RANSAC

Traditional Approaches

Ondřej Chum

Visual Recognition Group

Department of Cybernetics, Faculty of Electrical Engineering

Czech Technical University in Prague

RANSAC

In: $U = \{x_i\}$ set of data points, $|U| = N$

$f(S) : S \to p$ function f computes model parameters p given a sample S from U

$\rho(p, x)$ the cost function for a single data point x

Out: p^* p^*, parameters of the model maximizing the cost function

k := 0

Repeat until P{better solution exists} < η (a function of C^* and no. of steps k)

k := k + 1

I. Hypothesis

(1) select randomly set $S_k \subset U$, sample size $|S_k| = m$

(2) compute parameters $p_k = f(S_k)$

II. Verification

(3) compute cost $C_k = \sum_{x \in U} \rho(p_k, x)$

(4) if $C^* < C_k$ then $C^* := C_k$, $p^* := p_k$

end

Non-uniform sampling

Additional constraints

Randomized verification

Potential degeneracy tests

Improving precision

Outline

Non-uniform sampling
- NAPSAC
- PROSAC

Local Optimization (model refinement)

Degenerate configurations

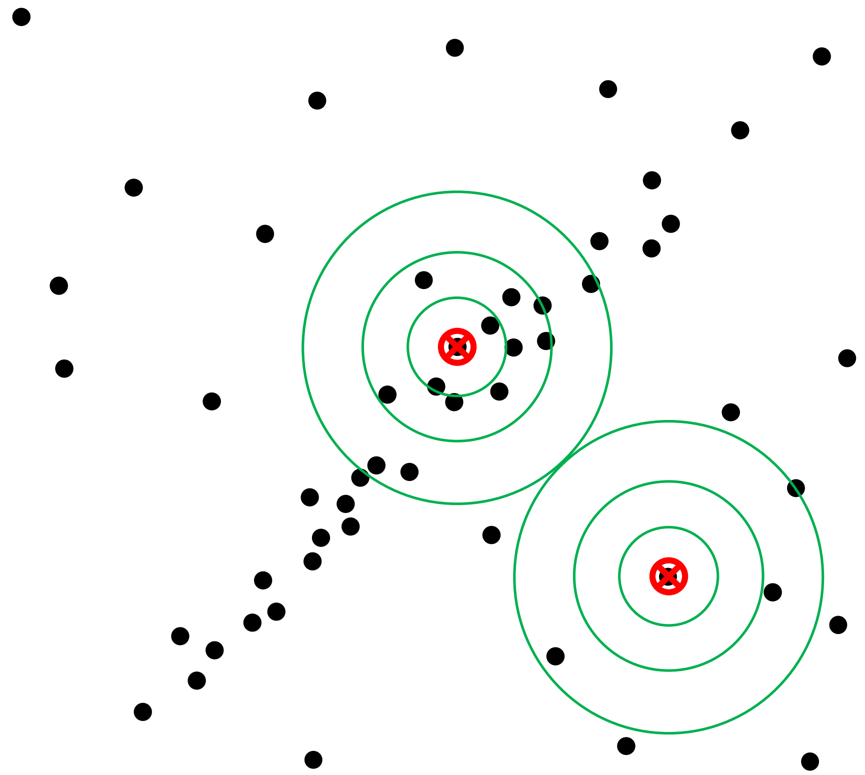
Checking the sample

Randomized verification

Sampling Locally

NAPSAC, …

Local Neighborhoods



Inliers tend to lie on densely populated manifolds

- Draw a first data point at random
- Draw the rest of the sample from some neighborhood of the initial point

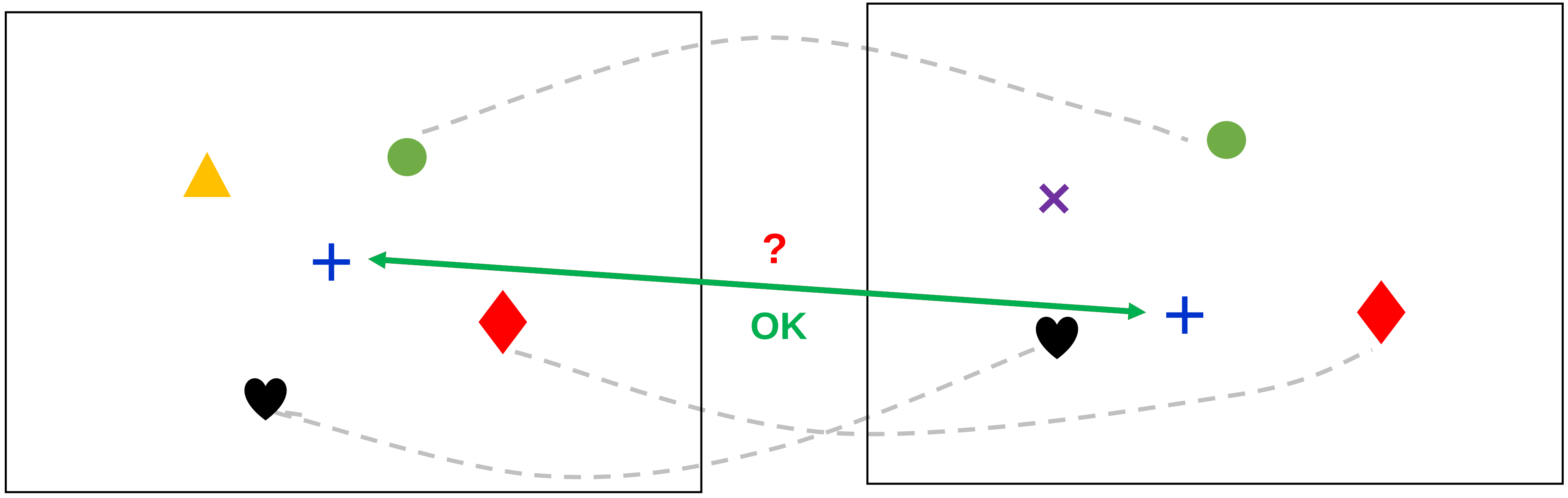
Ni, Jin, Dellaert: GroupSAC: Efficient consensus in the presence of groupings. ICCV 2009

Barath, Noskova, Ivashechkin, Matas: MAGSAC++, a fast, reliable and accurate robust estimator. CVPR 2020

Myatt, Torr, Nasuto, Bishop, Craddock: NAPSAC: High Noise, High Dimensional Robust Estimation - It's in the Bag. BMVC 2002

(Semi-) Local Geometry

Idea: verify a tentative match "+" by comparing neighboring features



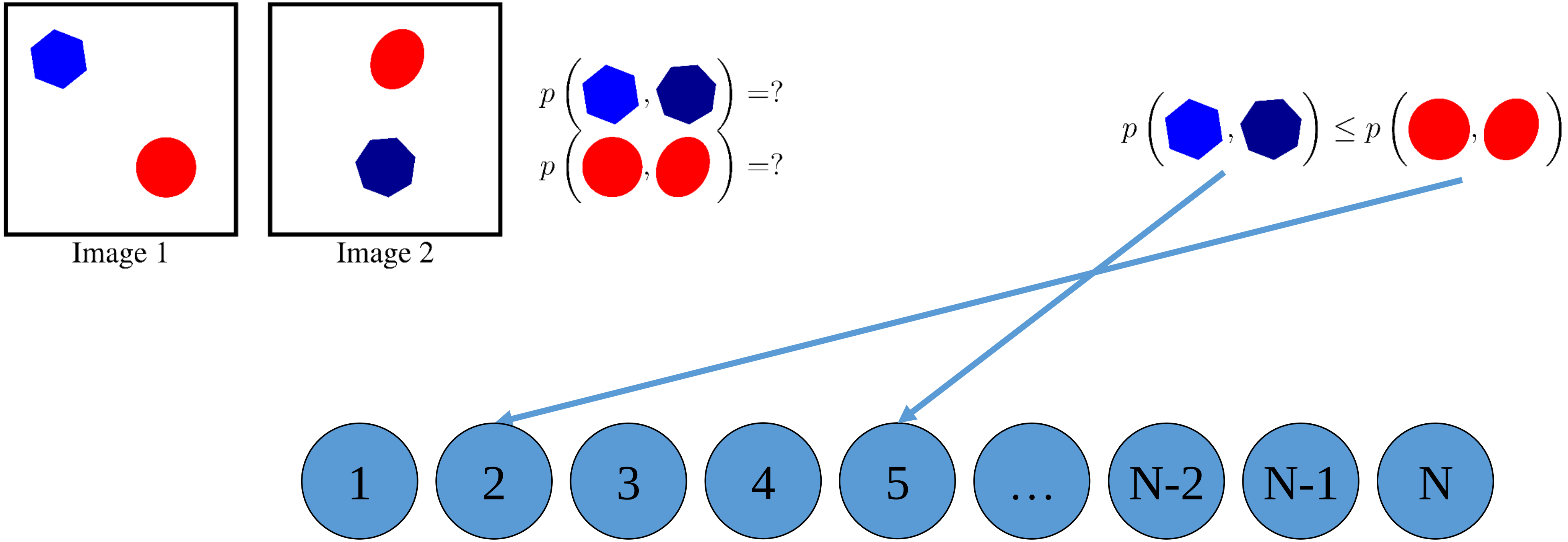
Schmid, Mohr: Local Greyvalue Invariants for Image Retrieval. PAMI 1997

PROSAC

Progressive Sample Consensus

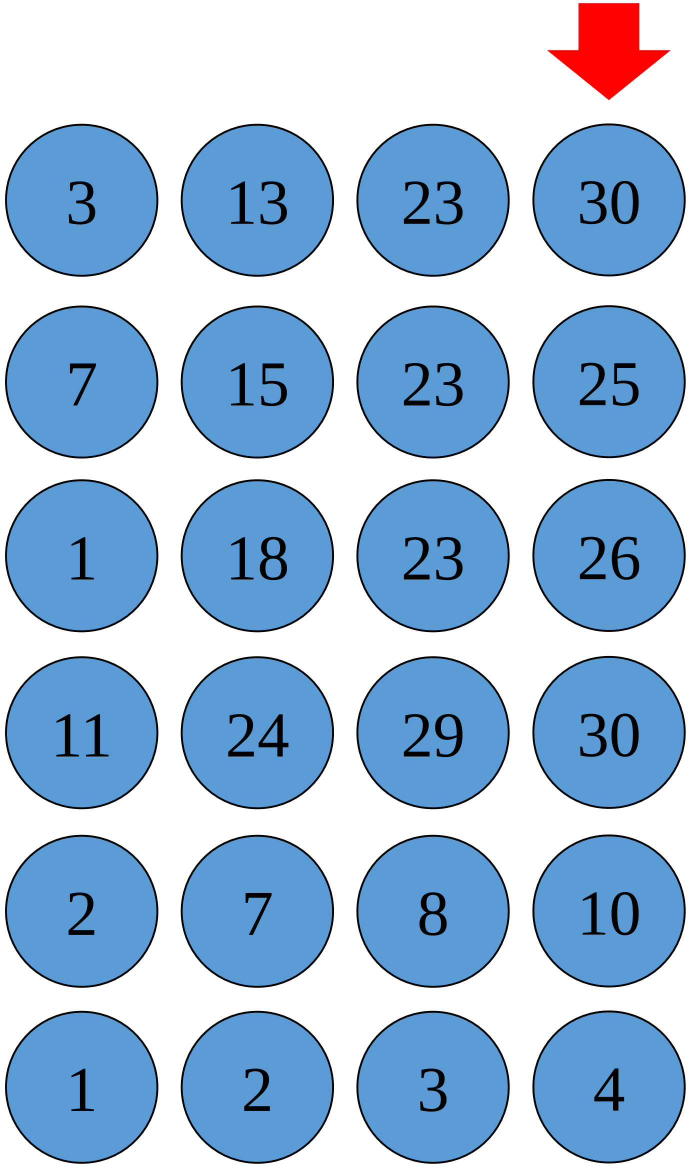
Quality of Correspondences

- Not all correspondences are created equally
- Some are better than others – are correct with higher probability
- Some quality is typically used to select tentative correspondences (similarity, first-to-second distance ratio, etc)



