

RANSAC in 2011

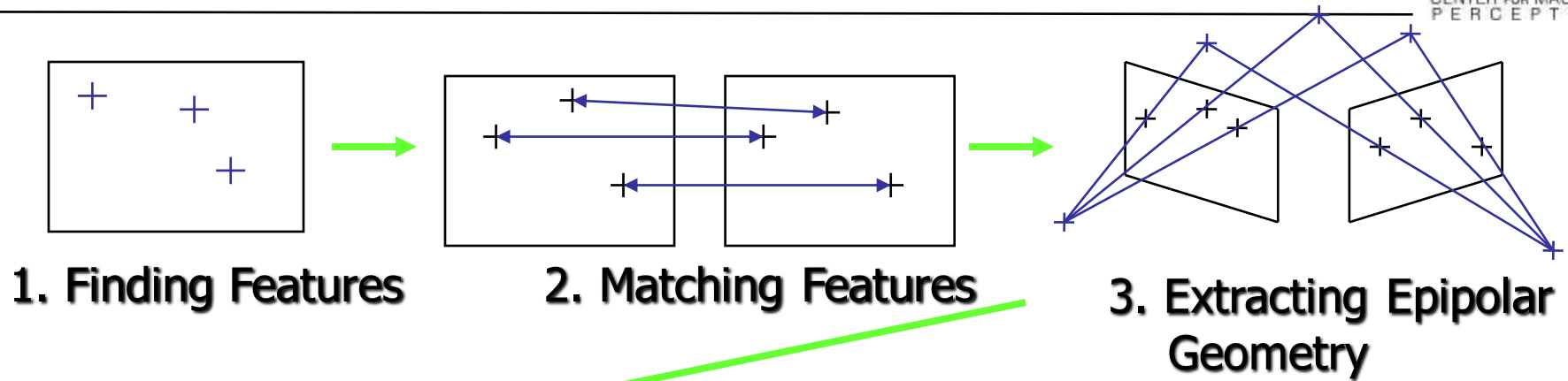
(30 years after)

Jiří Matas

Center for Machine Perception,
Department of Cybernetics,
Faculty of Electrical Engineering
Czech Technical University Prague

unless stated otherwise, slide credit goes to **Ondra Chum**

Robust Model Estimation, Inlier – Outlier Separation



INLIERS
good matches



OUTLIERS
mismatches

**You all know what
RANSAC is, don't you?**

The Acronym "RANSAC"

RANSAC

http://www.ransac.org/

Release Notes http://video.google.c... Plug-ins Extensions Support Mozilla Community ▾

RANSAC *making the world more secure*
NUCLEAR SECURITY ADVISORY COUNCIL

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WELCOME TO RANSAC

RANSAC is an independent, non-governmental research organization dedicated to increasing the security of weapons of mass destruction (WMD) and reducing proliferation risks. RANSAC's priority is supporting the cooperative threat reduction agenda between the U.S., Russia, and the other former Soviet states and promoting its expansion to address global proliferation dangers.

WHAT'S NEW

- > **5/12/2006** [Seizing the Moment: Using the US-India Nuclear Deal to Improve Fissile Material Security](#), Kenneth Luongo and Isabelle Williams
- > **5/12/2006** [Advancing International Cooperation on Bio-Initiatives in Russia and the CIS](#), Derek Averre, Kenneth Luongo, Maurizio Martellini

RANSAC
Profiled in
MacArthur Foundation's
25th Annual Report
[Read now!](#)

Featured in
National Journal's
Guide To The Web!

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

$f(S) : S \rightarrow p$ 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 $P\{\text{better solution exists}\} < \eta$ (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 parameter $p_k = f(S_k)$

