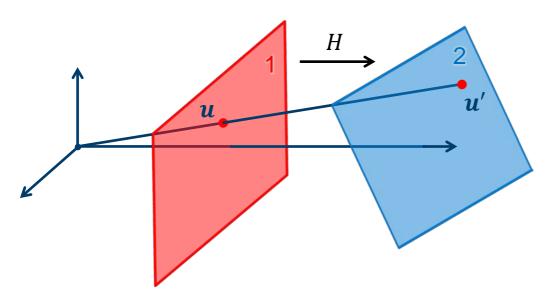


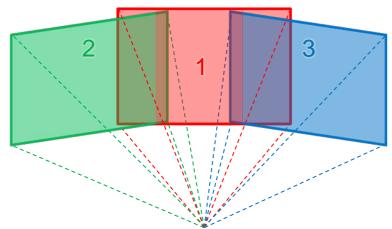
# Lecture 4.3 Estimating homographies from feature correspondences

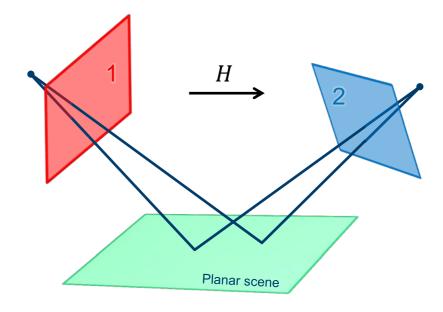
**Thomas Opsahl** 



# Homographies induced by central projection





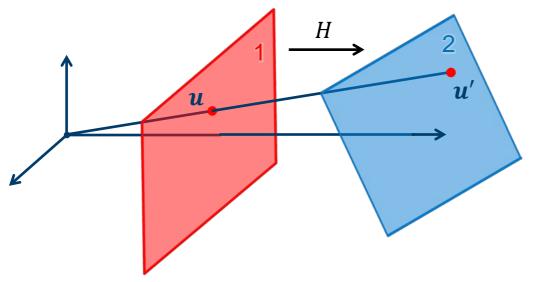


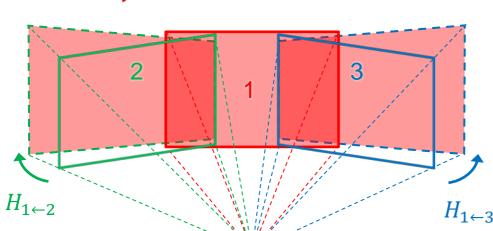
• Homography  $H\widetilde{u} = \widetilde{u}'$ 

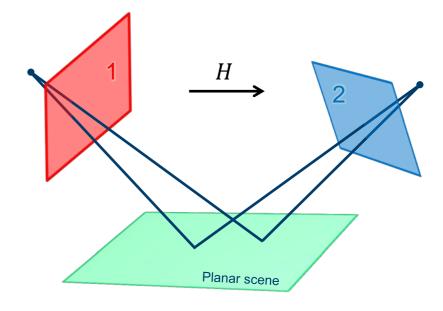
$$H = \begin{bmatrix} h_1 & h_2 & h_3 \\ h_4 & h_5 & h_6 \\ h_7 & h_8 & h_9 \end{bmatrix}$$

- Point-correspondences can be determined automatically
- Erroneous correspondences are common
- Robust estimation is required to find H

# Homographies induced by central projection







• Homography  $H\widetilde{u} = \widetilde{u}'$ 

$$H = \begin{bmatrix} h_1 & h_2 & h_3 \\ h_4 & h_5 & h_6 \\ h_7 & h_8 & h_9 \end{bmatrix}$$

- Point-correspondences can be determined automatically
- Erroneous correspondences are common
- Robust estimation is required to find H

