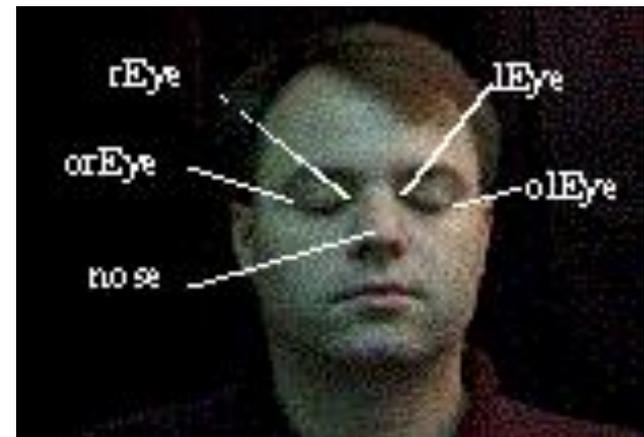
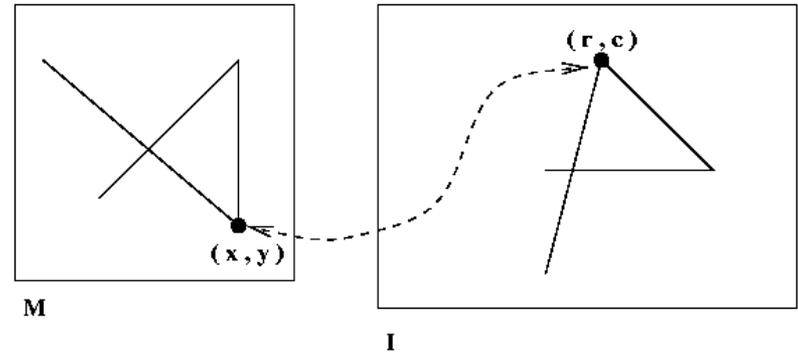


Point/feature matching methods 2

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Computer Science and Engineering
Michigan State University

Problems (review)

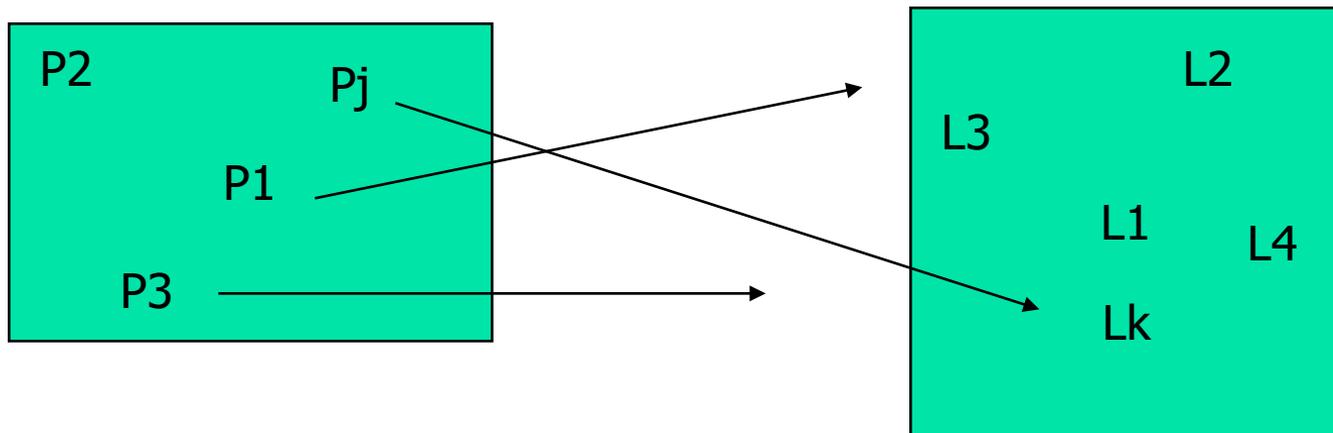
- How to find landmarks to match across two images?
- How to distinguish one landmark from another?
- How to match N landmarks from $I1$ to M landmarks from $I2$, assuming that $I2$ has more and less than $I1$?

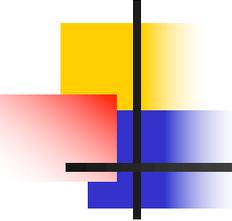


General matching notions

- P_j are points (or "parts") in first image
- L_k are labels in second image or model; these could be points, parts, or interpretations of them
- Need to match some pairs (P_j, L_k) : can be combinatorically expensive

There are many mappings from Image 1 pts to Image 2 labels.