Order all correspondences according to the quality

Evaluate “Better” Samples Earlier



Quality of a sample given by its worst correspondence

Draw all the samples first

Reorder with respect to the quality

Evaluate in the order of the sample quality

\+ Evaluates “better” samples first
\+ If the quality is uninformative ends up with uniform sampling

\- Inefficient

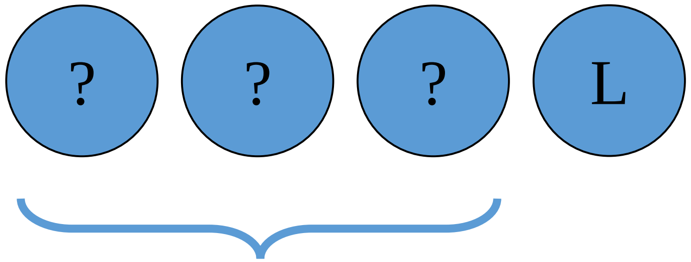
PROSAC Sampling

Drawing samples of m correspondences

L := m

Let T_L be the expected number of samples with quality L

Draw *ceil*(T_L) samples containing m-1 correspondences "better" than L and L



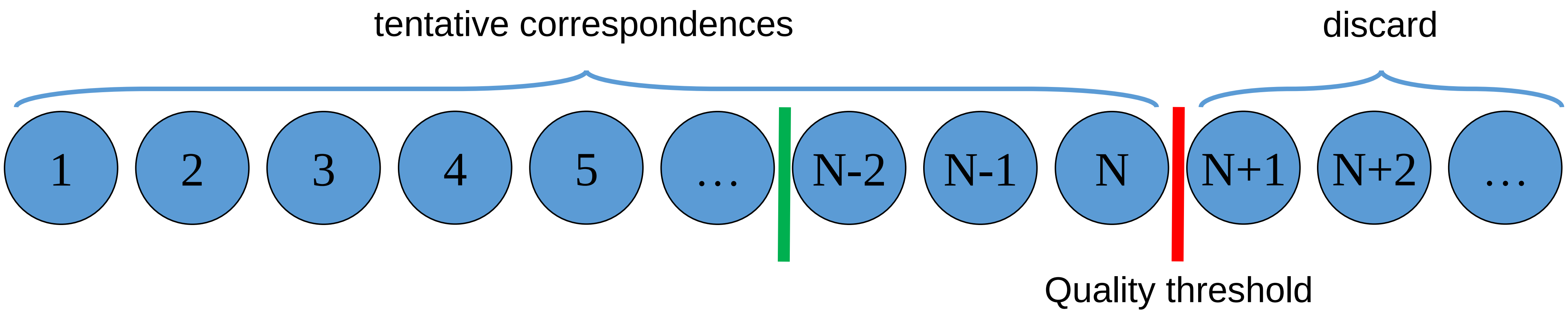
Draw uniformly from (1 … L-1)

L := L + 1

Stopping Criterion of PROSAC

Tentative correspondences commonly selected by thresholding their quality

Stopping criterion of RANSAC is based the fraction of inliers



Choose a threshold on the fly so that the fraction of inliers is maximized – earlier termination

Problems:

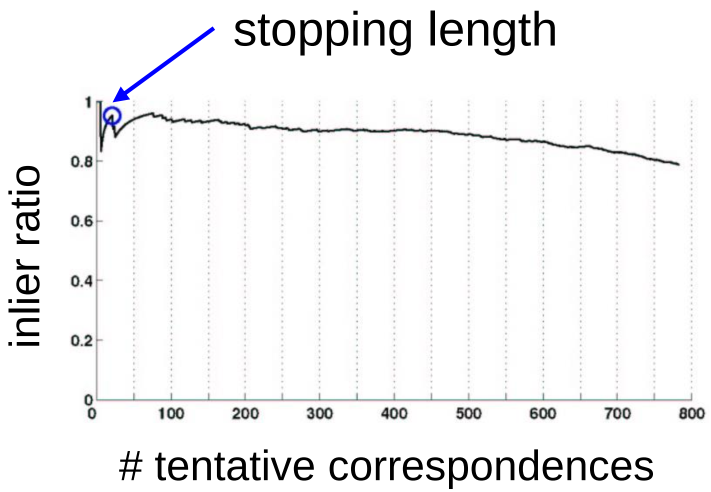
small sets of tentative correspondences (eg sample size) will have large inlier ratios – non-ramdomness
the ordering often introduces a bias (eg correspondences on a fronto-paralell plane match better)

Example

Epipolar geometry estimation

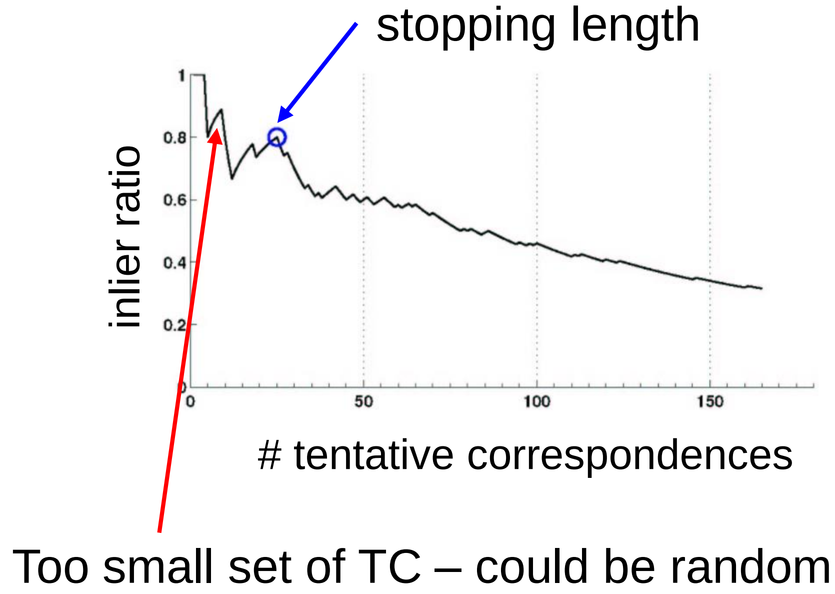
Executed on all TC

Background	$N = 783, \varepsilon = 79\%$		
	I	k	time [sec]
PROSAC	617	1.0	0.33
RANSAC	617	15	1.10



Executed on outliers to the background model

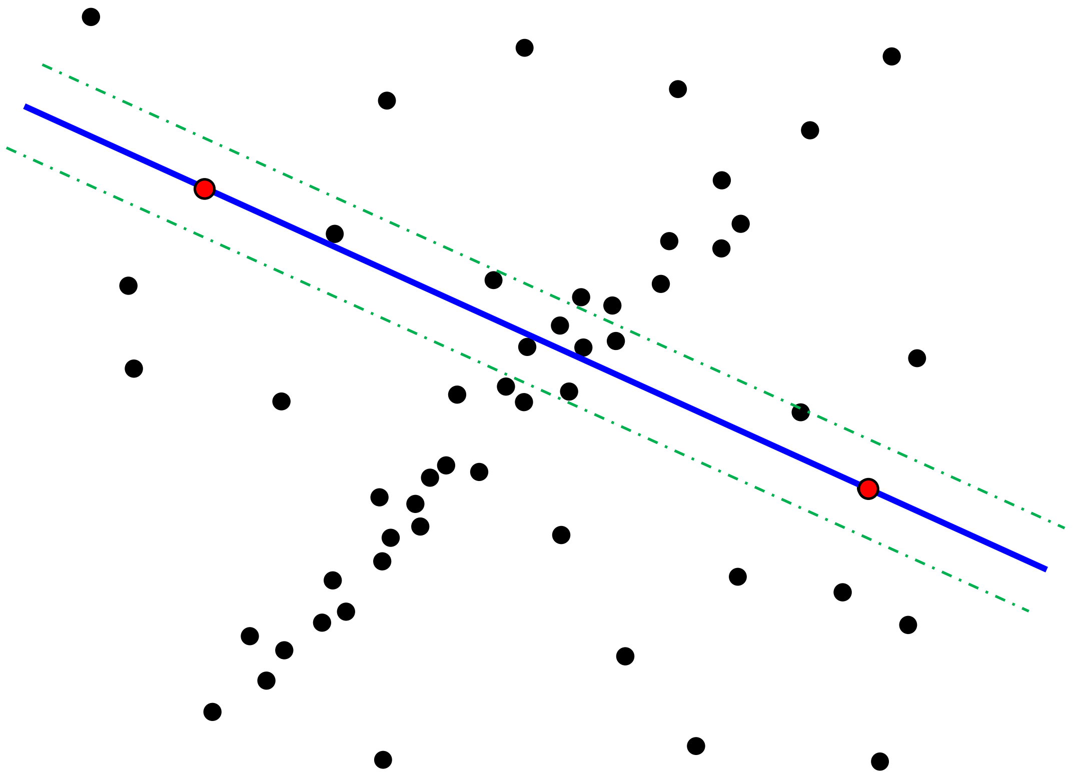
Mug	$N = 166, \varepsilon = 31\%$		
	I	k	time [sec]
PROSAC	51.6	18	0.12
RANSAC	52.3	10,551	0.96



LO-RANSAC

Locally Optimized RANSAC

RANSAC Recap



Select minimal sample at random

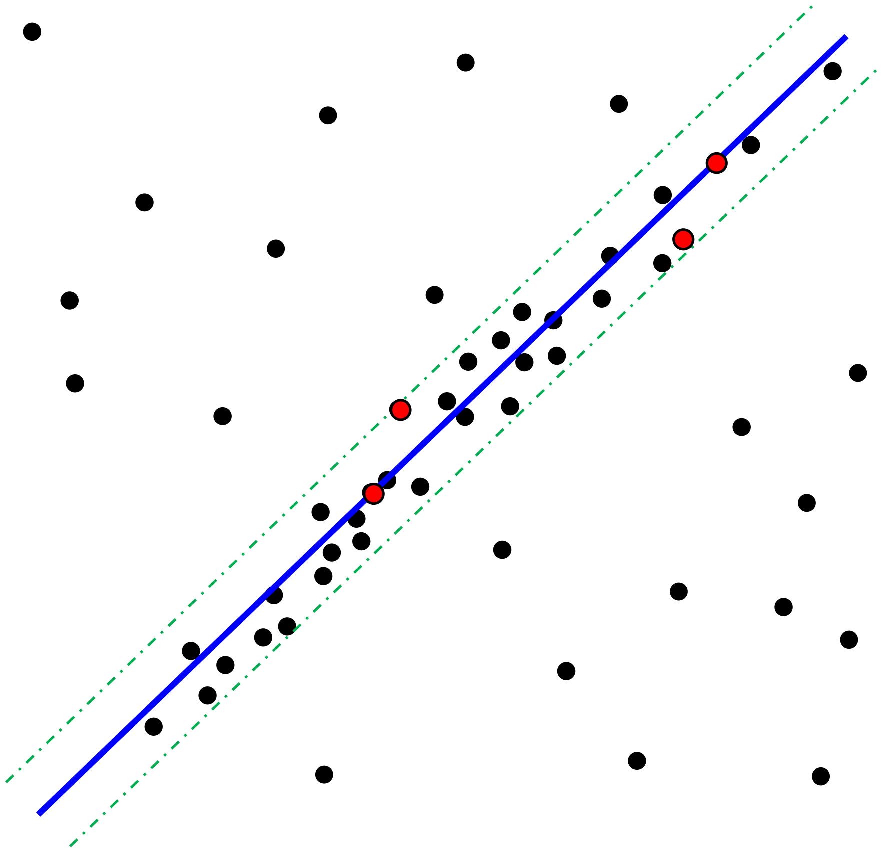
Calculate model parameters that fit the data in the sample

