

6. Homography



Mosaics: Stitching Images Together





















Image Alignment: a quick experiments





Translations are not enough to align the images



Motion Models



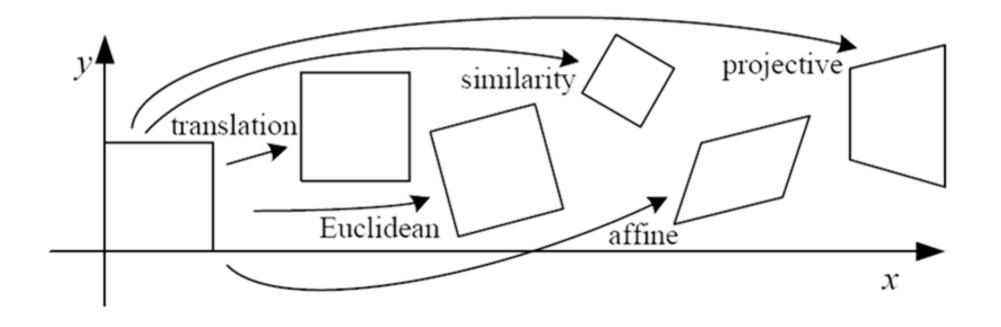
- What is an appropriate transformation:
 - translation?
 - rotation?
 - scale?
 - affine?
 - perspective?





Planar Linear Motion Models





Common Linear Transformations



• Uniform scaling by s:





$$\mathbf{S} = \left[egin{array}{ccc} s & 0 \\ 0 & s \end{array}
ight]$$

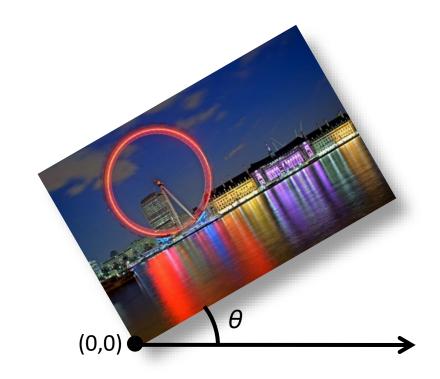
What is the inverse?

Common Linear Transformations



• Rotation by angle θ (about the origin)





$$\mathbf{R} = \begin{bmatrix} \cos \theta & -\sin \theta \\ \sin \theta & \cos \theta \end{bmatrix}$$

What is the inverse? For rotations: $\mathbf{R}^{-1} = \mathbf{R}^T$

2x2 Matrices



• What types of transformations can be represented with a 2x2 matrix?

2D mirror about Y axis?

2D mirror across line y = x?

$$x' = y$$
 $y' = x$
 $\mathbf{T} = \begin{bmatrix} 0 & 1 \\ 1 & 0 \end{bmatrix}$

2x2 Matrices



 What types of transformations can be represented with a 2x2 matrix?

2D Translation?

$$x' = x + t_x$$
 NO! $y' = y + t_y$

Homogeneous Coordinates



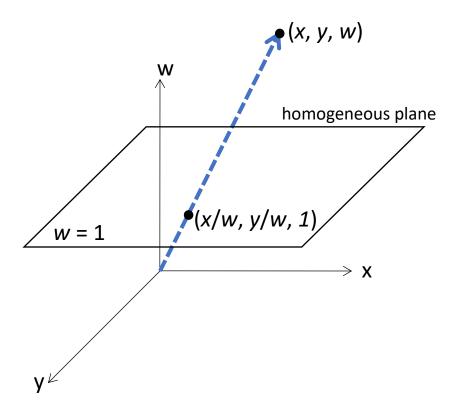
Trick: add one more coordinate:

$$(x,y) \Rightarrow \left[\begin{array}{c} x \\ y \\ 1 \end{array} \right]$$

homogeneous image coordinates

Converting from homogeneous coordinates

$$\left[\begin{array}{c} x \\ y \\ w \end{array}\right] \Rightarrow (x/w, y/w)$$



Translation



Solution: homogeneous coordinates to the rescue

$$\mathbf{T} = \left[egin{array}{cccc} 1 & 0 & t_x \ 0 & 1 & t_y \ 0 & 0 & 1 \end{array}
ight]$$

$$\begin{bmatrix} 1 & 0 & t_x \\ 0 & 1 & t_y \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} x \\ y \\ 1 \end{bmatrix} = \begin{bmatrix} x + t_x \\ y + t_y \\ 1 \end{bmatrix}$$

Affine Transformations



$$\mathbf{T} = \left[egin{array}{cccc} 1 & 0 & t_x \\ 0 & 1 & t_y \\ \hline 0 & 0 & 1 \end{array}
ight]$$
 any transformation with last row [0 0 1] we call an affine transformation

$$\left[egin{array}{cccc} a & b & c \ d & e & f \ 0 & 0 & 1 \end{array}
ight]$$

Basic Affine Transformations



$$\begin{bmatrix} x' \\ y' \\ 1 \end{bmatrix} = \begin{bmatrix} 1 & 0 & t_x \\ 0 & 1 & t_y \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} x \\ y \\ 1 \end{bmatrix}$$

Translate

$$\begin{bmatrix} x' \\ y' \\ 1 \end{bmatrix} = \begin{bmatrix} \cos \theta & -\sin \theta & 0 \\ \sin \theta & \cos \theta & 0 \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} x \\ y \\ 1 \end{bmatrix}$$

2D *in-plane* rotation

$$\begin{bmatrix} \mathbf{x'} \\ \mathbf{y'} \\ 1 \end{bmatrix} = \begin{bmatrix} 1 & 0 & t_x \\ 0 & 1 & t_y \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} \mathbf{x} \\ \mathbf{y} \\ 1 \end{bmatrix} = \begin{bmatrix} \mathbf{s}_x & 0 & 0 \\ 0 & \mathbf{s}_y & 0 \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} \mathbf{x} \\ \mathbf{y} \\ 1 \end{bmatrix}$$

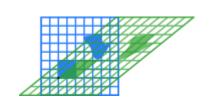
Scale

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

Shear (x direction)

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

Shear (y direction)



Affine Transformations



- Affine transformations are combinations of ...
 - Rotation, Scaling, Shearing, and
 - Translations

$$\begin{bmatrix} x' \\ y' \\ w \end{bmatrix} = \begin{bmatrix} a & b & c \\ d & e & f \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} x \\ y \\ w \end{bmatrix}$$

- 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

Is this an affine transformation?