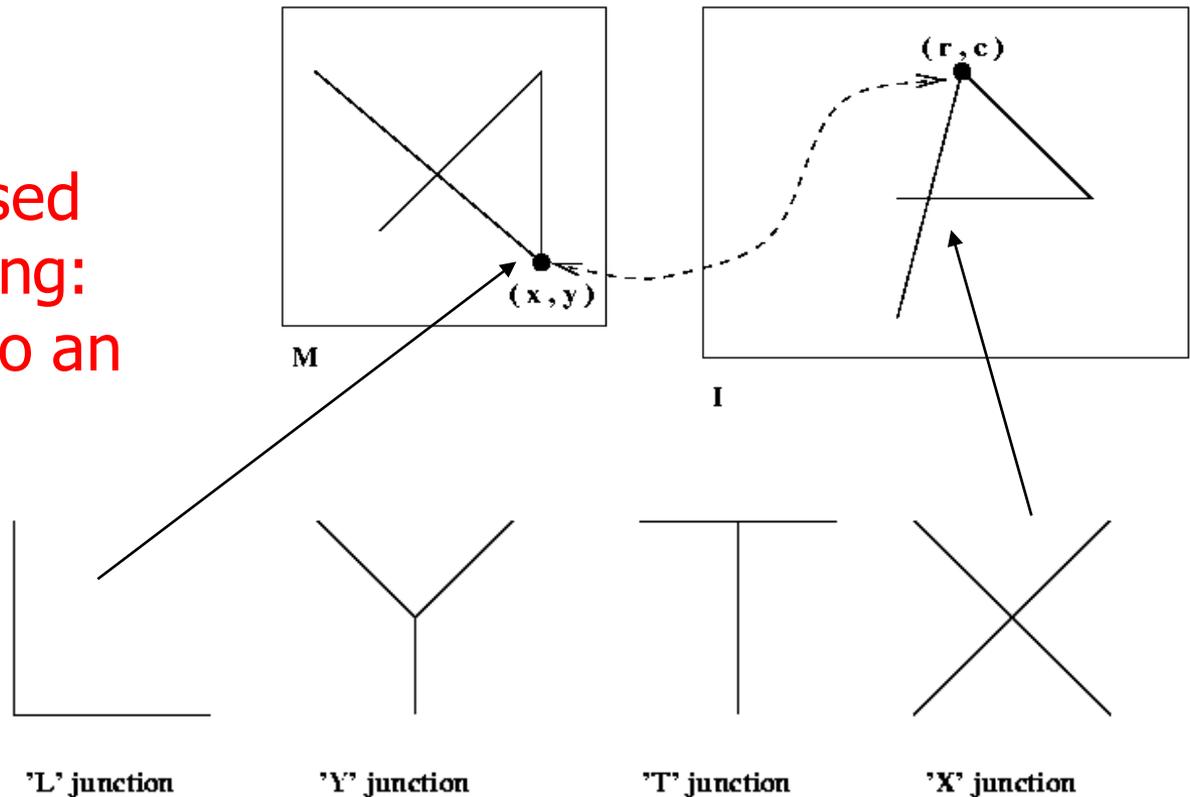
Constraining the mapping

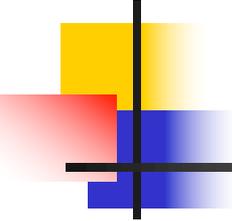
- Points may have distinguishing features
- Points may be distinguished by relations with neighbor points or regions
- Points may be distinguished by distance relations with distant points
- Points or corners might be connected to others

Point salience by topology/geometry

Junctions of a network can be used for reliable matching: never map an 'L' to an 'X', for example.

Might also use subtended angles or gradients across edges



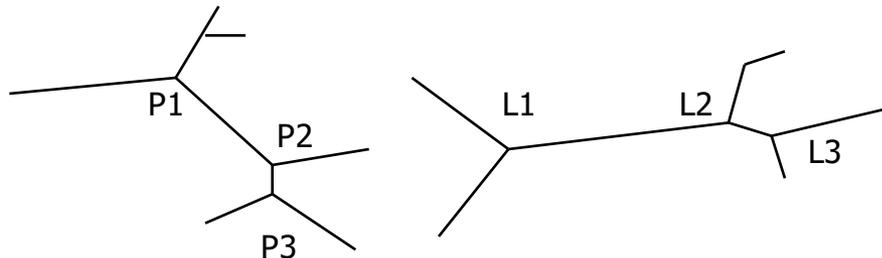


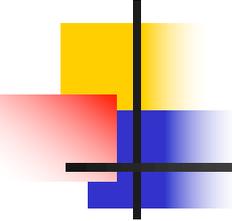
Other constraints on mapping

- Match centroids of similar regions, e.g. of dark regions in IR of similar area
- Match holes of same diameter
- Match corners of same angle and same contrast (gradient)
- Match points with similar RMTs

Can match minimal spanning trees (C. Zahn 1975)

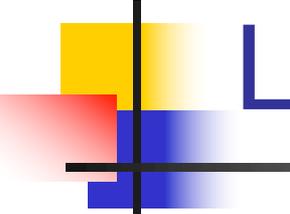
- Extract minimal spanning trees from points of I1 and of I2
- Assumption is that spanning tree structure is robust to some errors in point extraction
- Select tree nodes with high degree
- Below example: match 3 nodes of same degree and verify a consistent RS&T mapping





Local focus feature (Bolles)

- Identify several “focus features” that are close together
- Match only the focus features
- Can a consistent RS&T be derived from them?
- If so, can find more distant features to refine the RS&T
- Method robust against occlusions/errors



Local focus feature matching

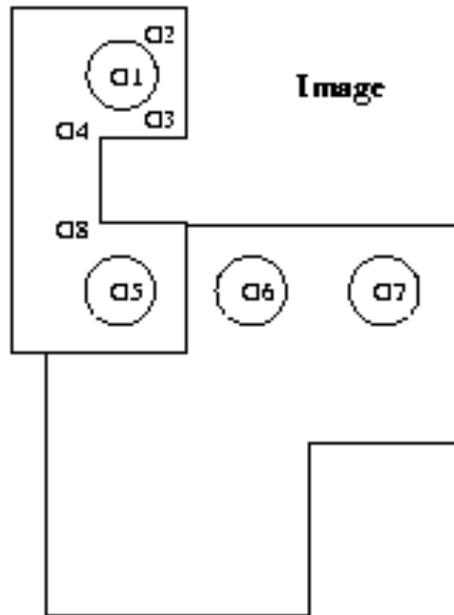
Let $G_i, i = 1, I$ be the detected image features.

Let $F_m, m = 1, M$ be the focus features of the model.

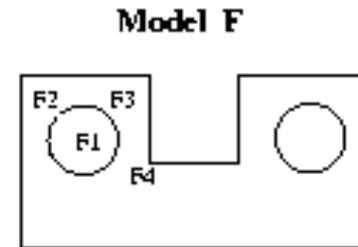
Let $S(f)$ be the set of nearby features for any feature f .

```
procedure local_feature_focus(G,F);  
{  
  for each focus feature  $F_m$   
    for each image feature  $G_i$  of the same type as  $F_m$   
      {  
        Find the maximal subgraph  $S_m$  of  $S(F_m)$  that  
          matches a subgraph  $S_i$  of  $S(G_i)$ ;  
        Compute the transformation  $T$  that maps the points of  
          each feature of  $S_m$  to the corresponding feature of  $S_i$ ;  
        Apply  $T$  to the boundary segments of the model;  
        if enough of the transformed boundary segments find  
          evidence in the image then return( $T$ );  
      }  
};  
}
```

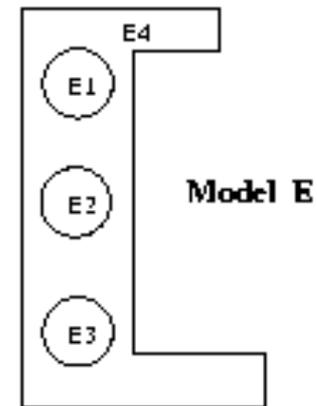
Try matching model to image



Image



Model F



Model E

Model feature F1 matches image hole a5. When rotated 90 degrees, two edges will align, but global match still wrong

Model E will match image fairly well also.