Calculate error function for each data point

Select data that support current hypothesis

Repeat sampling

RANSAC Recap



Repeat sampling

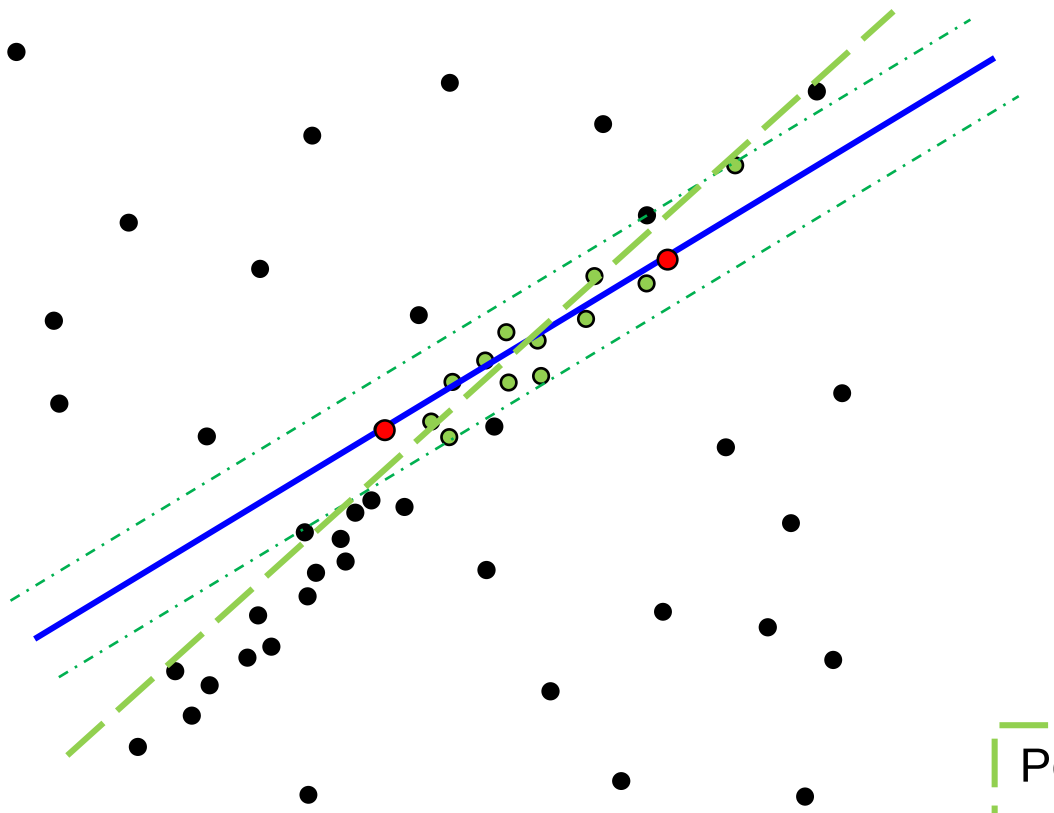
… until you hit an ALL INLIER sample

Get inliers consistent with the model

Make sure that there in no better model in the data

This is also ALL INLIER sample!

All-inlier Sample



Not every all-inlier sample gives a model consistent with all inliers

↓

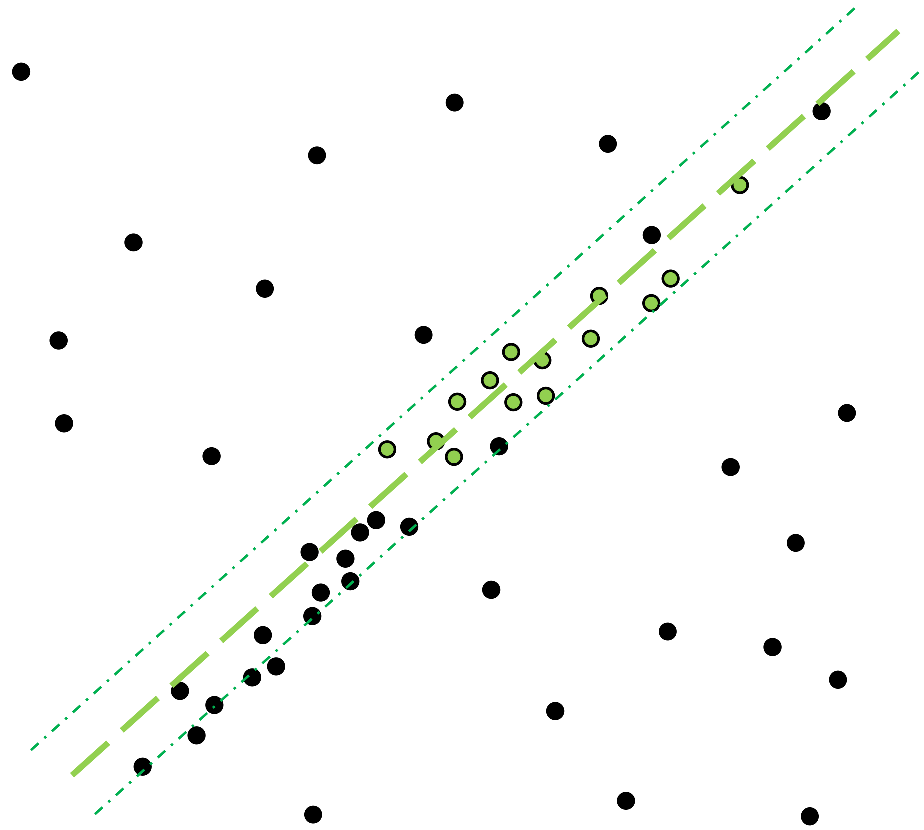
Lower number of inliers is detected

↓

RANSAC needs more samples

Post-processing of RANSAC inliers (least squares) often leads to a reasonable model

Local Optimization (LO)



Idea:
Insert optimization step into the hypothesis-verify loop

Use inliers of the LO step to determine the best model

Execute LO for so-far-the-best samples

$$\sum_{l=1}^{k} P_l = \sum_{l=1}^{k} \frac{1}{l} \leq \int_{1}^{k} \frac{1}{x} dx + 1 = \log k + 1$$

The LO step can be relatively complex, eg:

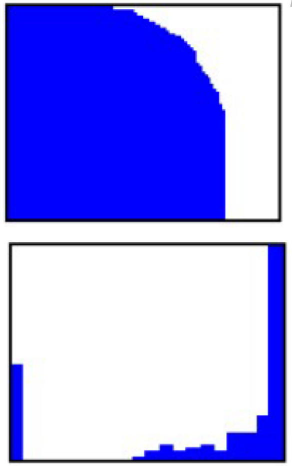
- least squares fit
- iteratively re-weighted least squares
- inlier re-sampling (inner RANSAC)
- graph-cup

Chum, Matas, Kittler: Locally Optimized RANSAC. DAGM 2003

Stability of LO-RANSAC

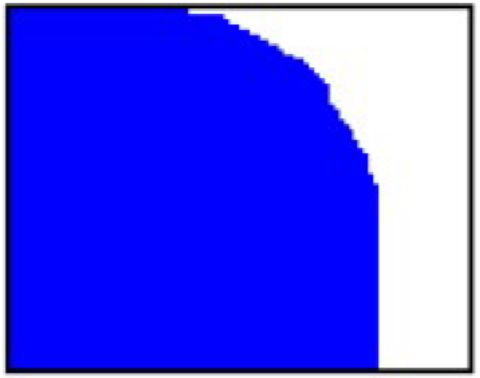
Homography

RANSAC



Statistics over 10 000 executions

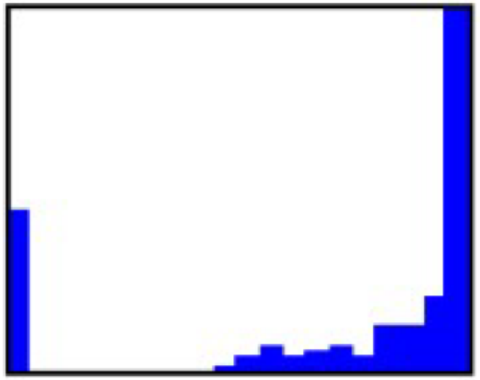
P(inlier)



correspondence id

Ideally, inliers are always detected as inliers, outliers as outliers

\# correspondences



P(inlier)

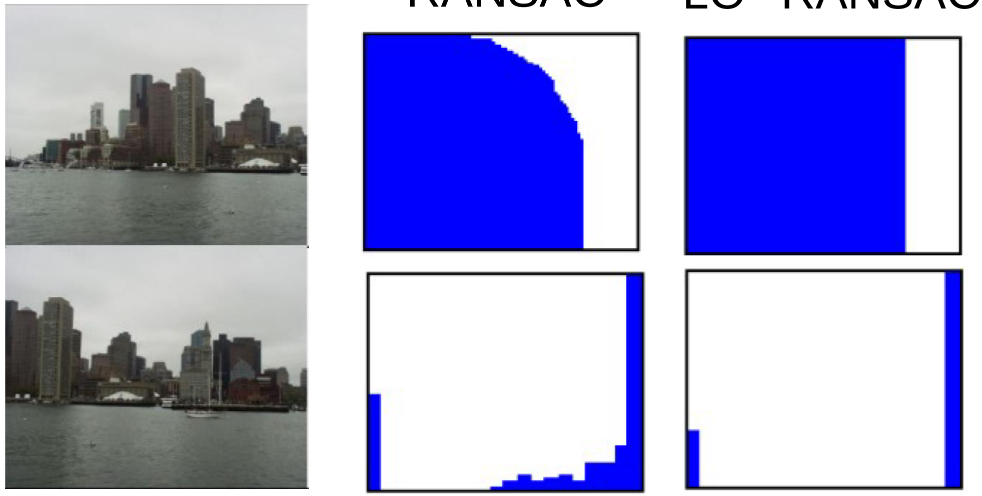
Ideally, inliers have probability one, outliers probability zero

