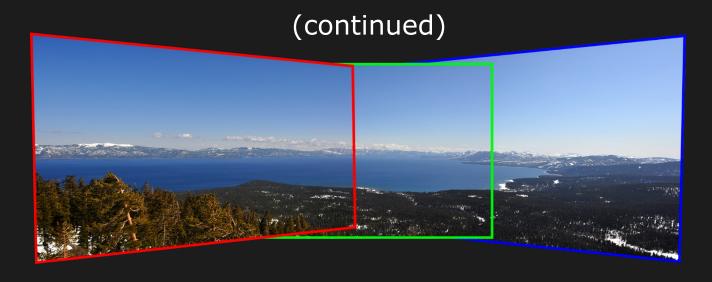
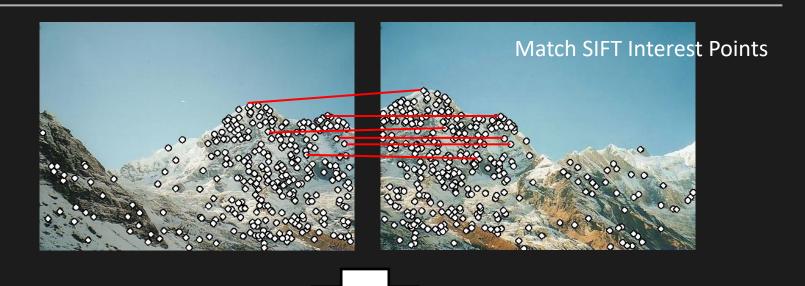
# CS/ECE 766: Computer Vision

University of Wisconsin-Madison

# Image Alignment and Stitching

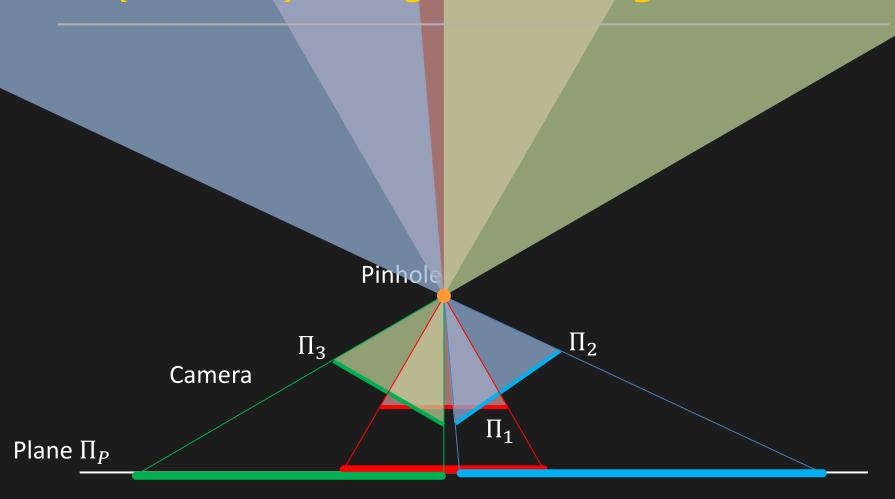


## (Review) Panorama Stitching

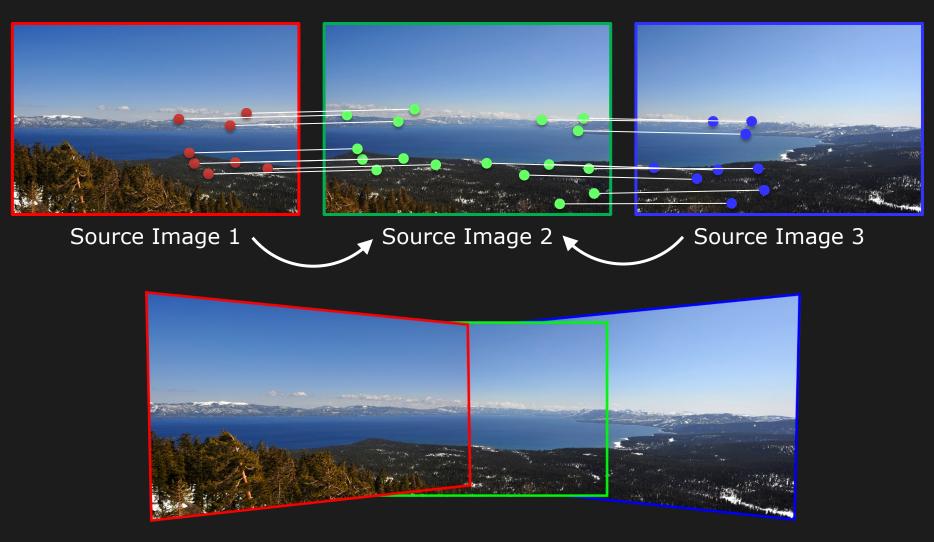




# (Review) Image Stitching Process

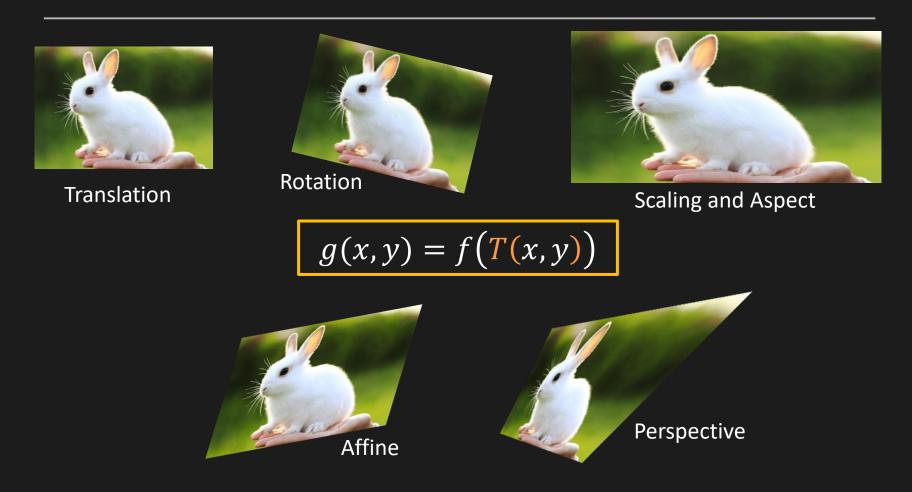


### (Review) Image Stitching Process



Warp images so that corresponding points align.