II. Verification

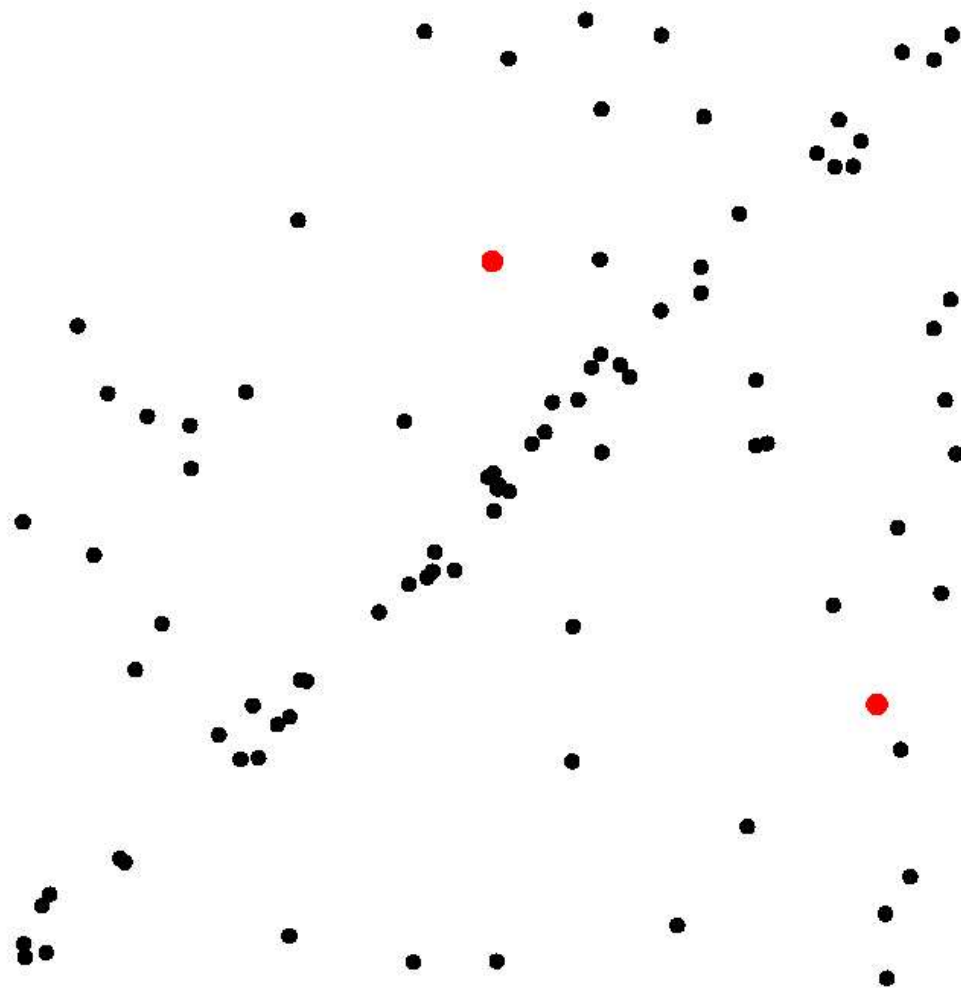
(3) compute cost $C_k = \sum_{x \in U} \rho(p_k, x)$

