



Geometry for Computer Vision

Lecture 6b

Sample Consensus Strategies

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Overview

- Issues with standard RANSAC
- Maximum-likelihood scoring
- LO-RANSAC
- Preemptive RANSAC
- DEGENSAC

Not covered here: All the other variants

RANDOMIZED RANSAC, G-SAC, NAPSAC etc.

Paper to read for next week: PROSAC



RANSAC issues

In lecture 3 we introduced RANSAC (Fischler&Bolles 81).

It finds a **model with maximal support** in the presence of **outliers**

Approach: randomly **generate hypotheses** and **score** them.

Most novelties since 1981 covered in thesis by:
Ondrej Chum, *Two-View Geometry Estimation by Random Sample and Consensus*, July 2005



RANSAC issues

S - correspondence set, K - number of trials

```
for k=1:K
```

```
    s=sample_draw_minimal(S)
```

```
    m=model_estimate(s)
```

```
    [v,inliers]=model_score(m,S)
```

```
    if v>best_v
```

```
        best_inlier_set=inliers
```

```
        best_v=v
```

```
        best_m=m
```

```
    end
```

```
end
```



RANSAC issue #1

Underlying optimization problem:

$$\varepsilon = \sum_k \sum_l v_k \|\mathbf{x}_{kl} - \text{proj}(\mathbf{X}_k, \theta_l)\|^2 \quad v_k \in \{0, 1\}$$

score is a discrete inlier count:

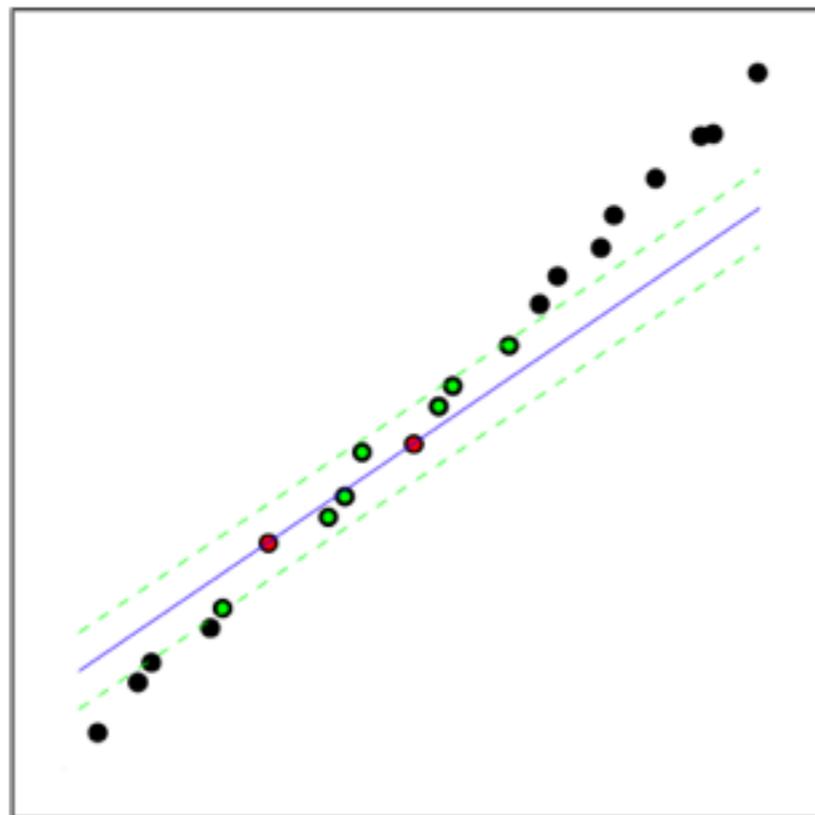
$$s = \sum_k v_k$$

there may be many equally good optima!