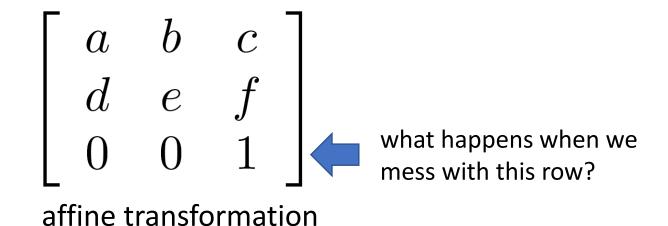






Where do we go from here?





Projective Transformations aka Homographies aka Planar Perspective Maps



$$\mathbf{H} = \left[egin{array}{cccc} a & b & c \ d & e & f \ g & h & 1 \end{array}
ight]$$

Called a homography (or planar perspective map)



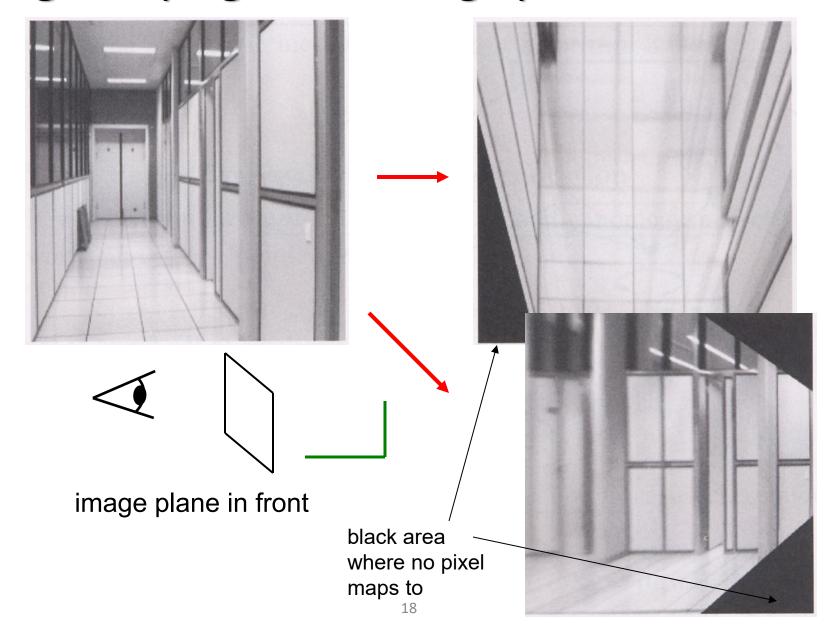






Image warping with homographies





Homographies











Projective Transformations



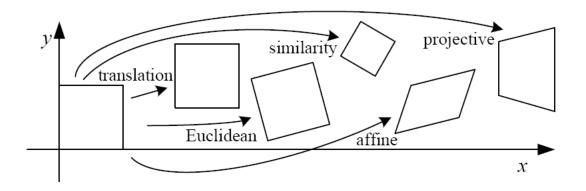
- Projective transformations ...
 - Affine transformations, and
 - Projective warps

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

- Properties of projective transformations:
 - Origin does not necessarily map to origin
 - Lines map to lines
 - Parallel lines do not necessarily remain parallel
 - Ratios are not preserved
 - Closed under composition

2D Linear Transformations





Name	Matrix	# D.O.F.	Preserves:	Icon
translation	$egin{bmatrix} ig[egin{array}{c c} ig[egin{array}{c c} I & t \end{bmatrix}_{2 imes 3} \end{array}$	2	orientation $+\cdots$	
rigid (Euclidean)	$igg[egin{array}{c c} R & t \end{bmatrix}_{2 imes 3}$	3	lengths $+\cdots$	\Diamond
similarity	$\left[\begin{array}{c c} sR & t\end{array}\right]_{2\times 3}$	4	$angles + \cdots$	\Diamond
affine	$\left[egin{array}{c} oldsymbol{A} \end{array} ight]_{2 imes 3}$	6	parallelism $+\cdots$	
projective	$\left[egin{array}{c} ilde{m{H}} \end{array} ight]_{3 imes 3}$	8	straight lines	

These transformations are a nested set of groups

• Closed under composition and inverse is a member

Examples





distant camera, zoomed in

Examples





synthetic rotations





original view

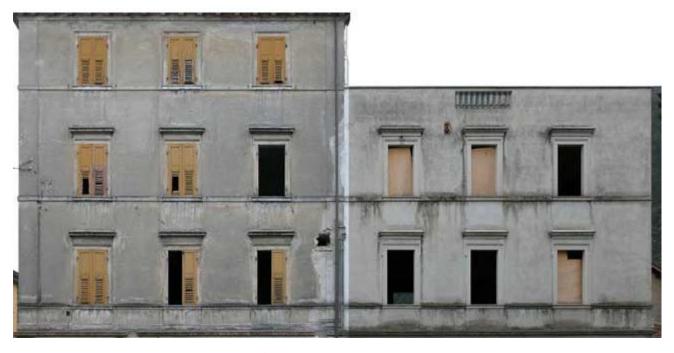
Examples



two original images







rectified and stitched

Questions?

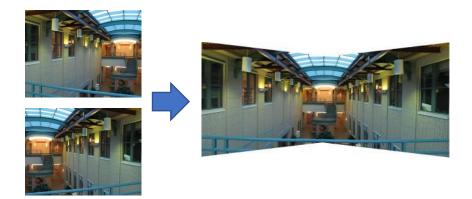


Homography Warping



The matrix representation

$$w \begin{bmatrix} x' \\ y' \\ 1 \end{bmatrix} = \begin{bmatrix} * & * & * \\ * & * & * \\ * & * & * \end{bmatrix} \begin{bmatrix} x \\ y \\ 1 \end{bmatrix}$$
$$X' \qquad \qquad H \qquad X$$



w means x and x' are equal up to a scale;w does not affect the results (per definition of homogenous coordinates)

- To apply a homography H
 - Compute x' = Hx (regular matrix multiply)
 - Convert x' from homogeneous to image coordinates
 - divide by w (third) coordinate

Solving for Homographies -- the basic idea



$$x' = Hx \qquad \longrightarrow \qquad \begin{bmatrix} x' \\ y' \\ 1 \end{bmatrix} = \begin{bmatrix} a & b & c \\ d & e & f \\ g & h & i \end{bmatrix} \begin{bmatrix} x \\ y \\ 1 \end{bmatrix}$$