Lebeda, Matas, Chum: Fixing the Locally Optimized RANSAC. BMVC 2012

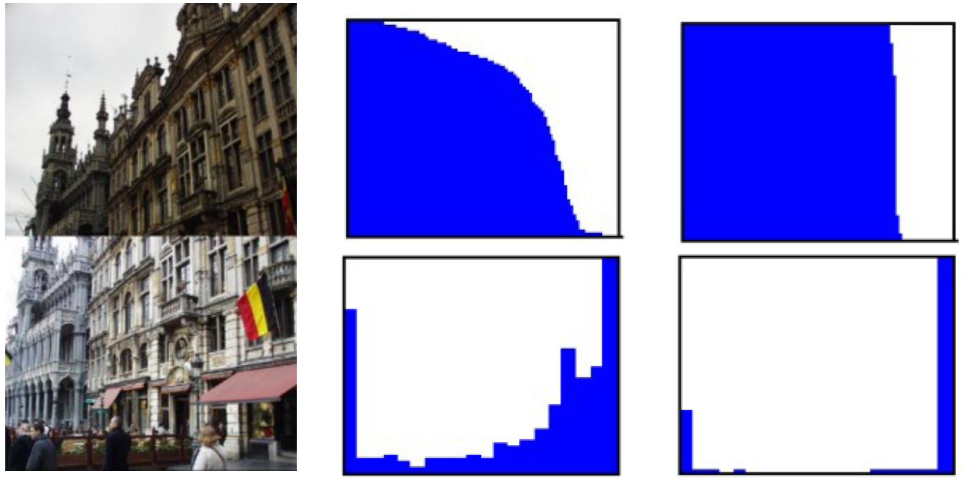
Stability of LO-RANSAC

Homography

RANSAC LO$^+$-RANSAC

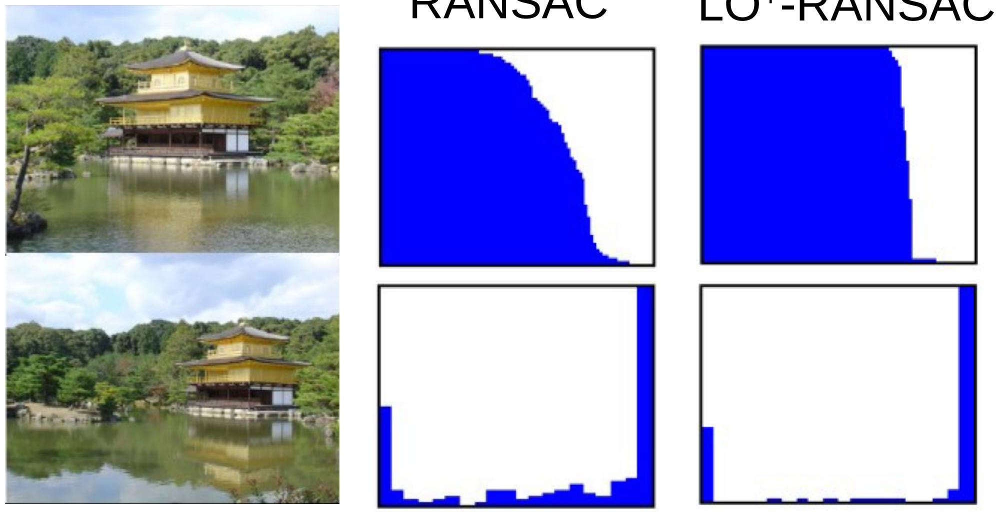


RANSAC LO$^+$-RANSAC

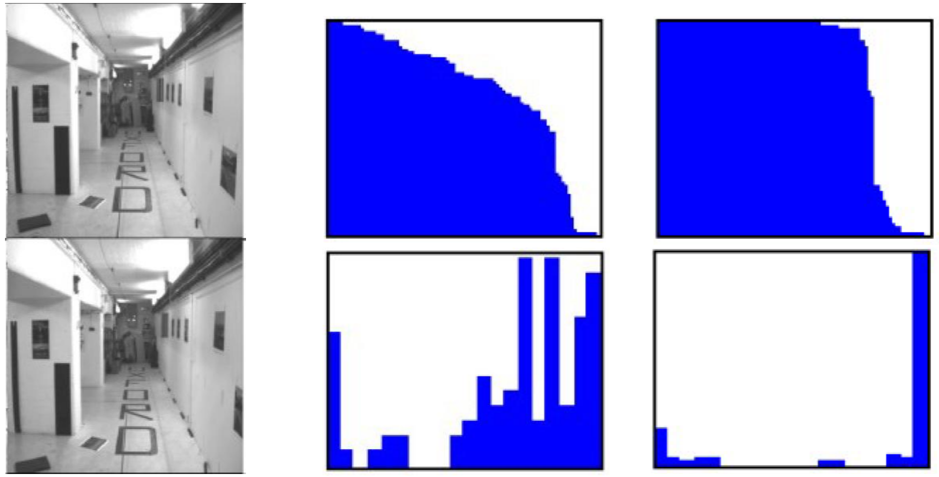


Epipolar geometry

RANSAC LO$^+$-RANSAC



RANSAC LO$^+$-RANSAC



Lebeda, Matas, Chum: Fixing the Locally Optimized RANSAC. BMVC 2012

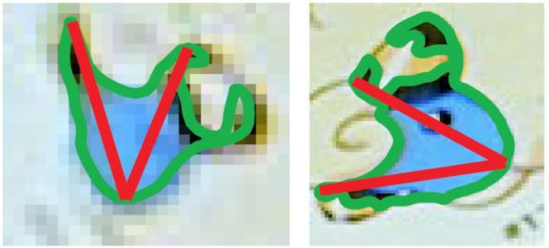
Hierarchical Model Estimation

Sample to estimate an imprecise / approximate model
In LO step, use inliers to the sampled model to estimate the full model

SPEED-UP by reducing the SAMPLE SIZE

EG from 3 Local Affine Frame (LAF) correspondences

Each region provides 3 points
3 LAFs determine EG
Points are close to each other (low precision)



Local Affine Frames

Epipolar geometry through Affine Epipolar Geometry

LO-RANSAC:

1. Approximated by affine EG only 2 LAF correspondences needed
2. In LO step, estimate the full EG from multiple correspondeces

Chum, Matas, Obdržálek: Enhancing RANSAC by Generalized Model Optimization. ACCV 2004
Pritts, Chum, Matas: Approximate Models for Fast and Accurate Epipolar Geometry Estimation. IVCNZ 2013

How Many Samples?

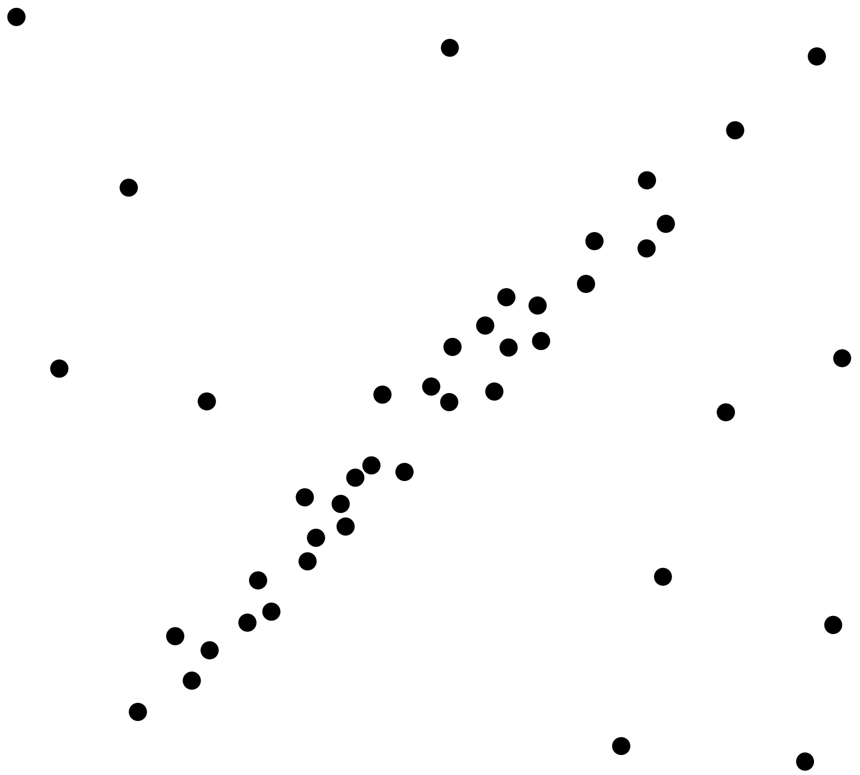
I / N [%]

Size of the sample m

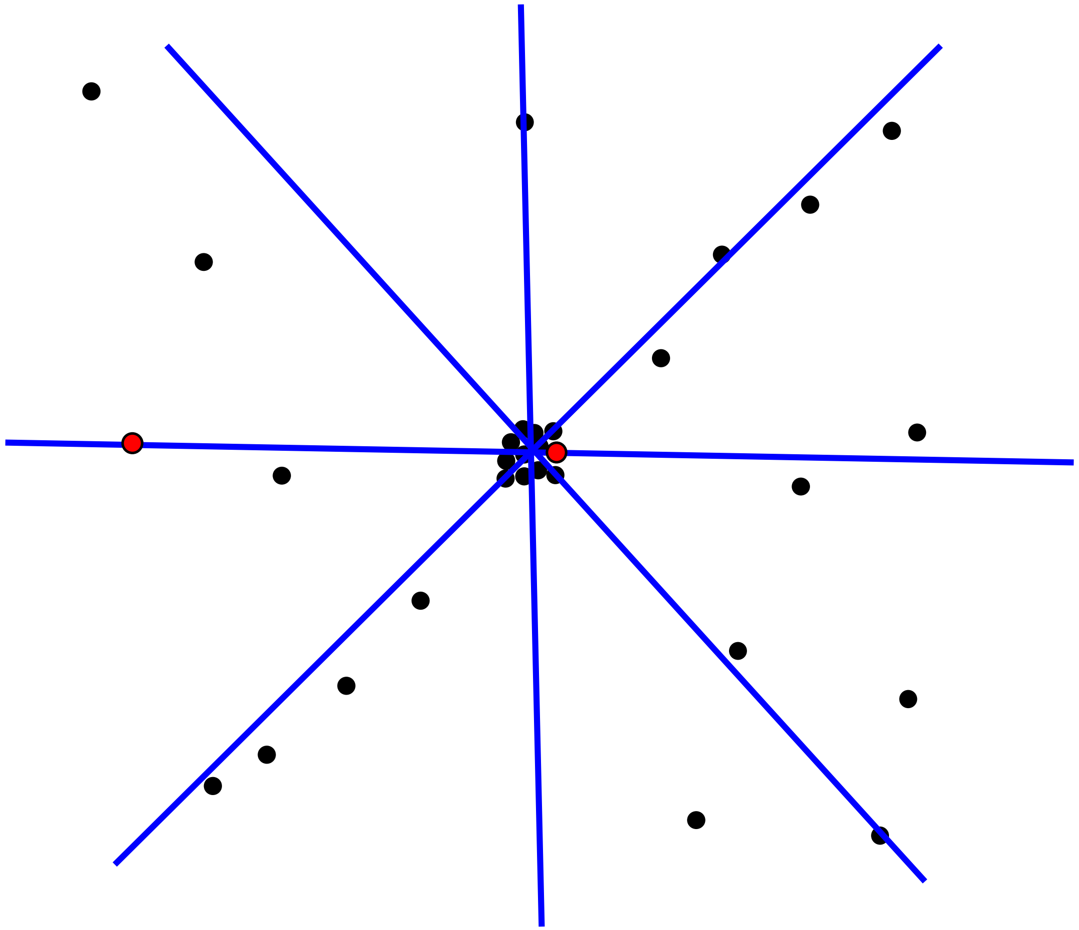
	15%	20%	30%	40%	50%	70%	
2	132	73	32	17	10	4	affine EG 2 LAF + LO
4	5916	1871	368	116	46	11	
7	$1.75 \cdot 10^6$	$2.34 \cdot 10^5$	$1.37 \cdot 10^4$	1827	382	35	EG 7pt algorithm
8	$1.17 \cdot 10^7$	$1.17 \cdot 10^6$	$4.57 \cdot 10^4$	4570	765	50	
12	$2.31 \cdot 10^{10}$	$7.31 \cdot 10^8$	$5.64 \cdot 10^6$	$1.79 \cdot 10^5$	$1.23 \cdot 10^4$	215	
18	$2.08 \cdot 10^{15}$	$1.14 \cdot 10^{13}$	$7.73 \cdot 10^9$	$4.36 \cdot 10^7$	$7.85 \cdot 10^5$	1838	
30	∞	∞	$1.35 \cdot 10^{16}$	$2.60 \cdot 10^{12}$	$3.22 \cdot 10^9$	$1.33 \cdot 10^5$	
40	∞	∞	∞	$2.70 \cdot 10^{16}$	$3.29 \cdot 10^{12}$	$4.71 \cdot 10^6$	