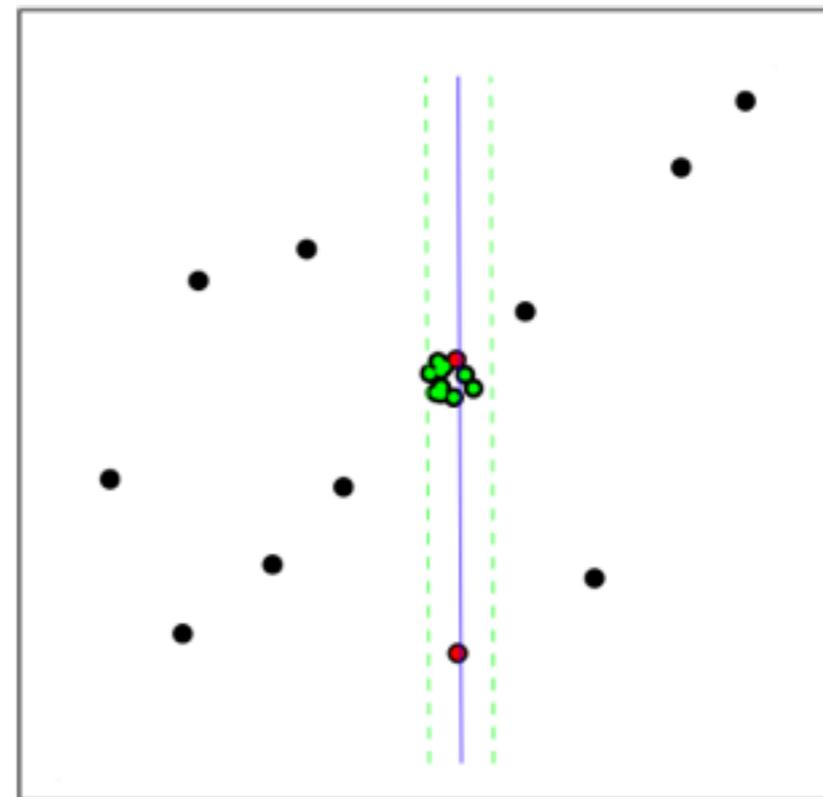
RANSAC issues #2 and #3

Two more problems with the original approach:



(a)

Inlier noise



(b)

Near degeneracies



RANSAC issue #3

Near degeneracies can be dealt with by sampling non-randomly, e.g.

- DEGENSAC, for F estimation in plane dominant scenes. **Chum et al., *Two-view Geometry estimation unaffected by a Dominant Plane*, CVPR05**

-



RANSAC issue #3

Near degeneracies can be dealt with by sampling non-randomly, e.g.

- DEGENSAC, for F estimation in plane dominant scenes. **Chum et al., *Two-view Geometry estimation unaffected by a Dominant Plane*, CVPR05**
- Distance constraint for points used in E estimation. **Hedborg et al., *Fast and Accurate Structure and Motion Estimation*, ISVC09**
Reduces #iterations by 50% in forward motion.



Maximum likelihood scoring

Underlying optimization problem:

$$\varepsilon = \sum_k \sum_l v_k ||\mathbf{x}_{kl} - \text{proj}(\mathbf{X}_k, \theta_l)||^2 \quad v_k \in \{0, 1\}$$

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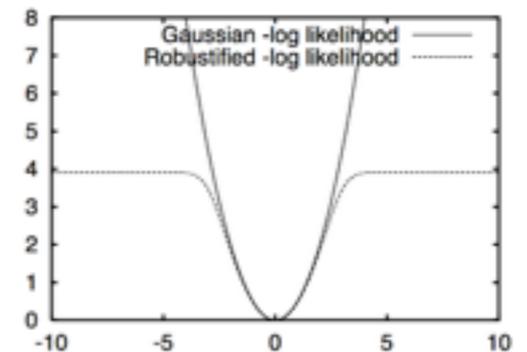
there may be many equally good optima!



Maximum likelihood scoring

Better to use a robust error norm:

$$\varepsilon = \sum_k \sum_l \rho(\mathbf{x}_{kl} - \text{proj}(\mathbf{X}_k, \theta_l))$$

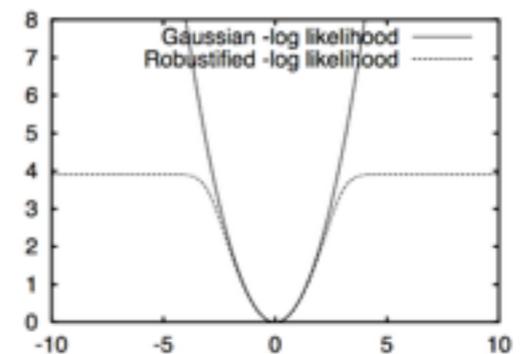




Maximum likelihood scoring

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and as score, the minimum error (MLE-SAC):