## Estimating the homography between overlapping images

- Establish point correspondences  $u_i \leftrightarrow u'_i$ 
  - Find key points  $\{u_i \in \text{Img1}\}\$ and  $\{u'_i \in \text{Img2}\}\$
  - Represent key points by suitable descriptors
  - Determine correspondences  $u_i \leftrightarrow u'_i$  by matching descriptors
  - Some wrong correspondences are to be expected
- Estimate the homography H such that  ${m u'}_i = H{m u}_i \ orall i$ 
  - Robust estimation with RANSAC
  - Improved estimation based on RANSAC inliers
- This homography enables us to compose the images into a larger image
  - Image mosaicing
  - Panorama







## **Adaptive RANSAC**

#### **Objective**

To robustly fit a model  $y = f(x; \alpha)$  to a data set S containing outliers

#### **Algorithm**

- 1. Let  $N = \infty$ ,  $S_{IN} = \emptyset$  and #iterations = 0
- 2. while N > #iterations repeat 3-5
- 3. Estimate parameters  $\alpha_{tst}$  from a random n-tuple from S
- 4. Determine inlier set  $S_{tst}$ , i.e. data points within a distance t of the model  $y = f(x; \alpha_{tst})$
- 5. If  $|S_{tst}| > |S_{IN}|$ , set  $S_{IN} = S_{tst}$ ,  $\alpha = \alpha_{tst}$ ,  $\omega = \frac{|S_{IN}|}{|S|}$  and  $N = \frac{log(1-p)}{log(1-\omega^n)}$  with p = 0.99 Increase #iterations by 1



### **Estimating the homography**

- Estimating the homography in a RANSAC scheme requires
  - 1. A basic homography estimation method for n point-correspondences
  - 2. A way to determine the inlier set of point-correspondences for a given homography



### **Estimating the homography**

- Estimating the homography in a RANSAC scheme requires
  - 1. A basic homography estimation method for n point-correspondences
  - 2. A way to determine the inlier set of point-correspondences for a given homography
- The homography has 8 degrees of freedom, but it is custom to treat all 9 entries of the matrix as unknowns instead of setting one of the entries to 1 which excludes all potential solutions where this entry is 0
- Let us solve the equation  $H\widetilde{\boldsymbol{u}}=\widetilde{\boldsymbol{u}}'$  for the entries of the homography matrix

$$H\widetilde{\boldsymbol{u}} = \widetilde{\boldsymbol{u}}'$$

$$\begin{bmatrix} h_1 & h_2 & h_3 \\ h_4 & h_5 & h_6 \\ h_7 & h_8 & h_9 \end{bmatrix} \begin{bmatrix} u \\ v \\ 1 \end{bmatrix} = \begin{bmatrix} u' \\ v' \\ 1 \end{bmatrix}$$

$$\begin{bmatrix} h_1 & h_2 & h_3 \\ h_4 & h_5 & h_6 \\ h_7 & h_8 & h_9 \end{bmatrix} \begin{bmatrix} u \\ 1 \end{bmatrix} = \begin{bmatrix} u' \\ v' \\ 1 \end{bmatrix} \Leftrightarrow \begin{cases} uh_1 + vh_2 + h_3 = u' \\ uh_4 + vh_5 + h_6 = v' \\ uh_7 + vh_8 + h_9 = 1 \end{cases} \Leftrightarrow \begin{bmatrix} 0 & 0 & 0 & -u & -v & -1 & v'u & v'v & v' \\ u & v & 1 & 0 & 0 & 0 & -u'u & -u'v & -u' \\ -v'u & -v'v & -v' & u'u & u'v & u' & 0 & 0 & 0 \end{cases} \begin{pmatrix} h_1 \\ h_2 \\ h_3 \\ h_4 \\ h_5 \\ h_6 \\ h_7 \\ h_8 \\ h_9 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \Leftrightarrow A\mathbf{h} = \mathbf{0}$$