Degenerate Configurations

Data with Outliers



Degenerate Data with Outliers



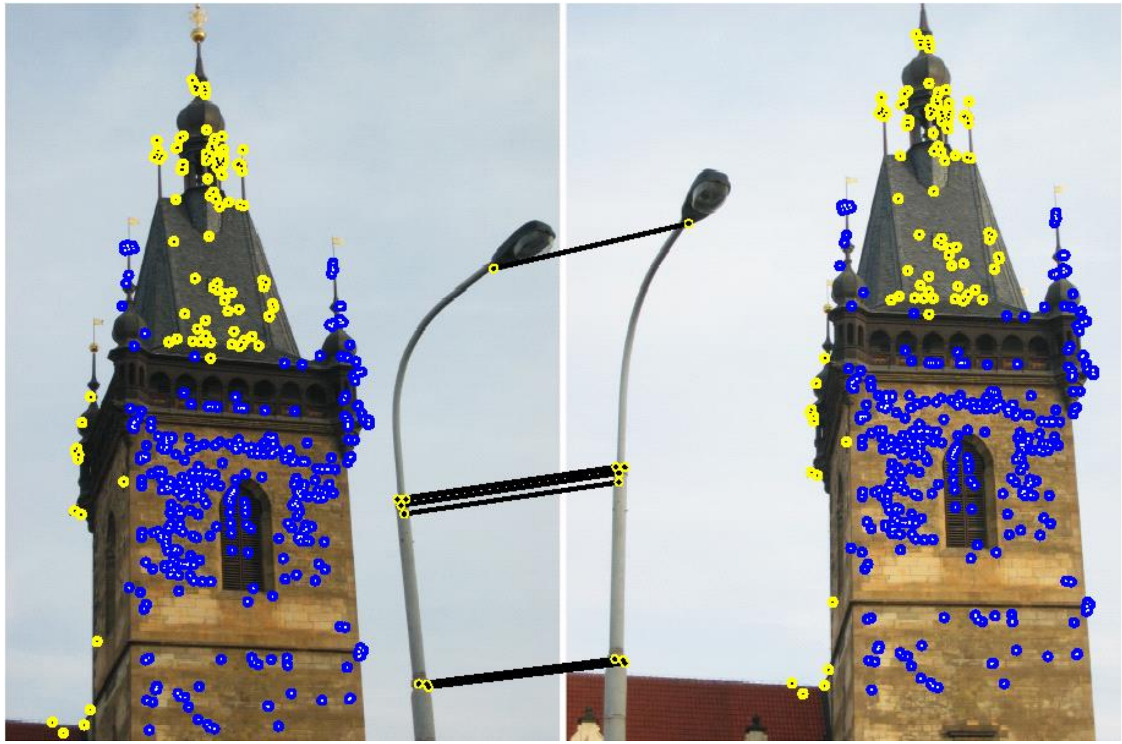
Infinite number of models passes through
a degenerate configuration

Sample from the degenerate configuration and outlier(s)
is a problem

It has higher than random support
(the degenerate whole of configuration)

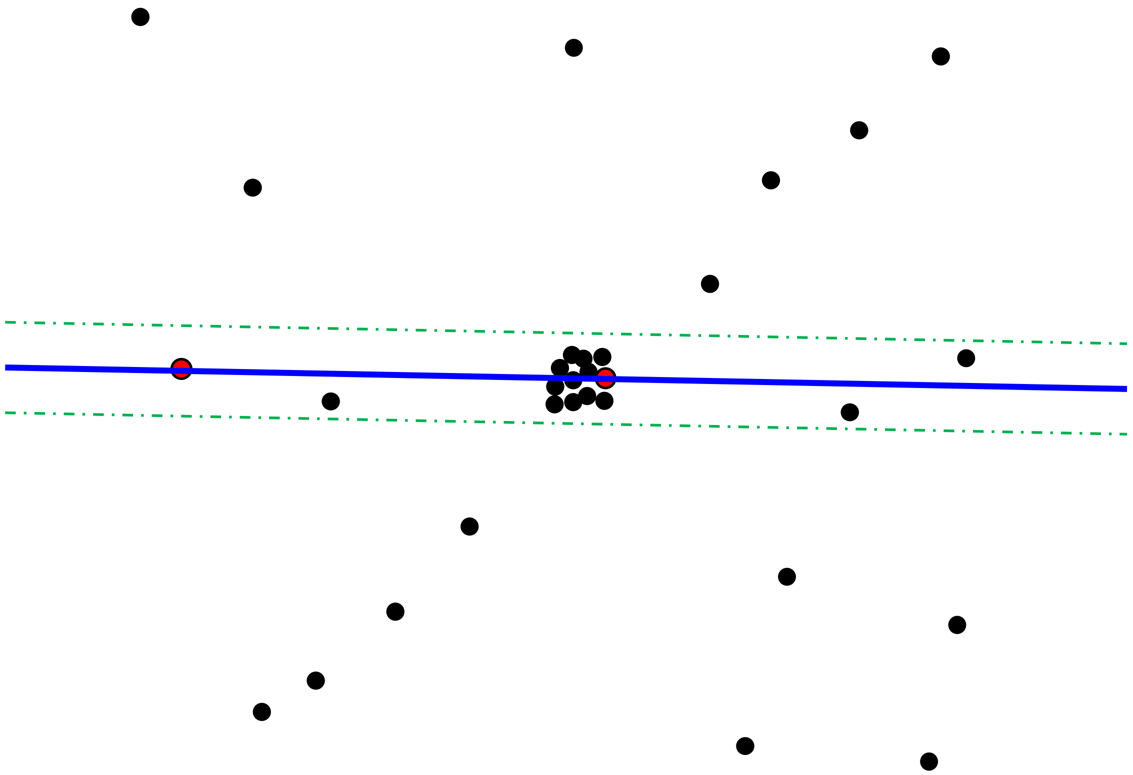
The Dominant Plane Problem

Given many (almost) coplanar points, a few points off the plane, and (possibly) many outliers estimate the epipolar geometry (EG), if possible.



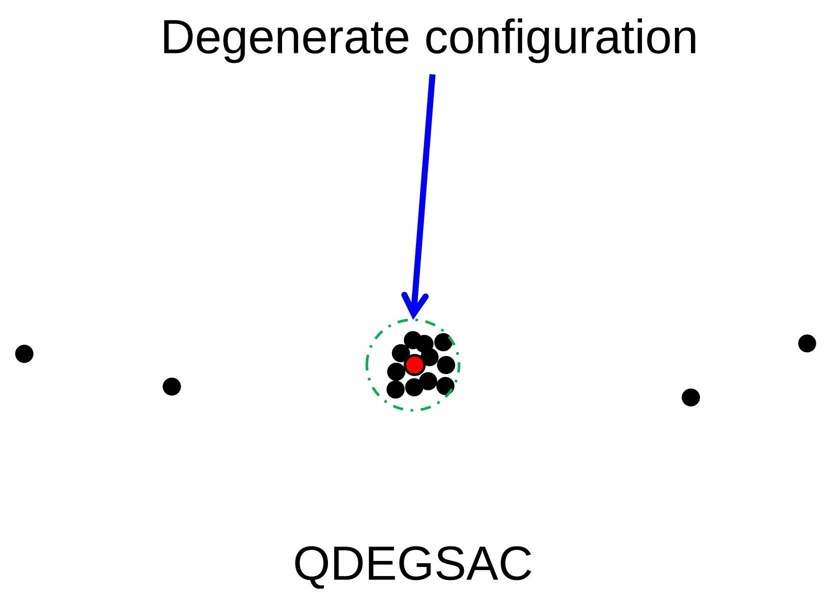
RANSAC run with 95% confidence actually finds the inliers on the lamppost in only 17% of executions

Dealing with Degenerate Configurations



Model with high number of inliers found

Dealing with Degenerate Configurations



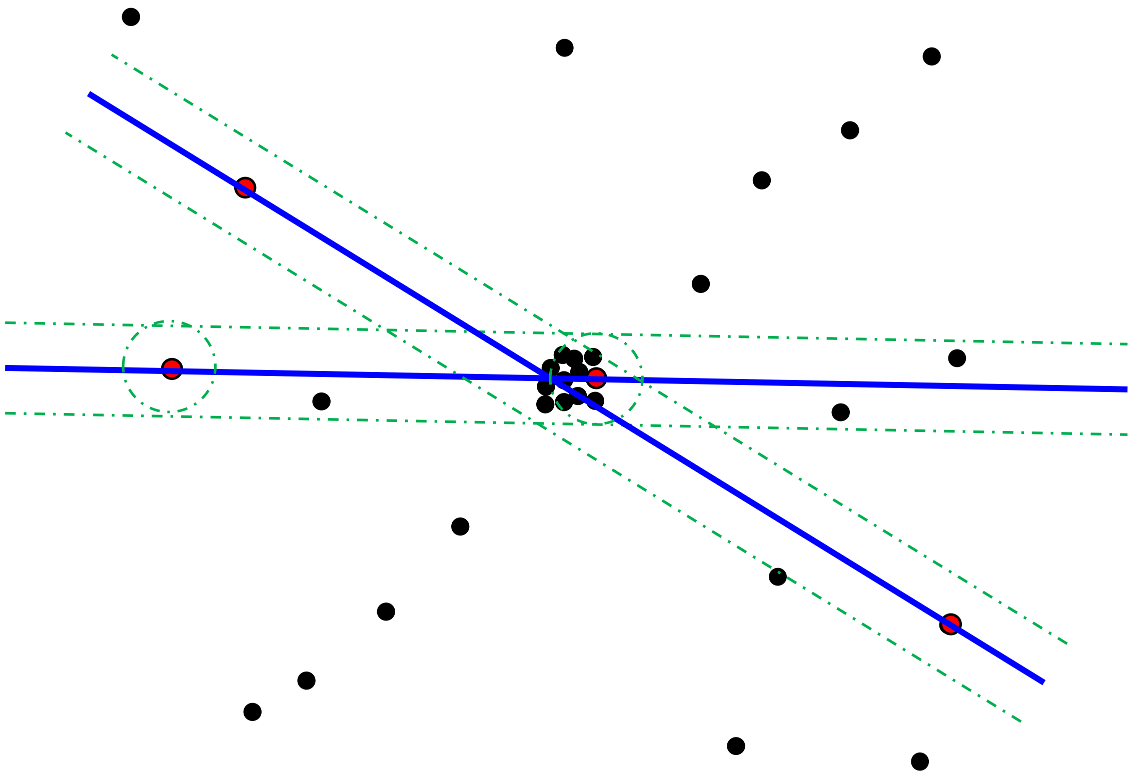
Model with high number of inliers found

Select inliers to the model

Execute RANSAC for model of lower dimensionality
to discover the presence of the degenerate configuration

Frahm, Pollefeys: RANSAC for (Quasi-)Degenereate Data (QDEGSAC). *CVPR 2006*

DEGENSAC



Assumption: Degenerate configuration hit by an all-outlier model - **unlikely**

The sample spans the degenerate configuration

Analyze the sample and the inliers for degenerate configuration – deterministic (no new RANSAC)

Chum, Werner, Matas: Epipolar Geometry Estimation Unaffected by the Dominant Plane. CVPR 2005

Dominant Plane

RANSAC draws minimal samples of 7 correspondences to hypothesize the epipolar geometry

When dominant plane is present, samples with more than 4 coplanar correspondences often appear

7 or 6 coplanar correspondences: the sample is consistent with a family of fundamental matrices. This case is easily be detected.