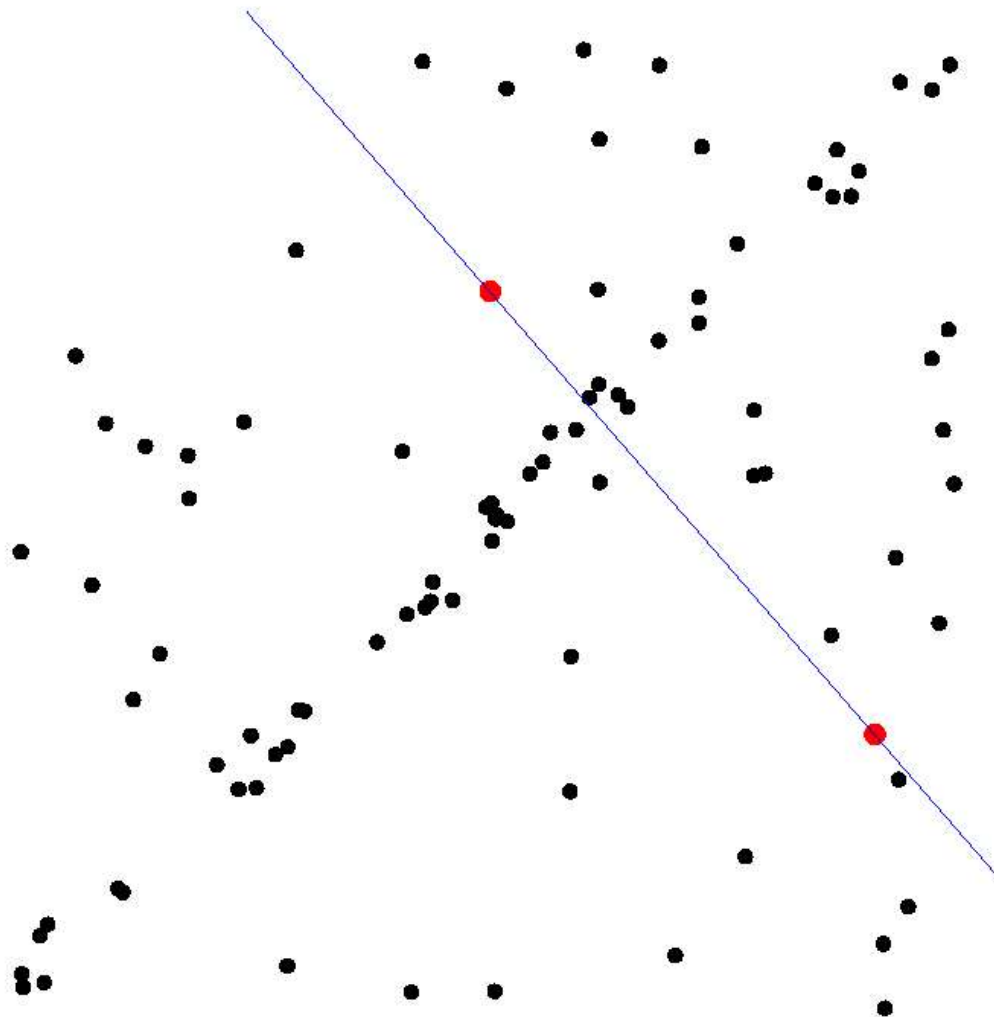
(4) if $C^* < C_k$ then $C^* := C_k$, $p^* := p_k$