- Find the homography *H* from feature correspondences
 - E.g. pairs of matched SIFT/Harris corners, x and x'
- How?
 - Reshape \boldsymbol{H} to a vector $\boldsymbol{h} = [a, b, c, d, e, f, g, h]^T$
 - -x and x' are both known parameters
 - Each pair of feature points provide linear equations of h
 - More pairs provide linear equations: Ah = b
 - How many correspondences do we need?



$$\mathbf{x}_{i} = (x_{i}, y_{i}, 1)^{\mathsf{T}} \quad \mathbf{x}'_{i} = (x'_{i}, y'_{i}, 1)^{\mathsf{T}}$$

$$\mathbf{x}'_{i} \propto \mathbf{H} \mathbf{x}_{i} \qquad \mathbf{x}'_{i} \times \mathbf{H} \mathbf{x}_{i} = 0$$

$$\mathbf{H} = \begin{pmatrix} \mathbf{h}^{1\mathsf{T}} \\ \mathbf{h}^{2\mathsf{T}} \\ \mathbf{h}^{3\mathsf{T}} \end{pmatrix} \qquad \mathbf{H} \mathbf{x}_{i} = \begin{pmatrix} \mathbf{h}^{1\mathsf{T}} \mathbf{x}_{i} \\ \mathbf{h}^{2\mathsf{T}} \mathbf{x}_{i} \\ \mathbf{h}^{3\mathsf{T}} \mathbf{x}_{i} \end{pmatrix}$$

$$\mathbf{x}_{i}' \times \mathbf{H} \mathbf{x}_{i} = \begin{pmatrix} y_{i}' \mathbf{h}^{3\mathsf{T}} \mathbf{x}_{i} - \mathbf{h}^{2\mathsf{T}} \mathbf{x}_{i} \\ \mathbf{h}^{1\mathsf{T}} \mathbf{x}_{i} - x_{i}' \mathbf{h}^{3\mathsf{T}} \mathbf{x}_{i} \\ x_{i}' \mathbf{h}^{2\mathsf{T}} \mathbf{x}_{i} - y_{i}' \mathbf{h}^{1\mathsf{T}} \mathbf{x}_{i} \end{pmatrix}$$



$$\mathbf{x'}_{i} \times \mathbf{H} \mathbf{x}_{i} = \begin{bmatrix} \mathbf{0}^{\mathsf{T}} & -\mathbf{x}_{i}^{\mathsf{T}} & y_{i}' \mathbf{x}_{i}^{\mathsf{T}} \\ \mathbf{x}_{i}^{\mathsf{T}} & \mathbf{0}^{\mathsf{T}} & -x_{i}' \mathbf{x}_{i}^{\mathsf{T}} \end{bmatrix} \begin{pmatrix} \mathbf{h}^{1} \\ \mathbf{h}^{2} \\ -y_{i}' \mathbf{x}_{i}^{\mathsf{T}} & x_{i}' \mathbf{x}_{i}^{\mathsf{T}} & \mathbf{0}^{\mathsf{T}} \end{bmatrix} \begin{pmatrix} \mathbf{h}^{1} \\ \mathbf{h}^{2} \\ \mathbf{h}^{3} \end{pmatrix} = \mathbf{0}$$

$$\mathbf{A}_{i}\mathbf{h}=0$$



- Equations are linear in \mathbf{h} , $\mathbf{A}_i \mathbf{h} = 0$
- Only 2 out of 3 are linearly independent (indeed, 2 eq/pt)

$$\begin{bmatrix} \mathbf{0}^{\mathsf{T}} & -\mathbf{x}_i^{\mathsf{T}} & y_i' \mathbf{x}_i^{\mathsf{T}} \\ \mathbf{x}_i^{\mathsf{T}} & \mathbf{0}^{\mathsf{T}} & -x_i' \mathbf{x}_i^{\mathsf{T}} \\ -y_i' \mathbf{x}_i^{\mathsf{T}} & x_i' \mathbf{x}_i^{\mathsf{T}} & \mathbf{0}^{\mathsf{T}} \end{bmatrix} \begin{pmatrix} \mathbf{h}^1 \\ \mathbf{h}^2 \\ \mathbf{h}^3 \end{pmatrix} = 0$$

(only drop third row if $w_i' \neq 0$)



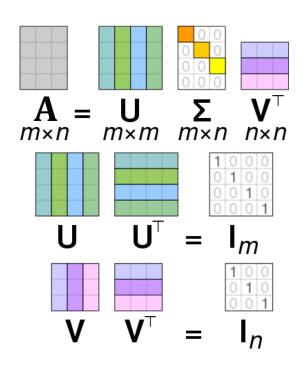
 \bullet Solving for H from 4 points (each point provide two independent equations of h)

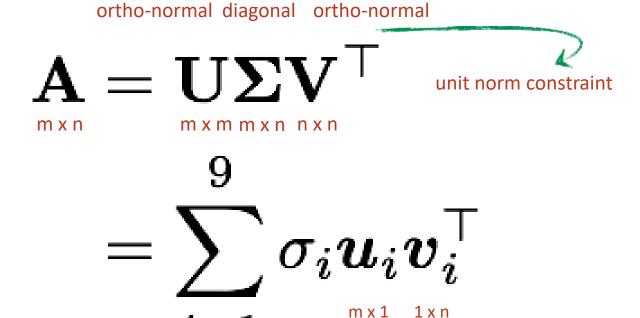
$$\mathbf{Ah} = 0$$

- size A is 8x9 or 12x9, but rank 8
- Trivial solution is **h**=0
- 1-D null-space yields solution of interest
 - pick for example the one with $\|\mathbf{h}\| = 1$
- No exact solution because of inexact measurement, i.e. "noise"
 - Minimize $\|\mathbf{A}\mathbf{h}\|$ with constraint $\|\mathbf{h}\|=1$ (solution is to take the SVD of **A**, and get the last column of the matrix **V**)

Singular Value Decomposition







Each column of V represents a solution for $\mathbf{A}h=\mathbf{0}$ where the singular value represents the reprojection error

DLT Algorithm



Objective

Given $n \ge 4$ 2D to 2D point correspondences $\{x_i \leftrightarrow x_i'\}$, determine the 2D homography matrix H such that $x_i' = Hx_i$

Algorithm

- (i) For each correspondence $x_i \leftrightarrow x_i$ compute A_i . Usually only two first rows needed.
- (ii) Assemble n 2x9 matrices A_i into a single 2nx9 matrix A_i
- (iii) Obtain SVD of A. Solution for h is last column of V
- (iv) Determine H from h

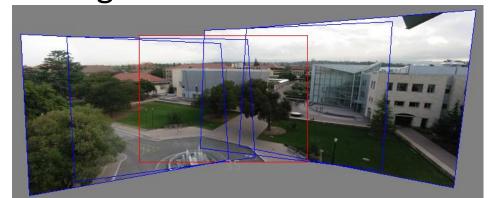
Questions?