Using distance constraints

Correct labeling is

$\{ (H1, E), (H2, A), (H3, B) \}$

(Left) Model object and (right) three holes detected in an image.
Model Point Locations and Interpoint Distances

point	coordinates †	to A	to B	to C	to D	to E
A	(8,17)	0	12	15	37	21
B	(16,26)	12	0	12	30	26
C	(23,16)	15	12	0	22	15
D	(45,20)	37	30	22	0	30
E	(22,1)	21	26	15	30	0

$12(P_1, P_2)$ means that $d(P_1, P_2) = 12$

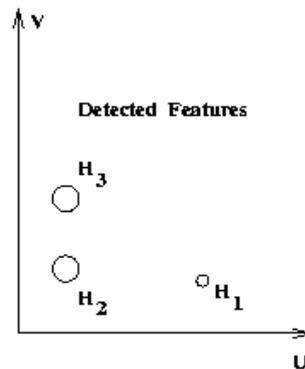
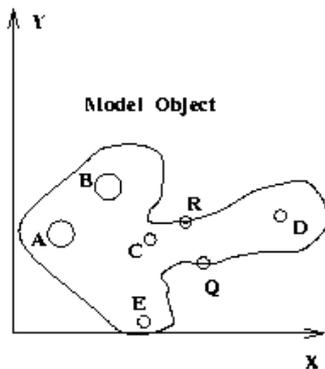


Image Point Locations and Interpoint Distances

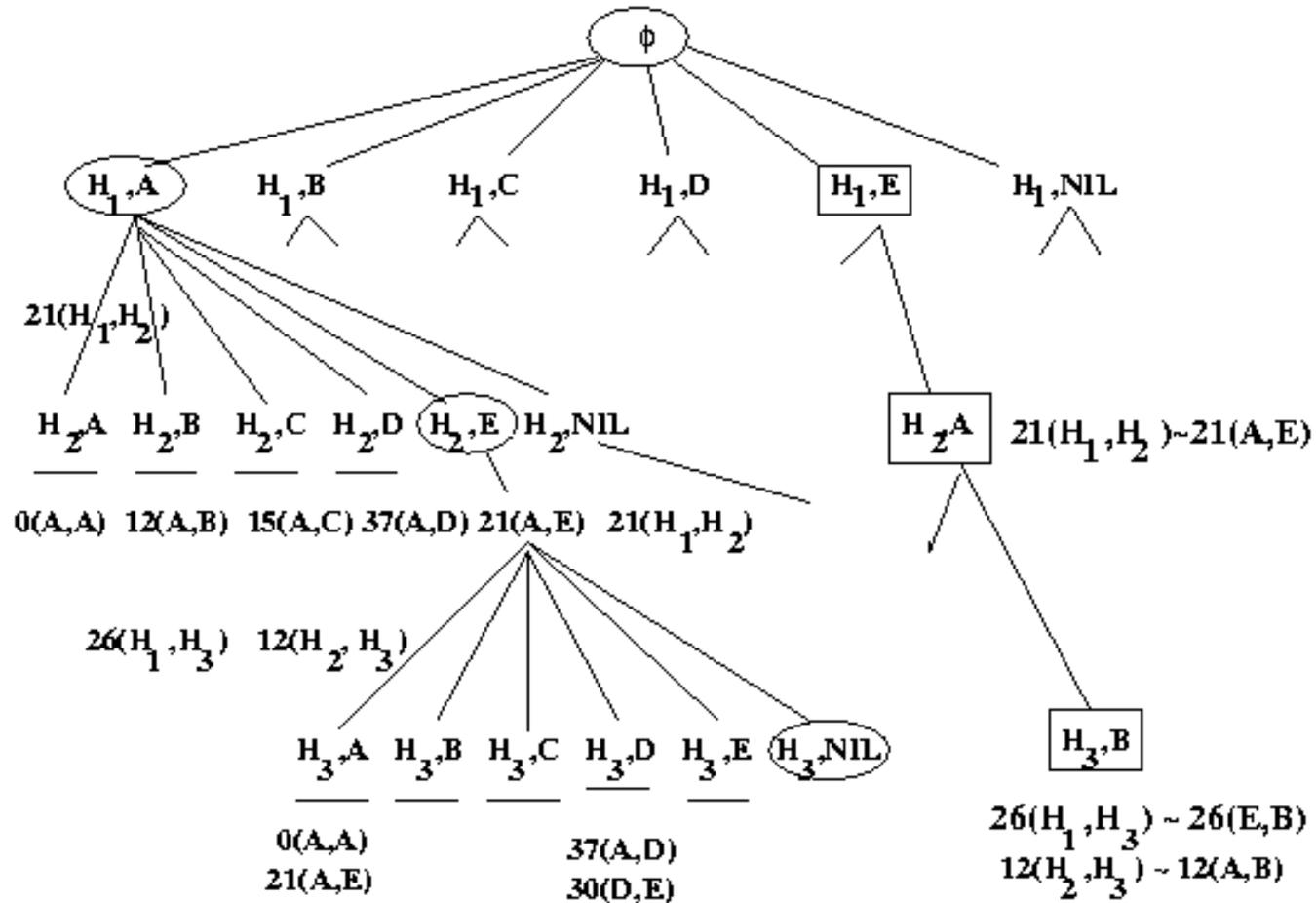
point	coordinates †	to H1	to H2	to H3
H1	(31,9)	0	21	26
H2	(10,12)	21	0	12
H3	(10,24)	26	12	0

Distances observed in the image must be explained in the model.

Backtracking search for consistent labeling of {H1, H2, H3}

If H1 is A,
then H2 must
be E to
explain
distance 21.
Then, there is
no label to
explain H3.

If H1 is E,
then H2 and
H3 can both
be
consistently
labeled.



Let's call features of image 1 "parts" and features of image 2 "labels"

1 DEFINITION Given a set of parts P , a set of labels for those parts L , a relation R_P over P , and a second relation R_L over L , a consistent labeling f is an assignment of labels to parts that satisfies:

If $(p_i, p_j) \in R_P$, then $(f(p_i), f(p_j)) \in R_L$.

**Labels of related parts
should be related**

I1: S1 above S4

I2: S_j above S_n

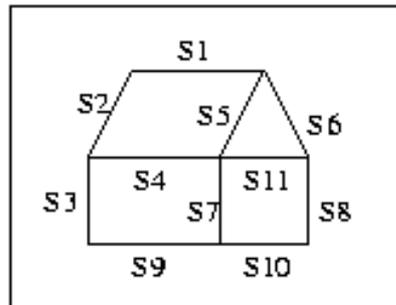


Image 1

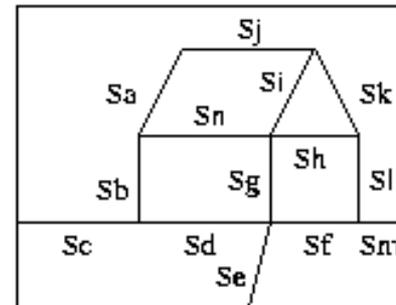
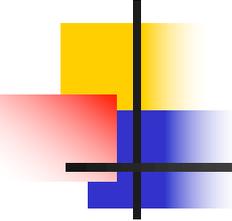


