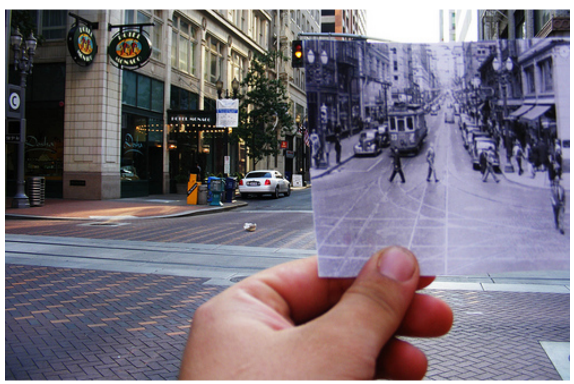
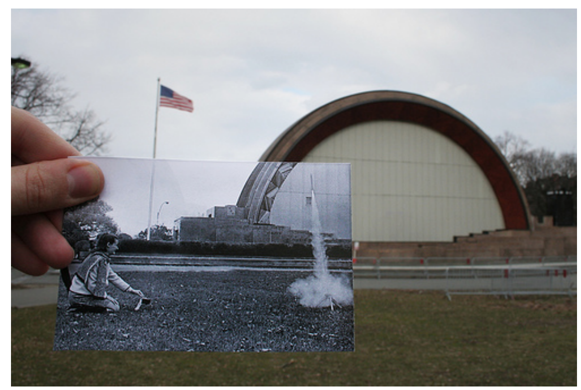
Image alignment

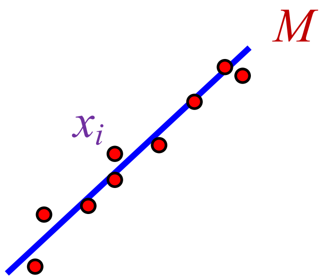


[Source]

Alignment: Fitting of transformations

- Previously: fitting a model to features in one image



- Given: points $x_1, \dots, x_n$
- Find: model M that minimizes

$$\sum_i \text{residual}(x_i, M)$$

Alignment: Fitting of transformations

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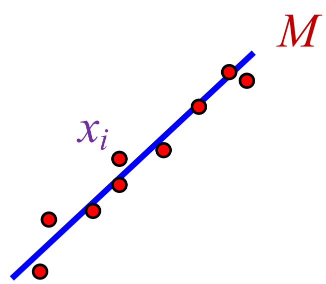
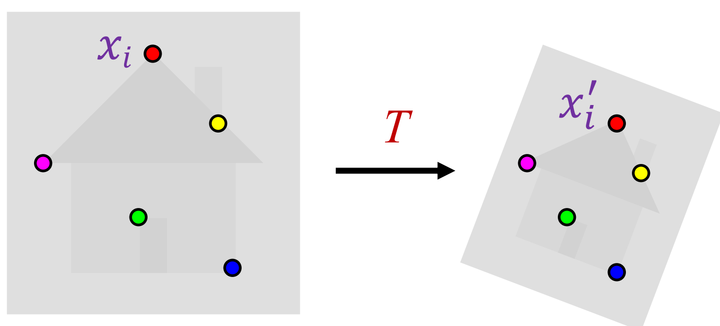


- Given: points $x_1, \dots, x_n$
- Find: model M that minimizes

$$\sum_i \text{residual}(x_i, M)$$

- Alignment: fitting a model to a transformation between pairs of features (*matches*) in two images



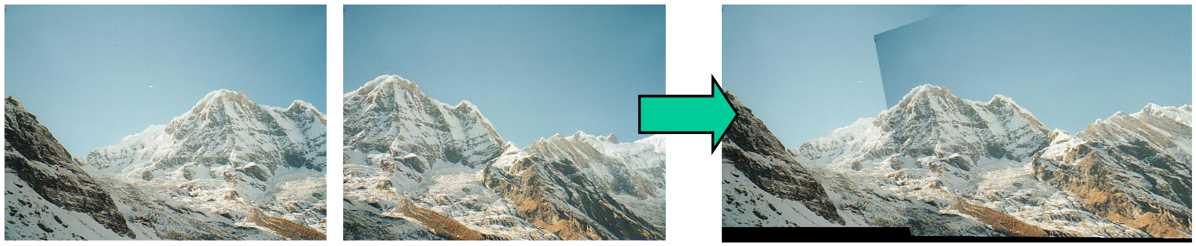
- Given: matches $(x_1, x_1'), \dots, (x_n, x_n')$
- Find: transformation T that minimizes

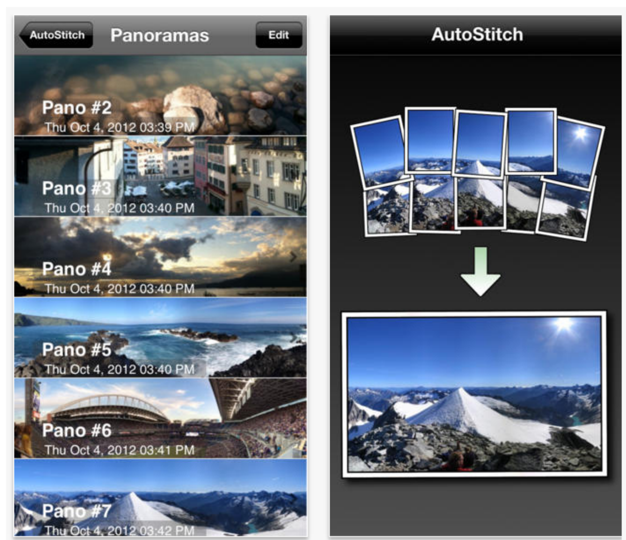
$$\sum_i \text{residual}(T(x_i), x_i')$$

Alignment: Overview

- Motivation
- Fitting of transformations
  - Affine transformations
  - Homographies
- Robust alignment
  - Descriptor-based feature matching
  - RANSAC
- Large-scale alignment
  - Inverted indexing
  - Vocabulary trees

Alignment applications: Panorama stitching

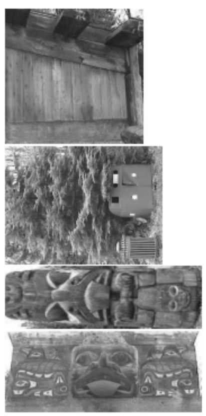




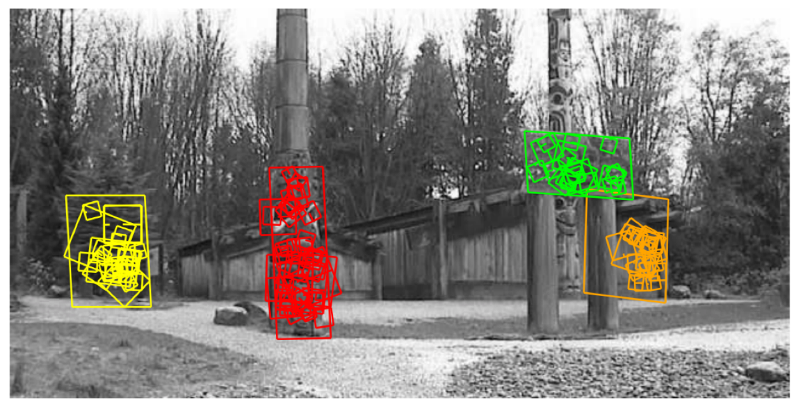
http://matthewalunbrown.com/autostitch/autostitch.html

Alignment applications: Instance recognition

Model images



Test image



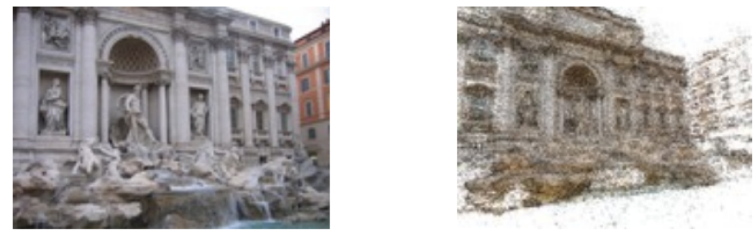
David G. Lowe. [Distinctive image features from scale-invariant keypoints](). *IJCV* 60 (2), pp. 91-110, 2004

Alignment applications: Instance recognition

T. Weyand and B. Leibe, [Visual landmark recognition from Internet photo collections: A large-scale evaluation](), CVIU 2015

Alignment applications: Large-scale reconstruction

Colosseum: 2,097 images, 819,242 points



Trevi Fountain: 1,935 images, 1,055,153 points

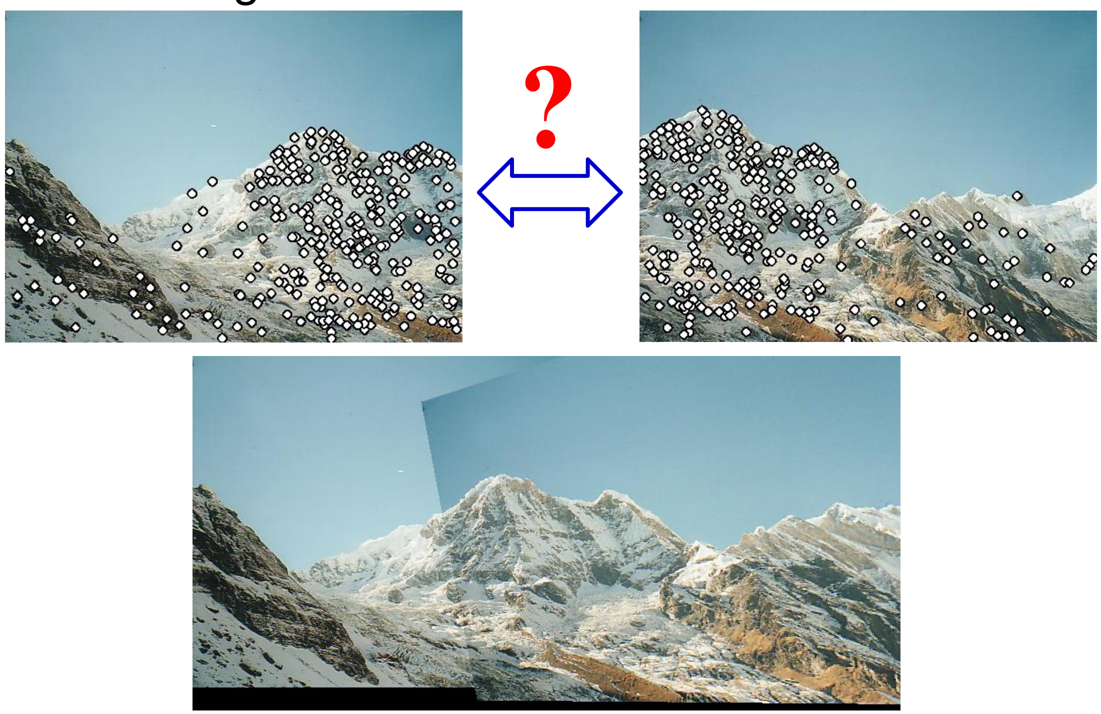
Pantheon: 1,032 images, 530,076 points

Hall of Maps: 275 images, 230,182 points

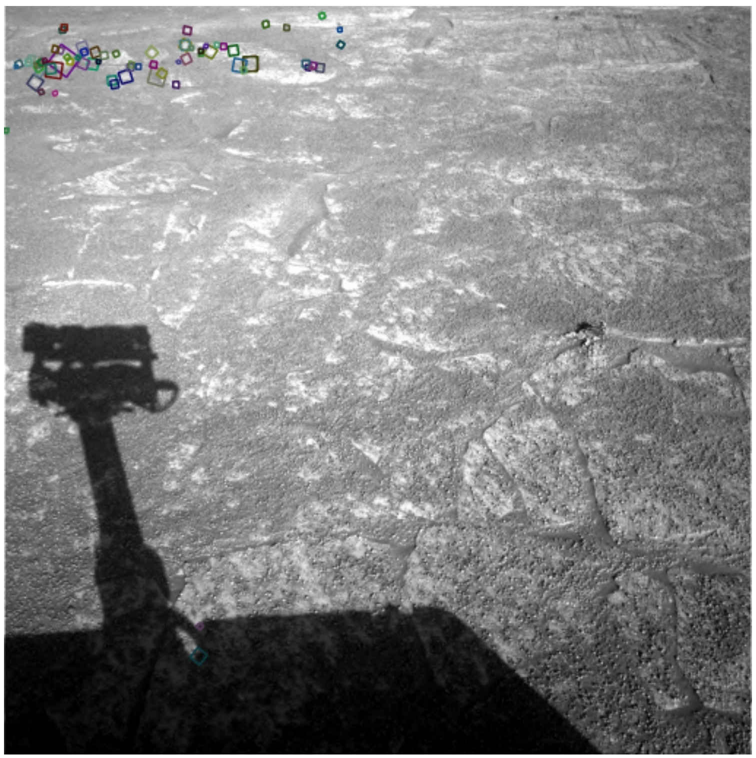
S. Agarwal et al. Building Rome in a Day. ICCV 2009

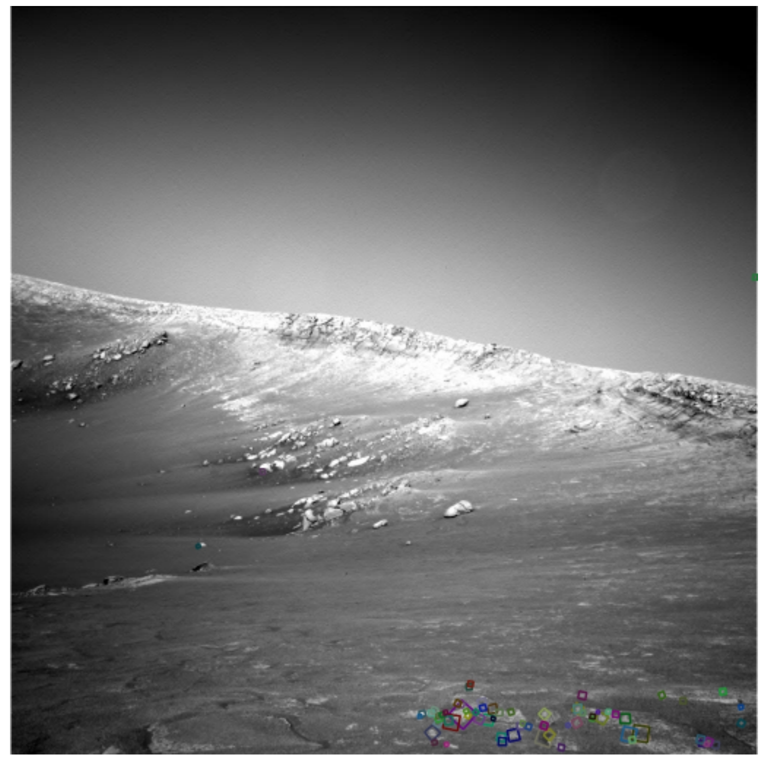
Feature-based alignment

- Find a set of of feature matches that agree in terms of:
  a) Local appearance
  b) Geometric configuration



Feature-based alignment *really works*!