$$\begin{bmatrix} h_1 & h_2 & h_3 \\ h_4 & h_5 & h_6 \\ h_7 & h_8 & h_9 \end{bmatrix} \begin{bmatrix} u \\ 1 \end{bmatrix} = \begin{bmatrix} u' \\ v' \\ 1 \end{bmatrix} \Leftrightarrow \begin{cases} uh_1 + vh_2 + h_3 = u' \\ uh_4 + vh_5 + h_6 = v' \\ uh_7 + vh_8 + h_9 = 1 \end{cases} \Leftrightarrow \begin{bmatrix} 0 & 0 & 0 & -u & -v & -1 & v'u & v'v & v' \\ u & v & 1 & 0 & 0 & 0 & -u'u & -u'v & -u' \\ -v'u & -v'v & -v' & u'u & u'v & u' & 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} h_1 \\ h_2 \\ h_3 \\ h_4 \\ h_5 \\ h_6 \\ h_7 \\ h_8 \\ h_9 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \Leftrightarrow A\mathbf{h} = \mathbf{0}$$

$$\begin{bmatrix} h_1 \\ h_2 \\ h_3 \\ h_4 \\ h_7 \\ h_8 \\ h_9 \end{bmatrix}$$
Observe that the third row in  $A$  is a linear combination of the first and second row 
$$row_3 = -u' \cdot row_1 - v' \cdot row_2$$

Hence every correspondence  $u_i \leftrightarrow u'_i$  contribute with 2 equations in the 9 unknown entries



- Since H (and thus h) is homogeneous, we only need the matrix A to have rank 8 in order to determine h up to scale
- It is sufficient with 4 point correspondences where no 3 points are collinear
- We can calculate the non-trivial solution to the equation  $A\mathbf{h} = \mathbf{0}$  by SVD  $\operatorname{svd}(A) = USV^T$
- The solution is given by the right singular vector without a singular value which is the last column of V, i.e.  $\mathbf{h} = \mathbf{v}_9$

```
\begin{bmatrix} 0 & 0 & 0 & -u_{1} & -v_{1} & -1 & v'_{1}u_{1} & v'_{1}v_{1} & v'_{1} \\ u_{1} & v_{1} & 1 & 0 & 0 & 0 & -u'_{1}u_{1} & -u'_{1}v_{1} & -u'_{1} \\ 0 & 0 & 0 & -u_{2} & -v_{2} & -1 & v'_{2}u_{2} & v'_{2}v_{2} & v'_{2} \\ u_{2} & v_{2} & 1 & 0 & 0 & 0 & -u'_{2}u_{2} & -u'_{2}v_{2} & -u'_{2} \\ \vdots & \vdots \end{bmatrix} \begin{bmatrix} h_{2} \\ h_{3} \\ h_{4} \\ h_{5} \\ h_{6} \\ h_{7} \\ h_{8} \\ h_{9} \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \\ \vdots \end{bmatrix}
A\mathbf{h} = \mathbf{0}
```

- Estimating the homography in a RANSAC scheme requires
  - 1. A basic homography estimation method for n point-correspondences
  - 2. A way to determine which of the point correspondences that are inliers for a given homography

#### **Direct Linear Transform**

$$A = \begin{bmatrix} 0 & 0 & 0 & -u_1 & -v_1 & -1 & v_1'u_1 & v_1'v_1 & v_1' \\ u_1 & v_1 & 1 & 0 & 0 & 0 & -u_1'u_1 & -u_1'v_1 & -u_1' \\ \vdots & \vdots \end{bmatrix}$$

- 1. Build the matrix A from at least 4 point-correspondences  $(u_i, v_i) \leftrightarrow (u'_i, v'_i)$
- 2. Obtain the SVD of A:  $A = USV^T$
- 3. If S is diagonal with positive values in descending order along the main diagonal, then h equals the last column of V
- 4. Reconstruct *H* from *h*



- The basic DLT algorithm is never used with more than 4 point-correspondences
- This is because the algorithm performs better when all the terms of A has a similar scale
  - Note that some of the terms will always be of scale 1
- To achieve this, it is common to extend the algorithm with a normalization and a denormalization step

#### **Normalized Direct Linear Transform**

- 1. Normalize the set of points  $u_i = [u_i, v_i]^T$  by computing a similarity transform T that translates the centroid to the origin and scales such that the average distance from the origin is  $\sqrt{2}$
- 2. In the same way normalize the set of points  $u'_i = [u'_i, v'_i]^T$  by computing a similarity transform T'
- 3. Apply the basic DLT algorithm on the normalized points to obtain a homography  $\widehat{H}$
- 4. Denormalize to get the homography:  $H = T'^{-1}\widehat{H}T$