## (Review) Global Warping/Transformation



Transformation T is the same over entire domain. Linear Transformation of Homogeneous Coordinates

#### (Review) Scaling, Rotation, Skew, Translation

$$\begin{bmatrix} x_2 \\ y_2 \end{bmatrix} = \begin{bmatrix} a & 0 \\ 0 & b \end{bmatrix} \begin{bmatrix} x_1 \\ y_1 \end{bmatrix}$$

Scaling

$$\begin{bmatrix} x_2 \\ y_2 \end{bmatrix} = \begin{bmatrix} 1 & m_x \\ 0 & 1 \end{bmatrix} \begin{bmatrix} x_1 \\ y_1 \end{bmatrix}$$

Horizontal Skew

$$\begin{bmatrix} x_2 \\ y_2 \end{bmatrix} = \begin{bmatrix} \cos\theta & -\sin\theta \\ \sin\theta & \cos\theta \end{bmatrix} \begin{bmatrix} x_1 \\ y_1 \end{bmatrix}$$

Rotation

Translations cannot be represented!

#### (Review) 2x2 Matrix Transformations

Any transformation of the form:

$$\begin{bmatrix} x_2 \\ y_2 \end{bmatrix} = \begin{bmatrix} a_{11} & a_{12} \\ a_{21} & a_{22} \end{bmatrix} \begin{bmatrix} x_1 \\ y_1 \end{bmatrix}$$

- Origin maps to the origin
- Lines map to lines
- Parallel lines remain parallel
- Closed under composition

$$\begin{array}{c}
\mathbf{p}_{2} = T_{21}\mathbf{p}_{1} \\
\mathbf{p}_{3} = T_{32}\mathbf{p}_{2} \\
\mathbf{p}_{3} = T_{31}\mathbf{p}_{1}
\end{array}$$

$$\mathbf{p}_{3} = T_{32}\mathbf{p}_{2} = T_{32}T_{21}\mathbf{p}_{1} \implies T_{31} = T_{32}T_{21}$$

### (Review) Homogenous Coordinates

The homogenous representation of a 2D point  $\mathbf{p} = (x, y)$  is a 3D point  $\widetilde{\mathbf{p}} = (\widetilde{x}, \widetilde{y}, \widetilde{z})$ . The third coordinate  $\widetilde{z} \neq 0$  is fictitious such that:

$$x = \frac{\tilde{x}}{\tilde{z}} \qquad y = \frac{\tilde{y}}{\tilde{z}}$$

$$x = \frac{\widetilde{x}}{\widetilde{z}}$$
  $y = \frac{\widetilde{y}}{\widetilde{z}}$   $\mathbf{p} \equiv \begin{bmatrix} x \\ y \\ 1 \end{bmatrix} \equiv \begin{bmatrix} \widetilde{z}x \\ \widetilde{z}y \\ \widetilde{z} \end{bmatrix} \equiv \begin{bmatrix} \widetilde{x} \\ \widetilde{y} \\ \widetilde{z} \end{bmatrix} = \widetilde{\mathbf{p}}$ 

Converting to homogeneous:

$$(x,y) = \left(\frac{\tilde{x}}{\tilde{z}}, \frac{\tilde{y}}{\tilde{z}}\right)$$

Converting from homogeneous:

$$(\tilde{x}, \tilde{y}, \tilde{z}) = (x, y, 1)$$

#### (Review) Scaling, Rotation, Skew, Translation

$$\begin{bmatrix} \tilde{x}_2 \\ \tilde{y}_2 \\ \tilde{z}_2 \end{bmatrix} = \begin{bmatrix} s_x & 0 & 0 \\ 0 & s_y & 0 \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} x_1 \\ y_1 \\ 1 \end{bmatrix}$$

Scaling

$$\begin{bmatrix} \tilde{x}_2 \\ \tilde{y}_2 \\ \tilde{z}_2 \end{bmatrix} = \begin{bmatrix} 1 & m_{\chi} & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} x_1 \\ y_1 \\ 1 \end{bmatrix}$$

Horizontal Skew

$$\begin{bmatrix} \tilde{x}_2 \\ \tilde{y}_2 \\ \tilde{z}_2 \end{bmatrix} = \begin{bmatrix} 1 & 0 & t_x \\ 0 & 1 & t_y \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} x_1 \\ y_1 \\ 1 \end{bmatrix}$$

**Translation** 

$$\begin{bmatrix} \tilde{x}_2 \\ \tilde{y}_2 \\ \tilde{z}_2 \end{bmatrix} = \begin{bmatrix} 1 & 0 & t_x \\ 0 & 1 & t_y \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} x_1 \\ y_1 \\ 1 \end{bmatrix} \qquad \begin{bmatrix} \tilde{x}_2 \\ \tilde{y}_2 \\ \tilde{z}_2 \end{bmatrix} = \begin{bmatrix} \cos\theta & -\sin\theta & 0 \\ \sin\theta & \cos\theta & 0 \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} x_1 \\ y_1 \\ 1 \end{bmatrix}$$