Source: N. Snavely

Feature-based alignment *really works*!

Source: N. Snavely

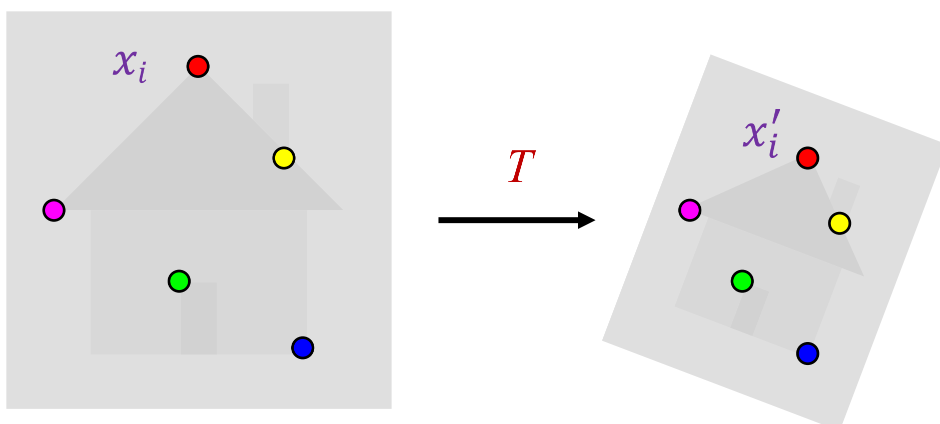
Alignment: Overview

- Motivation
- Fitting of transformations
  - Affine transformations
  - Homographies

Alignment: Fitting of transformations

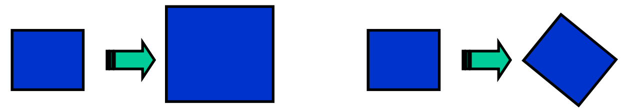
- Given: matches $(x_1, x_1'), \ldots, (x_n, x_n')$
- Find: transformation T that minimizes

$$\sum_i \text{residual}(T(x_i), x_i')$$

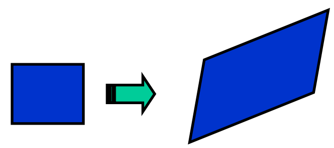


2D transformation models

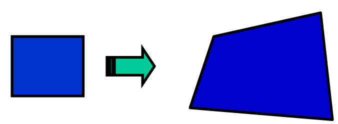
- Similarity (translation, scale, rotation)



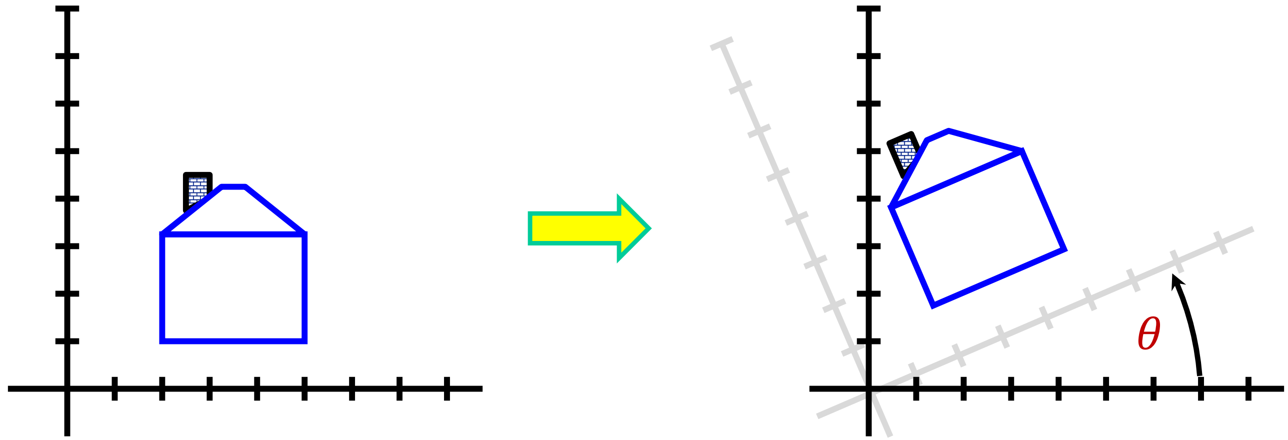
- Affine



- Projective (homography)



Recall: Rotation

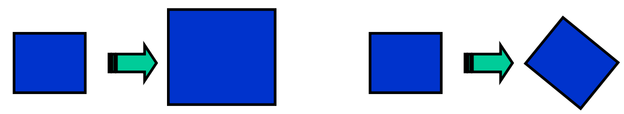


$$\begin{pmatrix} x' \\ y' \end{pmatrix} = \begin{bmatrix} \cos(\theta) & -\sin(\theta) \\ \sin(\theta) & \cos(\theta) \end{bmatrix} \begin{pmatrix} x \\ y \end{pmatrix}$$

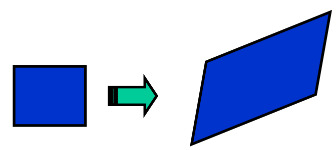
- Estimating the rotation matrix requires enforcing nonlinear constraints, so we will skip the details

2D transformation models

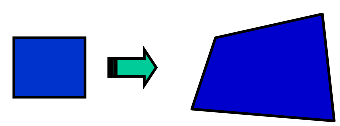
- Similarity (translation, scale, rotation)



- Affine

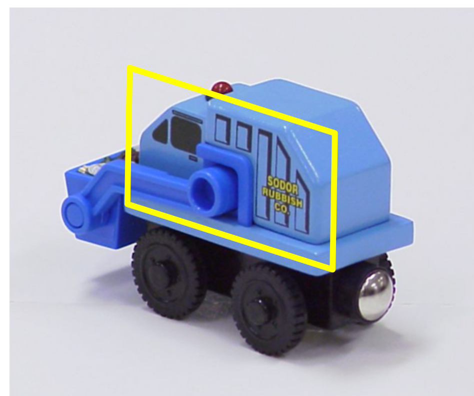


- Projective (homography)



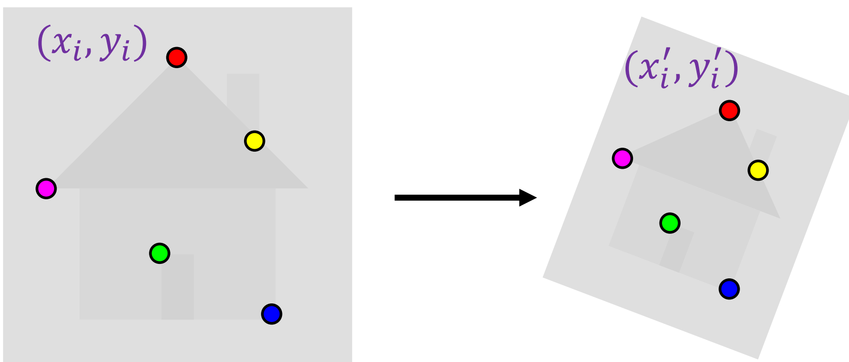
Let’s start with affine transformations

- Simple fitting procedure: linear least squares
- Approximates viewpoint changes for roughly planar objects and roughly orthographic cameras
- Can be used to initialize fitting for more complex models



Fitting an affine transformation

- Assume we know the correspondences, how do we get the transformation?



$$\begin{pmatrix} x'_i \\ y'_i \end{pmatrix} = \begin{bmatrix} m_1 & m_2 \\ m_3 & m_4 \end{bmatrix} \begin{pmatrix} x_i \\ y_i \end{pmatrix} + \begin{pmatrix} t_1 \\ t_2 \end{pmatrix}$$

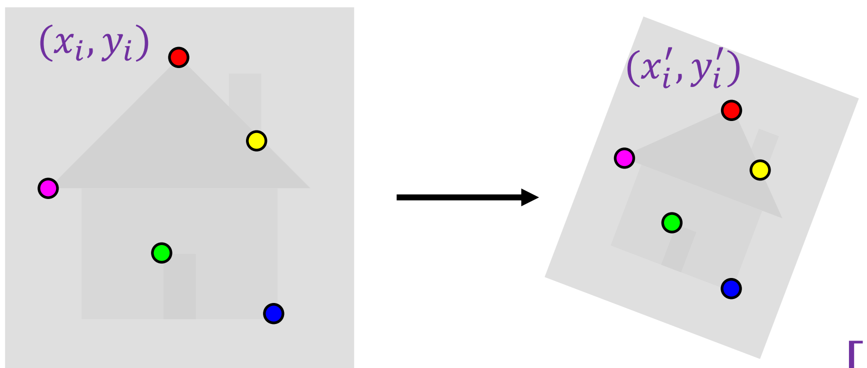
$\boldsymbol{x}'_i$ $\quad$ $\boldsymbol{M}$ $\quad$ $\boldsymbol{x}_i$ $\quad$ $\boldsymbol{t}$

Want to find $\boldsymbol{M}$, $\boldsymbol{t}$ to minimize

$$\sum_{i=1}^{n} \|\boldsymbol{x}'_i - \boldsymbol{M}\boldsymbol{x}_i - \boldsymbol{t}\|^2$$

Fitting an affine transformation

- Assume we know the correspondences, how do we get the transformation?



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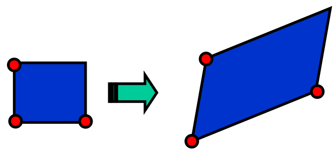
$$\begin{bmatrix} \quad & & & & & \quad \end{bmatrix} \begin{pmatrix} m_1 \\ m_2 \\ m_3 \\ m_4 \\ t_1 \\ t_2 \end{pmatrix} = \begin{pmatrix} \cdots \\ x'_i \\ y'_i \\ \cdots \end{pmatrix}$$

Fitting an affine transformation

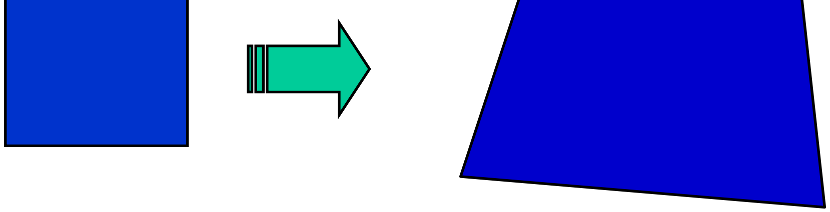
- How many matches do we need to solve for the transformation parameters?



$$\begin{bmatrix} & & \cdots & & & \\ x_i & y_i & 0 & 0 & 1 & 0 \\ 0 & 0 & x_i & y_i & 0 & 1 \\ & & \cdots & & & \end{bmatrix} \begin{pmatrix} m_1 \\ m_2 \\ m_3 \\ m_4 \\ t_1 \\ t_2 \end{pmatrix} = \begin{pmatrix} \cdots \\ x_i' \\ y_i' \\ \cdots \end{pmatrix}$$

Fitting a homography

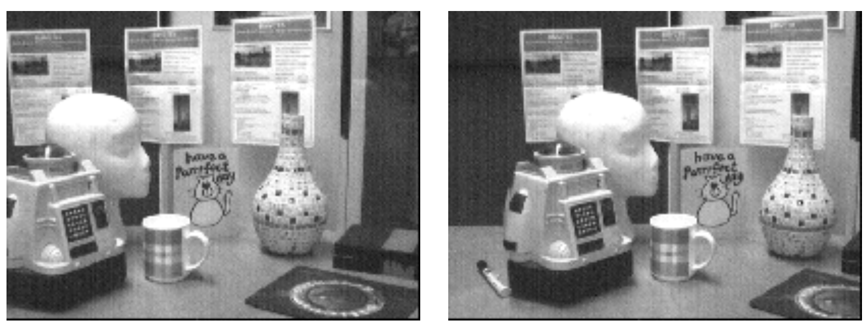
- A *homography* is a plane projective transformation (transformation taking a quad to another arbitrary quad)