end

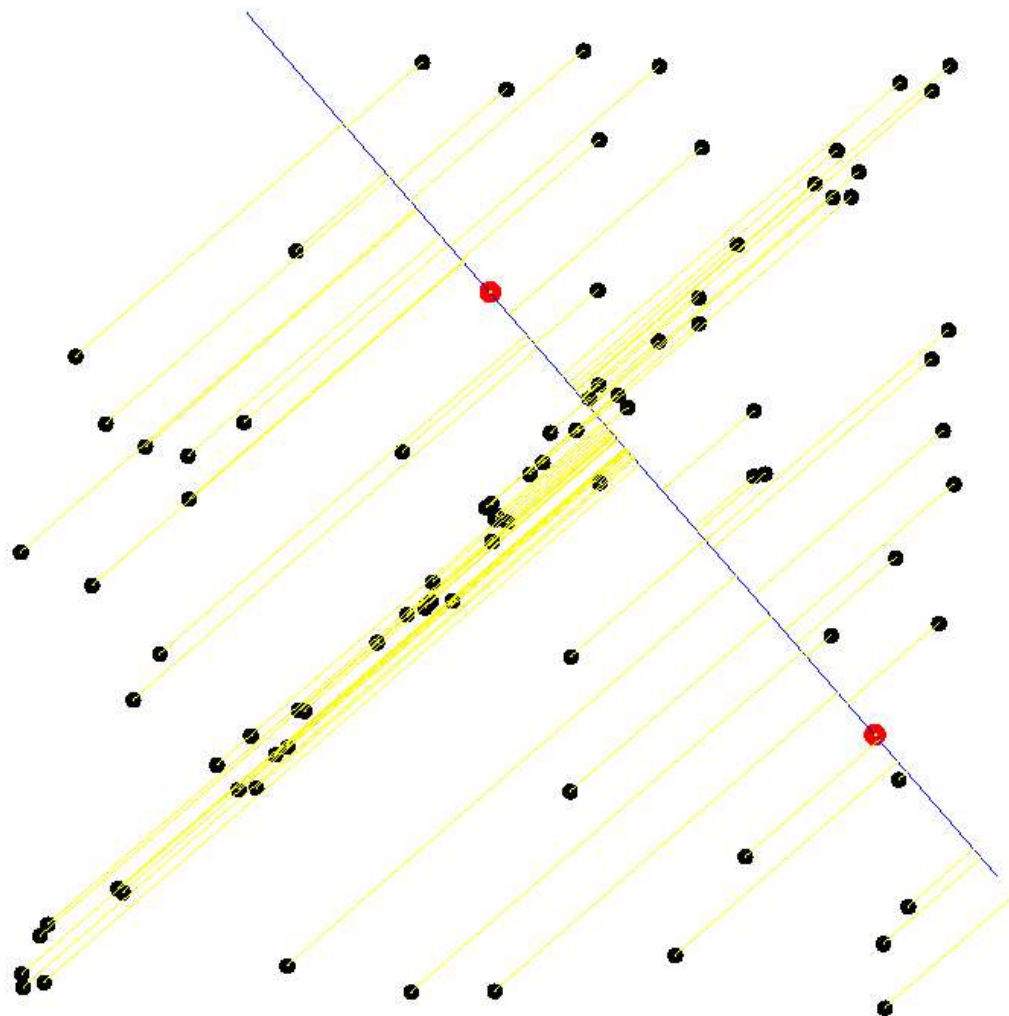


- Select sample of m points at random

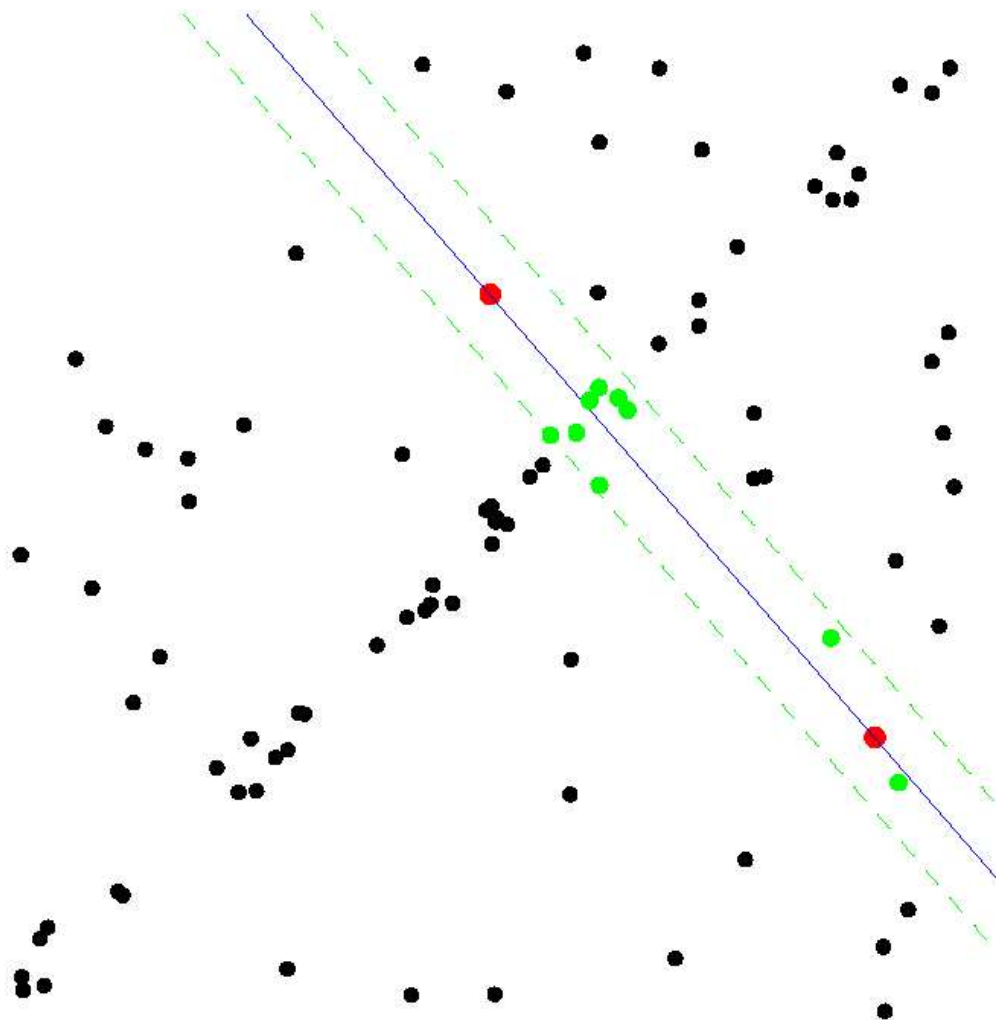