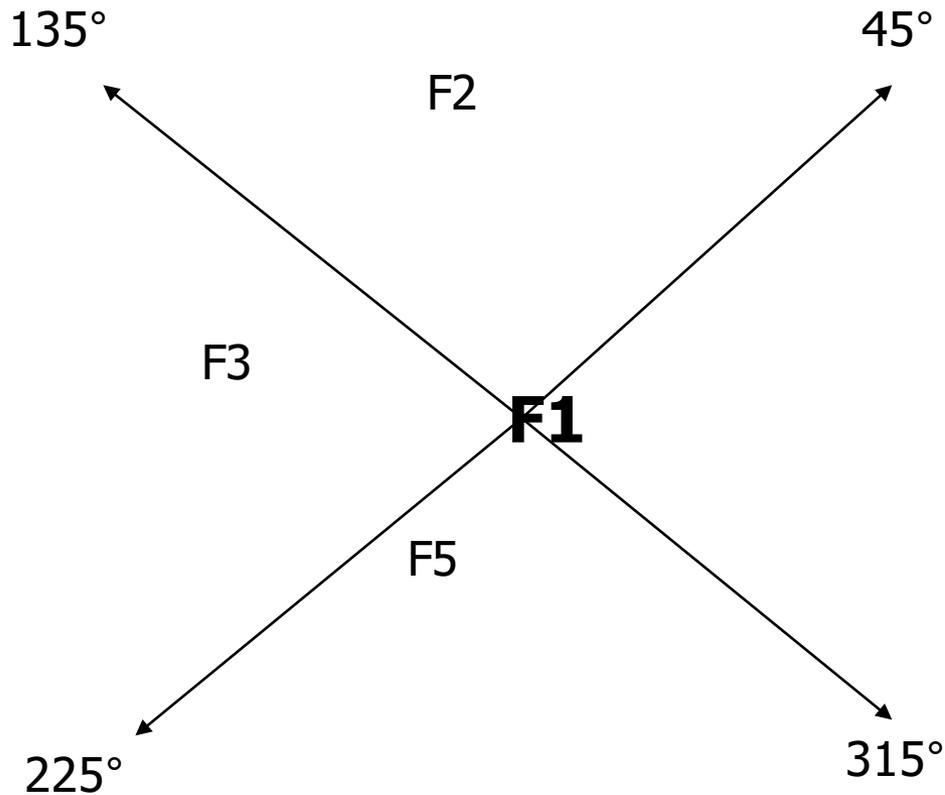
Image 2



What relations?

- We have been using rigid geometry – distance and angle
- Topological: F1 connects to F2; F1 inside of F2; F1 crosses F2; ...
- Other relations are useful when rigid mapping does not exist: F1 left of F2; F1 above F2; F1 between F2

Simple definitions of ...



- F2 above F1**
- F1 below F2**
- F5 below F1**
- F1 above F5**
- F1 left_of F4**
- F1 right_of F3**
- F4 right_of F1**
- F3 left_of F1**

IT backtracks over part-label pairs to get consistent set

- A stack holds all pairings $\{(P_1, L_1), \dots, (P_j, L_k)\}$
- check all relations on P_j and L_k
- if relation is violated, retract pairing (P_j, L_k) and try a new one

In general, IT Search is exponential in effort; however, in 2D or 3D alignment, Grimson and Lozano Perez have shown the bound to be $O(N^3)$

```
procedure Interpretation_Tree_Search( $P, L, R_P, R_L, f$ );
{
 $p := \text{first}(P)$ ;
for each  $l$  in  $L$ 
{
 $f' = f \cup \{(p, l)\}$ ; /* add part-label to interpretation */
OK = true;
for each N-tuple  $(p_1, \dots, p_N)$  in  $R_P$  containing component  $p$ 
and whose other components are all in domain( $f$ )
/* check on relations */
if  $(f(p_1), \dots, f(p_N))$  is not in  $R_L$  then
{
OK := false;
break;
}
if OK then
{
 $P' = \text{rest}(P)$ ;
if isempty( $P'$ ) then output( $f'$ );
else Interpretation_Tree_Search( $P', L, R_P, R_L, f'$ );
}
}
}
```

Discrete relaxation deletes part labels that are inconsistent with observations

(Left) Model object and (right) three holes detected in an image.
Model Point Locations and Interpoint Distances

Kleep model
distances

point	coordinates †	to A	to B	to C	to D	to E
A	(8,17)	0	12	15	37	21
B	(16,26)	12	0	12	30	26
C	(23,16)	15	12	0	22	15
D	(45,20)	37	30	22	0	30
E	(22,1)	21	26	15	30	0

Image Point Locations and Interpoint Distances

Features and
distances
observed in
the image

point	coordinates †	to H1	to H2	to H3
H1	(31,9)	0	21	26
H2	(10,12)	21	0	12
H3	(10,24)	26	12	0

Label A, B, C cannot match H1 since observed distances 26, 21 have not been observed. Also, H2 cannot be B.

Label Sets Midway through first pass of relaxation labeling.

	A	B	C	D	E
H_1	no $N \ni$ $d(A, N) = 26$	no $N \ni$ $d(B, N) = 21$	no $N \ni$ $d(C, N) = 26$	possible	possible
H_2	$21(H_2, H_1)$ $E \in L(H_1)$ $12(H_2, H_3)$ $B \in L(H_3)$	no $N \ni$ $d(B, N) = 21$	$21(H_2, H_1)$ $D \in L(H_1)$ $12(H_2, H_3)$ $B \in L(H_3)$		
H_1	no $N \ni$ $d(A, N) = 26$	$12(H_3, H_2)$ $A \in L(H_2)$ $26(H_3, H_1)$ $E \in L(H_1)$			

Impossible labels cause additional “filtering” out of possible labels

After completion of the second pass of relaxation labeling

Failed relationships cause labels to be dropped

	A	B	C	D	E
H_1	no	no	no	no	possible
H_2	possible	no	possible	no	no
H_3	no	possible	no	no	no

After completion of the third pass of relaxation labeling

During any pass filtering can be done in parallel; creating a separate output matrix for the next pass