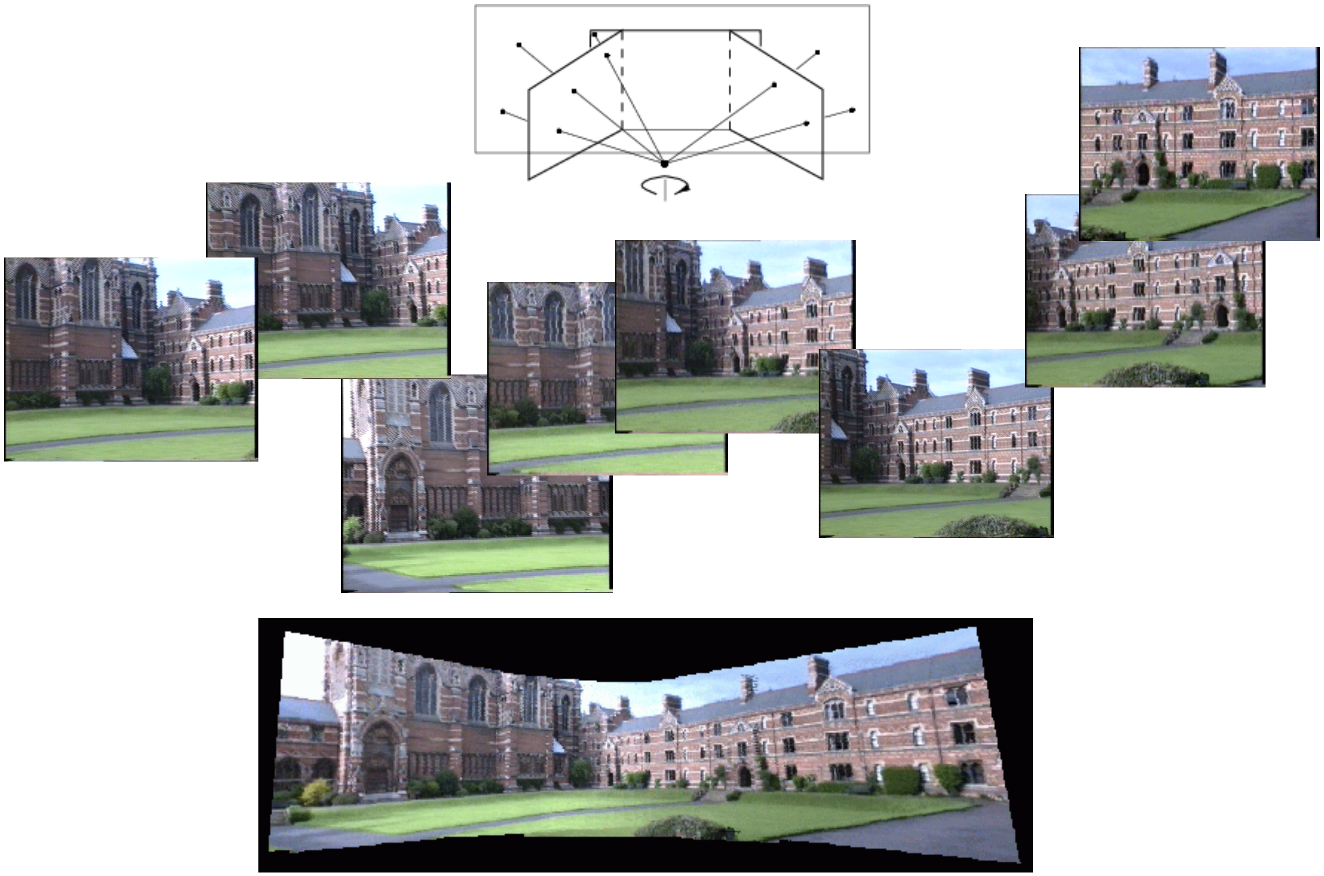
Homography in the real world

- The transformation between two views of a planar surface

- The transformation between images from two cameras that share the same center



Application: Panorama stitching

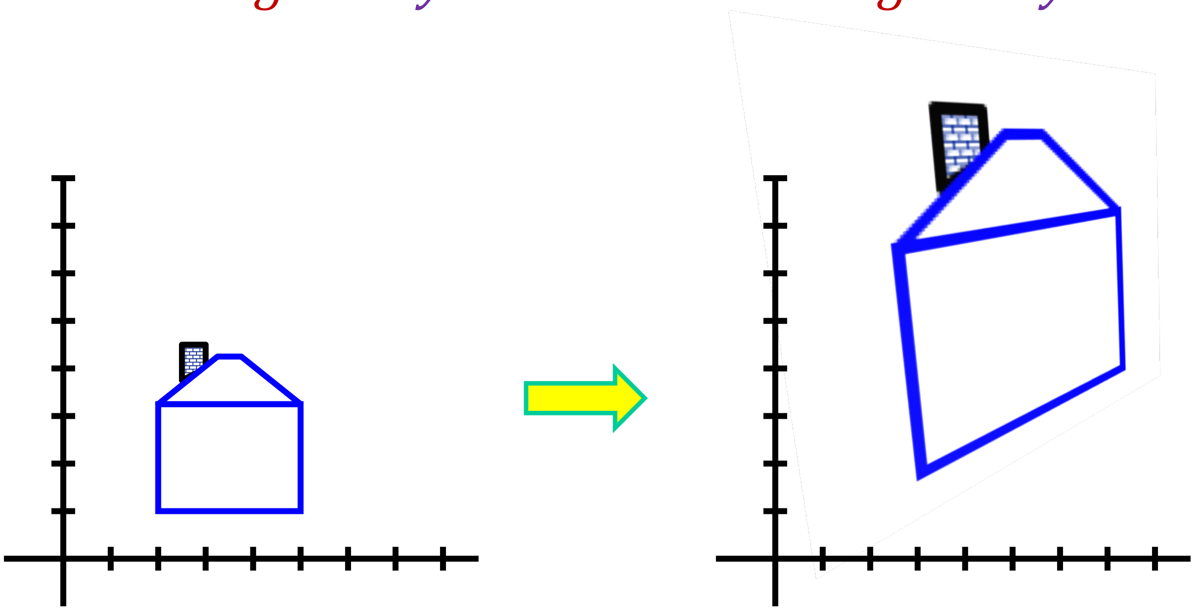


Source: Hartley & Zisserman

Fitting a homography

- Recall:

$$x' = \frac{ax + by + c}{gx + hy + i}, \qquad y' = \frac{dx + ey + f}{gx + hy + i}$$



Last time: Alignment

- Motivation
- Fitting of transformations
  - Affine transformations
  - Homographies

Fitting a homography

- We need 2D *homogeneous coordinates:*

$$(x, y) \Longrightarrow \begin{pmatrix} x \\ y \\ 1 \end{pmatrix}$$

Converting *to* homogeneous coordinates

$$\begin{pmatrix} x \\ y \\ w \end{pmatrix} \Longrightarrow (x/w, y/w)$$

Converting *from* homogeneous coordinates

  - All homogeneous coordinate vectors that are scalar multiples of each other represent the same point!

- Equation for homography in homogeneous coordinates:

$$\begin{pmatrix} x' \\ y' \\ 1 \end{pmatrix} \cong \begin{bmatrix} h_{11} & h_{12} & h_{13} \\ h_{21} & h_{22} & h_{23} \\ h_{31} & h_{32} & h_{33} \end{bmatrix} \begin{pmatrix} x \\ y \\ 1 \end{pmatrix}$$

$$\boldsymbol{x}' \cong \boldsymbol{H}\boldsymbol{x}$$

"equal up to scale"

Fitting a homography

- Constraint from a match $(\boldsymbol{x}_i, \boldsymbol{x}_i')$: $\boldsymbol{x}_i' \cong \boldsymbol{H}\boldsymbol{x}_i$
- How can we get rid of the scale ambiguity?
- Cross product trick: $\boldsymbol{x}_i' \times \boldsymbol{H}\boldsymbol{x}_i = \boldsymbol{0}$
- Recall cross product:

$$\begin{pmatrix} a \\ b \\ c \end{pmatrix} \times \begin{pmatrix} a' \\ b' \\ c' \end{pmatrix} = \begin{pmatrix} bc' - b'c \\ ca' - c'a \\ ab' - a'b \end{pmatrix}$$

- Let $\boldsymbol{h}_1^T$, $\boldsymbol{h}_2^T$, $\boldsymbol{h}_3^T$ be the rows of $\boldsymbol{H}$. Then

$$\boldsymbol{x}_i' \times \boldsymbol{H}\boldsymbol{x}_i = \begin{pmatrix} x_i' \\ y_i' \\ 1 \end{pmatrix} \times \begin{pmatrix} \boldsymbol{h}_1^T\boldsymbol{x}_i \\ \boldsymbol{h}_2^T\boldsymbol{x}_i \\ \boldsymbol{h}_3^T\boldsymbol{x}_i \end{pmatrix} = \begin{pmatrix} y_i'\boldsymbol{h}_3^T\boldsymbol{x}_i - \boldsymbol{h}_2^T\boldsymbol{x}_i \\ \boldsymbol{h}_1^T\boldsymbol{x}_i - x_i'\boldsymbol{h}_3^T\boldsymbol{x}_i \\ x_i'\boldsymbol{h}_2^T\boldsymbol{x}_i - y_i'\boldsymbol{h}_1^T\boldsymbol{x}_i \end{pmatrix}$$

Fitting a homography

- Constraint from a match $(\boldsymbol{x}_i, \boldsymbol{x}_i')$:

$$\boldsymbol{x}_i' \times \boldsymbol{H}\boldsymbol{x}_i = \begin{pmatrix} x_i' \\ y_i' \\ 1 \end{pmatrix} \times \begin{pmatrix} \boldsymbol{h}_1^T \boldsymbol{x}_i \\ \boldsymbol{h}_2^T \boldsymbol{x}_i \\ \boldsymbol{h}_3^T \boldsymbol{x}_i \end{pmatrix} = \begin{pmatrix} y_i' \boldsymbol{h}_3^T \boldsymbol{x}_i - \boldsymbol{h}_2^T \boldsymbol{x}_i \\ \boldsymbol{h}_1^T \boldsymbol{x}_i - x_i' \boldsymbol{h}_3^T \boldsymbol{x}_i \\ x_i' \boldsymbol{h}_2^T \boldsymbol{x}_i - y_i' \boldsymbol{h}_1^T \boldsymbol{x}_i \end{pmatrix}$$

- Rearranging the terms:

$$\begin{bmatrix} \boldsymbol{0}^T & -\boldsymbol{x}_i^T & y_i' \boldsymbol{x}_i^T \\ \boldsymbol{x}_i^T & \boldsymbol{0}^T & -x_i' \boldsymbol{x}_i^T \\ -y_i' \boldsymbol{x}_i^T & x_i' \boldsymbol{x}_i^T & \boldsymbol{0}^T \end{bmatrix} \begin{pmatrix} \boldsymbol{h}_1 \\ \boldsymbol{h}_2 \\ \boldsymbol{h}_3 \end{pmatrix} = \boldsymbol{0}$$

- Are these equations independent?

Fitting a homography

- Final linear system:

$$\begin{bmatrix} \mathbf{0}^T & \boldsymbol{x}_1^T & -y_1' \boldsymbol{x}_1^T \\ \boldsymbol{x}_1^T & \mathbf{0}^T & -x_1' \boldsymbol{x}_1^T \\ \dots & \dots & \dots \\ \mathbf{0}^T & \boldsymbol{x}_n^T & -y_n' \boldsymbol{x}_n^T \\ \boldsymbol{x}_n^T & \mathbf{0}^T & -x_n' \boldsymbol{x}_n^{\boldsymbol{T}} \end{bmatrix} \begin{pmatrix} \boldsymbol{h}_1 \\ \boldsymbol{h}_2 \\ \boldsymbol{h}_3 \end{pmatrix} = \mathbf{0} \qquad A\boldsymbol{h} = \mathbf{0}$$

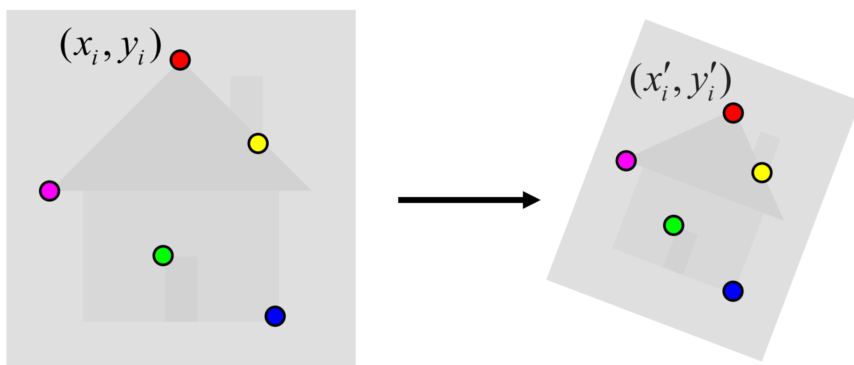
- Homogeneous least squares: find $\boldsymbol{h}$ minimizing $\|A\boldsymbol{h}\|^2$
  - Solution is eigenvector of $A^T A$ corresponding to smallest eigenvalue
- What is the minimum number of matches needed for a solution?
  - Four: A has 8 degrees of freedom (9 parameters, but scale is arbitrary), one match gives us two linearly independent equations

Alignment: Overview

- Motivation
- Fitting of transformations
  - Affine transformations
  - Homographies
- Robust alignment
  - Descriptor-based feature matching
  - RANSAC

Robust feature-based alignment

- So far, we've assumed that we are given a set of correspondences between the two images we want to align
- What if we don't know the correspondences?