Rotation

#### Any transformation of the form:

$$\begin{bmatrix} \tilde{x}_2 \\ \tilde{y}_2 \\ \tilde{z}_2 \end{bmatrix} = \begin{bmatrix} h_{11} & h_{12} & h_{13} \\ h_{21} & h_{22} & h_{23} \\ h_{31} & h_{32} & h_{33} \end{bmatrix} \begin{bmatrix} \tilde{x}_1 \\ \tilde{y}_1 \\ \tilde{z}_1 \end{bmatrix} \qquad \qquad \widetilde{\mathbf{p}}_2 = H \widetilde{\mathbf{p}}_1$$

$$\widetilde{\mathbf{p}}_2 = H\widetilde{\mathbf{p}}_1$$

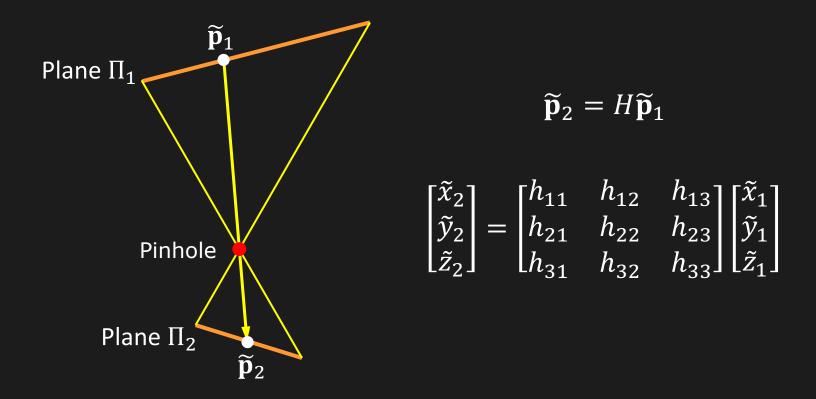






Also called Homography.

Mapping of one plane to another through a pinhole



Same as imaging a plane through a pinhole.

Homography can only be defined up to a scale.

$$\begin{bmatrix} h_{11} & h_{12} & h_{13} \\ h_{21} & h_{22} & h_{23} \\ h_{31} & h_{32} & h_{33} \end{bmatrix} \begin{bmatrix} \tilde{x}_1 \\ \tilde{y}_1 \\ \tilde{z}_1 \end{bmatrix} \equiv \begin{bmatrix} \tilde{x}_2 \\ \tilde{y}_2 \\ \tilde{z}_2 \end{bmatrix}$$

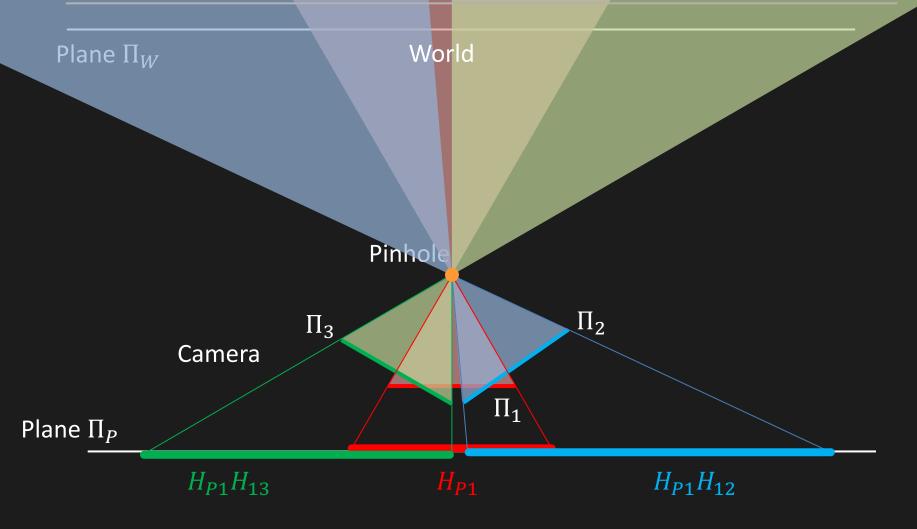
Because homogeneous coordinates are only defined up to a scale.

If we fix scale such that  $\sqrt{\Sigma(h_{ij})^2} = 1$  then 8 free parameters

Transformation that represents mapping a plane into another through a pinhole.

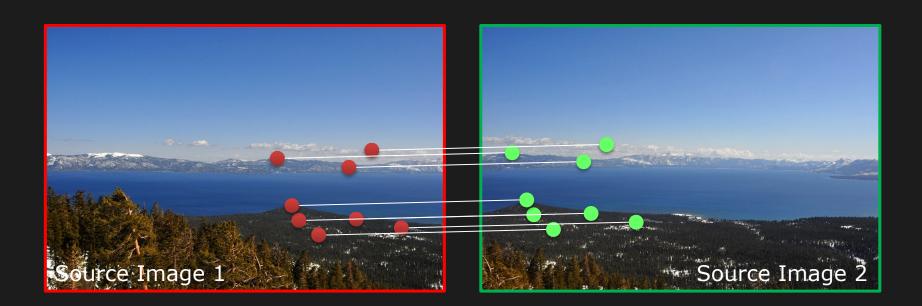
- Origin does not necessarily map to the origin
- Lines map to lines
- Parallel lines do not necessarily remain parallel
- Closed under composition

## (Review) Homography Composition



Useful in stitching planar panoramas.