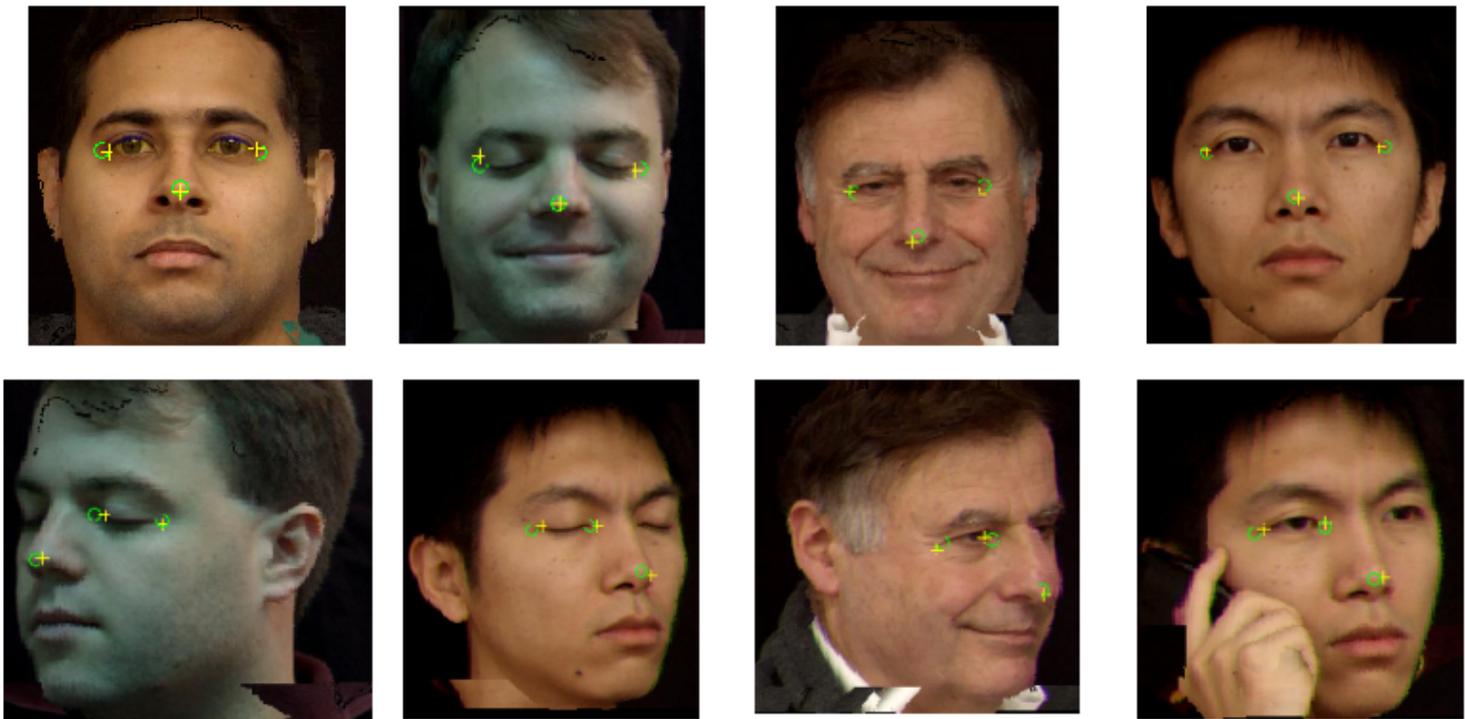
	A	B	C	D	E
H_1	no	no	no	no	possible
H_2	possible	no	no	no	no
H_3	no	possible	no	no	no

Discrete relaxation deletes inconsistent labels in stages

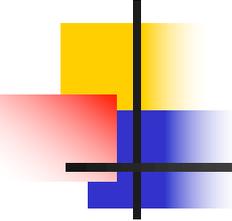
Let $P_i, i = 1, D$ be the detected image features.
Let $S(P_i), i = 1, D$ be the set of initially compatible labels.

```
procedure Relaxation_Labeling(P, S );  
{  
repeat  
  for each ( $P_i, S(P_i)$ ) do in parallel  
  {  
    for each label  $L_k \in S(P_i)$   
      for each relation  $R(P_i, P_j)$  in the image parts  
        if  $\exists L_m \in S(P_j)$  with  $R(L_k, L_m)$  in model  
          then keep  $L_k$  in  $S(P_i)$   
          else delete  $L_k$  from  $S(P_i)$   
  }  
until no change in any set  $S(P_i)$   
return(S);  
}
```

Face points filtered by known L-R, up-down, and distance relationships



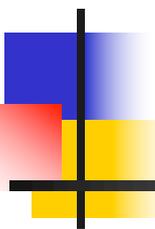
Points identified by surface curvature in neighborhood and filtered by location relative to other salient points. **These 3 points are then used for iterative 3D alignment (ICP algorithm) of the scan to a 3D model face.**



Face relationship filtering

TABLE 3
Relaxation Matrix after First Relaxation

		Interpretation						
		nose	rEye	lEye	orEye	olEye	centroid	null
Observation	Pt 1	1	0	0	1	0	0	1
	Pt 2	0	0	0	0	0	0	1
	Pt 3	0	1	1	1	0	0	1

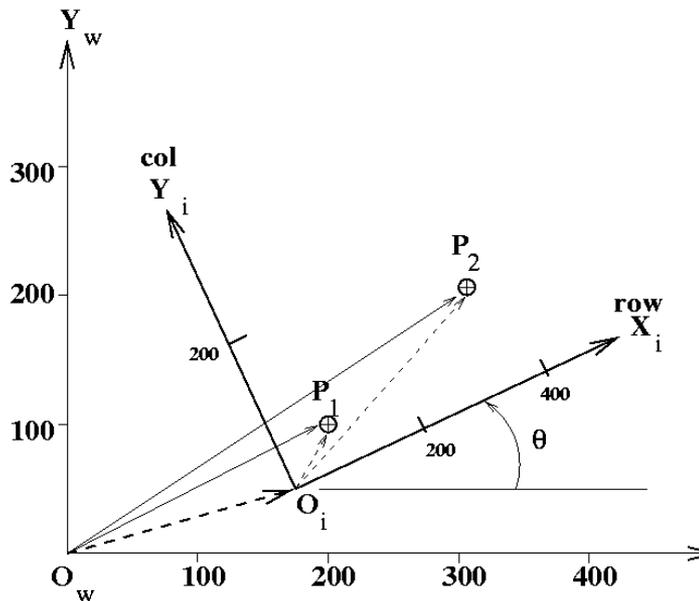


Notes on deriving a rigid mapping of P_j to P_k

- For 2D to 2D, match 2 points
- For 3D to 3D, match 3 points
- compute transform, then refine it to a best fit using least squares and many more matching points

Match of 2 points in 2D can determine R, S, and T

Rotation, Scaling and Translation



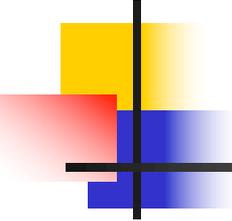
Assume two corresponding control points iP_j and wP_j

1. determine rotation θ
 - (a) direction of the vector $\mathbf{P}_1\mathbf{P}_2$ in I is determined as $\theta_i = \arctan(({}^iy_2 - {}^iy_1)/({}^ix_2 - {}^ix_1))$
 - (b) direction of the vector in W is determined as $\theta_w = \arctan(({}^wy_2 - {}^wy_1)/({}^wx_2 - {}^wx_1))$.
 - (c) $\theta = \theta_w - \theta_i$.
2. θ is determined: all \sin and \cos elements are known
3. solve 3 equations and 3 unknowns for s and x_0, y_0 .