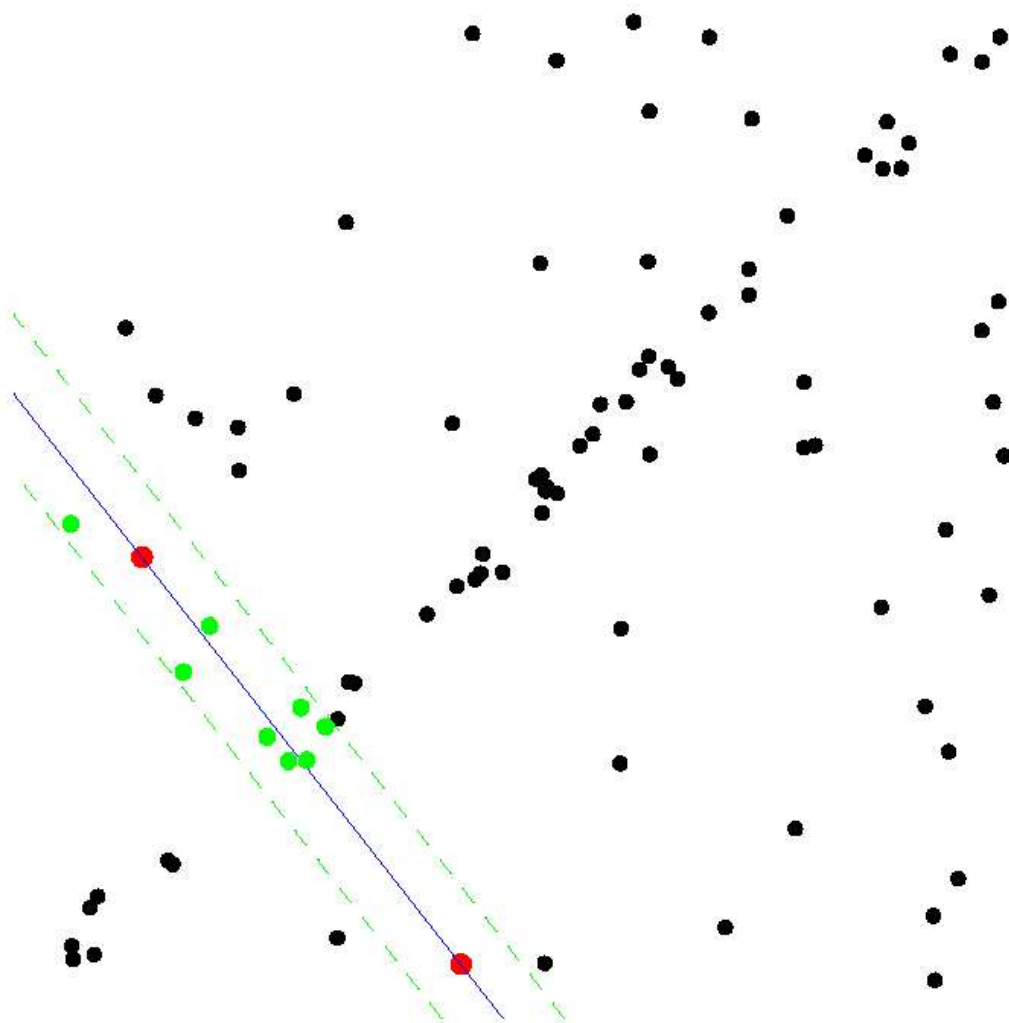
- Select sample of m points at random
- Calculate model parameters that fit the data in the sample