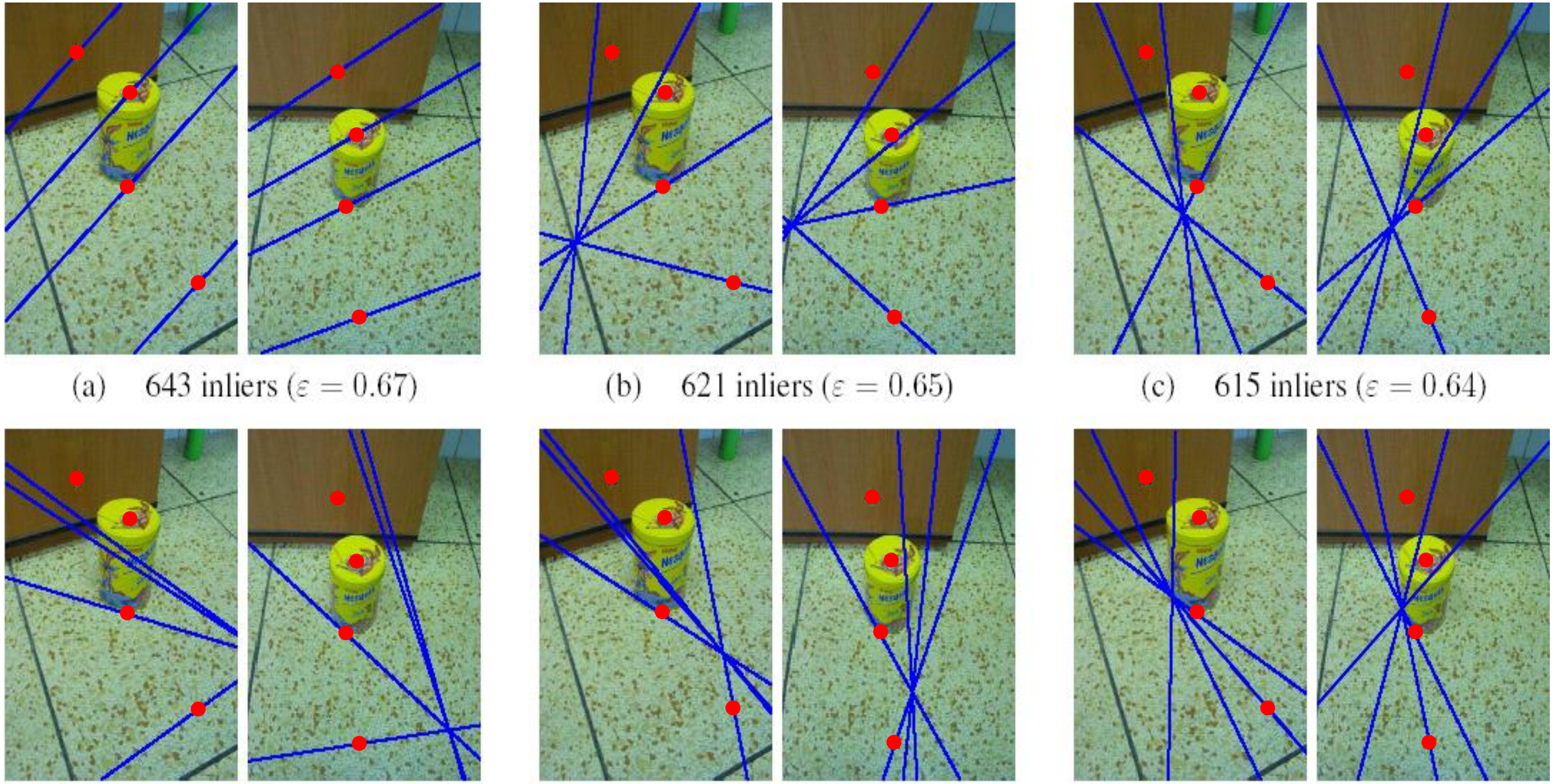
It was shown that the epipolar geometry hypothesised from 5 coplanar points from the dominant plane and 2 off the plane (a so called **H-degenerate** sample) has a large RANSAC support.

If at least one of the off-plane correspondences is an outlier, the EG is incorrect.

Chum, Werner, Matas: Epipolar Geometry Estimation Unaffected by the Dominant Plane. CVPR 2005

Different Solutions by RANSAC

Similar number of inliers, very different geometries



(a) 643 inliers ($\varepsilon = 0.67$) (b) 621 inliers ($\varepsilon = 0.65$) (c) 615 inliers ($\varepsilon = 0.64$)

(d) 614 inliers ($\varepsilon = 0.64$) (e) 616 inliers ($\varepsilon = 0.64$) (f) 615 inliers ($\varepsilon = 0.64$)

• Manually selected correspondences

DEGENSAC

Core of the algorithm:

1. Draw samples of 7 correspondences and estimate 1-3 fundamental matrices by the 7-point algorithm
2. Test samples with the largest support so far for H-degeneracy
3. When **H-degeneracy** was detected, use plane-and-parallax algorithm

Note: the plane-and-parallax needs to draw samples of only 2 correspondences to hypothesize EG, therefore its complexity is negligible compared to RANSAC where 7 correspondences are drawn into a sample

Irani, Anadan: Parallax geometry of pairs of points for 3D scene analysis. ECCV 1997

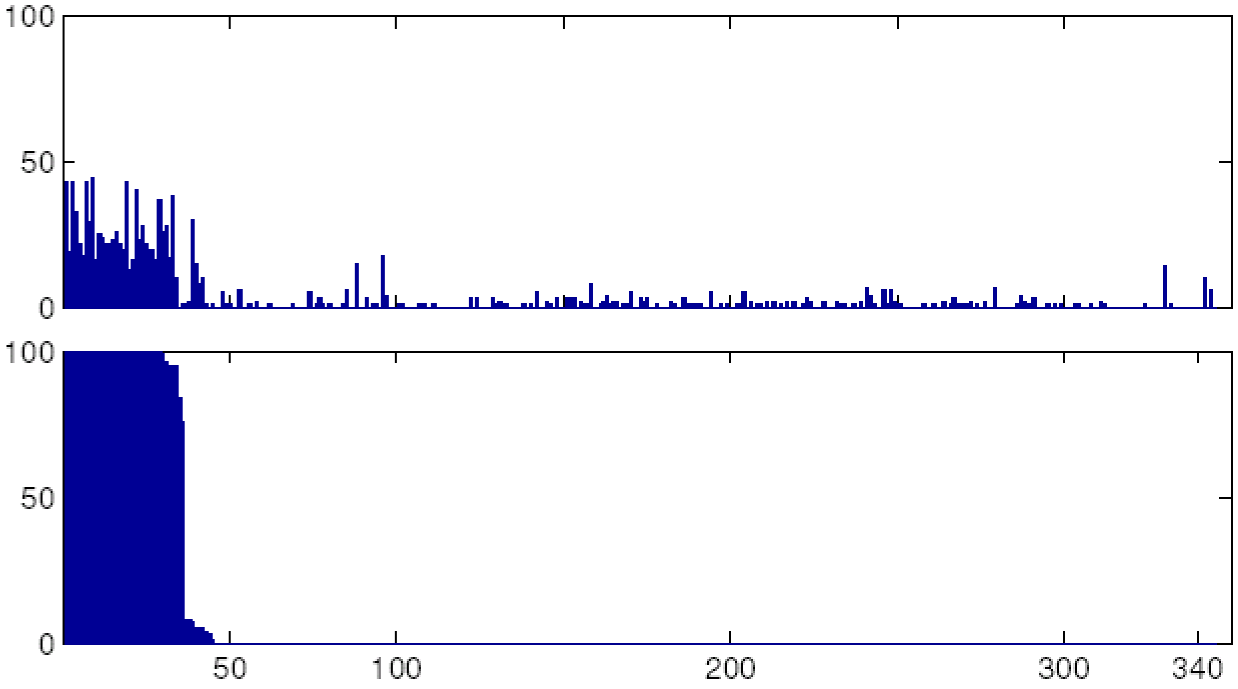
Stability of the Results

How many times will a correspondence be labeled as an inlier, if we run the experiment 100 times?

Off the plane correspondences

RANSAC

DEGENSAC



Correspondence number

Non-minimal Samples

Finding lines in 3D via plane fitting
(the line being a degenerate configuration of the plane)

Assumption: Outliers are uniformly distributed in 3D

Algorithm:

- Draw samples of three points & fit a plane to them
- Calculate the support of the plane
- Check the three lines defined by the points of samples with the largest support so far

Advantage: it is more likely to draw at least 2 inliers out of 3 than 2 out of 2 when fitting a line

Disadvantage: does not work if all points occupy a single plane
(all outlier model - off the line - hits the degenerate configuration)

Non-minimal Samples for Homography

Finding homographies via EG fitting

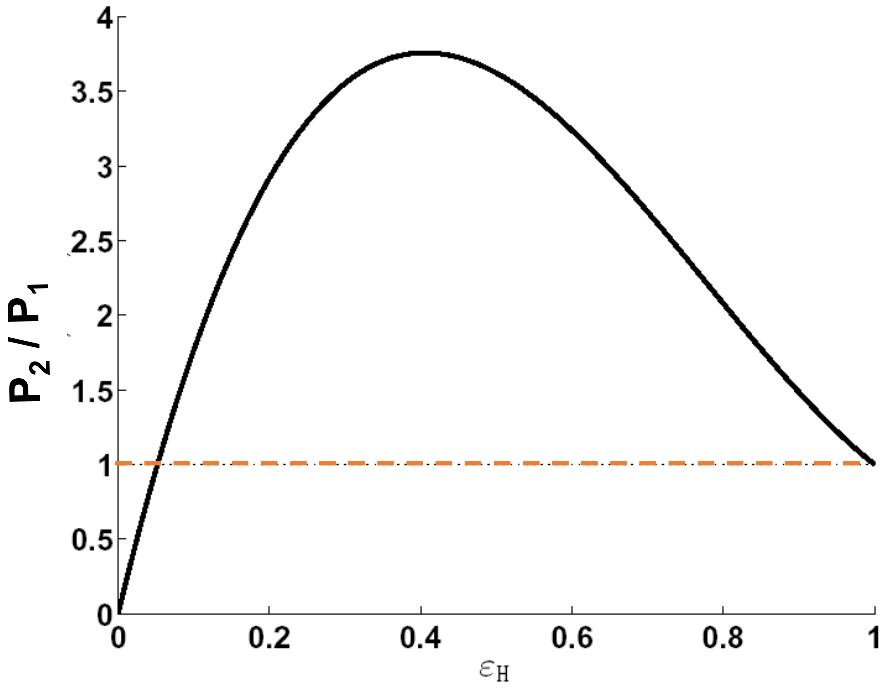
Ratio of the number of samples needed to estimate homography by drawing samples of four and seven correspondences respectively

Probability of drawing 4 inlierers

$$P_1 = \varepsilon_H^4$$

Probability of drawing a 7-tuple with at least 5 inliers

$$P_2 = \sum_{i=5}^{7} \binom{7}{i} \varepsilon_H^i (1 - \varepsilon_H)^{7-i}$$



Fraction of inliers

Sample Checks

Oriented Constraints

Constraints

Constraints on the model parameters that do not reduce the model complexity exist in some problems.

model complexity - the number of data points that define the model ‘uniquely’ (sample size)

e.g. line segment of a fixed length (2 points are still needed)

Possible approaches:

Sample so that only hypotheses satisfying the constraints are generated

- may be time demanding or even intractable

Ignore additional constraints

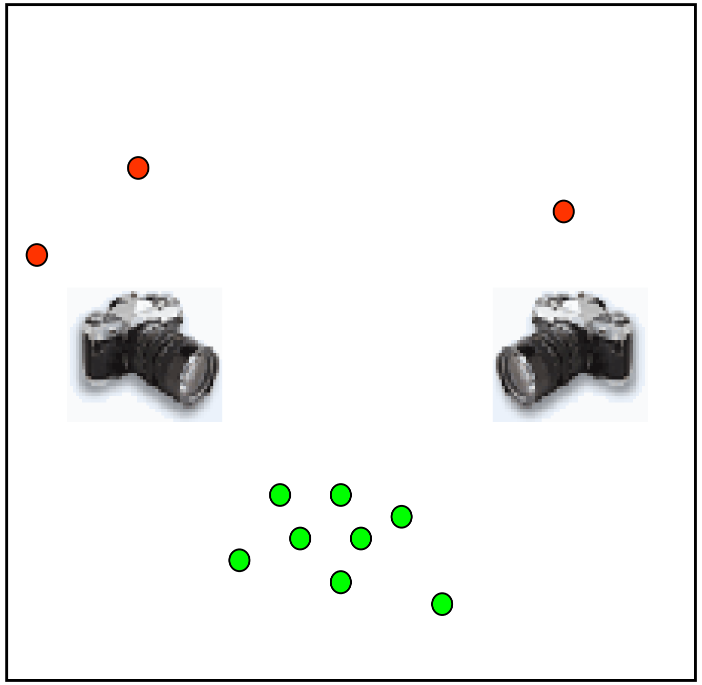
- typically works OK since models that are not allowed do not have sufficient support