$$\begin{bmatrix} x_w \\ y_w \\ 1 \end{bmatrix} = \begin{bmatrix} 1 & 0 & x_0 \\ 0 & 1 & y_0 \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} s & 0 & 0 \\ 0 & s & 0 \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} \cos \theta & -\sin \theta & 0 \\ \sin \theta & \cos \theta & 0 \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} x_i \\ y_i \\ 1 \end{bmatrix}$$

$$x_w = x_i s \cos \theta - y_i s \sin \theta + x_0$$

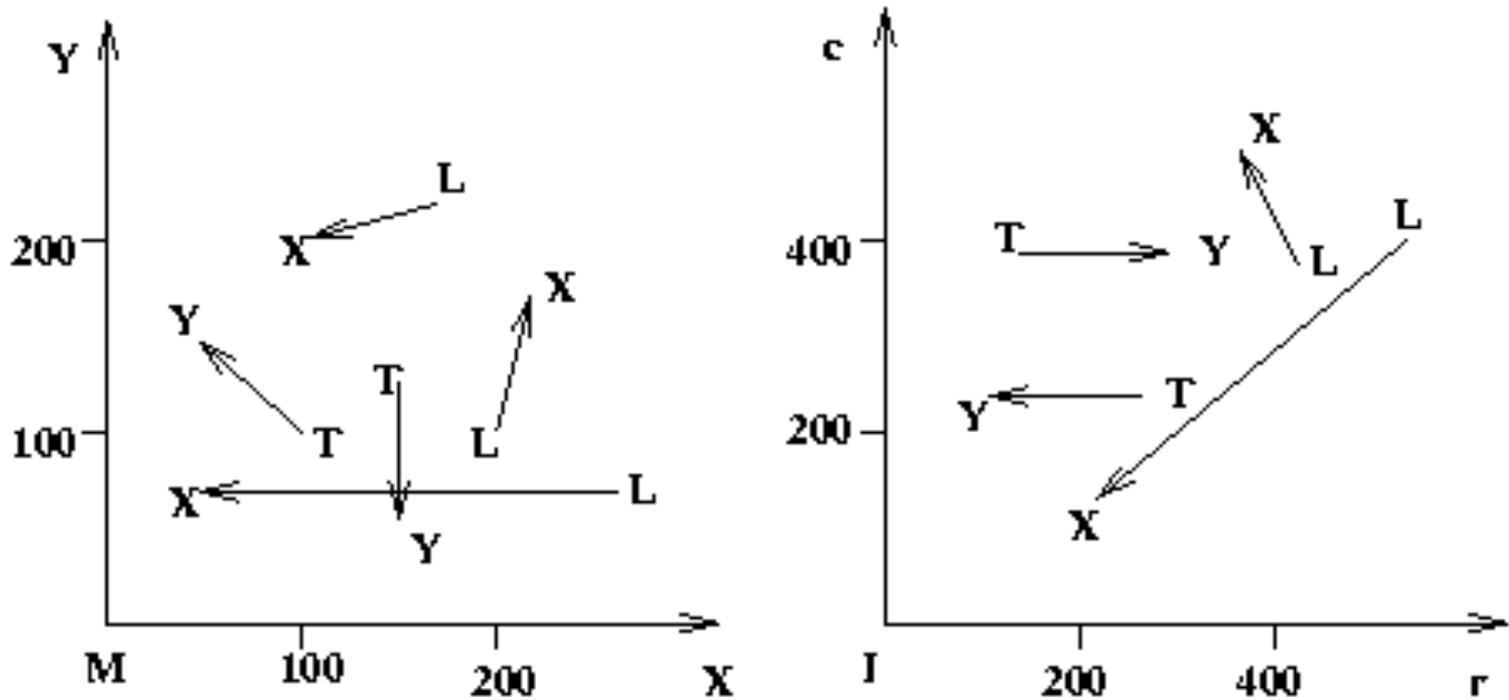
$$y_w = x_i s \sin \theta + y_i s \cos \theta + y_0$$



Transform derived from 2 points can fit badly for other points

- Better if original 2 points are far apart
- An error of $\Delta\theta$ in the rotation implies an error in point location of $r\Delta\theta$ where r is the distance to the point from the center of rotation.
- Can use crude transformation to pair points and then refit the transformation using least squares

Synthetic example of map to image correspondence



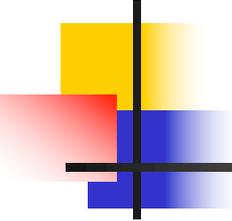
Assuming point labels must match, derive the RS&T matching each pair of similar vectors \rightarrow 10 possible mappings.

Clusters in pose space show correct transform & error!

Cluster space formed from 10 pose computations.

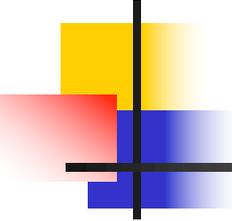
Model Pair	Image Pair	θ	s	u_0	v_0	
L(170,220),X(100,200)	L(545,400),X(200,120)	0.403	6.10	118	-1240	
L(170,220),X(100,200)	L(420,370),X(360,500)	5.14	2.05	-97	514	
T(100,100),Y(40,150)	T(260,240),Y(100,245)	0.663	2.05	225	-48	*
T(100,100),Y(40,150)	T(140,380),Y(300,380)	3.87	2.05	166	669	
L(200,100),X(220,170)	L(545,400),X(200,120)	2.53	6.10	1895	200	
L(200,100),X(220,170)	L(420,370),X(360,500)	0.711	1.97	250	-36	*
L(260, 70),X(40, 70)	L(545,400),X(200,120)	0.682	2.02	226	-41	*
L(260, 70),X(40, 70)	L(420,370),X(360,500)	5.14	0.651	308	505	
T(150,125),Y(150, 50)	T(260,240),Y(100,245)	4.68	2.13	3	568	
T(150,125),Y(150, 50)	T(140,380),Y(300,380)	1.57	2.13	407	60	

3 of the 10 vector pairings produce approximately the same RS&T transformation: examine the variance of parameters.



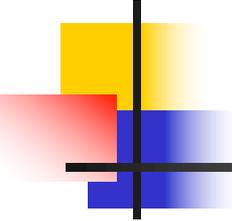
Pose-clustering concept

- Match minimal set of (points) features F_s between I and M
- Compute alignment transformation ω from F_s and contribute to cluster space
- Repeat this for “all” or “many” corresponding feature sets
- Identify the best cluster centers ω_i and attempt to verify those on other features
- * minimal basis means that ω_i will have error; cluster center is better, but iterative refinement of ω_i using many more features is better yet



Pose clustering in 2D and 3D

- 2D: Can get 4 parameter RS&T ω from only two matching points (as above)
- 3D: can get 6 parameter rigid trans. from 3 matching points (S&S text 13.2.6)
- 3D: or 2 lines and one point, or 3 lines



RANSAC: random sample and consensus (Fischler and Bolles)

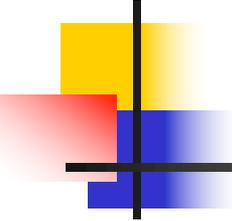
- Randomly choose minimal set of matching points $\{P_j\}$ and $\{L_j\}$
- Compute aligning transformation T from these points so that $T(P_j) = L_j$ for all j
- Check that this transformation maps other points correctly: $T(P_i) = L_i$ for more i &
- Repeat until some transformation is verified (or no more choices remain)

& best to refine T on all correspondences as they are checked.