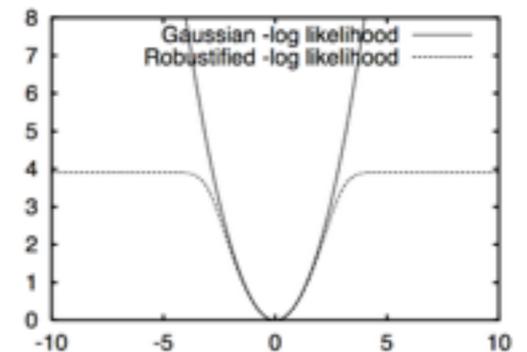
$$s = -\varepsilon$$



Maximum likelihood scoring

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called **maximum likelihood scoring**

See: Torr & Zisserman, *MLE-SAC: A new robust estimator with application to estimating image geometry*, CVIU'00



LO-RANSAC

Inlier noise means that the heuristic for number of samples to draw:

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

is overly optimistic.

A small modification makes the heuristic work again: **Chum et al., *Locally Optimized RANSAC*, DAGM03**



LO-RANSAC

Small modification:

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```
    if v>best_v
```

```
        [inliers,v,m]=local_optimization(inliers,v,m)
```

```
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```
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```

```
        best_m=m
```

```
    end
```

```
end
```



LO-RANSAC

Chum tries four variants of local optimisation:

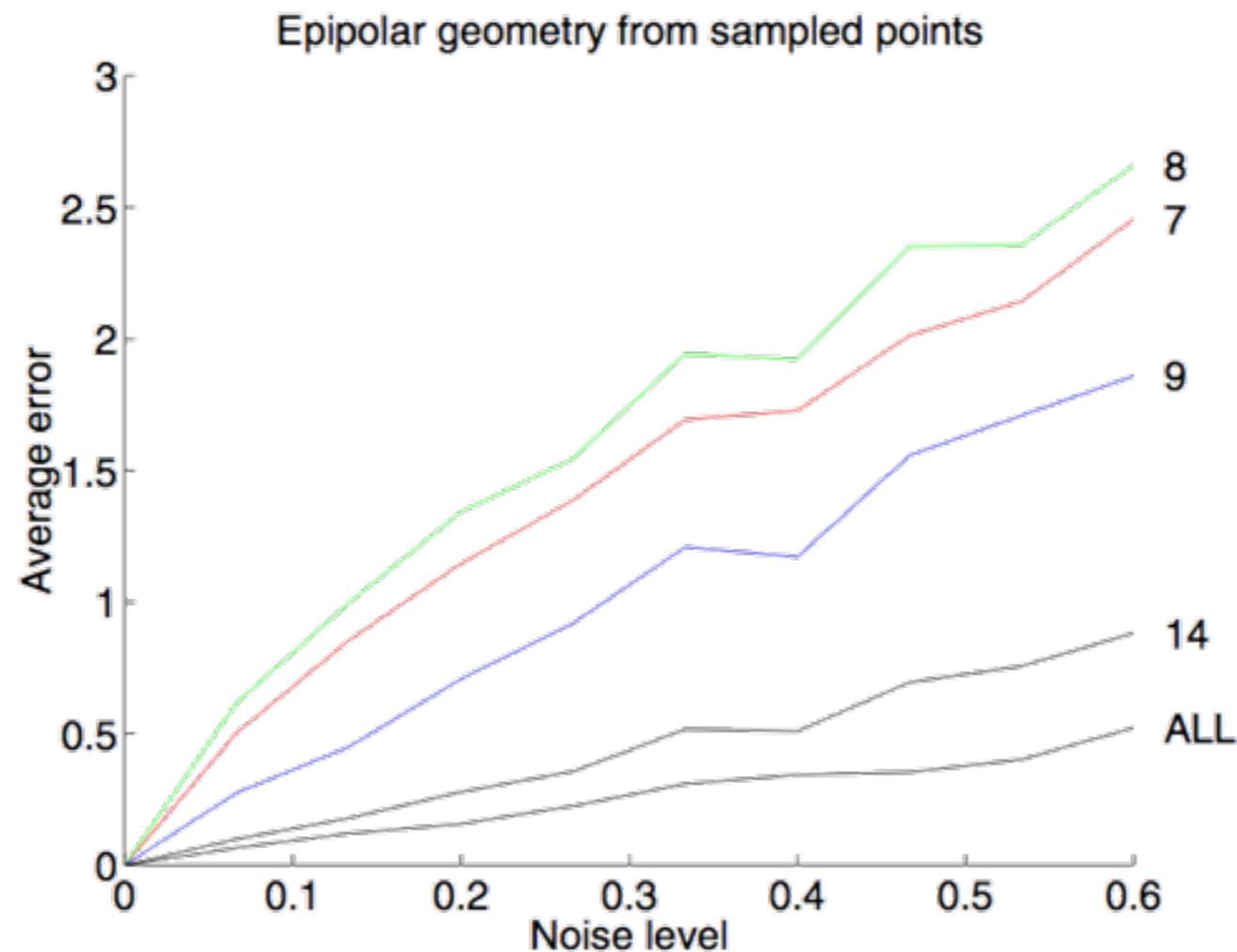
1. Linear estimation from all inliers
2. Iterative linear estimation with decreasing inlier threshold.
3. Inner RANSAC
4. Inner RANSAC with #2.