Check the constraints before verification step

- can save a lot of time on verification
- e.g. line segment of a fixed length, sampled points are further than the length

Oriented Constraints for Two-View Geometry

Cameras can only observe points in front of the camera – rays are half-lines



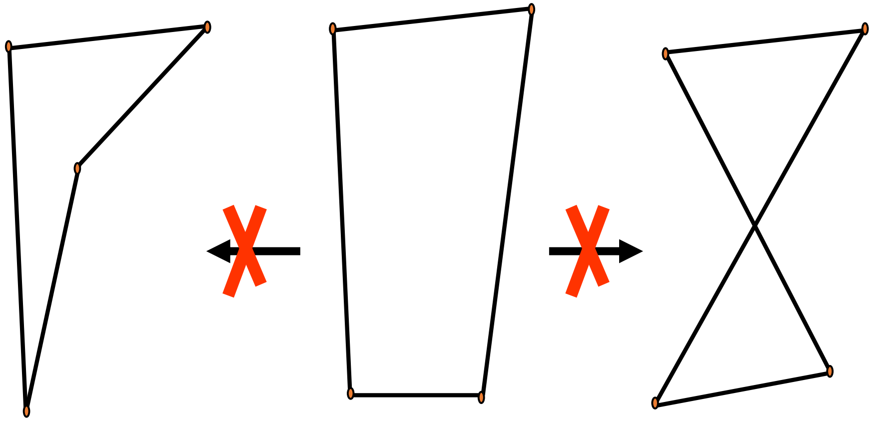
Stolfi: Oriented Projective Geometry: A Framework for Geometric Computations. Academic Press 1991

Laveau, Faugeras: 3-D scene representation as a collection of images. ICPR 1994

Werner, Pajdla: Oriented matching constraints. BMVC 2001

Oriented Constraints

Homography



Need to preserve convexity
Compare signs of two determinants (four times)
Can be performed prior to computing the H matrix

Epipolar Geometry

oriented constraint $\boxed{\mathbf{F}\mathbf{x} \stackrel{+}{\sim} \mathbf{e}' \times \mathbf{x}'}$ (1)

$$\Downarrow$$

$$\mathbf{x}'^{\top}\mathbf{F}\mathbf{x} \stackrel{+}{\sim} \mathbf{x}'^{\top}(\mathbf{e}' \times \mathbf{x}')$$

$$\Downarrow$$

standard constraint $\mathbf{x}'^{\top}\mathbf{F}\mathbf{x} = 0$ (2)

Estimate F using (2) – up to 3 solutions
Test all 7 points in the sample using (1)
Takes 27 – 81 floating point operations
Discards 5% – 45% of models

Chum, Werner, Matas: Epipolar Geometry Estimation via RANSAC Benefits from the Oriented Epipolar Constraint. ICPR 2004

Randomized Verification

Time Complexity of RANSAC

I. Hypothesis

(1) select randomly set $S_k \subset U$, sample size $|S_k| = m$

(2) compute parameters $p_k = f(S_k)$

II. Verification

(3) compute cost $C_k = \sum_{x \in U} \rho(p_k, x)$

(4) if $C^* < C_k$ then $C^* := C_k$, $p^* := p_k$

Time

t_M instantiate the model(s)

$\overline{m}_S \; N$

average # of models per sample

# of data points (correspondences)

Overall time spent in k samples

$$\boxed{t = k(\mathrm{t}_M + \overline{m}_S \; N)}$$

Randomized Verification

I. Hypothesis

Time

(1) select randomly set $S_k \subset U$, sample size $|S_k| = m$

(2) compute parameters $p_k = f(S_k)$

t_M

instantiate the model(s)

II.a Pre-verification

(3) reject weak hypotheses after a few randomly selected verification

II.b Verification $C_k = \sum_{x \in U} \rho(p_k, x)$

(4) compute cost

$\overline{m}_S \, t_V$

average # of models per sample

average # of verifications

(5) if $C^* < C_k$ then $C^* := C_k$, $p^* := p_k$

Overall time spent in k samples

$$\boxed{t = k(\mathrm{t}_M + \overline{m}_S \, t_V)}$$

Pre-verification Errors

False positive

- Incorrect model is not rejected
- Decreases efficiency (increases the average number of verifications)

False negative

- Correct model is rejected with probability α
- Decreases confidence in the solution (good model could have been discarded)

Increase # sample by factor 1 / (1 - α) to guarantee RANSAC confidence in the solution

$$\frac{k}{1-\alpha}(\mathrm{t}_M + \overline{m}_S\, t_V) \quad < \quad k(\mathrm{t}_M + \overline{m}_S\, N)$$

Efficient randomized verification strategy

RANSAC with the $T_{d,d}$ Test

Verify $d << N$ data points, reject the model if not all d data points are consistent with the model

For most problems and inlier ratios, the optimal value is $d = 1$, that is $T_{1,1}$

d	samples	models	tests	inliers
0	1866	4569	6821218	600
1	4717	11536	16311	600
2	11849	28962	33841	600

Synthetic experiment on 1500 correspondences, 40% inliers, 30 repetitions

Chum, Matas: Randomized RANSAC with T_d,d Test. BMVC 2002

Bail out Test

After each verification, check the current number of inliers I_n against the expected number of inliers of a good model

Exact probabilities intractable

Approximate by a Normal distribution

$$I_n \sim \mathrm{N}(\mu, \sigma^2) = \mathrm{N}\left(n\varepsilon_i, n\varepsilon_i(1-\varepsilon_i)\left(\frac{N-n}{N-1}\right)\right)$$

Test with a threshold $I_n^{\min} = \lfloor n\varepsilon_i - z_c\sigma \rfloor$, where z_c is a quantile of the Normal distribution

Capel: An Effective Bail-Out Test for RANSAC Consensus Scoring. BMVC 2005

WaldSAC: Optimal Randomized Verification

Minimize # observations to guarantee bounds on FP and FN

		Randomized verification:
Sequential decision making	Reject	Discard the model
	Accept	Never taken – always verify all
	Take another observation	Verify next data point

A. Wald: Sequential Analysis. Dover, 1947

Optimal strategy in sequential decision making is based on sequential probability ratio test (SPRT)

Single parameter A:

probability of rejecting a good model $\alpha = 1/A$

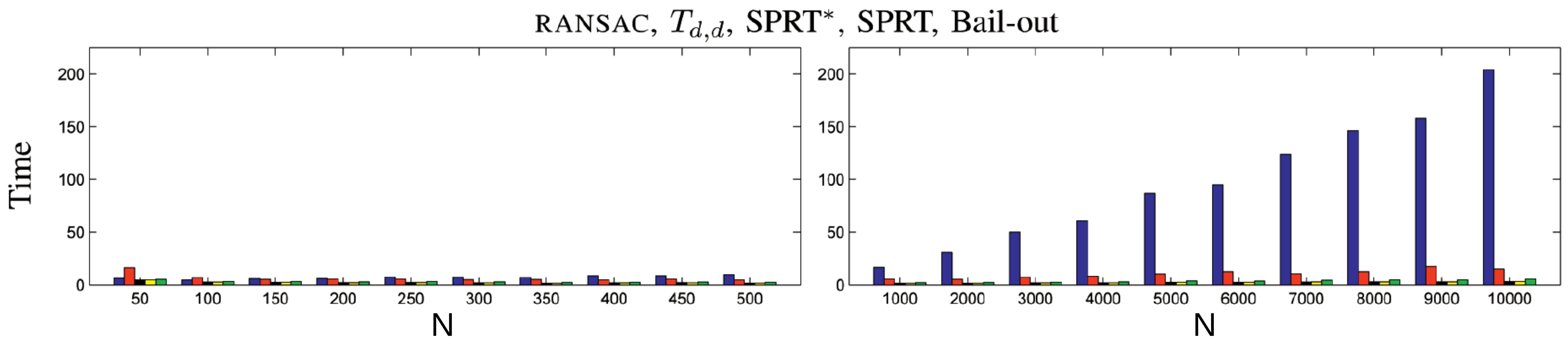
average number of measurements before rejection $C \log(A)$

$$\boxed{t(A) = \frac{k}{(1 - 1/A)}(t_M + \overline{m}_S C \log A)}$$

Chum, Matas: Optimal Randomized RANSAC. TPAMI 2008

Experimental Comparison

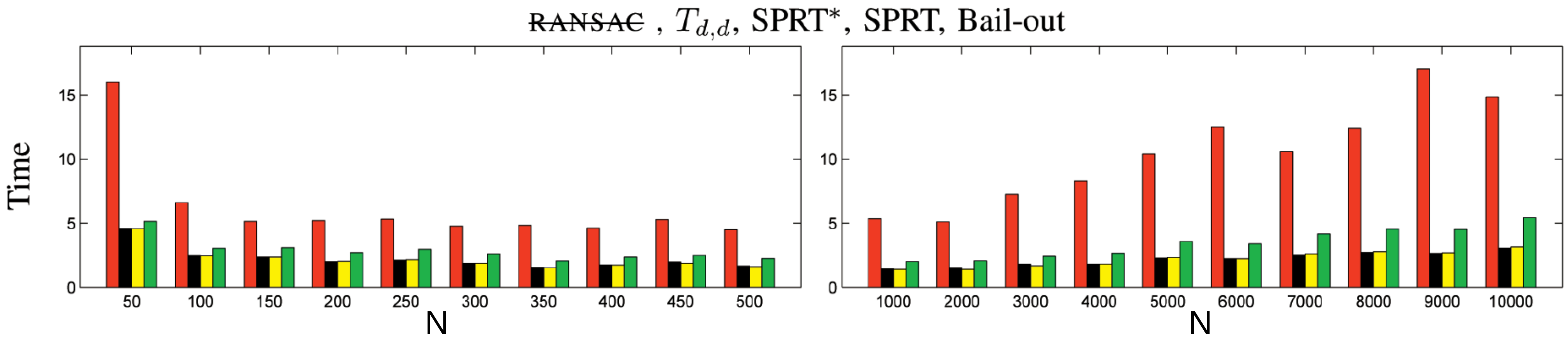
Synthetic data, 30% inliers, varying N, epipolar geometry estimation



SPRT* optimal setting, fraction of inliers known beforehand
SPRT estimated fraction of inliers updated on the fly