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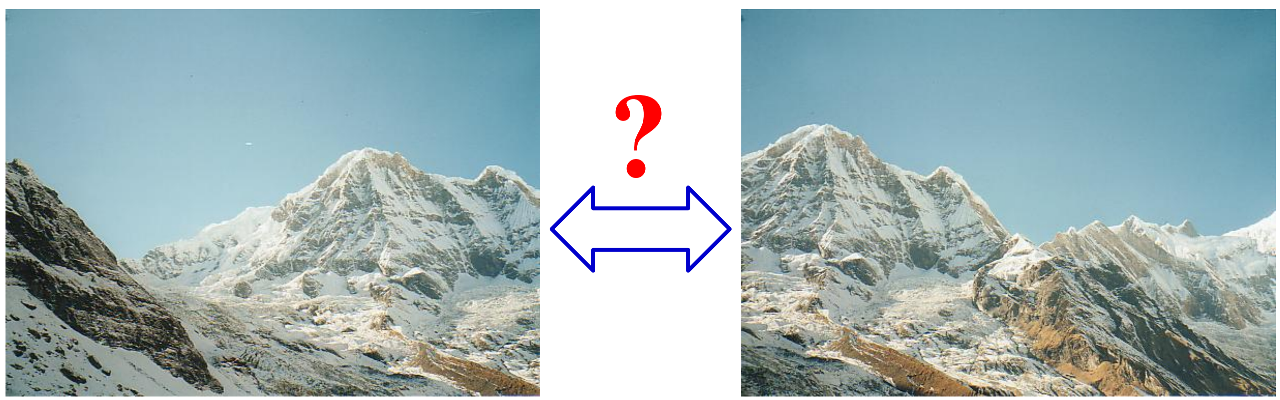
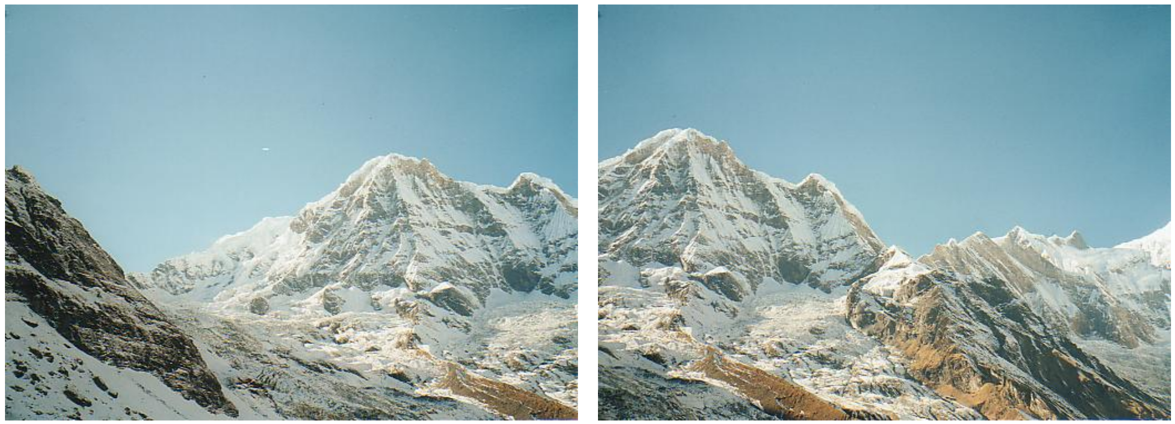
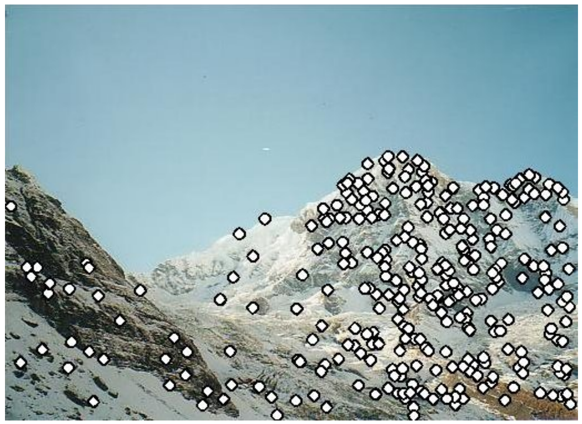
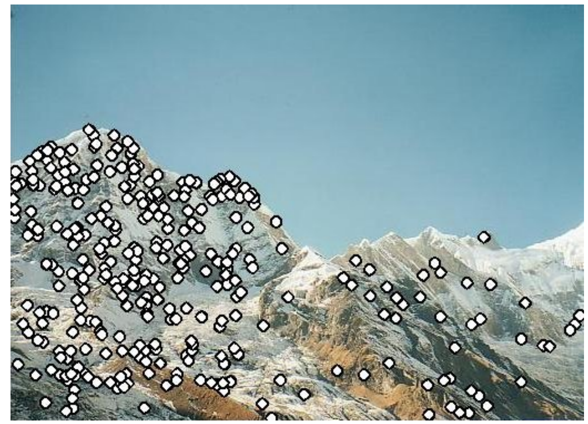


Robust feature-based alignment



Robust feature-based alignment



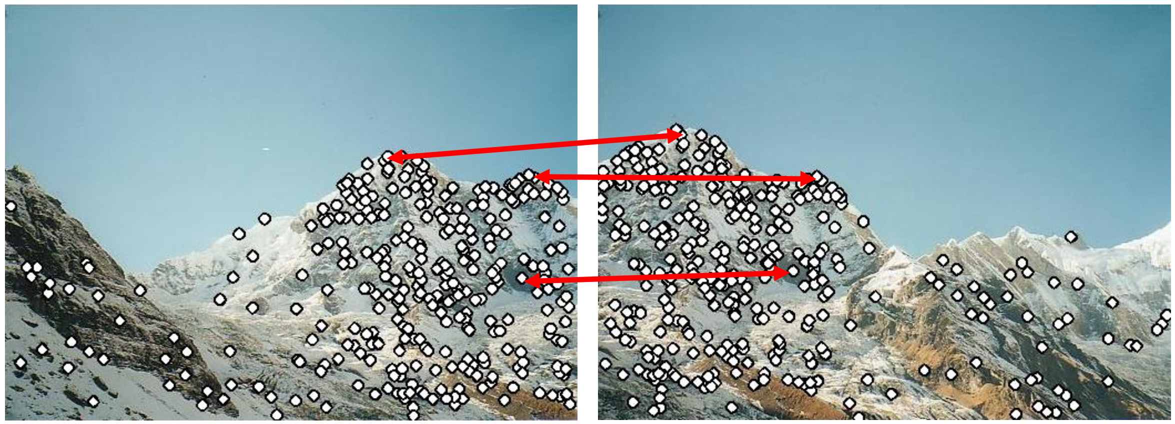


- Extract features

Robust feature-based alignment

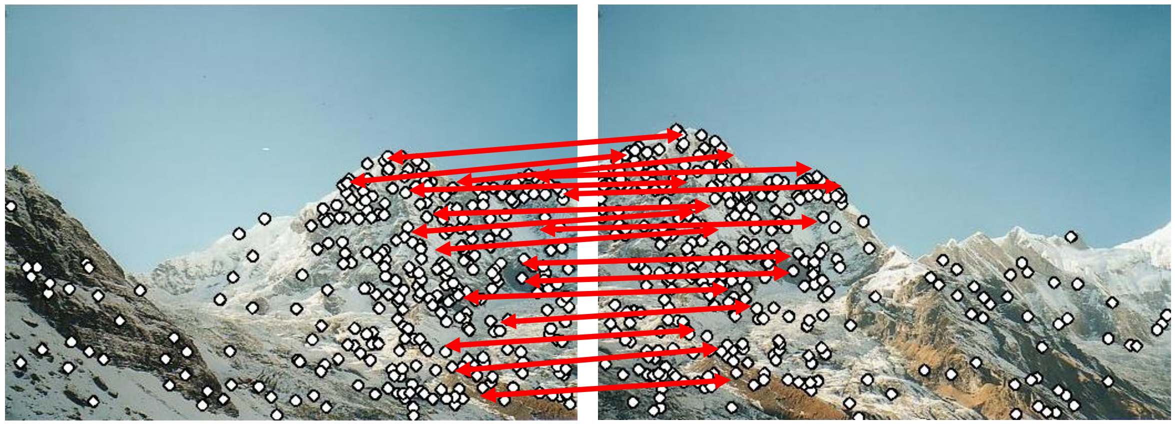
- Extract features
- Compute *putative matches*

Robust feature-based alignment



- Extract features
- Compute *putative matches*
- Loop:
  - *Hypothesize* transformation T

Robust feature-based alignment



- Extract features
- Compute *putative matches*
- Loop:
  - *Hypothesize* transformation T
  - *Verify* transformation (search for other matches consistent with T)

Robust feature-based alignment

- Extract features
- Compute *putative matches*
- Loop:
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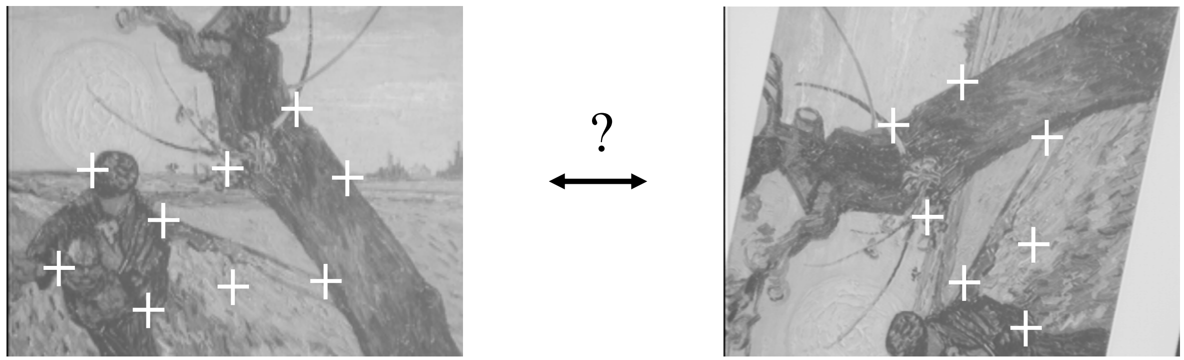
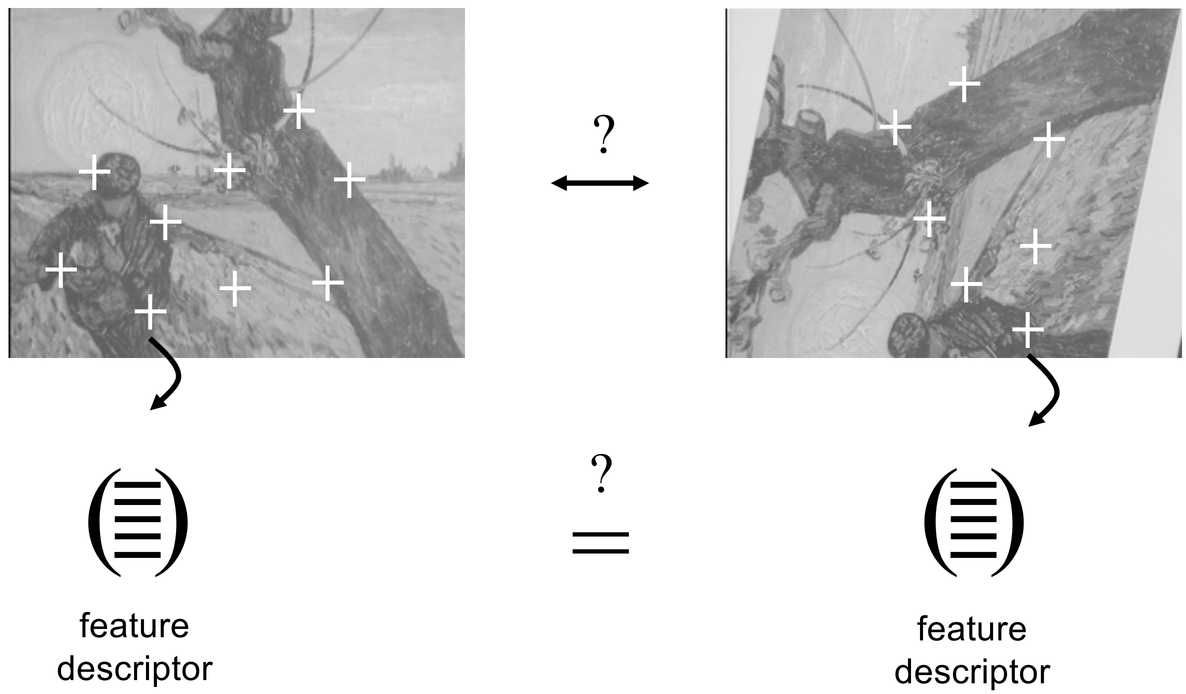
Generating putative correspondences



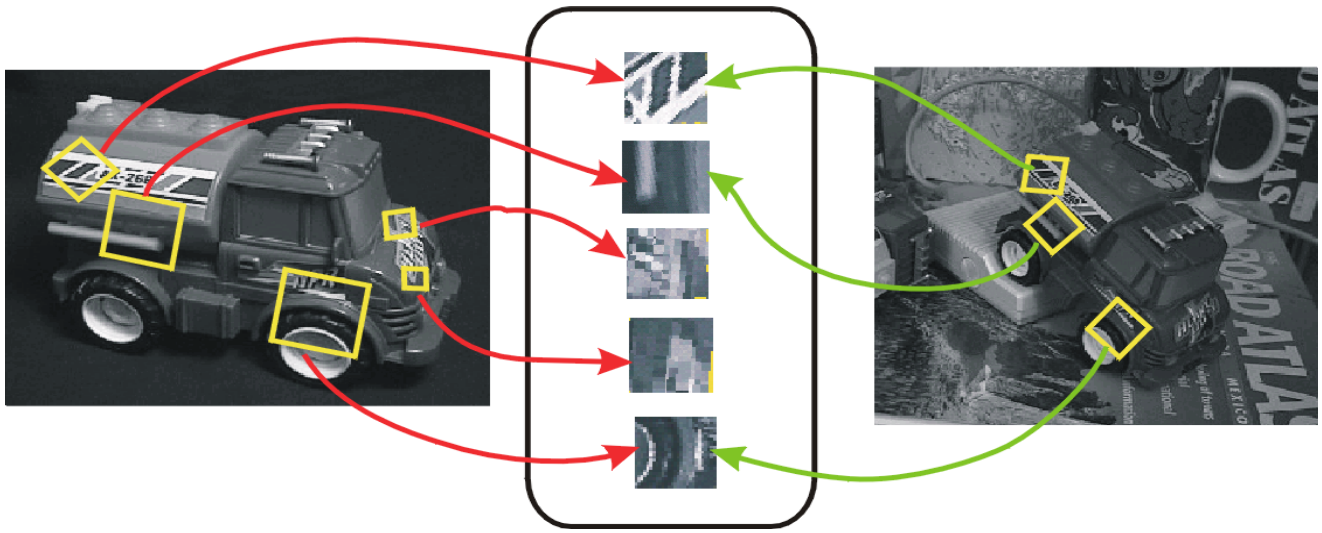
Generating putative correspondences



- Need to compare *feature descriptors* of local patches surrounding interest points