#3 and #4 worked best, and #4 came close to the heuristically expected #samples.



LO-RANSAC

The inner RANSAC step uses non-minimal sample sets. Errors for linear F estimation:





Open source

Lebeda, Matas, Chum, *Fixing the Locally Optimized RANSAC*, BMVC'12

C/C++ library available on the web. Source code on request. The "Fixes" are:

1. Maximum likelihood scoring (i.e. MLESAC)
2. Iterative Reweighted Least-Squares on random subsets of bounded size (`7xmin_subset`)



Preemptive Ransac

David Nister, *Preemptive RANSAC for live structure and motion estimation*, ICCV03

Total time for RANSAC is given by:

$$t = k(t_M + E[m_S]t_V)$$

k- #iterations t_M -model estimation time,
 t_V -verification time. m_S - #models/iteration



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 t_V -verification time. m_S - #models/iteration

If many correspondences, t_V will dominate.



Preemptive Ransac

Idea: Do a probabilistic verification instead.

$$t = k(t_M + E[m_S]t_V)$$

- In a **real-time system**, t is fixed, so if we reduce t_V we may increase k .
- Preemptive RANSAC does this by evaluating all hypotheses in parallel.
- In each step, a fixed number of most promising hypotheses are kept.



Preemptive Ransac

Preemptive RANSAC:

1. Generate $f(1)$ hypotheses in parallel.
2. For $n=1$ to N
3. Evaluate $f(n)$ hypotheses on a random correspondence
4. Keep the $f(n+1)$ best hypotheses according to accumulated score.

$$f(1)=M \quad \text{and} \quad f(n+1) \leq f(n)$$



Preemptive Ransac

$f(n)$ - the preemption function

$$f(n) = \lfloor M 2^{-\lfloor \frac{n}{B} \rfloor} \rfloor$$

B - block size (f only changes every B steps)