Overall Pipeline



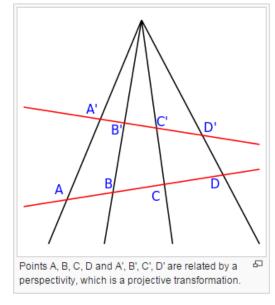
- 3D rotation → homography image transformation
 - Using homogeneous coordinates to represent pixel position
- Use feature correspondence
- Solve the homography model
- Warp all images to a reference one
 - 1. Pick one image (red)
 - 2. Warp the other images towards it by solving the homography transformation (usually, one by one)
- Use your favorite blending



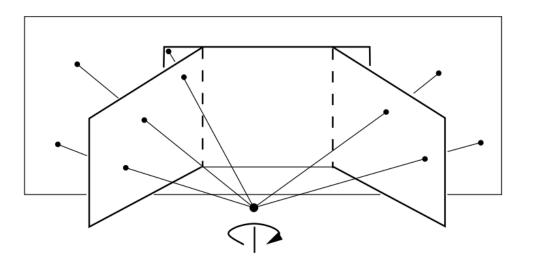
Why the Homography Model?



- Projective Transformation
 - Historically developed from the study of central projection
 - Maps lines to lines, points to points, but does not preserve parallelism
- The two images of a rotating camera



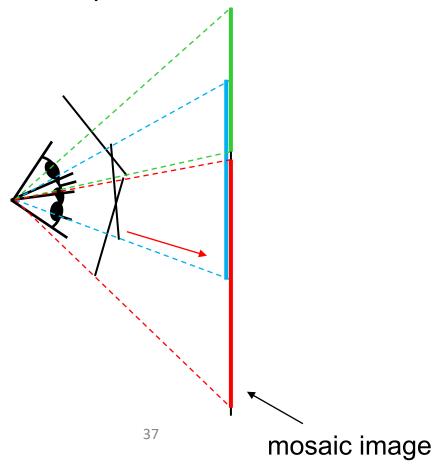
From Wikipedia



An Intuitive Explanation

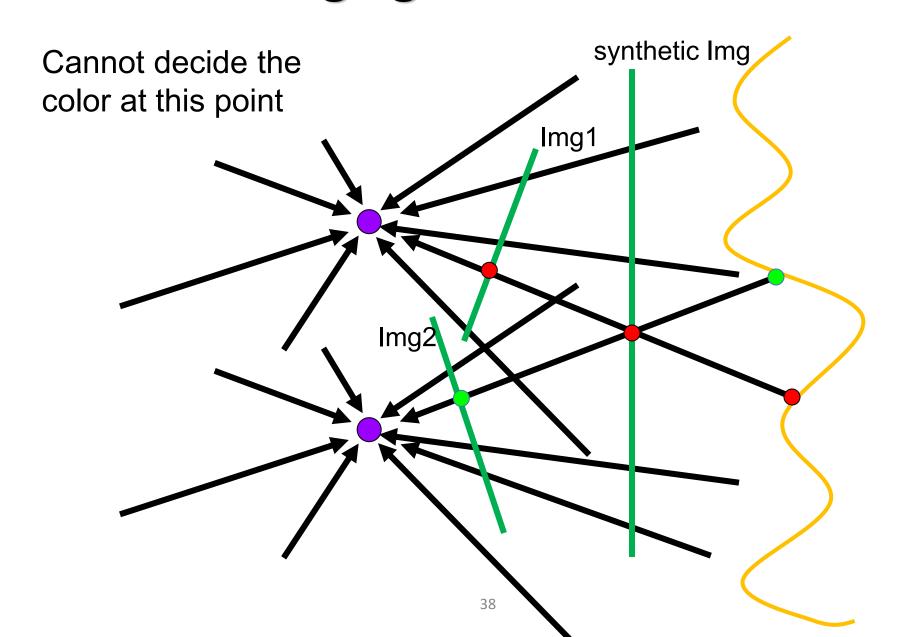


- The mosaic has a natural interpretation in 3D
 - The images are reprojected onto a common plane
 - The mosaic is the image of that plane



Mosaic for Changing Camera Center?

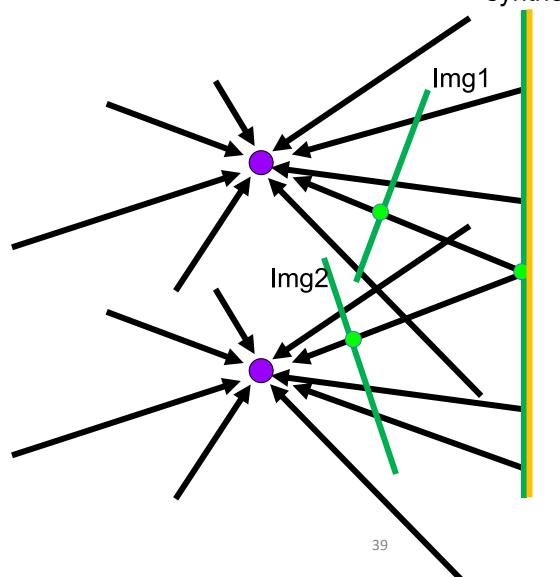




Works for Planar Scenes











Questions?