Feature descriptors

- Recall: feature detection vs. feature description



Comparing feature descriptors

- Simplest descriptor: vector of raw intensity values
- How to compare two such vectors $\boldsymbol{u}$ and $\boldsymbol{v}$?
  - **Sum of squared differences** (SSD):

$$\mathrm{SSD}(\boldsymbol{u},\boldsymbol{v}) = \sum_i (u_i - v_i)^2$$

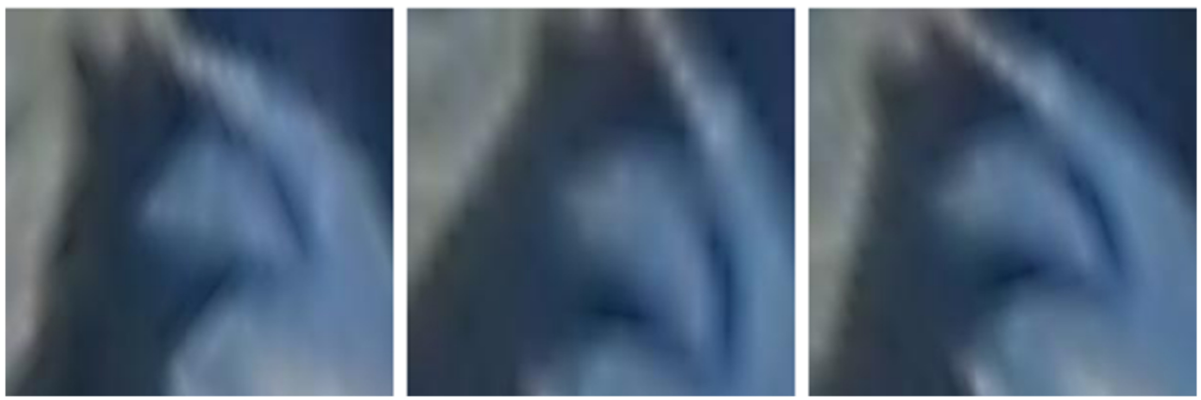
  - **Normalized correlation**: dot product between $\boldsymbol{u}$ and $\boldsymbol{v}$ normalized to have zero mean and unit norm:

$$\rho(\boldsymbol{u},\boldsymbol{v}) = \frac{\sum_i (u_i - \overline{\boldsymbol{u}})(v_i - \overline{\boldsymbol{v}})}{\sqrt{\left(\sum_j (u_j - \overline{\boldsymbol{u}})^2\right)\left(\sum_j (v_j - \overline{\boldsymbol{v}})^2\right)}}$$

  - Why would we prefer normalized correlation over SSD?

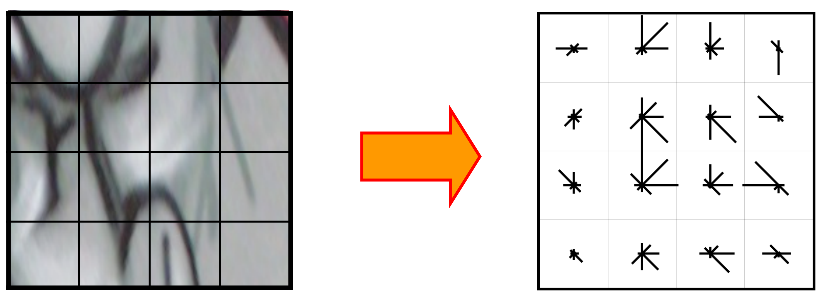
Disadvantage of intensity vectors as descriptors

- Small deformations can affect the matching score a lot



Feature descriptors: SIFT

- Descriptor computation:
  - Divide patch into 4×4 sub-patches
  - Compute histogram of gradient orientations (8 reference angles) inside each sub-patch
  - Resulting descriptor: $4 \times 4 \times 8 = 128$ dimensions



David G. Lowe. Distinctive image features from scale-invariant keypoints. *IJCV* 60 (2), pp. 91-110, 2004.

Feature descriptors: SIFT

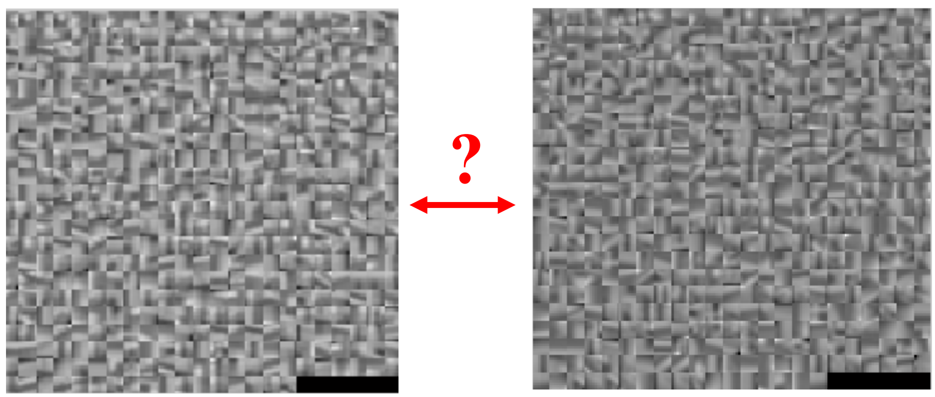
- Descriptor computation:
  - Divide patch into 4×4 sub-patches
  - Compute histogram of gradient orientations (8 reference angles) inside each sub-patch
  - Resulting descriptor: $4\times4\times8 = 128$ dimensions

- What are the advantages of SIFT descriptor over raw pixel values?
  - Gradients are less sensitive to illumination change
  - Pooling of gradients over the sub-patches achieves robustness to small shifts, but still preserves some spatial information

David G. Lowe. [Distinctive image features from scale-invariant keypoints](). *IJCV* 60 (2), pp. 91-110, 2004.

Generating putative correspondences

- For each patch in one image, find a short list of patches in the other image that could match it based solely on appearance



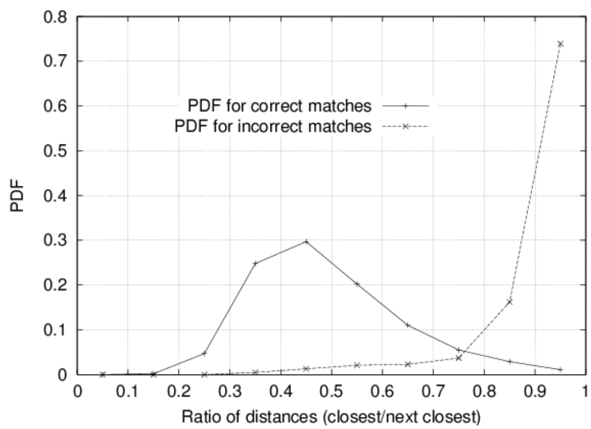
Rejection of ambiguous matches

- How can we tell which putative matches are more reliable?
- Heuristic: compare distance of **nearest** neighbor to that of **second nearest** neighbor

Source: Y. Furukawa

Rejection of ambiguous matches

- How can we tell which putative matches are more reliable?
- Heuristic: compare distance of **nearest** neighbor to that of **second nearest** neighbor
  - Ratio of closest distance to second-closest distance will be high for features that are not distinctive



Threshold of 0.8 found to provide good separation

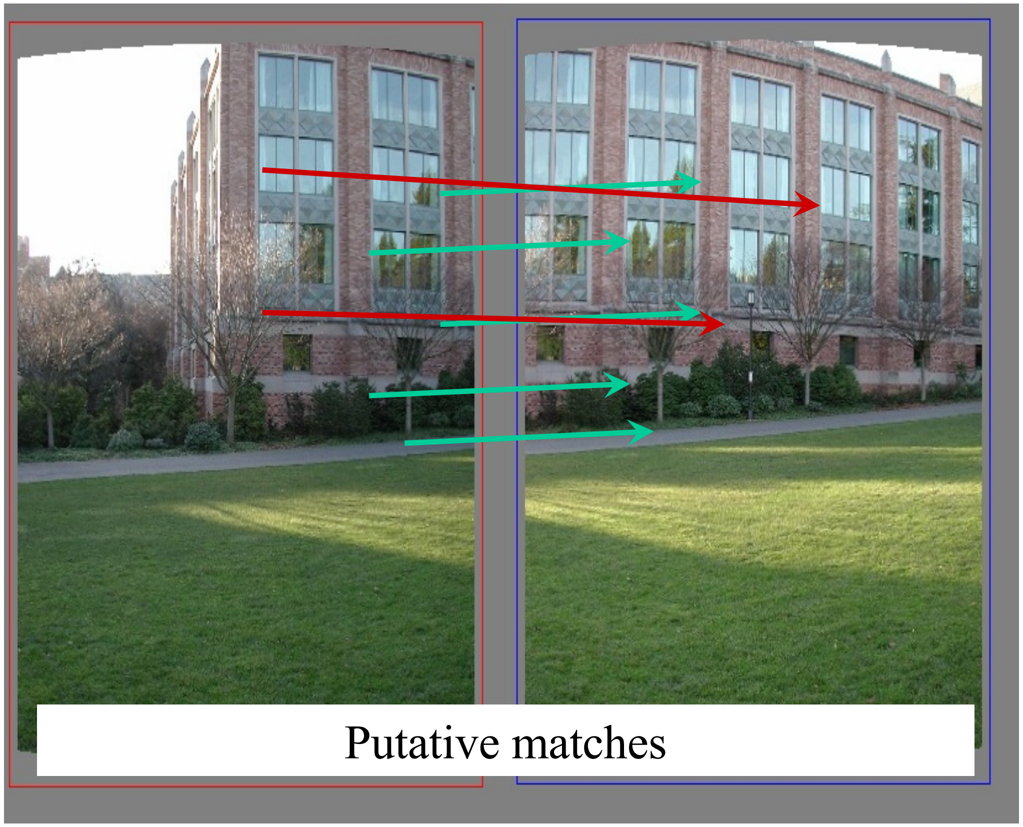
David G. Lowe. Distinctive image features from scale-invariant keypoints. *IJCV* 60 (2), pp. 91-110, 2004.

Robust alignment

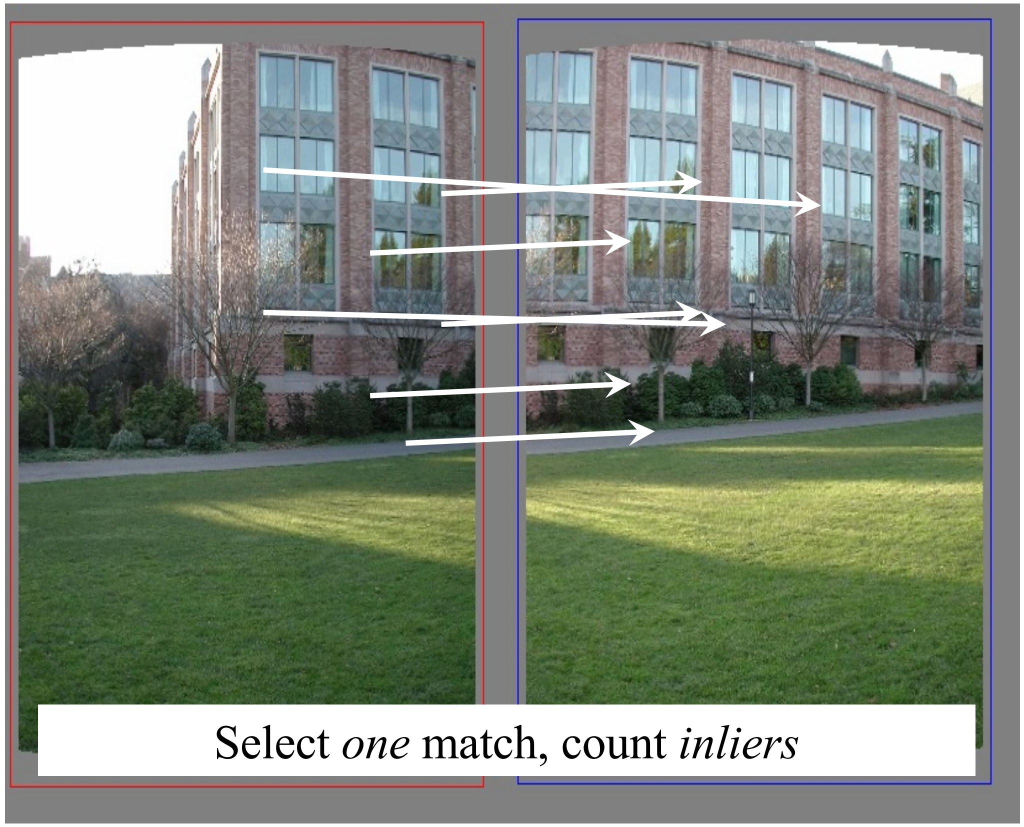
- Even after filtering out ambiguous matches, the set of putative matches still contains a very high percentage of outliers

- Solution: RANSAC
- RANSAC loop:
  1. Randomly select a *seed group* of matches
  2. Compute transformation from seed group
  3. Find *inliers* to this transformation
  4. If the number of inliers is sufficiently large, re-compute least-squares estimate of transformation on all of the inliers
- At the end, keep the transformation with the largest number of inliers