- Estimating the homography in a RANSAC scheme requires
  - 1. A basic homography estimation method for n point-correspondences
  - 2. A way to determine the inlier set of point-correspondences for a given homography
- For a point correspondence  $(u_i, v_i) \leftrightarrow (u'_i, v'_i)$  and homography H, we can choose from several errors
  - Algebraic error:  $\varepsilon_i = ||A_i \boldsymbol{h}||$  where

$$A_{i} = \begin{bmatrix} 0 & 0 & 0 & -u_{i} & -v_{i} & -1 & v'_{i}u_{i} & v'_{i}v_{i} & v'_{i} \\ u_{i} & v_{i} & 1 & 0 & 0 & 0 & -u'_{i}u_{i} & -u'_{i}v_{i} & -u'_{i} \end{bmatrix}$$

Geometric errors:

1. 
$$\varepsilon_i = d(H\boldsymbol{u}_i, \boldsymbol{u'}_i) + d(\boldsymbol{u}_i, H^{-1}\boldsymbol{u'}_i)$$
 (Reprojection error)

2. 
$$\varepsilon_i = d(\boldsymbol{u}_i, H^{-1}\boldsymbol{u}'_i)$$

3. 
$$\varepsilon_i = d(H\boldsymbol{u}_i, \boldsymbol{u'}_i)$$

Notation	
Euclidean distance	$d(\cdot,\cdot)$
Inhomogenous $H\widetilde{m{u}}_i$	$H\mathbf{u}_i$
Inhomogeneous $H^{-1}\widetilde{\pmb{u}}'_i$	$ H^{-1}u'_i $



## Robust homography estimation

#### **RANSAC** estimation of homography

For a set of point-correspondences  $S = \{u_i \mapsto u'_i\}$ , perform N iterations, where N is determined adaptively

- 1. Estimate  $H_{tst}$  from 4 random correspondences  $u_i \mapsto u'_i$  using the basic DLT algorithm
- 2. Determine the set of inlier-correspondences  $S_{tst} = \{ \boldsymbol{u_i} \mapsto \boldsymbol{u'_i} \text{ such that } \epsilon_i < t \}$ Here one can choose  $\epsilon_i = d(H\boldsymbol{u_i}, \boldsymbol{u'_i}) + d(\boldsymbol{u_i}, H^{-1}\boldsymbol{u'_i})$  and  $t = \sqrt{5.99}\sigma$  where  $\sigma$  is the expected uncertainty in key-point positions
- 3. If  $|S_{tst}| > |S_{IN}|$  update N, homography and inlier set:  $H = H_{tst}$ ,  $S_{IN} = S_{tst}$

- Finally we would typically re-estimate H from all correspondences in  $S_{IN}$ 
  - Normalized DLT
  - Minimize  $\epsilon = \sum \epsilon_i$  in an iterative optimization method like Levenberg Marquardt