M - number of models

Accumulated scoring $L(m) = \sum_{n=1}^N \rho(n, m)$

Log-likelihood of sample n given model m

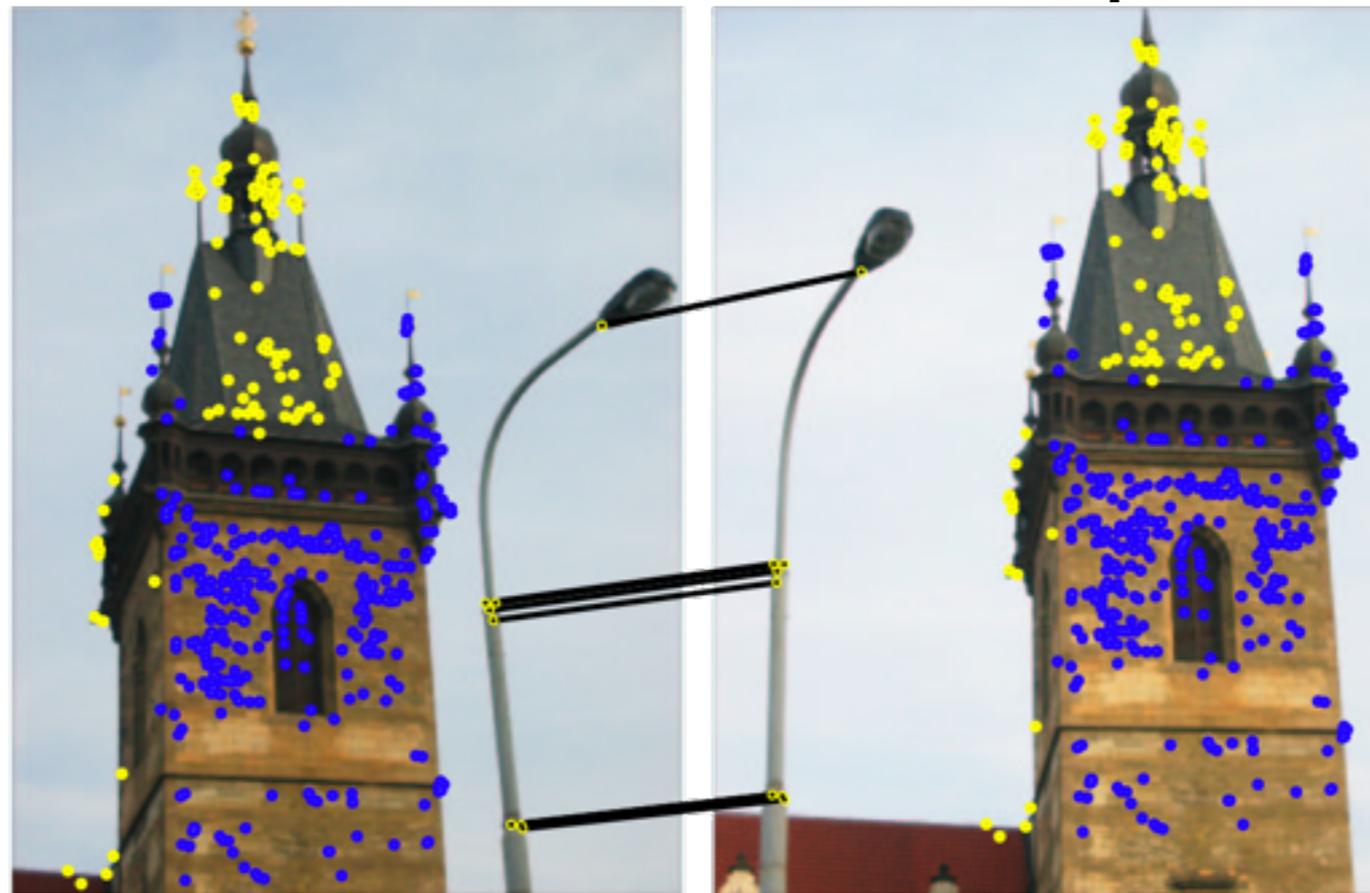
$$\rho(n, m)$$



Degensac

Chum, et al., *Two-view Geometry Estimation Unaffected by a Dominant Plane*, CVPR'05

Planar dominant scenes are also problematic





Degensac

Actually, the F estimation problem is even worse than it might appear, as 5 points in a plane +2 **arbitrary** correspondences gives an F compatible with the plane.



Degensac

Actually, the \mathbf{F} estimation problem is even worse than it might appear, as 5 points in a plane +2 *arbitrary* correspondences gives an \mathbf{F} compatible with the plane.

In le5 we saw that if all seven points are in a plane, then

$$\mathbf{x}_k^T \mathbf{F} \mathbf{y}_k = 0, \quad \mathbf{x}_k = \mathbf{H} \mathbf{y}_k, \quad k = 1 \dots 7$$