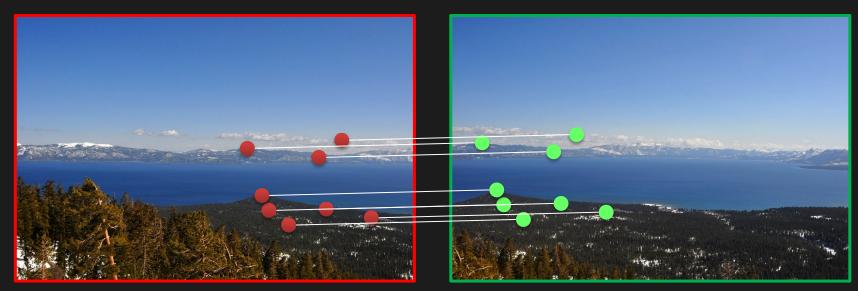
## (Review) Computing Homography



Given a set of matching points between images 1 and 2, find the homography *H* that best "agrees" with the matches.

The scene points should lie on a plane, or be distant (plane at infinity), or imaged from the same point.

## (Review) Computing Homography



Source Image

**Destination Image** 

$$\begin{bmatrix} x_d \\ y_d \\ 1 \end{bmatrix} \equiv \begin{bmatrix} \tilde{x}_d \\ \tilde{y}_d \\ \tilde{z}_d \end{bmatrix} = \begin{bmatrix} h_{11} & h_{12} & h_{13} \\ h_{21} & h_{22} & h_{23} \\ h_{31} & h_{32} & h_{33} \end{bmatrix} \begin{bmatrix} x_s \\ y_s \\ 1 \end{bmatrix}$$

How many pairs of points are needed to define the homography?

There are 9 unknowns, but only 8 degrees of freedom.

Each pair provides 2 constraints. So, 4 pairs are needed.

## (Review) Computing Homography

For a given pair i of corresponding points (2 constraints):

$$x_{d}^{(i)} = \frac{\tilde{x}_{d}^{(i)}}{\tilde{z}_{d}^{(i)}} = \frac{h_{11}x_{s}^{(i)} + h_{12}y_{s}^{(i)} + h_{13}}{h_{31}x_{s}^{(i)} + h_{32}y_{s}^{(i)} + h_{33}} \qquad y_{d}^{(i)} = \frac{\tilde{y}_{d}^{(i)}}{\tilde{z}_{d}^{(i)}} = \frac{h_{21}x_{s}^{(i)} + h_{22}y_{s}^{(i)} + h_{23}}{h_{31}x_{s}^{(i)} + h_{32}y_{s}^{(i)} + h_{33}}$$

Rearranging the terms and writing as linear equation:

$$\begin{bmatrix} x_s^{(1)} & y_s^{(1)} & 1 & 0 & 0 & 0 & -x_d^{(1)}x_s^{(1)} & -x_d^{(1)}y_s^{(1)} & -x_d^{(1)} \\ 0 & 0 & 0 & x_s^{(1)} & y_s^{(1)} & 1 & -y_d^{(1)}x_s^{(1)} & -y_d^{(1)}y_s^{(1)} & -y_d^{(1)} \\ \vdots & & & \vdots & & & & \\ x_s^{(i)} & y_s^{(i)} & 1 & 0 & 0 & 0 & -x_d^{(i)}x_s^{(i)} & -x_d^{(i)}y_s^{(i)} & -x_d^{(i)} \\ 0 & 0 & 0 & x_s^{(i)} & y_s^{(i)} & 1 & -y_d^{(i)}x_s^{(i)} & -y_d^{(i)}y_s^{(i)} & -x_d^{(i)} \\ 0 & 0 & 0 & x_s^{(i)} & y_s^{(i)} & 1 & -y_d^{(i)}x_s^{(i)} & -y_d^{(i)}y_s^{(i)} & -y_d^{(i)} \\ 0 & \vdots & & & \vdots & & \\ x_s^{(n)} & y_s^{(n)} & 1 & 0 & 0 & 0 & -x_d^{(n)}x_s^{(n)} & -x_d^{(n)}y_s^{(n)} & -x_d^{(n)} \\ 0 & 0 & 0 & x_s^{(n)} & y_s^{(n)} & 1 & -y_d^{(n)}x_s^{(n)} & -y_d^{(n)}y_s^{(n)} & -y_d^{(n)} \end{bmatrix} \begin{bmatrix} h_{11} \\ h_{12} \\ h_{13} \\ h_{21} \\ h_{22} \\ h_{23} \\ h_{31} \\ h_{32} \\ h_{33} \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ \vdots \\ 0 \\ 0 \end{bmatrix}$$

$$A$$
 (Known)

### (Review) Constrained Least Squares

Solve for h:

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

 $A \mathbf{h} = \mathbf{0}$  such that  $\|\mathbf{h}\|^2 = 1$ 

Define least squares problem:

$$\min_{\mathbf{h}}(\mathbf{h}^T A^T A \mathbf{h})$$
 such that  $\mathbf{h}^T \mathbf{h} = 1$ 

Solve (unconstrained) Lagrangian function  $L(\mathbf{h}, \lambda)$ :

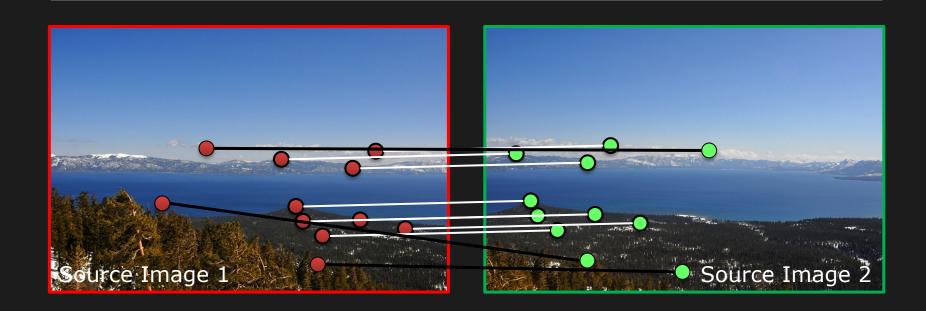
$$L(\mathbf{h}, \lambda) = \mathbf{h}^T A^T A \mathbf{h} - \lambda (\mathbf{h}^T \mathbf{h} - 1)$$