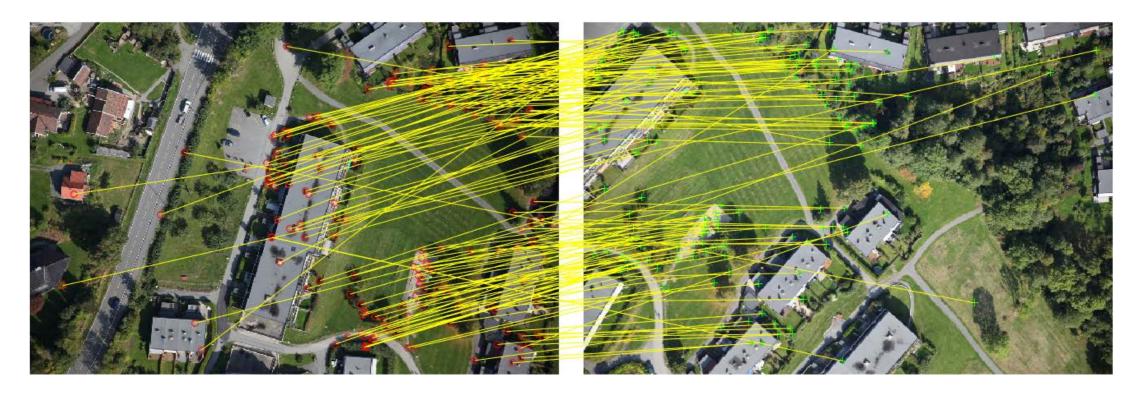


• Let us compose these two images into a larger image



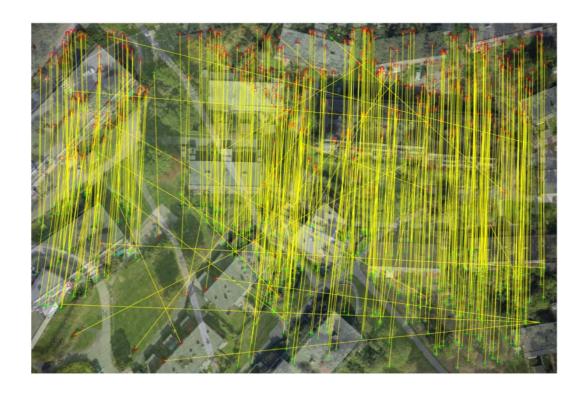


Find key points and represent by descriptors



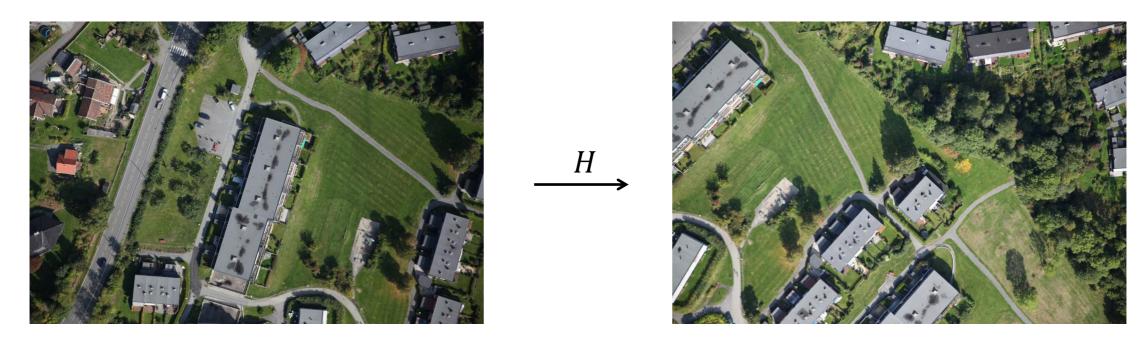
- Establish point-correspondences by matching descriptors
- Several wrong correspondences





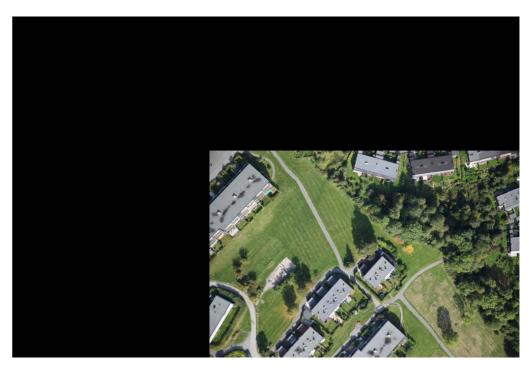
- Establish point-correspondences by matching descriptors
- Several wrong correspondences