Mosaic Stitching Algorithm



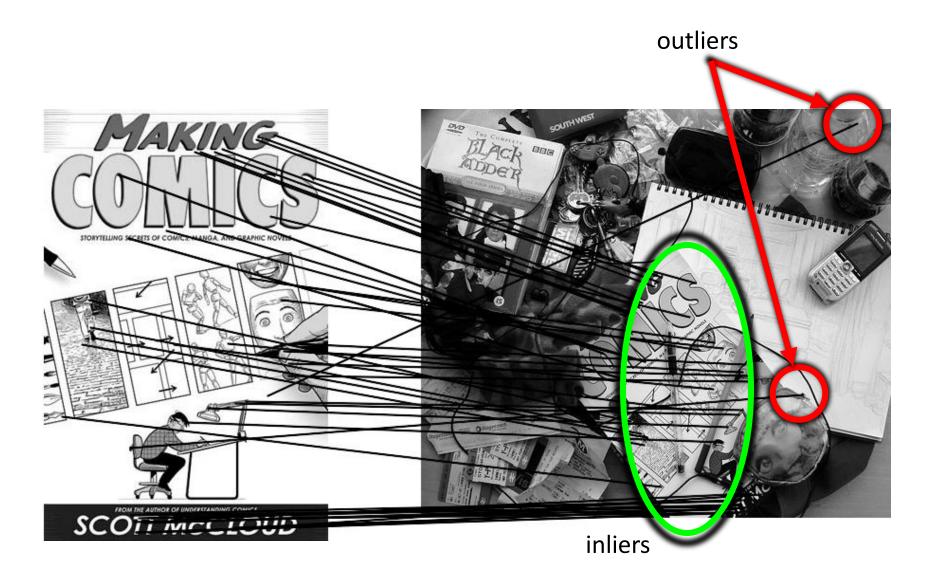
Given images A and B

- 1. Compute image features for A and B
- 2. Match features between A and B
- 3. Compute homography between A and B using least squares on set of matches

What could go wrong?

Outliers

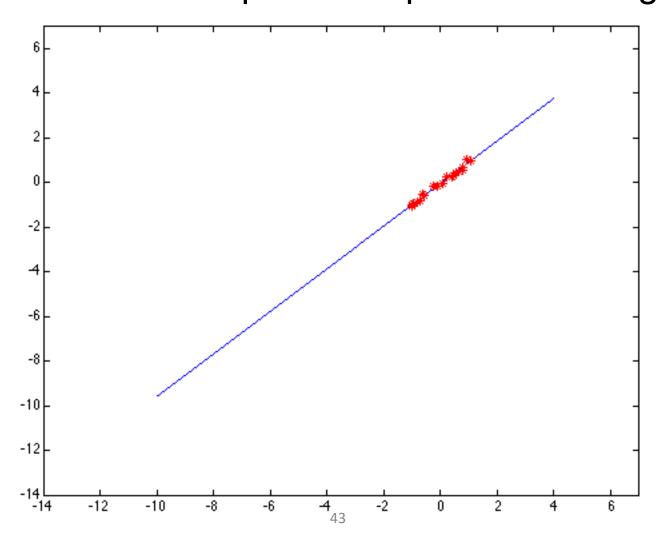




Problems of Least Square Fitting



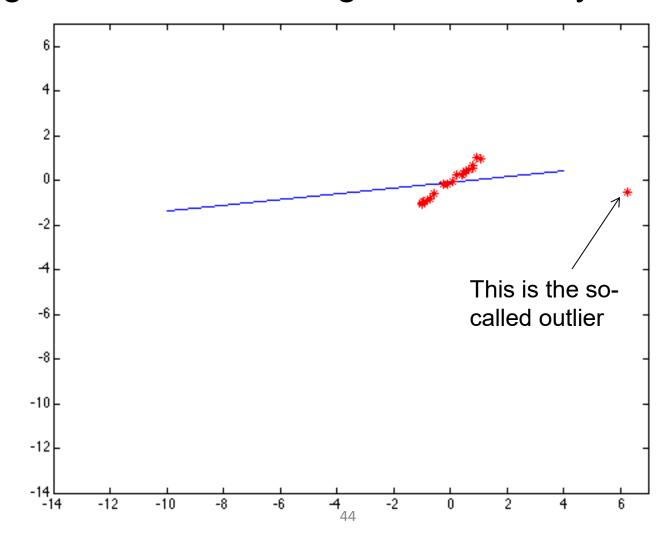
Let's consider a simpler example... linear regression



Problems of Least Square Fitting



A single outlier could 'drag' the line away....



Robust Fitting



- Squared penalty can be a source of bias in the presence of noise points
 - One is an M-estimator
 - A error function with an upper bound
 - Square nearby, threshold far away
 - Another is RANSAC
 - Search for good points

M-estimators

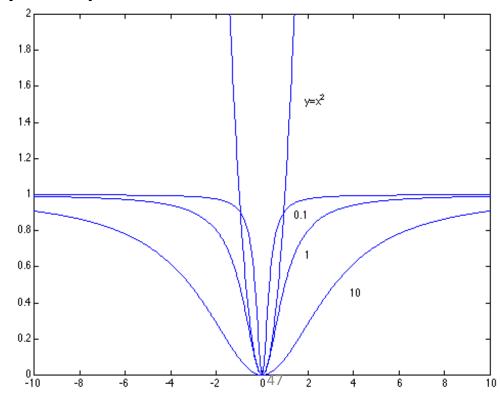


- Least square minimizes $\sum_i r^2(x_i, \theta)$
 - $r(x_i, \theta)$ is the residual/distance
 - In the case of line fitting, $r(\cdot) = (ax_i + by_i + c)$
- M-estimators minimize $\sum_i \rho(r(\cdot); \sigma)$
 - There are different choices of the function $\rho(\cdot)$
 - Typically, the result objective function is even more nonlinear!!
 - Harder to optimize

Typical Examples of ho

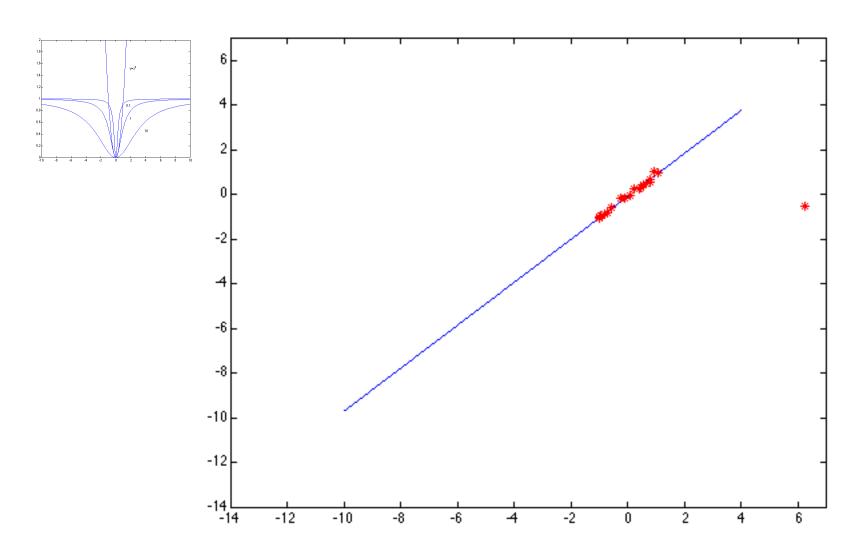


- A popular choice is $\rho(r;\sigma) = \frac{r^2}{r^2 + \sigma^2}$
 - When r is too large, ρ becomes saturated to 1
 - When r is small, ρ functions like r^2
- ρ is controlled by the parameter σ



Examples





Questions?