and $\mathbf{F} = [\mathbf{e}]_{\times} \mathbf{H}$ for any epipole \mathbf{e}

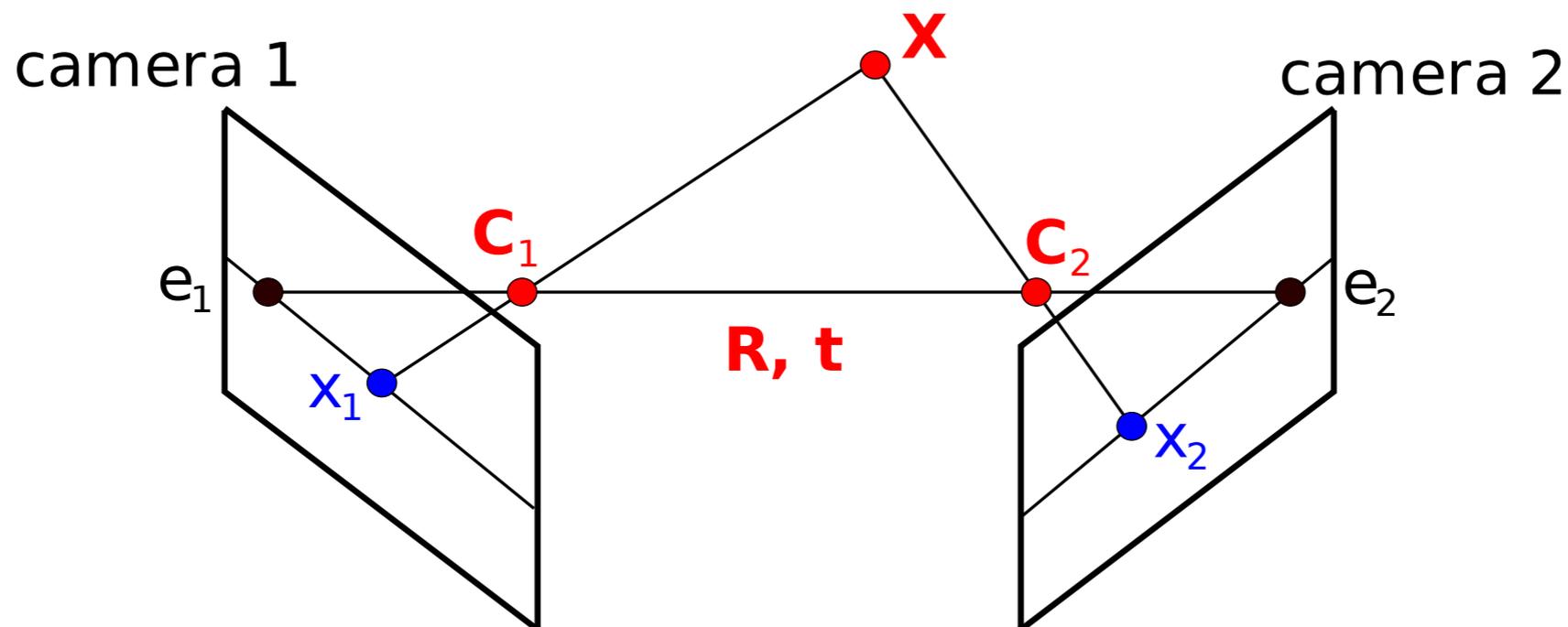


Degensac

If **six** points are in a plane

$$\mathbf{x}_k^T \mathbf{F} \mathbf{y}_k = 0, \quad k = 1 \dots 7 \quad \mathbf{x}_k = \mathbf{H} \mathbf{y}_k, \quad k = 1 \dots 6$$

$$\mathbf{F} = [\mathbf{e}]_{\times} \mathbf{H} \quad \text{for} \quad \mathbf{e} \in \mathbb{R}^3, \quad \mathbf{e}^T (\mathbf{H} \mathbf{x}_7 \times \mathbf{y}_7) = 0$$