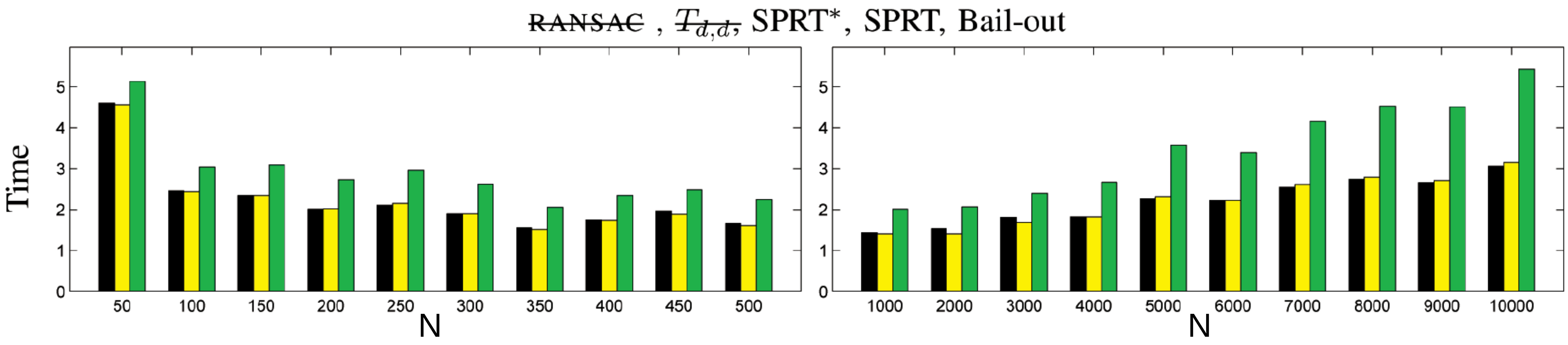
Experimental Comparison

Synthetic data, 30% inliers, varying N, epipolar geometry estimation



Experimental Comparison

Synthetic data, 30% inliers, varying N, epipolar geometry estimation



Latent RANSAC

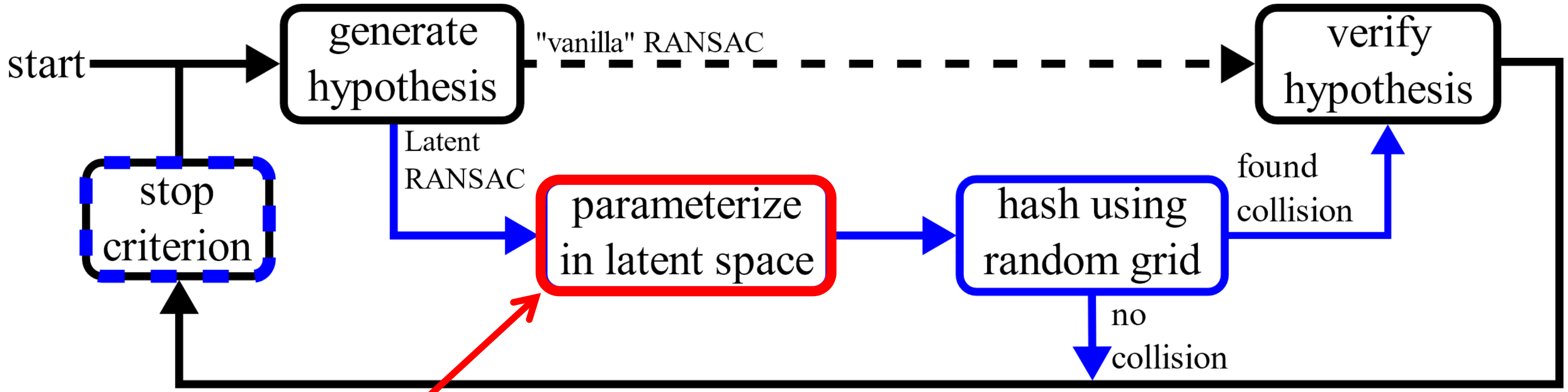


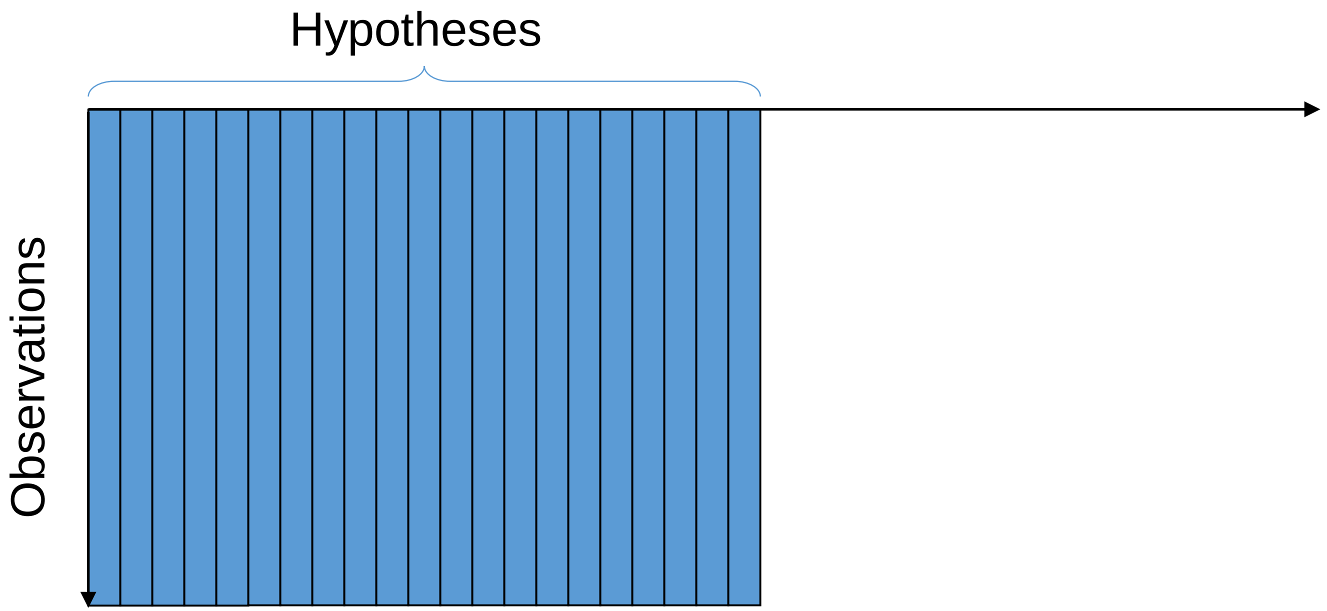
Image from Korman, Litman CVPR 2018

Problem: how to meaningfully parametrize high-dimensional models such as fundamental matrix
even homography is problematic – image points can be sent to infinity (or beyond)

Korman, Litman: Latent RANSAC. CVPR 2018
Xu, Oja, Kultanen: A new curve detection method: Randomized Hough transform (RHT). Pattern Recognition Letters 1990

Fixed Time Budget

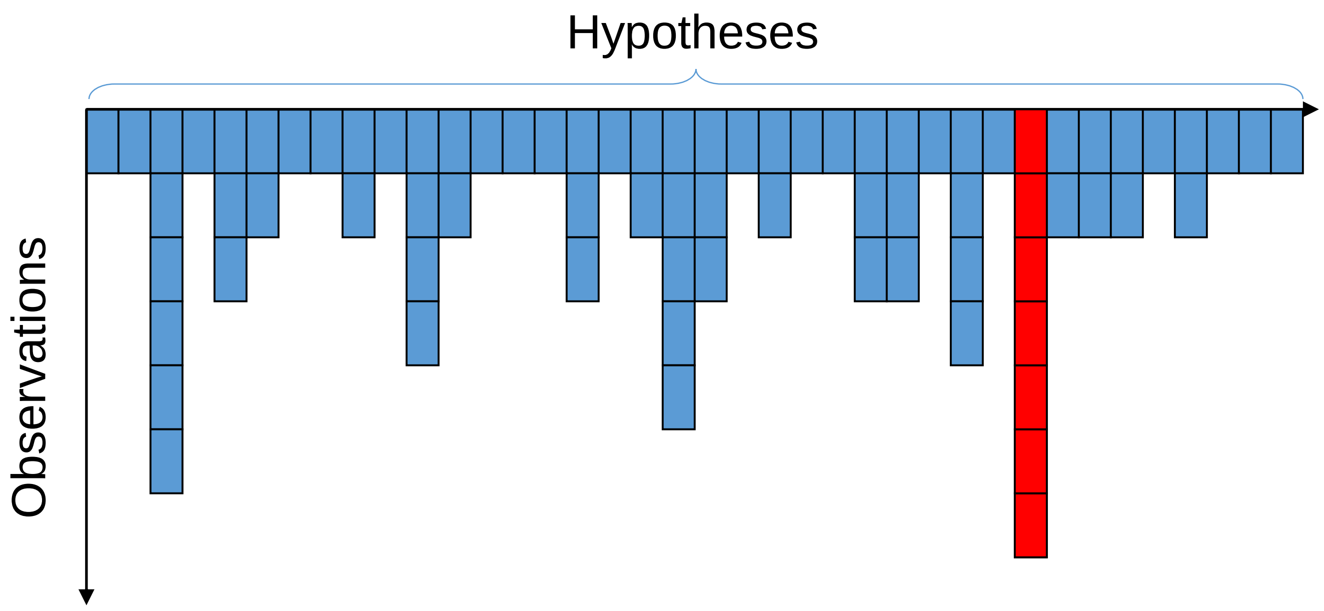
Real time system
Task: find the best model within given fixed time (not a confidence in the solution)
Solution: fixed number of hypotheses and fixed number of verifications



Animation courtesy of David Nistér

Idea: Better hypotheses are likely to be also better on a subset of data

Preemptive RANSAC



Animation courtesy of David Nistér

Nister: Preemptive RANSAC for Live Structure and Motion Estimation. ICCV 2003

Conclusions

Non-uniform sampling can speed-up RANSAC significantly
- Locality
- Quality

Local Optimization stabilizes the results and reduces the number of samples
- Approximate models bring significant speed-up

Degenerate Configurations
- Avoid wrong models with high number of inliers
- Efficiently detect models as degenerate configurations of higher dimensional models

Checking samples of additional constraints can avoid the verification
- Oriented constraints in two-view problems

Randomized verification
- Speed-up for problems with large number of correspondences

Most of the algorithms implemented in USAC

Raguram et al.: USAC: A Universal Framework for Random Sample Consensus. TPAMI 2013

Thanks!

References

Barath, Noskova, Ivashechkin, Matas: MAGSAC++, a fast, reliable and accurate robust estimator. CVPR 2020
Capel: An Effective Bail-Out Test for RANSAC Consensus Scoring. BMVC 2005
Chum, Matas: Optimal Randomized RANSAC. TPAMI 2008
Chum, Matas: Matching with PROSAC - Progressive Sampling Consensus. CVPR 2005
Chum, Matas, Obdrzalek: Enhancing RANSAC by Generalized Model Optimization, ACCV 2004
Chum, Matas, Kittler: Locally Optimized RANSAC. DAGM 2003
Chum, Matas: Randomized RANSAC with T_d,d Test. BMVC 2002
Chum, Werner, Matas: Epipolar Geometry Estimation Unaffected by the Dominant Plane. CVPR 2005
Chum, Werner, Matas: Epipolar Geometry Estimation via RANSAC Benefits from the Oriented Epipolar Constraint. ICPR 2004
Frahm, Pollefeys: RANSAC for (Quasi-)Degenereate Data (QDEGSAC). *CVPR 2006*
Irani, Anadan: Parallax geometry of pairs of points for 3D scene analysis. ECCV 1997
Korman, Litman: Latent RANSAC. CVPR 2018
Laveau, Faugeras: 3-D scene representation as a collection of images. ICPR 1994
Lebeda, Matas, Chum: Fixing the Locally Optimized RANSAC. BMVC 2012
P. M. Lee: Sequential Probability Ratio Test. Univ. of York, 2007

References

Myatt, Torr, Nasuto, Bishop, Craddock: NAPSAC: High Noise, High Dimensional Robust Estimation - It's in the Bag. BMVC 2002
Ni, Jin, Dellaert: GroupSAC: Efficient consensus in the presence of groupings. ICCV 2009
Nister: Preemptive RANSAC for Live Structure and Motion Estimation. ICCV 2003
Pritts, Chum, Matas: Approximate Models for Fast and Accurate Epipolar Geometry Estimation. IVCNZ 2013
Raguram et al.: USAC: A Universal Framework for Random Sample Consensus. TPAMI 2013
Schmid, Mohr: Local Greyvalue Invariants for Image Retrieval. PAMI 1997
Stolfi: Oriented Projective Geometry: A Framework for Geometric Computations. Academic Press 1991
A. Wald: Sequential Analysis. Dover, 1947
Werner, Pajdla: Oriented matching constraints. BMVC 2001
Xu, Oja, Kultanen: A new curve detection method: Randomized Hough transform (RHT). Pattern Recognition Letters 1990