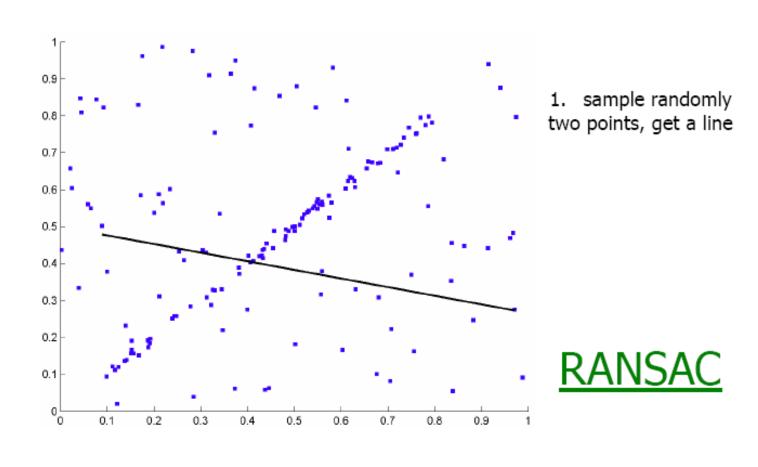
The Idea of RANSAC



- Choose a small set of samples at random
 - the set should be as small as possible, so that it is more likely outlier-free (e.g. two points for line fitting)
- Fit a model e.g. the line
- Count the number of inliers
 - Points that "agree" with the model are considered inliers
 - "Agree" = within a small distance of the line
- Repeat the random sampling many times, select the one with the largest number of inliers
- Take these inliers as true inliers and fit again

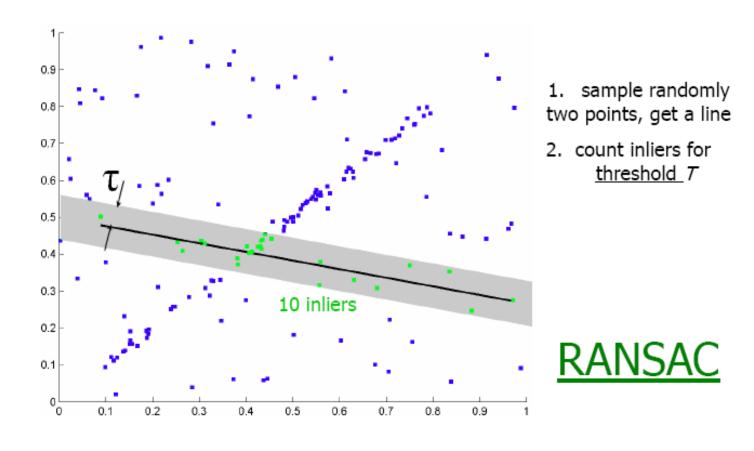
Example





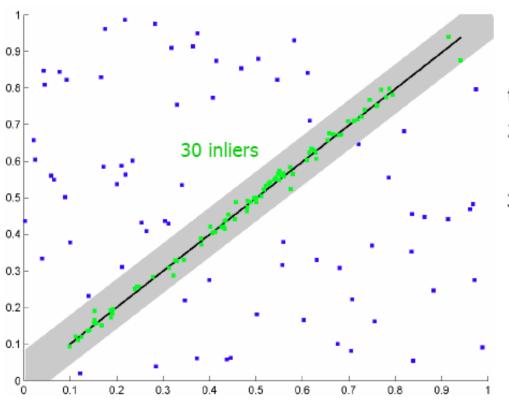
Example





Example





- 1. sample randomly two points, get a line
- 2. count inliers for threshold 7
- 3. repeat N times and select model with most inliers

RANSAC

RANSAC



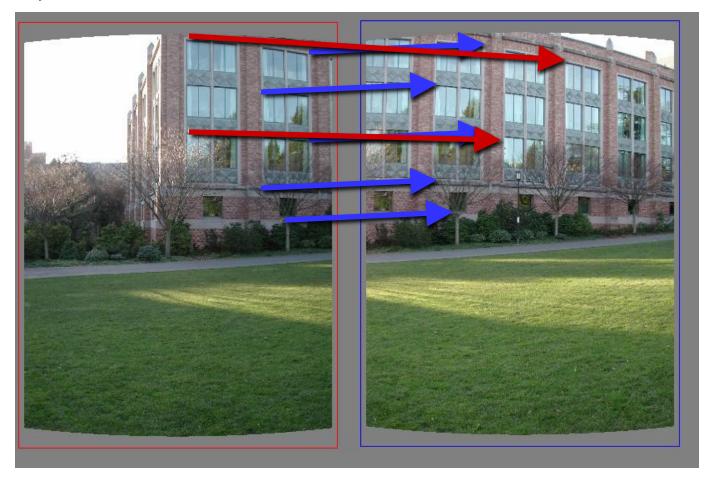
General version:

- 1. Randomly choose *s* samples
 - Typically s = minimum sample size that lets you fit a model
- 2. Fit a model (e.g., line) to those samples
- 3. Count the number of inliers that approximately fit the model
- 4. Repeat *N* times
- 5. Choose the largest set of inliers, and fit the model again

Translation Estimation



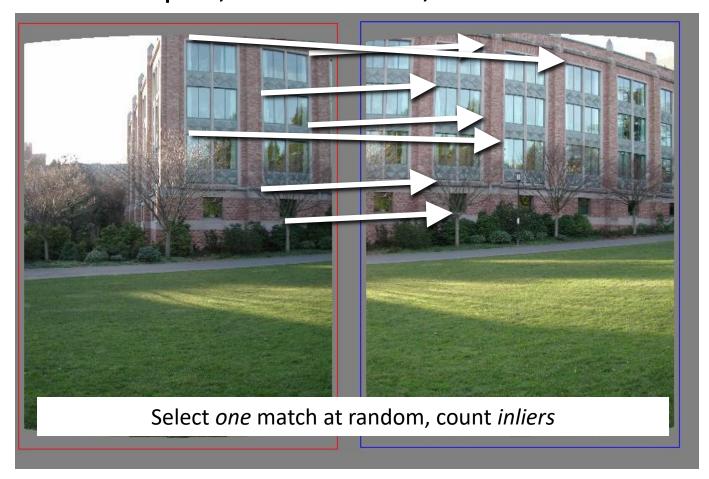
• Two "outlier", five "inliers"