Taking derivatives of  $L(\mathbf{h}, \lambda)$  w.r.t  $\mathbf{h}$ :  $2A^TA\mathbf{h} - 2\lambda\mathbf{h} = \mathbf{0}$ 

$$A^T A \mathbf{h} = \lambda \mathbf{h}$$
 Eigenvalue Problem

Eigenvector  $\mathbf{h}$  with smallest eigenvalue  $\lambda$  of matrix  $A^TA$ minimizes the loss function  $L(\mathbf{h})$ .

#### What Could Go Wrong?



#### **Outliers!**

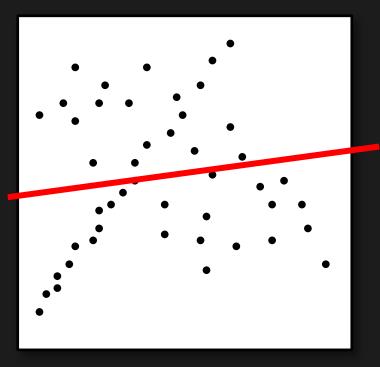
We need to robustly compute transformation in the presence of wrong matches.

How?

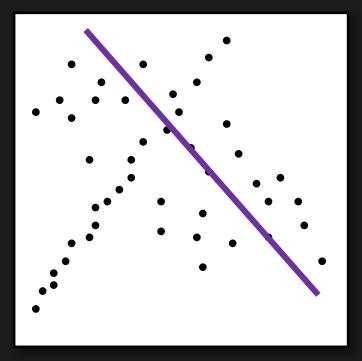
If number of outliers < 50%, then RANSAC to the rescue!

## RANSAC Example: Line Fitting

#### Robust line fitting:



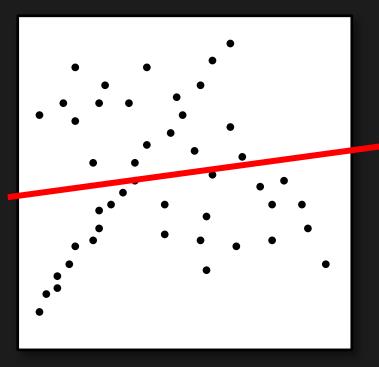
Least Squares Fitting Inliers: 2



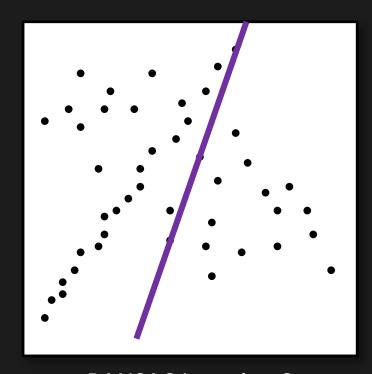
RANSAC Iteration 1
Inliers: 4

## RANSAC Example: Line Fitting

#### Robust line fitting:



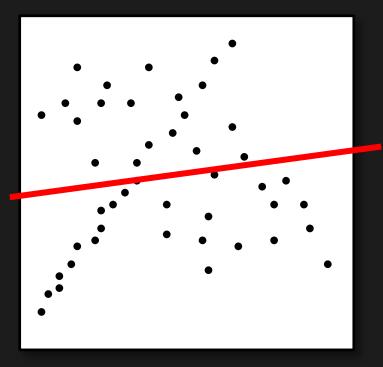
Least Squares Fitting Inliers: 2



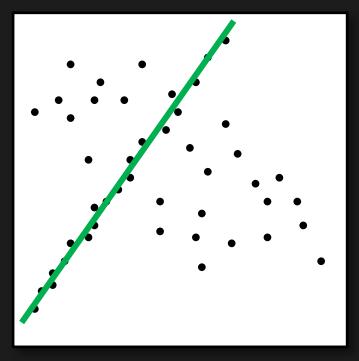
RANSAC Iteration 2
Inliers: 3

## RANSAC Example: Line Fitting

#### Robust line fitting:



Least Squares Fitting Inliers: 2



RANSAC Iteration i Inliers: 20

#### RANdom SAmple Consensus

#### General RANSAC Algorithm:

- 1. Randomly choose s samples. Typically s is the minimum samples to fit a model.
- 2. Fit the model to the randomly chosen samples.
- 3. Count the number M of data points (inliers) that fit the model within a measure of error  $\varepsilon$ .
- 4. Repeat Steps 1-3 N times
- 5. Choose the model that has the largest number *M* of inliers.

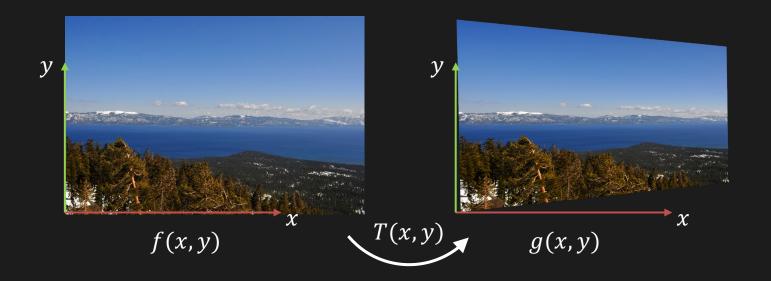
#### For homography:

s = 4 points.  $\epsilon$  is acceptable alignment error in pixels.