Corner features matched between aerial images

Registering Image ${}^1I_{t1}$ to ${}^2I_{t2}$





General affine transform

ANY COMBINATION of *scaling, rotation, translation, shearing, reflection* is modeled by matrix multiplication—with the combined form:

$$\begin{bmatrix} x \\ y \\ 1 \end{bmatrix} = \begin{bmatrix} a_{11} & a_{12} & a_{13} \\ a_{21} & a_{22} & a_{23} \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} u \\ v \\ 1 \end{bmatrix} \quad (8)$$

The transformation is rigid when the 2 x 2 matrix has orthonormal rows and columns.

$$\begin{bmatrix} a_{11} & a_{12} \\ a_{21} & a_{22} \end{bmatrix}$$

Derivation of least squares constraints on coefficients a_{jk}

Taking the six partial derivatives of the error function with respect to each of the six variables and setting this expression to zero gives us the six equations represented in matrix form.

$$\begin{bmatrix} \Sigma x_j^2 & \Sigma x_j y_j & \Sigma x_j & 0 & 0 & 0 \\ \Sigma x_j y_j & \Sigma y_j^2 & \Sigma y_j & 0 & 0 & 0 \\ \Sigma x_j & \Sigma y_j & \Sigma 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & \Sigma x_j^2 & \Sigma x_j y_j & \Sigma x_j \\ 0 & 0 & 0 & \Sigma x_j y_j & \Sigma y_j^2 & \Sigma y a_j \\ 0 & 0 & 0 & \Sigma x_j & \Sigma y_j & \Sigma 1 \end{bmatrix} \begin{bmatrix} a_{11} \\ a_{12} \\ a_{13} \\ a_{21} \\ a_{22} \\ a_{23} \end{bmatrix} = \begin{bmatrix} \Sigma u_j x_j \\ \Sigma u_j y_j \\ \Sigma u_j \\ \Sigma v_j x_j \\ \Sigma v_j y_j \\ \Sigma v_j \end{bmatrix} \quad (16)$$

Best affine transform matching the town images

**11 matching
point pairs**

Matching control point pairs are:

288	210	31	160	232	288	95	205	195	372	161	229	269	314	112	159
203	424	199	209	230	336	130	196	284	401	180	124	327	428	198	69
284	299	100	146	337	231	45	101	369	223	38	64				

The Transformation Matrix is:

```
[ -0.0414 , 0.773 , -119  
  -1.120 , -0.213 , 526  
   0.0 , 0.0 , 1.0 ]
```

**Ajk from the least
squares procedure**

Residuals (in pixels) for 22 equations are as follows:

Δx	0.18	-0.68	-1.22	0.47	-0.77	0.06	0.34	-0.51	1.09	0.04	0.96
Δy	1.51	-1.04	-0.81	0.05	0.27	0.13	-1.12	0.39	-1.04	-0.12	1.81

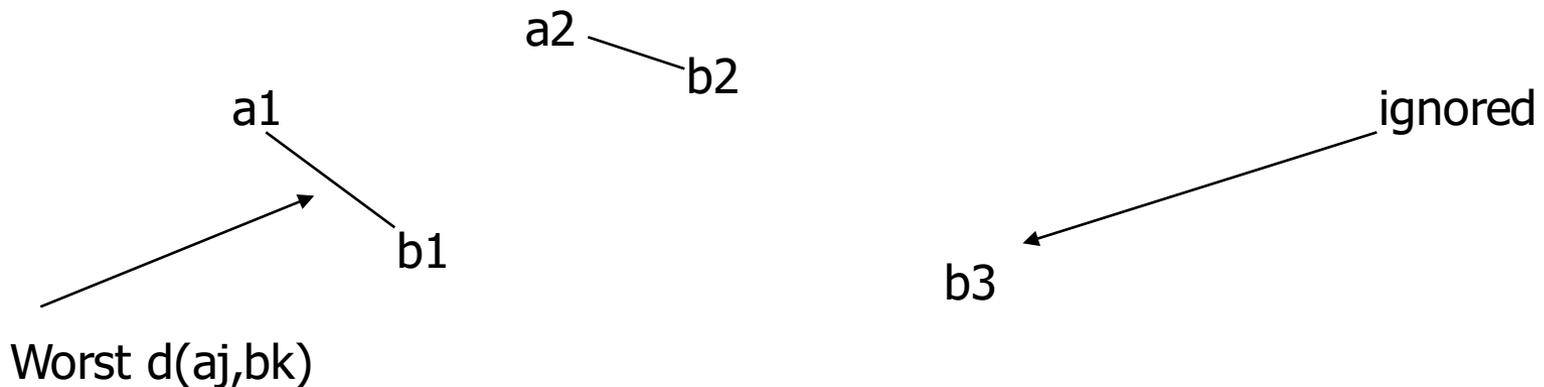
P1

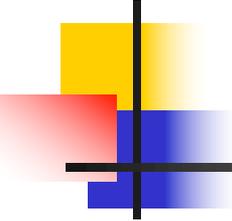
**Residuals of mapping are all less than 2
pixels in the right image space.**

P11

Euclidean distance between point sets measures their match: 2D or 3D

- set A has points from image 1
- set B has points from image 2
- assume every point from A should be observed in B also
- match measure can be the worst distance from any point in A to some point in B, or the root mean square of all such distances