RAndom SAmple Consensus



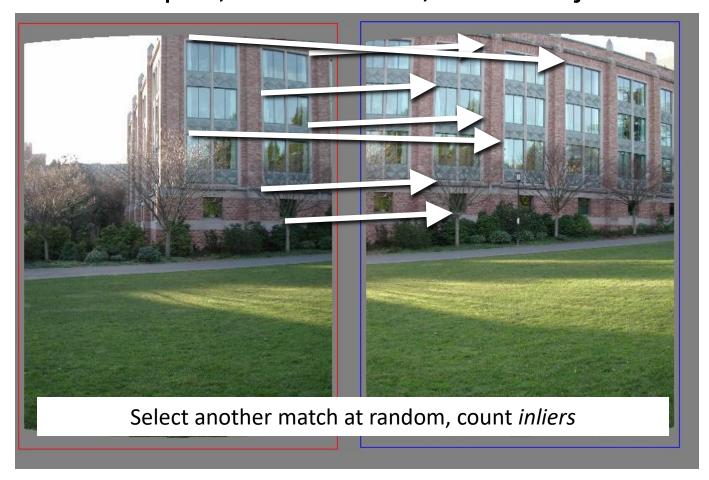
Randomly select one pair, count inliers, and find five inliers



RAndom SAmple Consensus



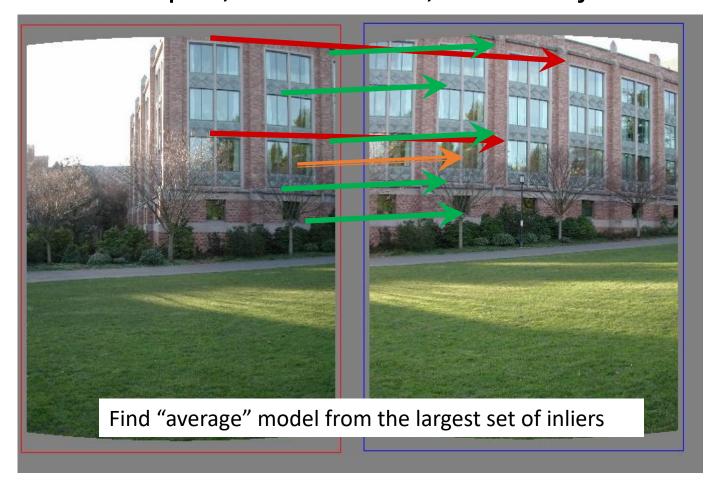
Randomly select one pair, count inliers, and find just one inlier



RAndom SAmple Consensus



Randomly select one pair, count inliers, and find just one inlier



RANSAC



- Idea:
 - 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

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?
 - I will explain the calculation soon

Questions?



How Many Iterations?



- Suppose each time s samples are selected to fit a model
- Suppose e is the percentage of outlier
- Suppose N iterations have been run
- Success = at least one set of samples is outlier-free
 - So what is the probability p of success?
- The math:
 - The probability q that a set is outlier-free $q = (1 e)^s$
 - The probability (1-p) that all sets have outliers $1-p=(1-q)^N$
- Decide the confidence probability p (e.g. 0.99), then determine N

$$N = \log(1 - p) / \log(1 - (1 - e)^{s})$$

How Many Iterations?



- Suppose each time s samples are selected to fit a model
- Suppose e is the percentage of outlier
- Decide the confidence probability p (e.g. 0.99), then determine N

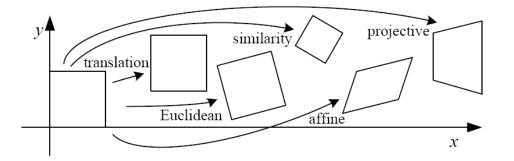
$$N = \log(1-p)/\log(1-(1-e)^s)$$

	proportion of outliers e							
S	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	16	24	37	97	293	
7	4	8	20	33	54	163	588	
8	5	9	26	44	78	272	1177	

How Big is s?



- For alignment, depends on the motion model
 - Here, each sample is a correspondence (pair of matching points)



Name	Matrix	# D.O.F.	Preserves:	Icon
translation	$egin{array}{ c c c c c c c c c c c c c c c c c c c$	2	orientation $+\cdots$	
rigid (Euclidean)	$igg igg[m{R} igg m{t} igg]_{2 imes 3}$	3	lengths +···	\Diamond
similarity	$\left[\begin{array}{c c} sR & t\end{array}\right]_{2\times 3}$	4	angles $+\cdots$	\Diamond
affine	$\left[egin{array}{c} oldsymbol{A} \end{array} ight]_{2 imes 3}$	6	parallelism + · · ·	
projective	$\left[egin{array}{c} ilde{m{H}} \end{array} ight]_{3 imes 3}$	8	straight lines	

Adaptively Determining N



e is often unknown a priori,

- so pick worst case, e.g. 50%,
- adapt if more inliers are found, e.g. 80% would yield e=0.2

The algorithm:

- N=∞, sample_count =0
- While N >sample_count repeat
 - Choose a sample and count the number of inliers
 - Set e=1-(number of inliers)/(total number of points)
 - Recompute *N* from *e*
 - Increment the sample_count by 1
- Terminate

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

Questions?