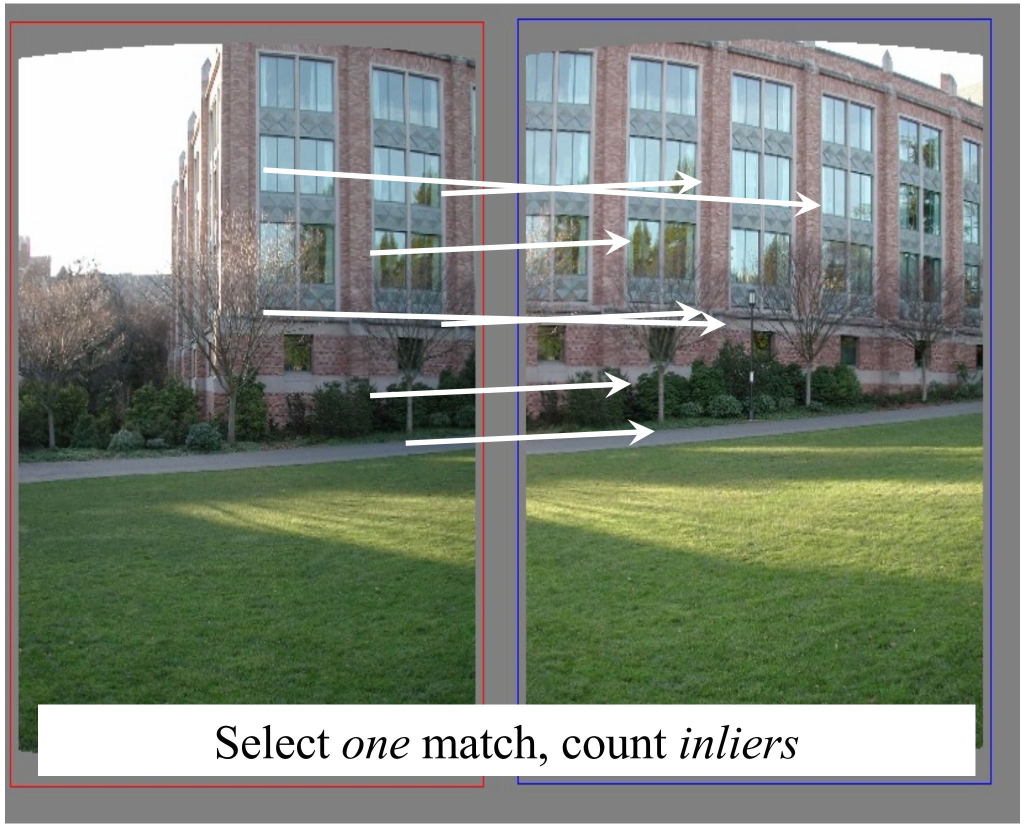
RANSAC example: Translation



RANSAC example: Translation

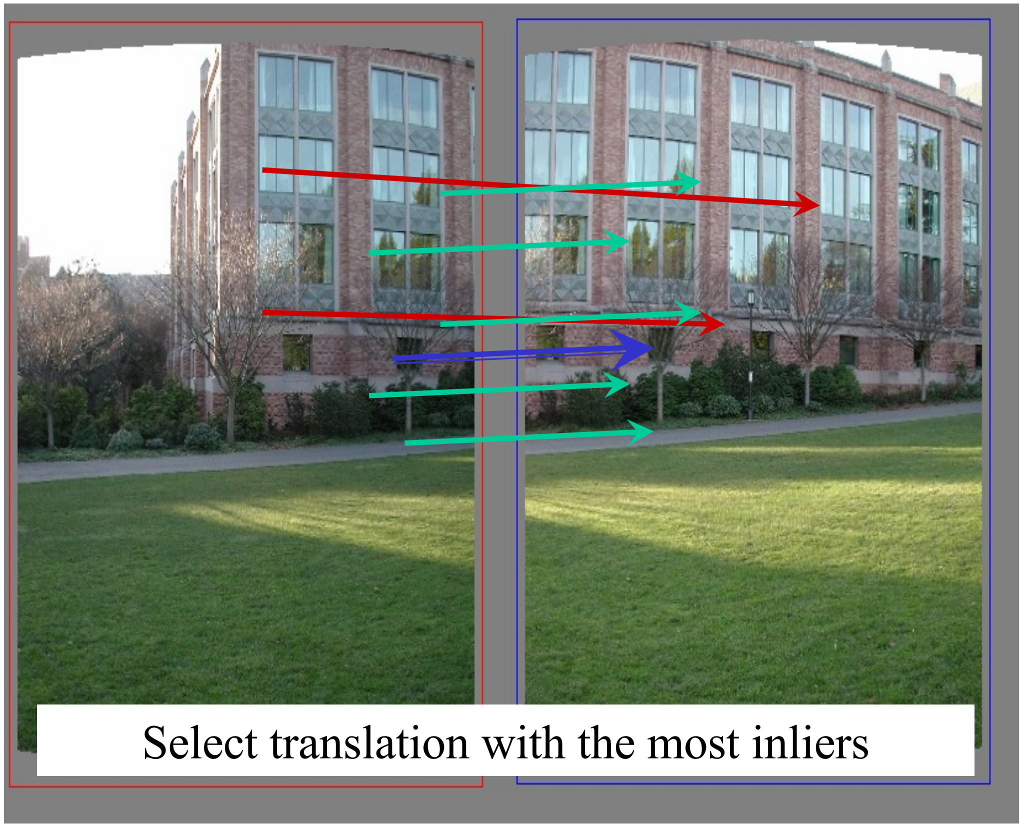


RANSAC example: Translation



Select *one* match, count *inliers*

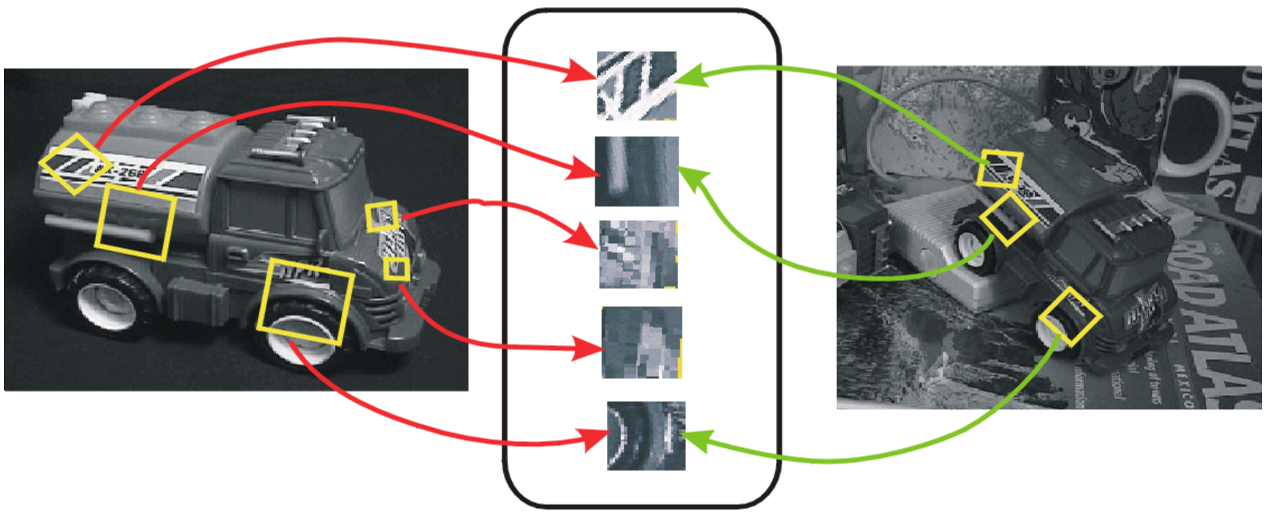
RANSAC example: Translation



Select translation with the most inliers

Alternative for robust alignment: Hough voting

- A single SIFT match can vote for translation, rotation, and scale parameters of a transformation between two images
  - Votes can be accumulated in a 4D Hough space with large bins
  - Clusters of matches falling into the same bin should undergo a more precise verification procedure



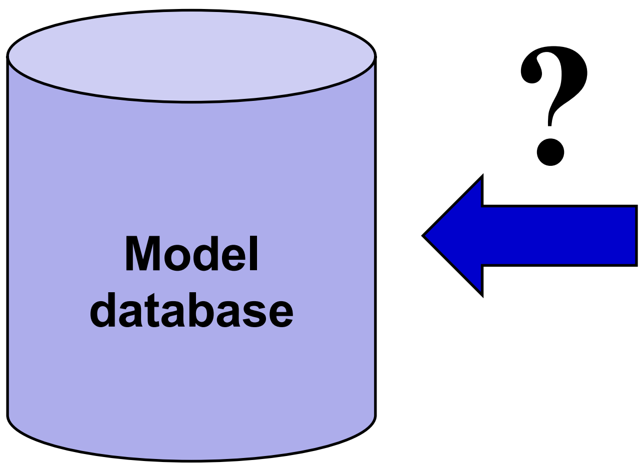
David G. Lowe. [Distinctive image features from scale-invariant keypoints](). *IJCV* 60 (2), pp. 91-110, 2004.

Alignment: Overview

- Motivation
- Fitting of transformations
  - Affine transformations
  - Homographies
- Robust alignment
  - Descriptor-based feature matching
  - RANSAC
- Large-scale alignment
  - Inverted indexing
  - Vocabulary trees

Scalability: Alignment to large databases

- What if we need to align a test image with thousands or millions of images in a model database?
  - Efficient putative match generation: approximate descriptor similarity search, inverted indices



Test image

Large-scale visual search

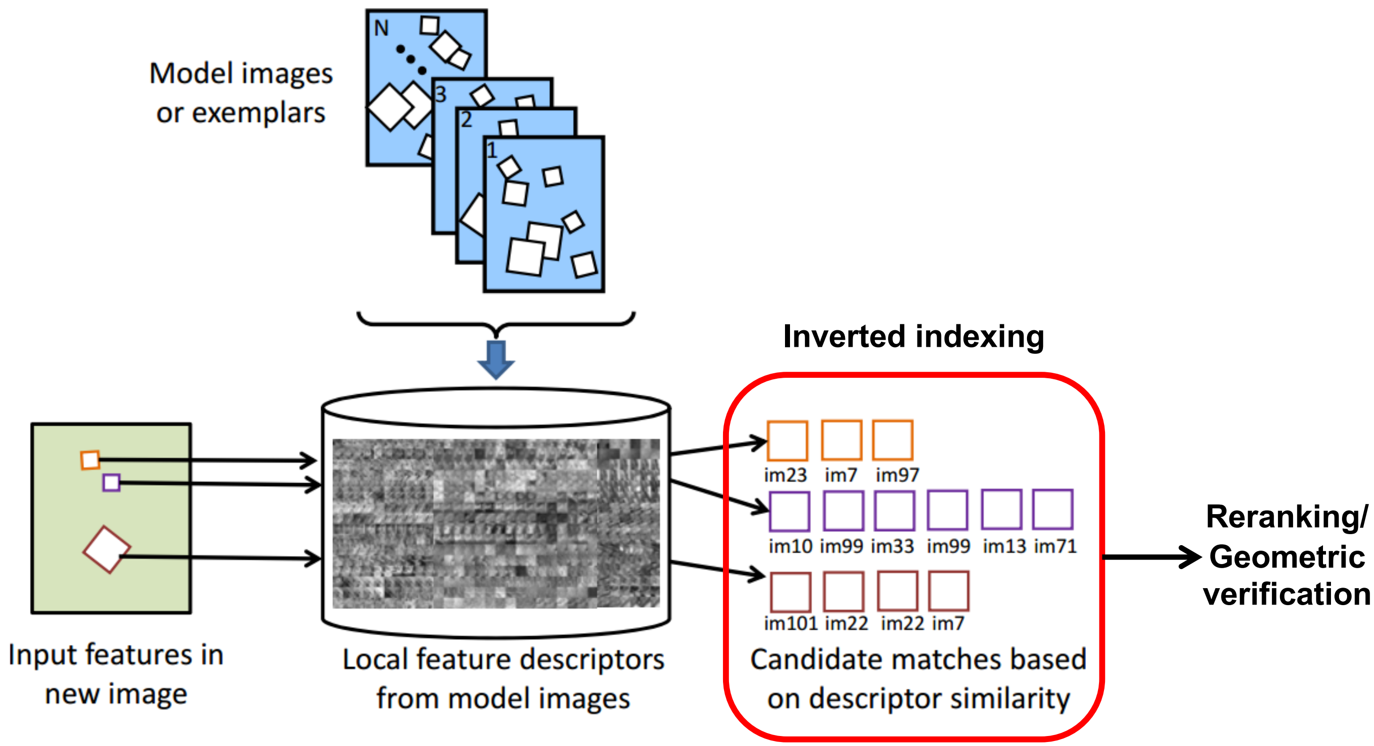
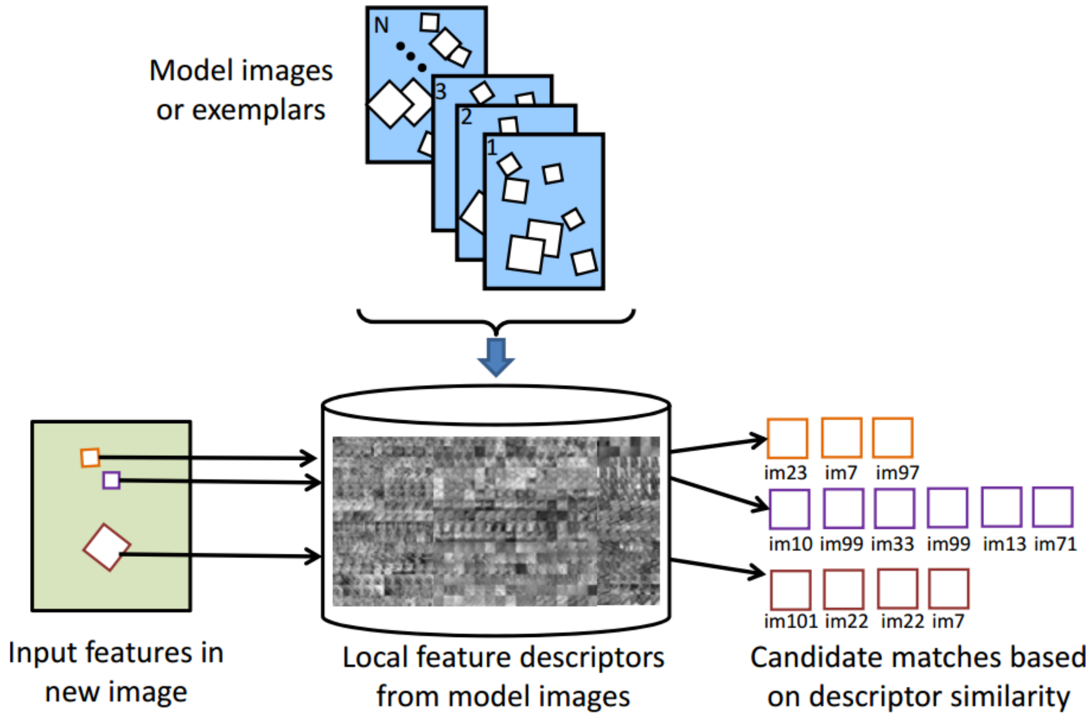


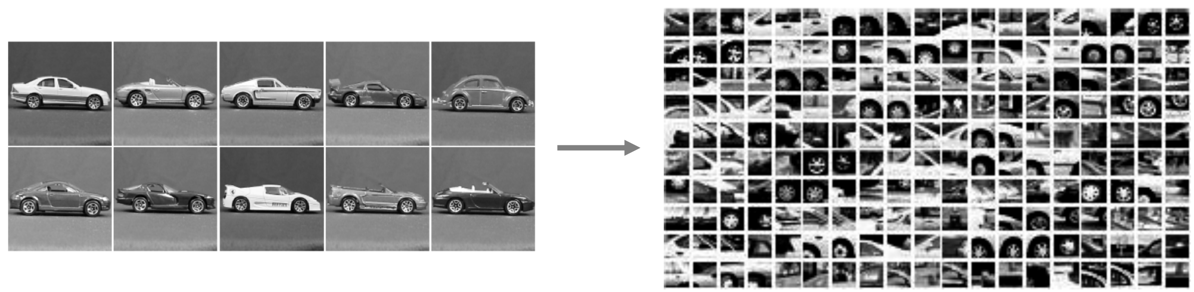
Figure from: Kristen Grauman and Bastian Leibe, [Visual Object Recognition], Synthesis Lectures on Artificial Intelligence and Machine Learning, April 2011, Vol. 5, No. 2, Pages 1-181

How to do the indexing?