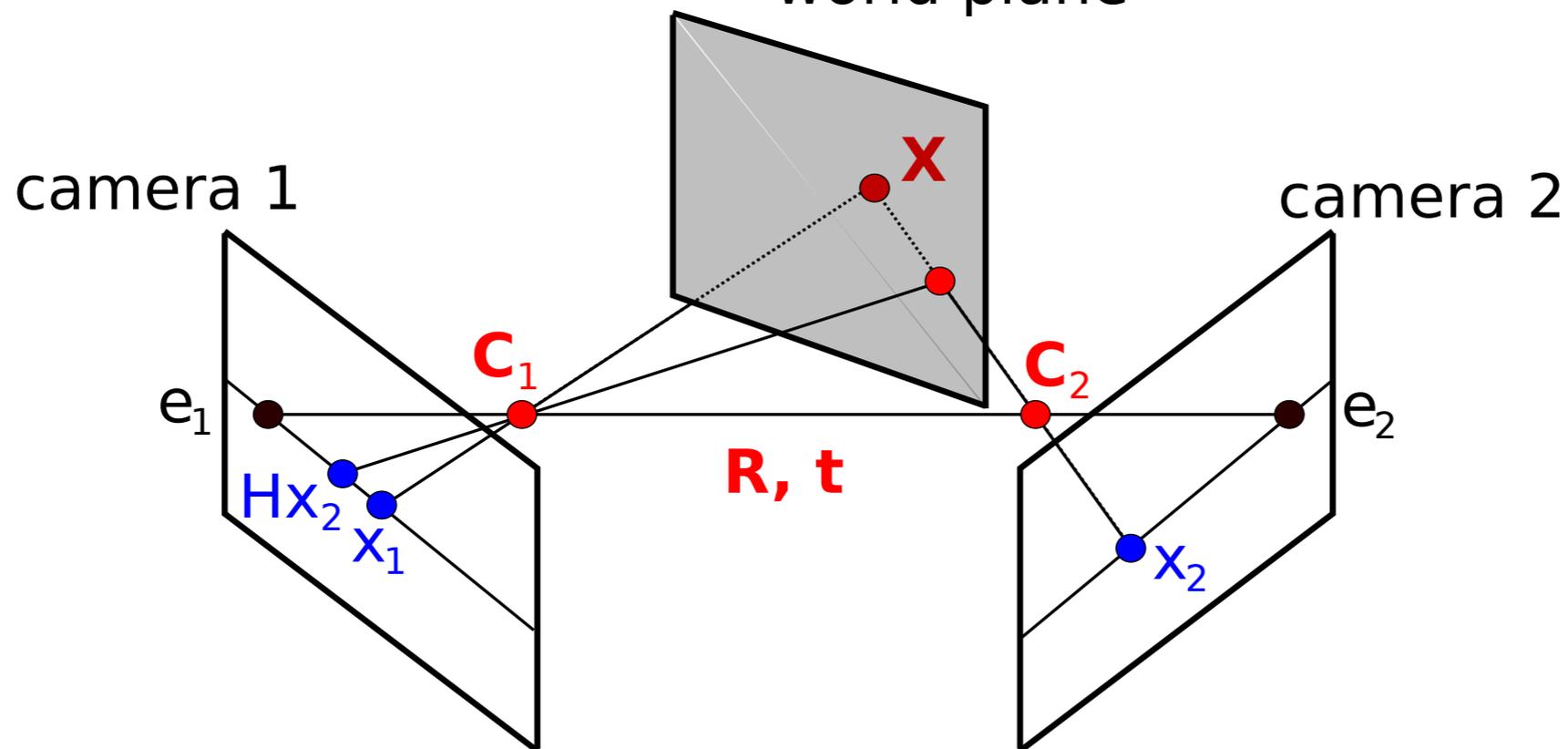
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world plane





Degensac

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For **five** points in the plane

$$\mathbf{x}_6 \times (\mathbf{H} \mathbf{y}_6) \quad \text{and} \quad \mathbf{x}_7 \times (\mathbf{H} \mathbf{y}_7)$$

define two lines that intersect in \mathbf{e} . \mathbf{F} will have all points consistent with \mathbf{H} as inliers.



Degensac

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Also used in plane+parallax algorithm



Degensac - detection

From \mathbf{F} and $\{\mathbf{x}_k \leftrightarrow \mathbf{y}_k\}_{k=1}^3$ we can compute a homography $\mathbf{H} = \mathbf{A} - \mathbf{e}_1(\mathbf{M}^{-1}\mathbf{b})^T$

where $\mathbf{A} = [\mathbf{e}_1]_{\times} \mathbf{F}$ $\mathbf{M} = [\mathbf{x}_1 \ \mathbf{x}_2 \ \mathbf{x}_3]^T$

and $b_k = (\mathbf{x}_k \times \mathbf{A}\mathbf{y}_k)^T (\mathbf{x}_k \times \mathbf{e}_1) \|\mathbf{x}_k \times \mathbf{e}_1\|^{-2}$



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This \mathbf{H} is now checked for two additional inliers. If found, \mathbf{F} is said to be \mathbf{H} -degenerate



Degensac - detection

There are $\binom{7}{5} = 21$ ways to pick five points from 7.

But, if we pick the 3 points that define **H** as
 $\{1, 2, 3\}, \{4, 5, 6\}, \{1, 2, 7\}, \{4, 5, 7\}, \{3, 6, 7\}$

We will have covered all 21 permutations.

Thus at most **five H** need to be computed and tested to find out if **F** is **H**-degenerate.



Degensac

DEGENSAC algorithm

1. Select 7 random correspondences and estimate F
2. IF best support this far
3. IF H -degeneracy
4. Do inner RANSAC and estimate F from H and 2 correspondences that are inconsistent with H (Plane+Parallax algorithm)
5. IF new F has even bigger support, store F
6. ELSE store H



Paper to discuss next week...

Ondrej Chum and Jiri Matas, *Matching with PROSAC -- Progressive Sample Consensus*, CVPR'05