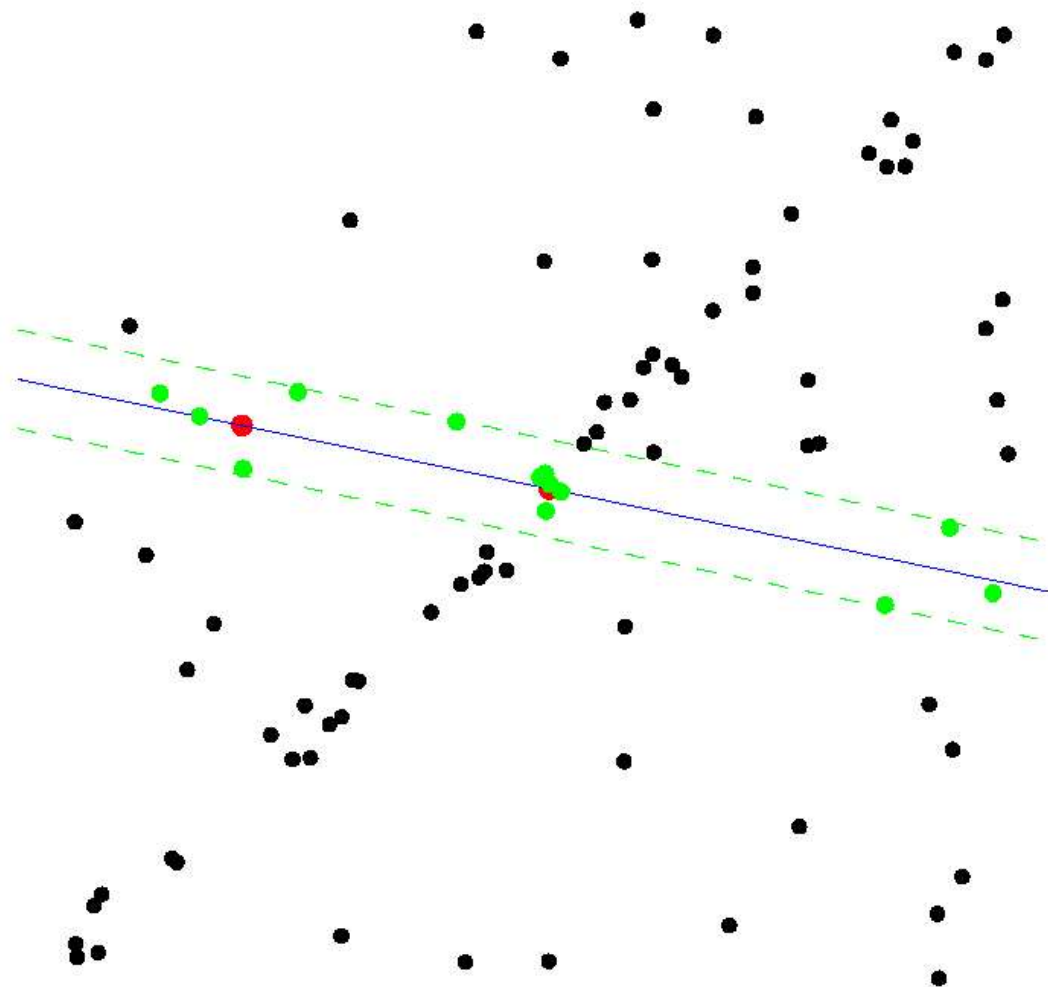
- Select sample of m points at random
- Calculate model parameters that fit the data in the sample
- **Calculate error function for each data point**