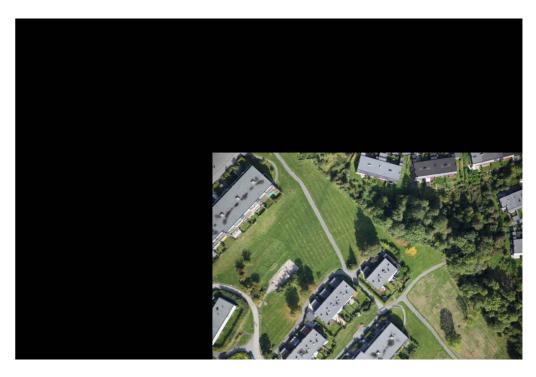
- Estimate homography  $H\widetilde{\boldsymbol{u}} = \widetilde{\boldsymbol{u}}'$ 
  - OpenCV
    #include "opencv2/calib3d.hpp"
    cv::findHomography(srcPoints, dstPoints, CV\_RANSAC);
  - Matlab
    tform = estimateGeometricTransform(srcPoints,dstPoints,'projective');





- Represent the images in common coordinates (Note the additional translation!)
  - OpenCV
    #include "opencv2/calib3d.hpp"
    cv::warpPerspective(img1, img2, H, output\_size);
  - Matlab
    img2 = imwarp(img1,tform);





Now we can compose the images









#### **Singular Value Decomposition**

The singular value decomposition of a real  $m \times n$  matrix A is a factorization  $A = USV^T$ 

Here U is a orthogonal  $m \times m$  matrix, V is a orthogonal  $n \times n$  matrix and S is a real positive diagonal  $m \times n$  matrix

The diagonal entries of  $S = \operatorname{diag}(s_1, \dots, s_{\min(m,n)})$  are known as the singular values of A and the columns of  $U = [\boldsymbol{u}_1, \dots, \boldsymbol{u}_m]$  and  $V = [\boldsymbol{v}_1, \dots, \boldsymbol{v}_n]$  are known as the left and right singular vectors of A respectively

The nullspace of A is the span of the right singular vectors  $v_i$  that corresponds to a zero singular value  $s_i$  (or does not have a corresponding singular value)

#### How to use

Matlab
 [U,S,V] = svd(A);
 Right singular vectors are columns in V

OpenCV

```
cv::SVD::compute(A, S, U, Vtranspose,
cv::SVD::FULL_UV);
Right singular vectors are rows in Vtranspose
```

Eigen

```
Eigen::JacobiSVD<Eigen::MatrixXd> svd(A,
Eigen::ComputeFullU | Eigen::ComputeFullV);
Right singular vectors are columns in svd.matrixV()
```



#### **Singular Value Decomposition**

The singular value decomposition of a real  $m \times n$  matrix A is a factorization  $A = USV^T$ 

Here U is a orthogonal  $m \times m$  matrix, V is a orthogonal  $n \times n$  matrix and S is a real positive diagonal  $m \times n$  matrix

The diagonal entries of  $S = \operatorname{diag}(s_1, \dots, s_{\min(m,n)})$  are known as the singular values of A and the columns of  $U = [\boldsymbol{u}_1, \dots, \boldsymbol{u}_m]$  and  $V = [\boldsymbol{v}_1, \dots, \boldsymbol{v}_n]$  are known as the left and right singular vectors of A respectively

The nullspace of A is the span of the right singular vectors  $v_i$  that corresponds to a zero singular value  $s_i$  (or does not have a corresponding singular value)

#### **Applications of SVD**

Solving homogeneous linear equations like Ah = 0

#### Method

For theoretical problems,  $\mathbf{h} \in \text{null}(A)$  so  $\mathbf{h}$  is a linear combination of the right singular vectors  $\mathbf{v}_i$  that correspond to a zero singular value  $s_i$ 

$$\mathbf{h} = \sum k_i \mathbf{v}_i$$
;  $k_i \in \mathbb{R}$ ,  $s_i = 0$  (or missing)

For practical problems, the presence of noise force us to expand the solution by including those right singular vectors that correspond to small singular values  $s_i \approx 0$ 

$$\mathbf{h} = \sum k_i \mathbf{v}_i; \ k_i \in \mathbb{R}, s_i \approx 0 \text{ (or missing)}$$



#### **Example**

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

$$\begin{bmatrix} 1 & 2 & 3 \\ 4 & 5 & 6 \end{bmatrix} \begin{bmatrix} x \\ y \\ z \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix}$$