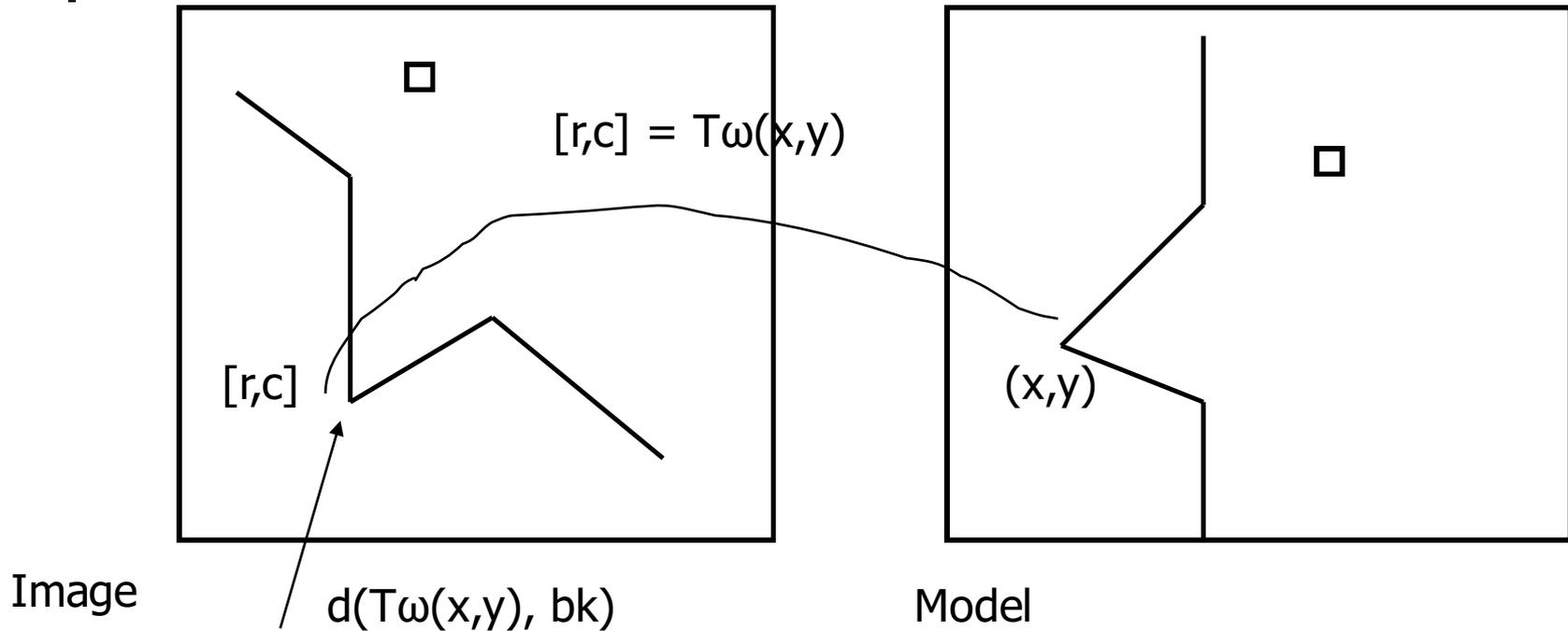


Example application

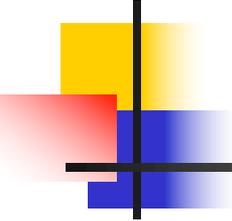
- Observed data A is 3D surface scan of face
- Model data B is 3D surface model of face
- Best match of A to B probably requires points of A to be rotated and translated at least slightly
- So, we have to search over a 6-parameter space ω
- For each parameter set, we need to transform points of A into the space of B and **then** find the best point matches.

$$\textit{compute} \quad d(T_{\omega}(a_j), b_k)$$

Example 2D case



To evaluate the value of the match of the Model in the Image for the pose parameters ω model points must be transformed and best matching image points located – how to do it?



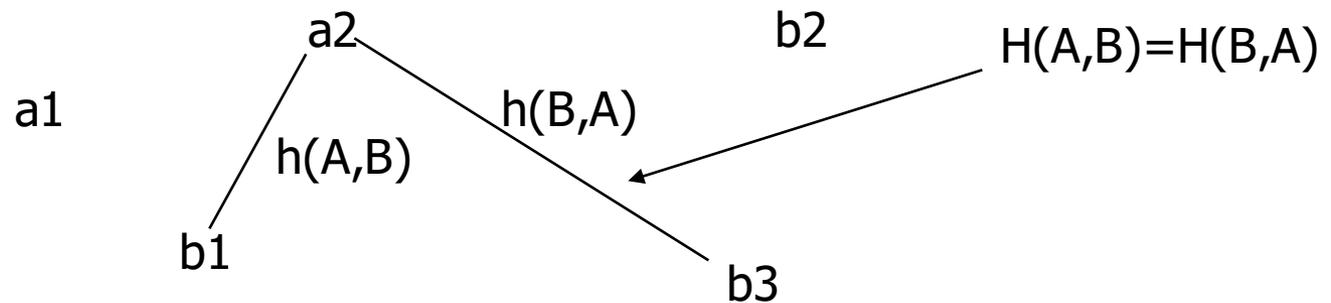
Distance transform helps

- Identify image feature points b_k ;
- Set image feature points to 0
- Set all neighbors of 0 values to 1
- Set all unset neighbors of 1 values to 2
- Set all unset neighbors of 2 to 3, etc.

$$match_{\omega}(A) = \sum_{(x,y) \in A} I_B[T(x,y)]$$

Sum all the distance penalties over all transformed points of the model: called "chamfer-matching" by Barrow and Tenenbaum

Hausdorff distance: take worst of the closest matches



$$h(A, B) = \max_{a \in A} \{ \min_{b \in B} \{ d(a, b) \} \}$$

in general $h(A, B) \neq h(B, A)$

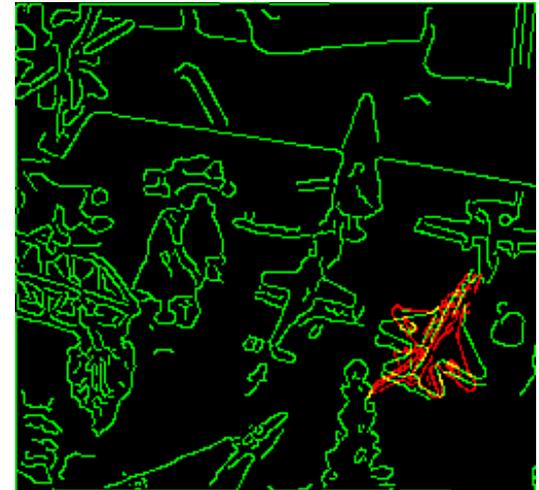
a symmetric dist. is

$$H(A, B) = \max \{ h(A, B), h(B, A) \}$$

Example use from Leventon



Edge points of
model plane image

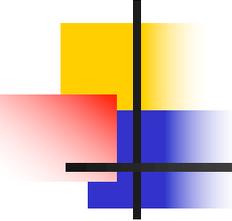


Left: Model scene
with objects

Images from Leventon web pages.

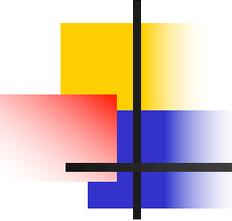
Best $h(\text{plane}, \text{scene})$
over all sets of
translated plane edge
points

Symmetric distance not wanted here since
most scene points should not be matched.



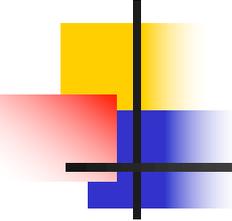
Variations on Hausdorff dist.

- Create histogram of all individual point distances of $h(A,B)$
- If, say 80%, of these are suitably small, then accept the match.
- Can define the 80% Hausdorff distance as that distance D such that $d(a_j, B) \leq D$ for 80% of the points a_j of A
- Perhaps we can now match the outline of a given pickup truck with and without a refrigerator in the back.
- See papers of Huttenlocher, Leventon



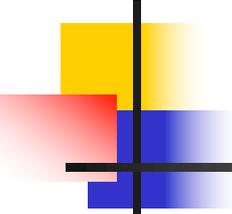
Summary of matching, Part 2

- Brute force matching of points is computationally expensive
- Strong constraints on matching from feature point type and relations with other features
- Some matching methods: focus features, RANSAC, relaxation, interpretation tree, pose clustering
- Best affine (RT&T) transformation from N pairs of matching points can be done in 2D or 3D.
- Chamfer-matching enables faster match evaluation



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