### Back to Warping Images

Given a transformation T and a source image f(x,y), compute the transformed image g(x,y)

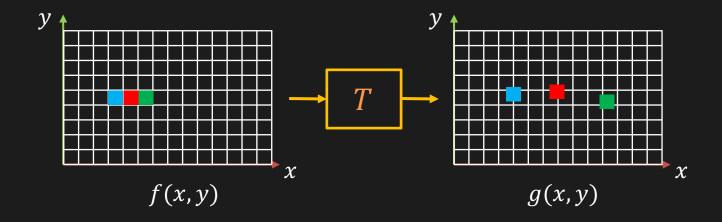
$$g(x,y) = f(T(x,y))$$



#### Forward Warping

Send each pixel (x,y) in f(x,y) to its corresponding location T(x,y) in g(x,y)

$$g(x,y) = f(T(x,y))$$

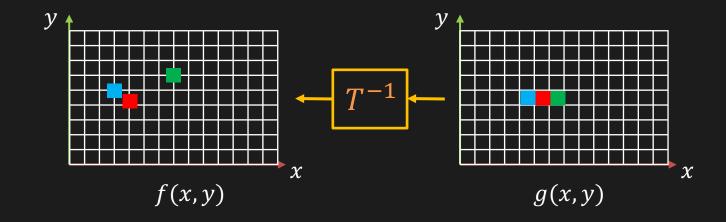


What if pixel lands in between pixels? What if not all pixels in g(x,y) are filled? Can result in holes!

#### **Backward Warping**

Get each pixel (x, y) in g(x, y) from its corresponding location  $T^{-1}(x, y)$  in f(x, y)

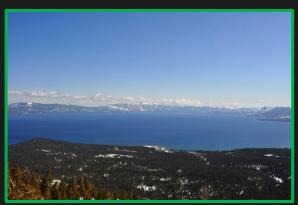
$$g(x,y) = f(T(x,y))$$



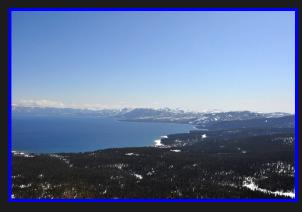
What if pixel lands between pixels?
No problem. Use Nearest Neighbor or
Interpolate (Weighted Average of Neighbors)!