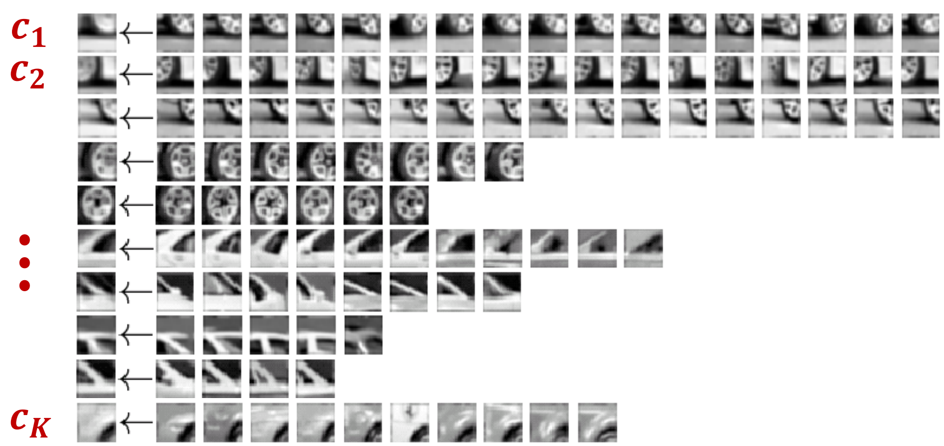


- Idea: find a set of *visual codewords* to which descriptors can be *quantized*

Recall: Visual codebook for implicit shape models



Appearance codebook



B. Leibe, A. Leonardis, and B. Schiele, Combined Object Categorization and Segmentation with an Implicit Shape Model, ECCV Workshop on Statistical Learning in Computer Vision 2004

K-means clustering

- We want to find K cluster centers and an assignment of points to cluster centers to minimize the sum of squared Euclidean distances between each point and its assigned cluster center:

$$\sum_i \sum_k a_{ik} \|\boldsymbol{x}_i - \boldsymbol{c}_k\|^2$$

Sum over all points

Sum over all clusters

Point $\boldsymbol{x}_i$ is assigned to cluster k

Center of cluster k

K-means clustering

- We want to find K cluster centers and an assignment of points to cluster centers to minimize the sum of squared Euclidean distances between each point and its assigned cluster center:

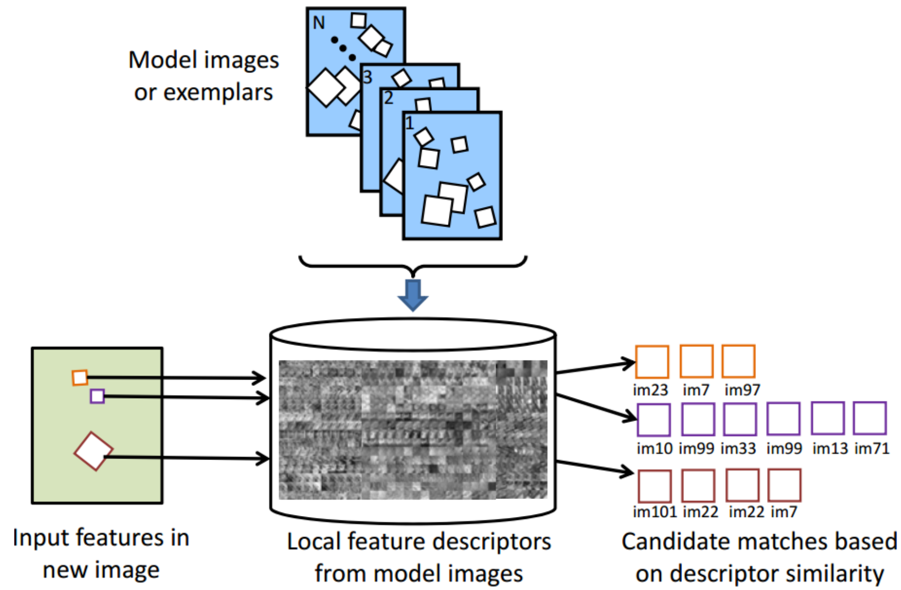
$$\sum_i \sum_k a_{ik} \|\boldsymbol{x}_i - \boldsymbol{c}_k\|^2$$

- Algorithm:
  - Randomly initialize K cluster centers
  - Iterate until convergence:
    – Assign each data point to its nearest center
    – Recompute each cluster center as the mean of all points assigned to it

K-means example

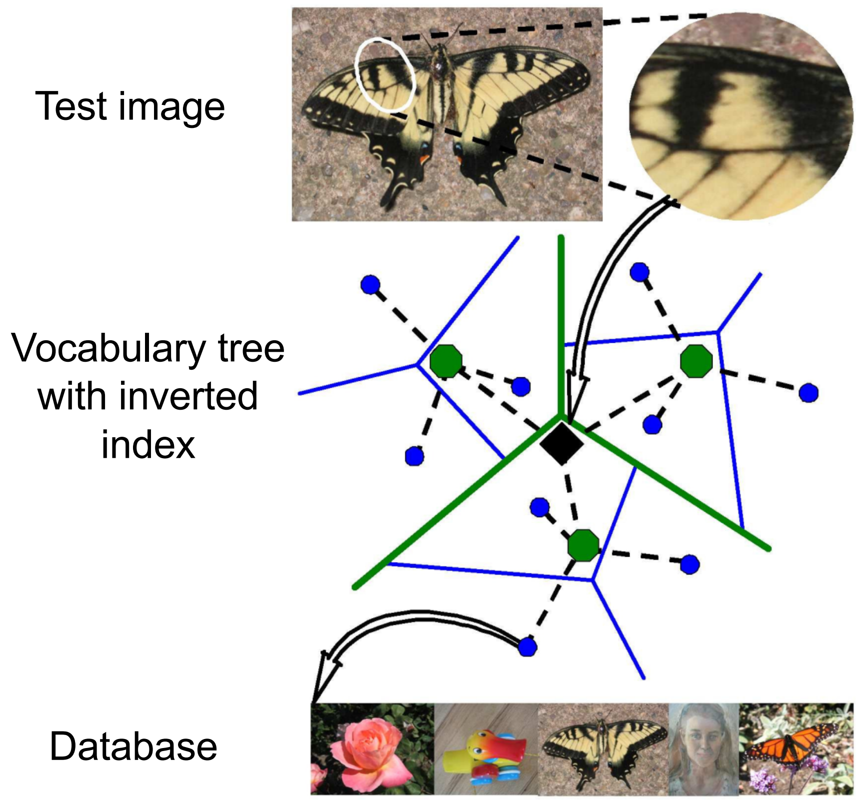
Source

How to do the indexing?

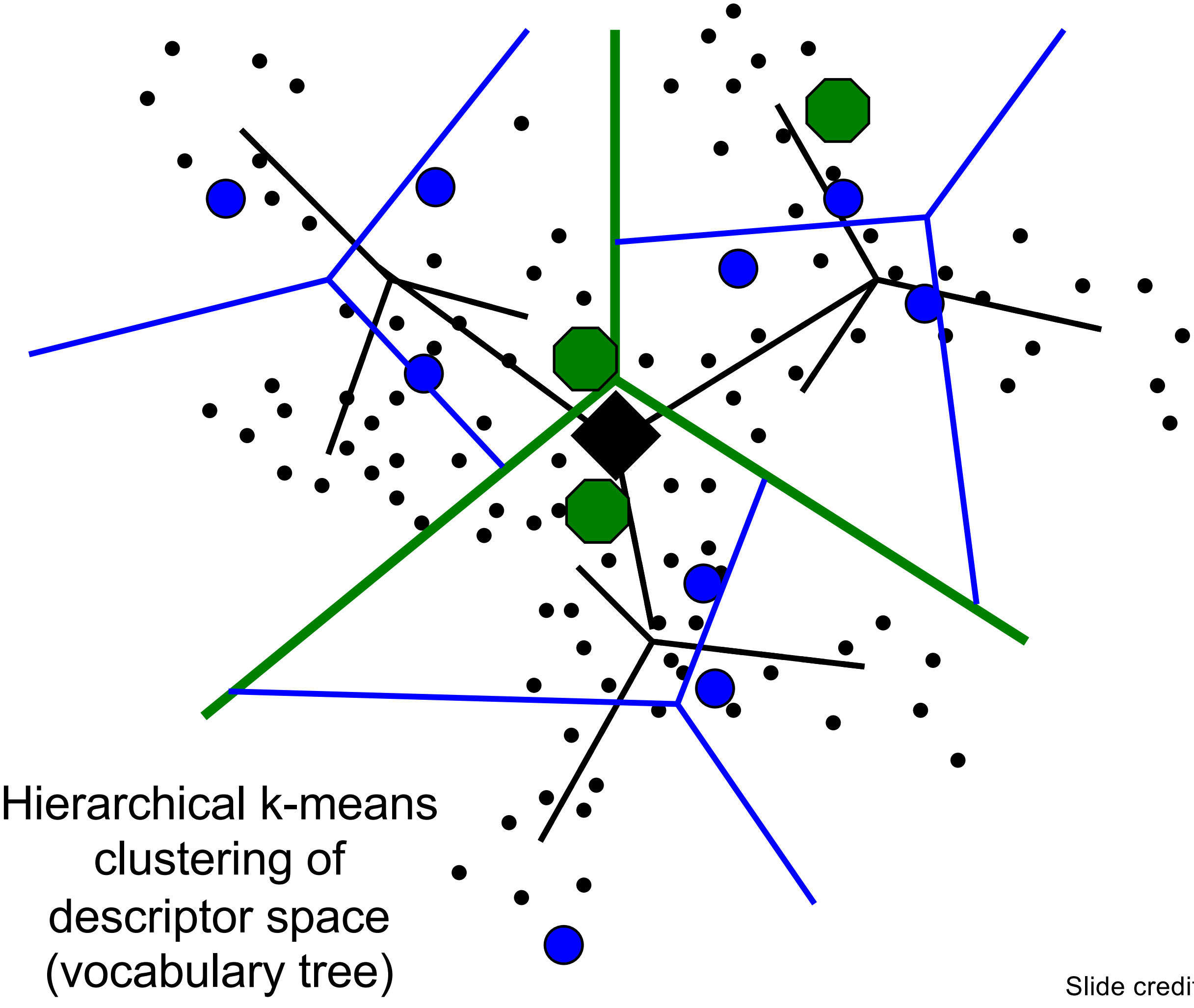


- Cluster descriptors in the database to form codebook
- At query time, quantize descriptors in query image to nearest codevectors
- Problem solved?