From [U,S,V] = svd(A); we get

$$U = \begin{bmatrix} -0.3863 & -0.9224 \\ -0.9224 & 0.3863 \end{bmatrix} \quad S = \begin{bmatrix} 9.5080 & 0 & 0 \\ 0 & 0.7729 & 0 \end{bmatrix}$$
$$V = \begin{bmatrix} -0.4287 & 0.8060 & 0.4082 \\ -0.5663 & 0.1124 & -0.8165 \\ -0.7039 & -0.5812 & 0.4082 \end{bmatrix}$$

#### From this we see that A has:

2 left singular vectors

$$\mathbf{u}_{1} = \begin{bmatrix} -0.3863 \\ -0.9224 \end{bmatrix} \quad \mathbf{u}_{2} = \begin{bmatrix} -0.9224 \\ 0.3863 \end{bmatrix}$$

2 nonzero singular values

$$s_1 = 9.5080$$
  $s_2 = 0.7729$ 

• 3 right singular vectors

$$\mathbf{v}_{1} = \begin{bmatrix} -0.4287 \\ -0.5663 \\ -0.7039 \end{bmatrix} \quad \mathbf{v}_{2} = \begin{bmatrix} 0.8060 \\ 0.1124 \\ -0.5812 \end{bmatrix} \quad \mathbf{v}_{3} = \begin{bmatrix} 0.4082 \\ -0.8165 \\ 0.4082 \end{bmatrix}$$

Since  $v_3$  does not have a corresponding singular value,  $x = v_3$  is a non-trivial solution to Ax = 0 and  $x = k \cdot v_3$ ;  $k \in \mathbb{R} \setminus \{0\}$  is the family of all non-trivial solutions

#### **Example**

$$\begin{bmatrix} 1.0792 & 2.0656 & 3.0849 \\ 4.0959 & 5.0036 & 6.0934 \\ 1.0679 & 2.0743 & 3.0655 \\ 4.0758 & 5.0392 & 6.0171 \end{bmatrix} \begin{bmatrix} x \\ y \\ z \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix}$$

This time singular value decomposition give us the following singular values and right singular vectors:

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

$$\mathbf{v}_{1} = \begin{bmatrix} -0.4336 \\ -0.5635 \\ -0.7032 \end{bmatrix} \quad \mathbf{v}_{2} = \begin{bmatrix} -0.8103 \\ -0.0975 \\ 0.5778 \end{bmatrix} \quad \mathbf{v}_{3} = \begin{bmatrix} 0.3942 \\ -0.8203 \\ 0.4143 \end{bmatrix}$$

This time all right singular vectors correspond to a non-zero singular value, so the equation does not have any non-trivial solutions! If this equation came from a practical problem, instead of looking for solutions to Ax = 0, we might be looking for the x that minimize ||Ax||

Since  $s_1 \not\approx 0$ ,  $s_2 \not\approx 0$ ,  $s_3 \approx 0$ , we would conclude that  $x = v_3$  solves the equation in a least-squares sense

Check:

$$A\mathbf{v}_3 = \begin{bmatrix} 0.0091\\ 0.4288\\ -0.0105\\ -0.0341 \end{bmatrix}$$

## **Summary**

• Homography  $H\widetilde{u} = \widetilde{u}'$ 

$$H = \begin{bmatrix} h_1 & h_2 & h_3 \\ h_4 & h_5 & h_6 \\ h_7 & h_8 & h_9 \end{bmatrix}$$

- Automatic point-correspondences
- Wrong correspondences are common
- RANSAC estimation
  - Basic DLT (Direct Linear Transform)
     on 4 random correspondences
  - Inliers determined from the reprojection error  $\epsilon_i = d(H\boldsymbol{u}_i, \boldsymbol{u'}_i) + d(\boldsymbol{u}_i, H^{-1}\boldsymbol{u'}_i)$

- Improve estimate by normalized DLT on inliers or iterative methods for an even better estimate
- Additional reading
  - Szeliski: 6.1.1 6.1.3