Cost functions



- Algebraic distance
- Geometric distance
- Reprojection error

- Comparison
- Geometric interpretation

Algebraic Distance



DLT minimizes ||Ah||

$$e = Ah$$
 residual vector

 \mathbf{e}_i the first two components of \boldsymbol{e}

$$d_{\text{alg}}(\mathbf{x}_i', \mathbf{H}\mathbf{x}_i)^2 = \left\| \mathbf{e}_i \right\|^2 = \left\| \begin{bmatrix} 0^{\mathsf{T}} & -\mathbf{x}_i^{\mathsf{T}} & -y_i'\mathbf{x}_i^{\mathsf{T}} \\ -\mathbf{x}_i^{\mathsf{T}} & 0^{\mathsf{T}} & -x_i'\mathbf{x}_i^{\mathsf{T}} \end{bmatrix} \mathbf{h} \right\|^2$$

The algebraic distance between x_1 , x_2 :

$$d_{\text{alg}}(\mathbf{x}_1, \mathbf{x}_2)^2 = a_1^2 + a_2^2$$
 where $\mathbf{a} = (a_1, a_2, a_3)^T = \mathbf{x}_1 \times \mathbf{x}_2$

$$\sum_{i} d_{\text{alg}}(\mathbf{x}'_{i}, \mathbf{H}\mathbf{x}_{i})^{2} = \sum_{i} \|\mathbf{e}_{i}\|^{2} = \|\mathbf{A}\mathbf{h}\|^{2} = \|\mathbf{e}\|^{2}$$

Not geometrically/statistically meaningful, but given good normalization it works fine and is very fast (use for initialization)

Geometric Distance



- X measured coordinates
- X estimated coordinates

d(.,.) Euclidean distance (in image)

Error in one image

$$\hat{\mathbf{H}} = \underset{\mathbf{H}}{\operatorname{argmin}} \sum_{i} d(\mathbf{x}'_{i}, \mathbf{H}\mathbf{x}_{i})^{2}$$

Symmetric transfer error

$$\hat{\mathbf{H}} = \underset{\mathbf{H}}{\operatorname{argmin}} \sum_{i} d(\mathbf{x}_{i}, \mathbf{H}^{-1}\mathbf{x}_{i}')^{2} + d(\mathbf{x}_{i}', \mathbf{H}\mathbf{x}_{i})^{2}$$

Reprojection error

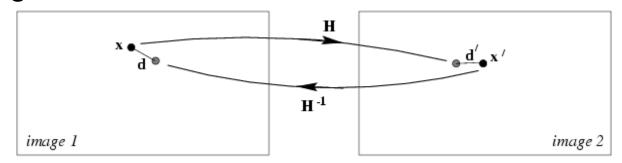
$$\left(\hat{\mathbf{H}}, \hat{\mathbf{x}}_{i}, \hat{\mathbf{x}}_{i}'\right) = \underset{\mathbf{H}, \hat{\mathbf{x}}_{i}, \hat{\mathbf{x}}_{i}'}{\operatorname{argmin}} \sum_{i} d(\mathbf{x}_{i}, \hat{\mathbf{x}}_{i})^{2} + d(\mathbf{x}_{i}', \hat{\mathbf{x}}_{i}')^{2}$$

subject to
$$\hat{\mathbf{x}}_i' = \hat{\mathbf{H}}\hat{\mathbf{x}}_i$$

Visualization

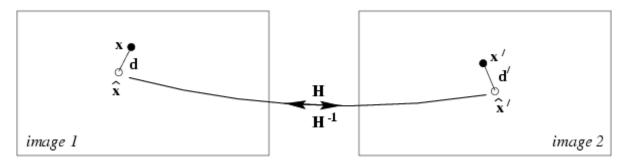


Symmetric geometric error



$$d(\mathbf{x}, \mathbf{H}^{-1}\mathbf{x}')^2 + d(\mathbf{x}', \mathbf{H}\mathbf{x})^2$$

Reprojection error



$$d(\mathbf{x}, \hat{\mathbf{x}})^2 + d(\mathbf{x}', \hat{\mathbf{x}}')^2$$

Minimize the re-projection error



The objective function

$$\{\mathbf{H}, \hat{\mathbf{x}}_{i}, \hat{\mathbf{x}}_{i}'\} = \arg\min \sum_{i} d(\mathbf{x}_{i}, \hat{\mathbf{x}}_{i})^{2} + d(\mathbf{x}_{i}', \hat{\mathbf{x}}_{i}')^{2}$$
$$= (x_{i} - \hat{x}_{i})^{2} + (y_{i} - \hat{y}_{i})^{2} + (x'_{i} - \hat{x}'_{i})^{2} + (y'_{i} - \hat{y}'_{i})^{2}$$

$$\hat{x}_{i}' = \frac{a\hat{x}_{i} + b\hat{y}_{i} + c}{g\hat{x}_{i} + h\hat{y}_{i} + i} \qquad \hat{y}_{i}' = \frac{d\hat{x}_{i} + e\hat{y}_{i} + f}{g\hat{x}_{i} + h\hat{y}_{i} + i} \qquad \begin{bmatrix} \hat{x}'_{i} \\ \hat{y}'_{i} \\ 1 \end{bmatrix} \propto \begin{bmatrix} a & b & c \\ d & e & f \\ g & h & i \end{bmatrix} \begin{bmatrix} x_{i} \\ y_{i} \\ 1 \end{bmatrix}$$

- Nonlinear, how do we minimize it?
 - General methods
 - Newton iteration
 - Levenberg-Marquardt

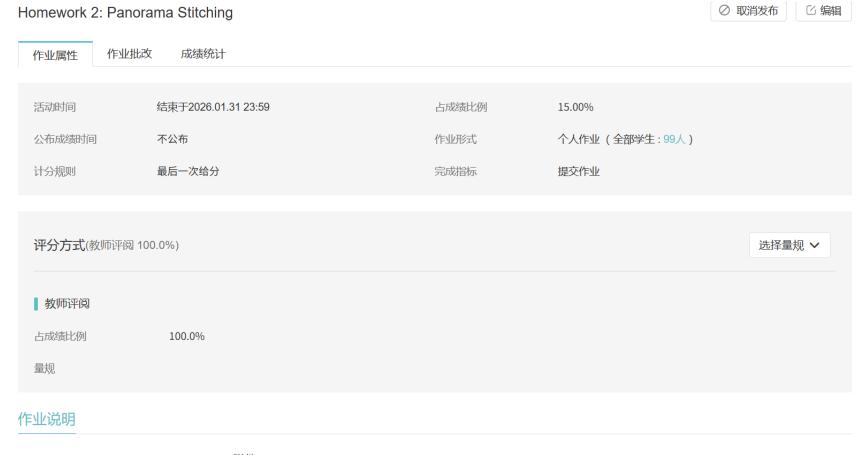
Questions?



Homework 1: Photometric Stereo



• Deadline: 2025.12.21 23:59



Please refer to the supplementary files (附件) for the detailed illustration of the homework (Homework2_2025.pdf) and the test data (Homework2.zip). The DDL is December 21, 2025.