Source Image 1



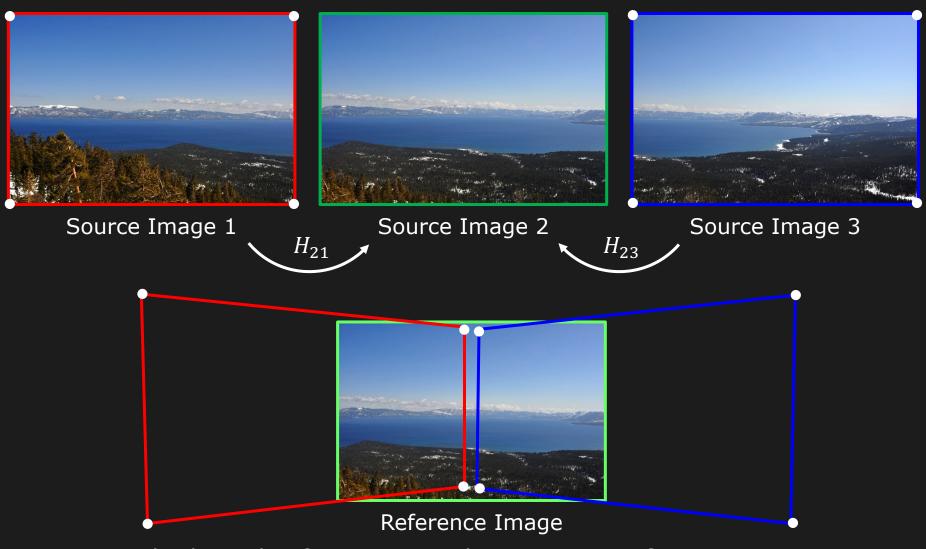
Source Image 2



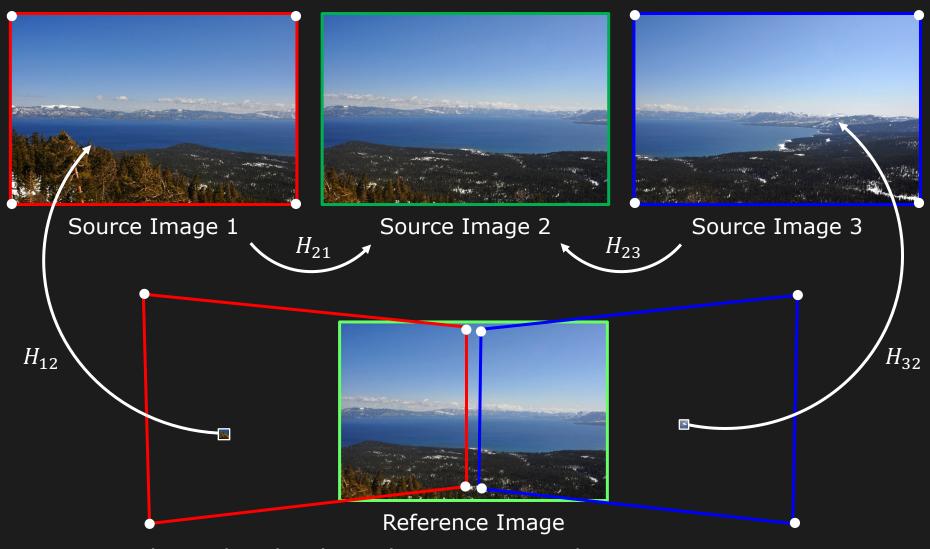
Source Image 3



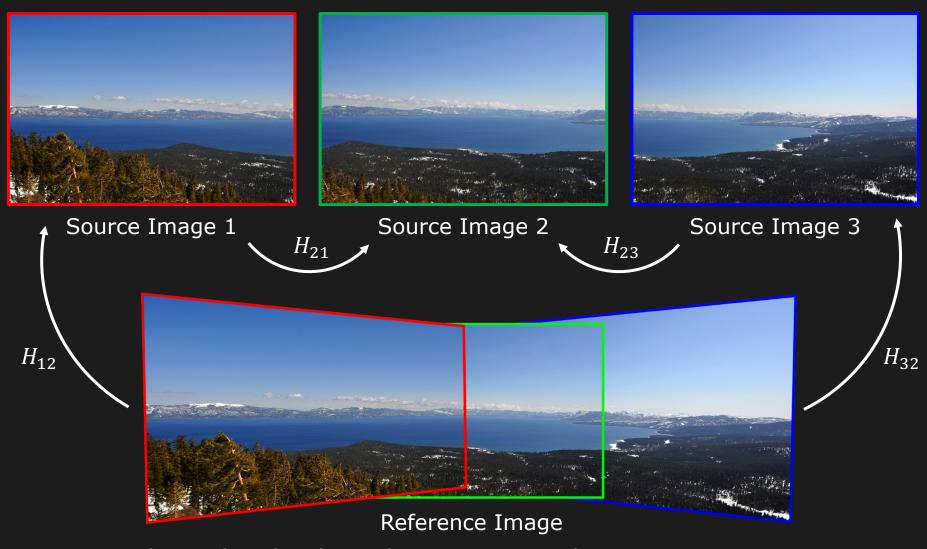
Reference Image (Source Image 2)



Compute the bounds of Image 1 and Image 3 in reference image space



For each pixel within bounds, compute its location in source image



For each pixel within bounds, compute its location in source image

## Blending Images



Overlaid Aligned Images

Hard seams due to vignetting, exposure differences, etc.

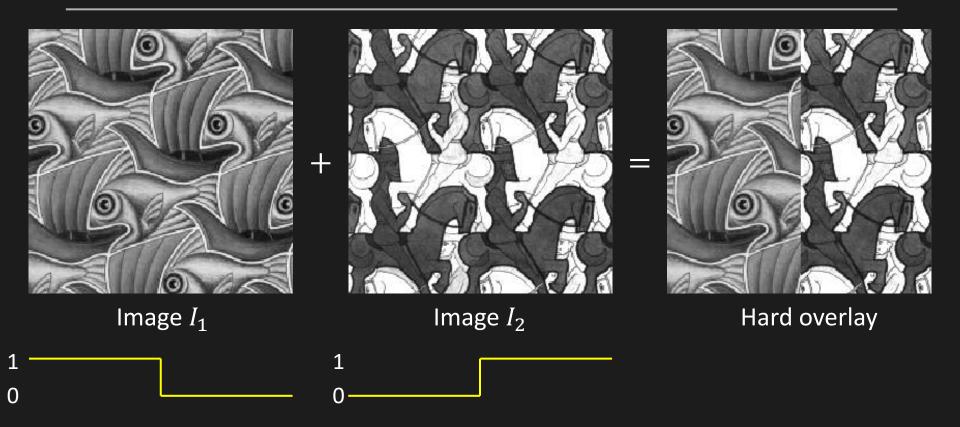
## Blending Images: Averaging



Averaged Images

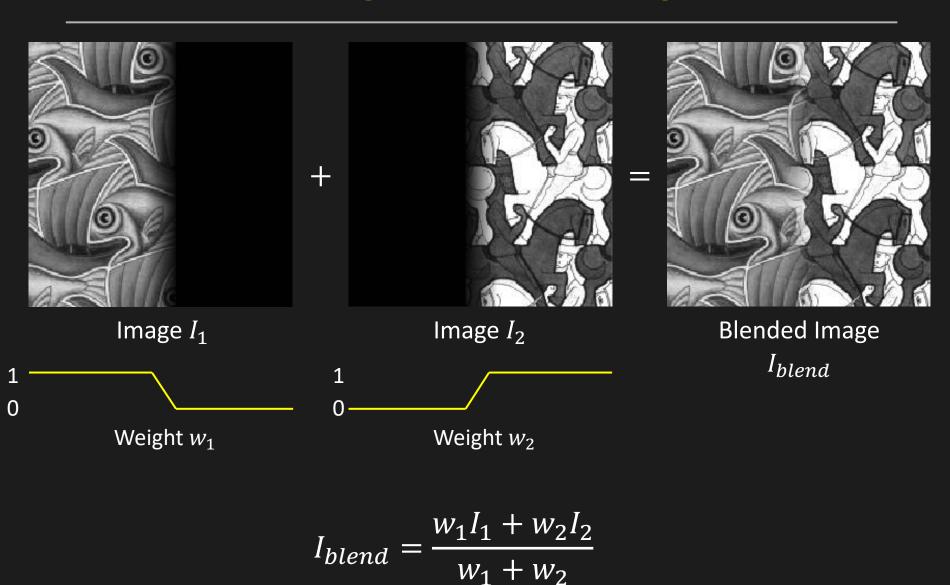
Seams still visible.

