RANSAC pros and cons

Pros

- Simple and general

RANSAC pros and cons

Pros

- Simple and general
- Applicable to many different problems

RANSAC pros and cons

Pros

- Simple and general
- Applicable to many different problems
- Often works well in practice

RANSAC pros and cons

Pros

- Simple and general
- Applicable to many different problems
- Often works well in practice

Cons

- Parameters to tune

RANSAC pros and cons

Pros

- Simple and general
- Applicable to many different problems
- Often works well in practice

Cons

- Parameters to tune
- Sometimes too many iterations are required

RANSAC pros and cons

Pros

- Simple and general
- Applicable to many different problems
- Often works well in practice

Cons

- Parameters to tune
- Sometimes too many iterations are required
- Can fail for extremely low inlier ratios

RANSAC pros and cons

Pros

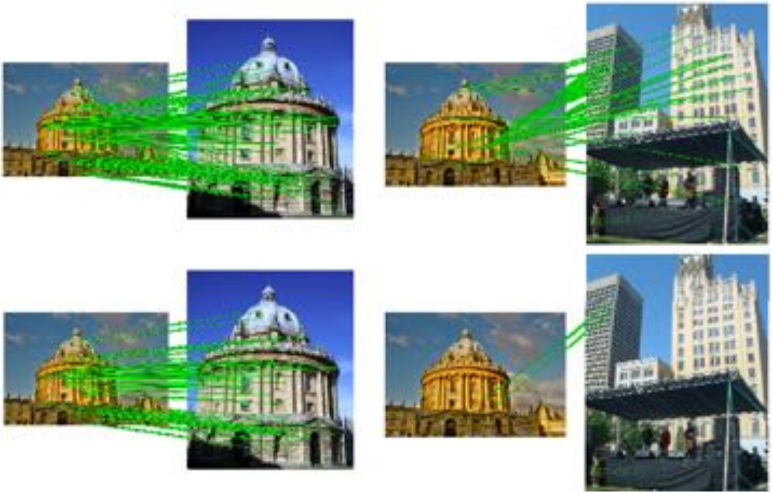
- Simple and general
- Applicable to many different problems
- Often works well in practice

Cons

- Parameters to tune
- Sometimes too many iterations are required
- Can fail for extremely low inlier ratios
- We can often do better than brute-force sampling

[Source: N. Snavely, slide credit: R. Urtasun]

Ransac Verification



[Source: K. Grauman, slide credit: R. Urtasun]

Summary – Stuff You Need To Know

To match image I and J under affine transformation:

- Compute scale and rotation invariant keypoints in both images
- Compute a (rotation invariant) feature vector in each keypoint (e.g., SIFT)
- Match all features in I to all features in J
- For each feature in reference image I find closest match in J
- If ratio between closest and second closest match is < 0.8, keep match
- Do RANSAC to compute affine transformation A:
  - Select 3 matches at random
  - Compute A
  - Compute the number of inliers
  - Repeat
  - Find A that gave the most inliers