Efficient indexing technique: Vocabulary trees

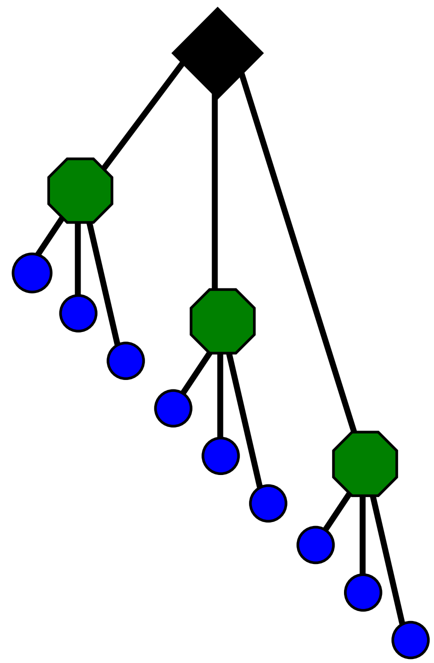


D. Nistér and H. Stewénius, Scalable Recognition with a Vocabulary Tree, CVPR 2006



Hierarchical k-means clustering of descriptor space (vocabulary tree)

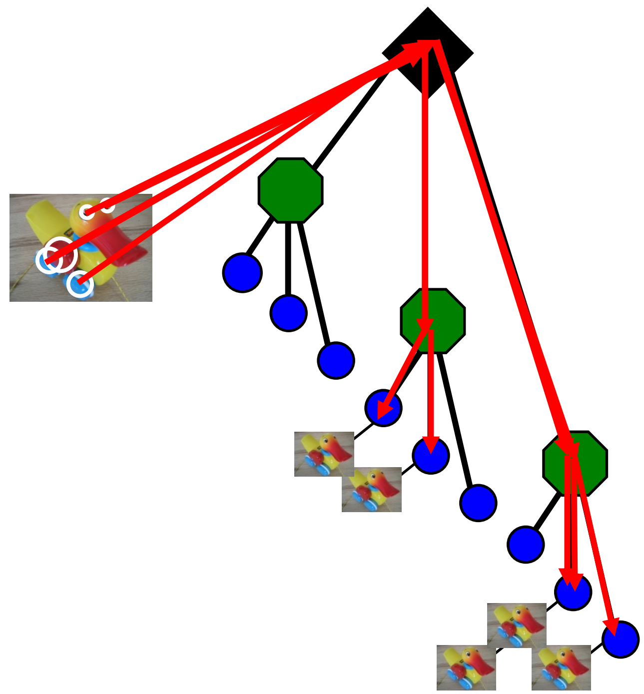
Slide credit: D. Nister



Vocabulary tree/inverted index

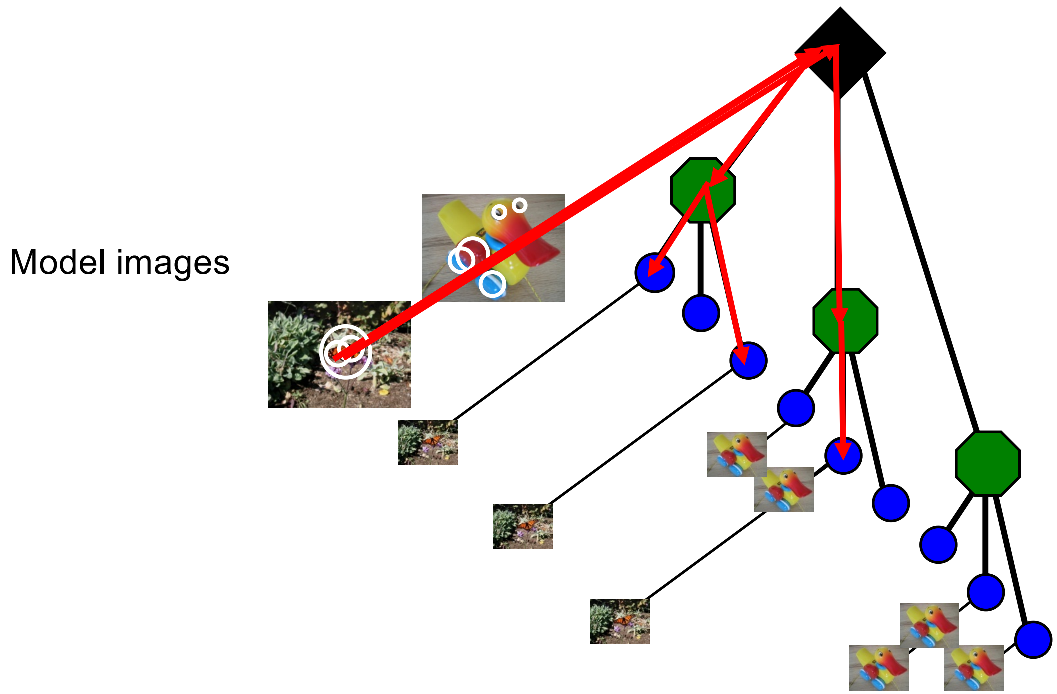
Slide credit: D. Nister

Model images



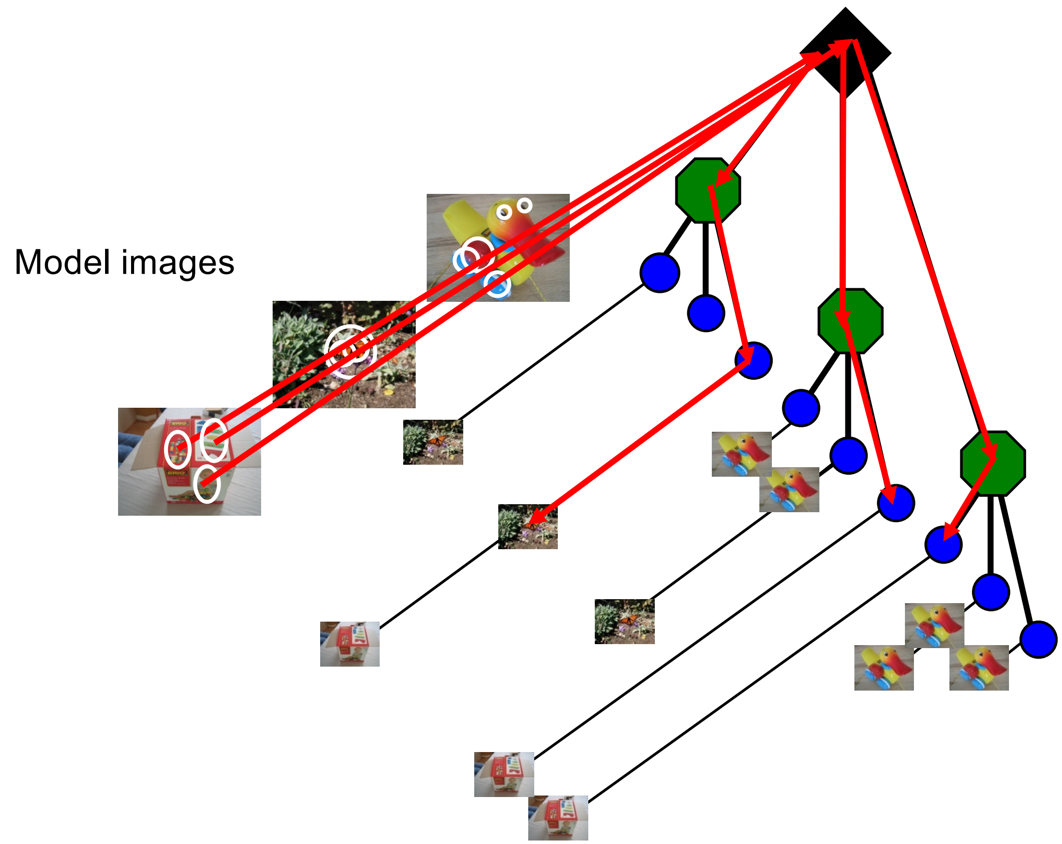
Populating the vocabulary tree/inverted index

Slide credit: D. Nister



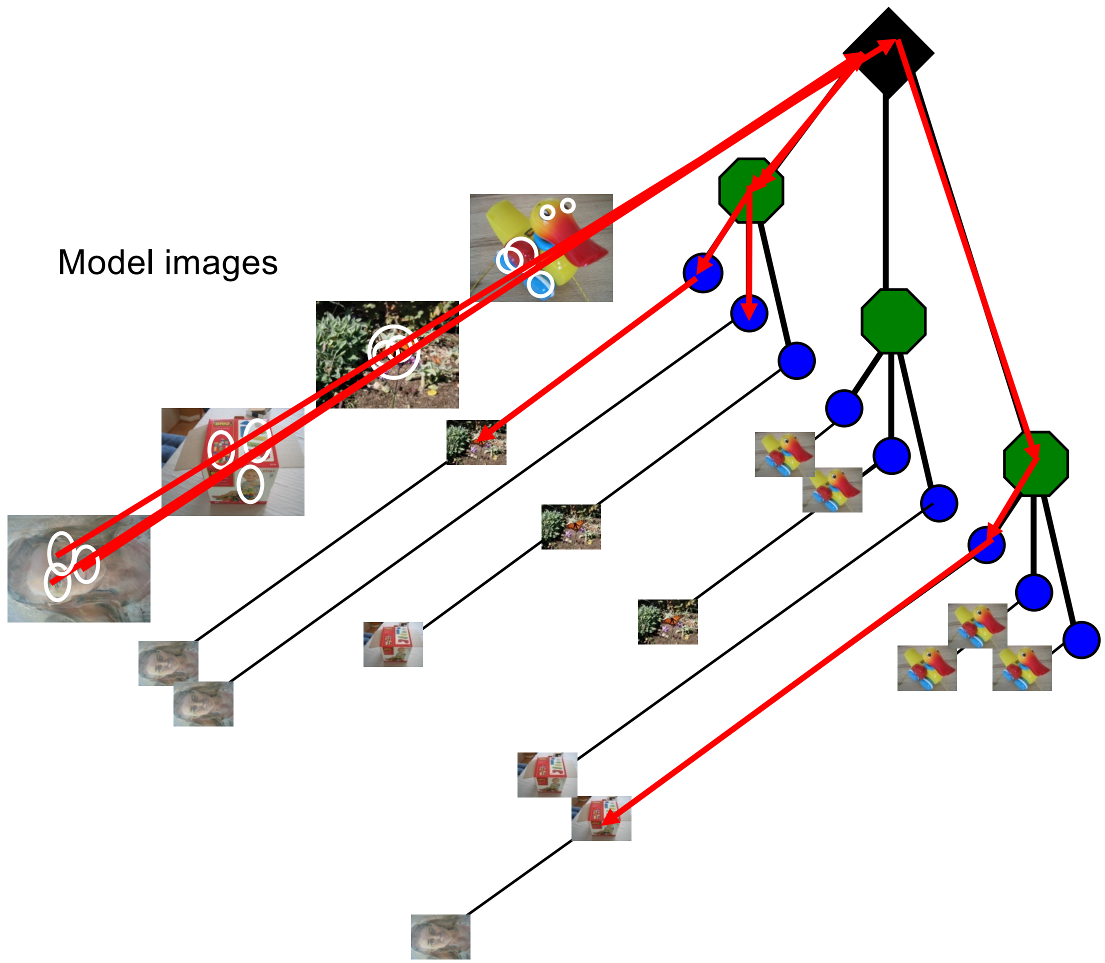
Populating the vocabulary tree/inverted index

Slide credit: D. Nister



Populating the vocabulary tree/inverted index

Slide credit: D. Nister



Populating the vocabulary tree/inverted index

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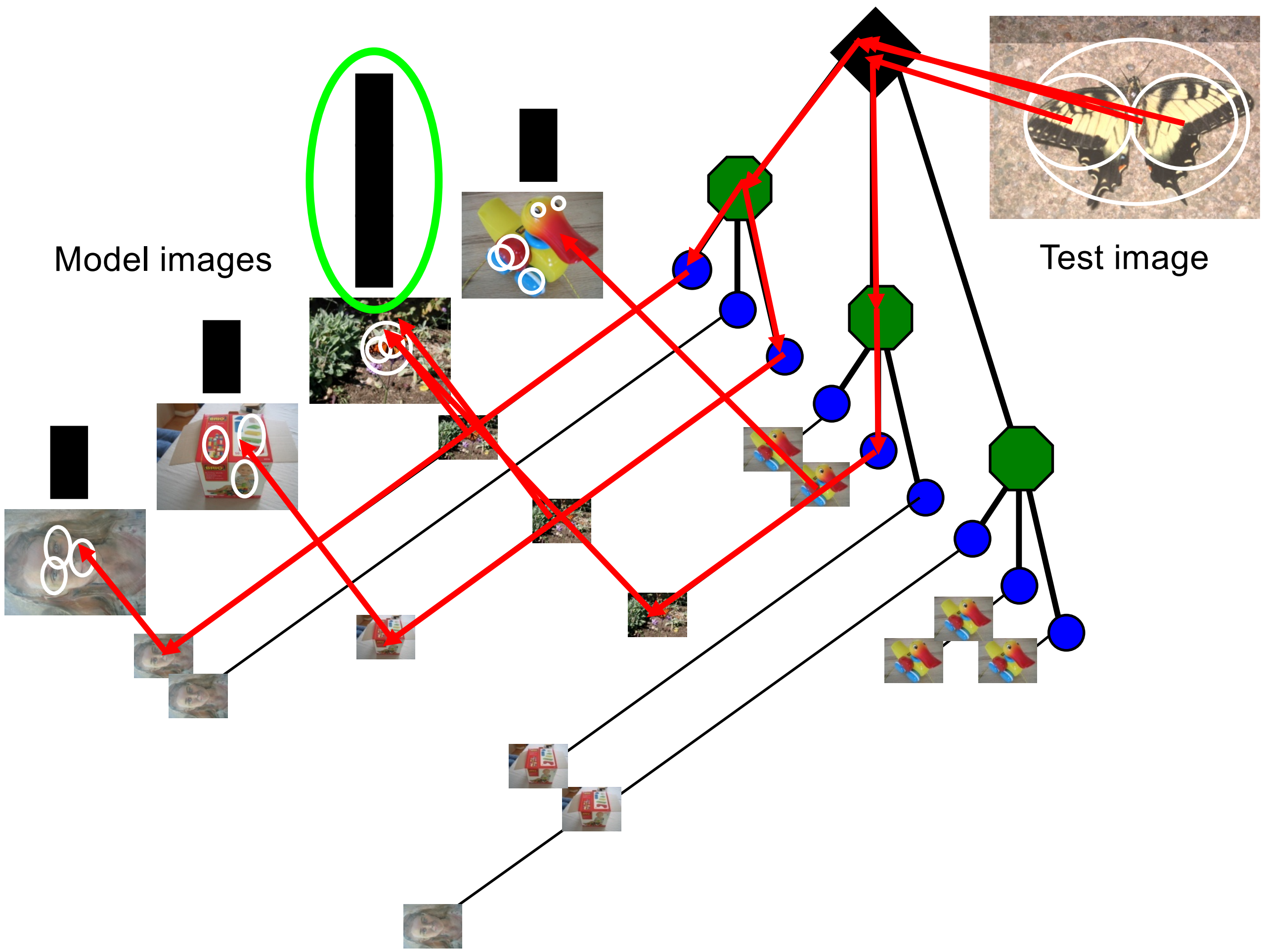

Looking up a test image

Slide credit: D. Nister