### Blending Images

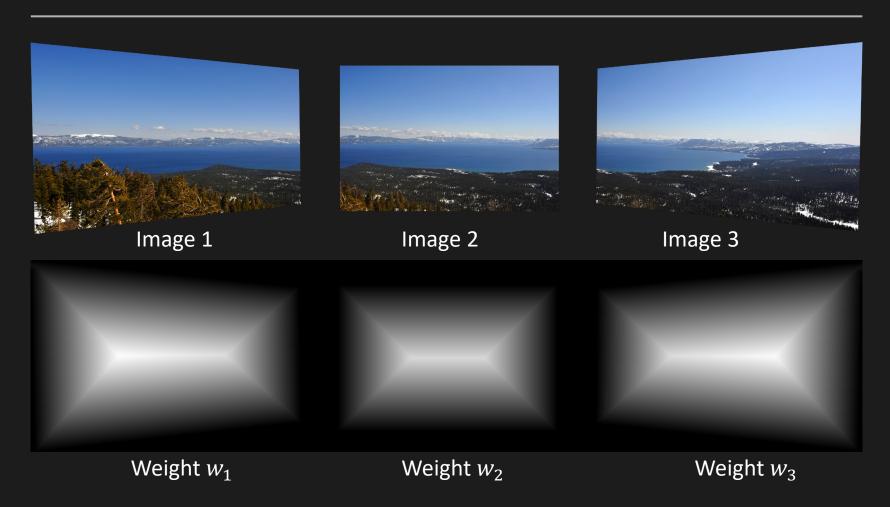


Say we want to blend images  $I_1$  and  $I_2$  at the center.

## Weighted Blending



### Weighted Blending



Pixels closer to the edge get a lower weight.

Python: scipy.ndimage.distance\_transform\_edt

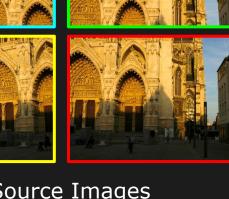
# Weighted Blending

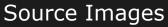


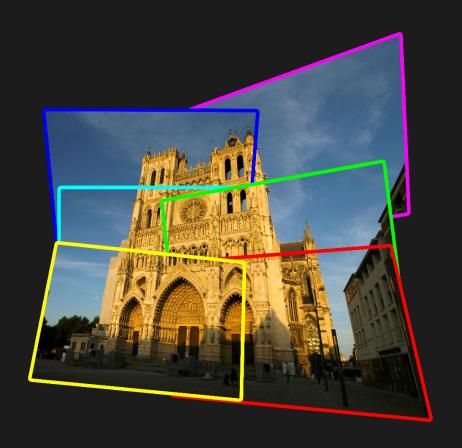


# Image Stitching Example



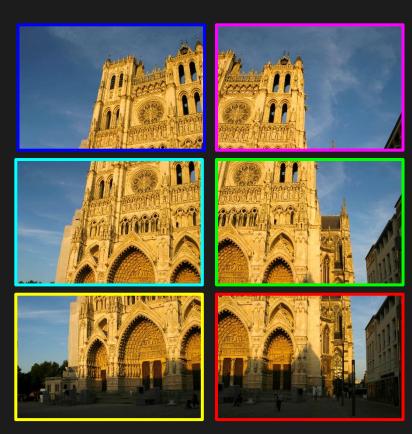


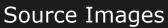




Aligned Images

# Image Stitching Example







Blended Images

#### References: Textbooks

Computer Vision: Algorithms and Applications (Chapter 2, 9) Szeliski, R., Springer

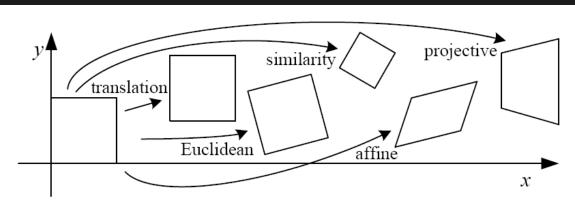
#### References: Papers

[Fischler 1981] Fischler M. A. and Bolles R. C. "Random Sample Consensus: A Paradigm for Model Fitting with Applications to Image Analysis and Automated Cartography", 1981.

#### **Image Credits**

- I.1 http://www.flickr.com/photos/byspice/4577634277
- 1.2 http://www.ptgui.com/examples/quicktour5/
- I.3 Figure 2.4, Table 2.1, Computer Vision: Algorithms and Applications, Szeliski, R., Springer

## Appendix A: Linear Transformations



Name	Matrix	# D.O.F.	Preserves:	Icon
translation	$egin{bmatrix} ig[ egin{array}{c c} ig[ oldsymbol{I} ig  oldsymbol{t} ig]_{2 imes 3} \end{array}$	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	$\left[egin{array}{c} oldsymbol{A} \end{array} ight]_{2 imes 3}$	$\begin{bmatrix} \boldsymbol{A} \end{bmatrix}_{2\times 3}$ 6 parallelism $+\cdots$		
projective	$\left[egin{array}{c}  ilde{m{H}} \end{array} ight]_{3 imes 3}$	8	straight lines	

#### Appendix B: RANSAC

How many iterations?

Suppose,

- p: probability or confidence with which we need the correct fit.
- $\alpha$ : probability of choosing an inlier while selecting the s samples.

If the s points are selected independently. Then,

Minimum number of iterations required:

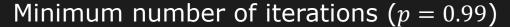
$$N = \frac{\log(1-p)}{\log(1-\alpha^s)}$$

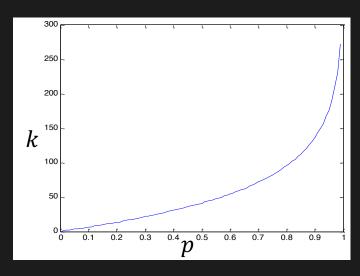
## Appendix B: RANSAC

Minimum number of iterations required:

$$k = \frac{\log(1-p)}{\log(1-\alpha^s)}$$

	Proportion of inliers $\alpha$							
S	95%	90%	80%	75%	70%	60%	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	





$$s = 8, \alpha = 60\%$$