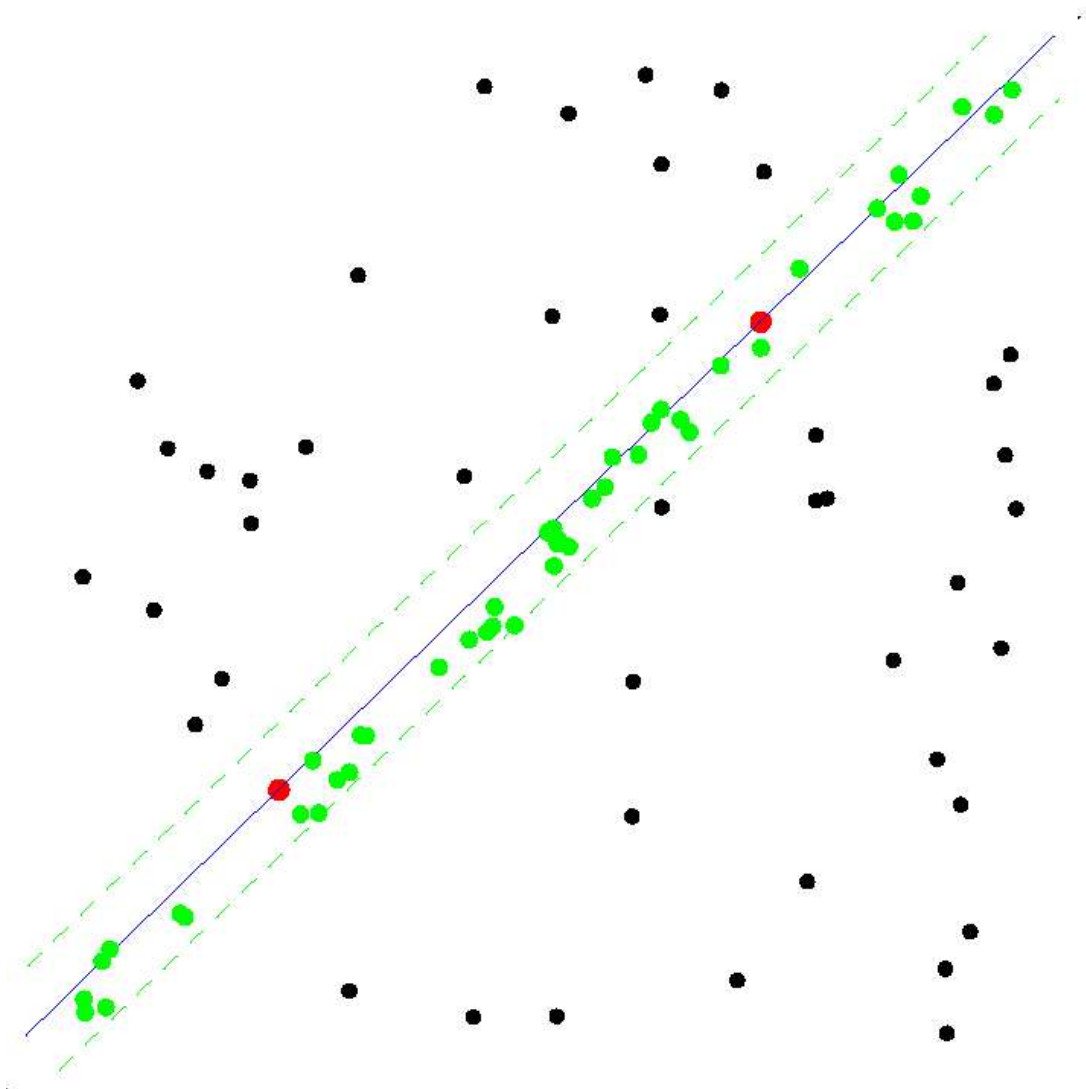
- Select sample of m points at random
- Calculate model parameters that fit the data in the sample
- Calculate error function for each data point
- **Select data that support current hypothesis**



- Select sample of m points 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**



- Select sample of m points 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**



ALL-INLIER SAMPLE

RANSAC time complexity

$$t = k(t_M + \bar{m}_s N)$$

k ... number of samples
drawn

N ... number of data
points

t_M ... time to compute a
single model

\bar{m}_s ... average number of
models per
sample

the “gold standard” algorithm:

In: $U = \{x_i\}$ set of **data points**, $|U| = N$
 $f(S) : S \rightarrow p$ 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 $P\{\text{better solution exists}\} < \eta$ (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

(4) if $C^* < C_k$ then $C^* := C_k$, $p^* := p_k$ $C_k = \sum_{x \in U} \rho(p_k, x)$

end Repeat

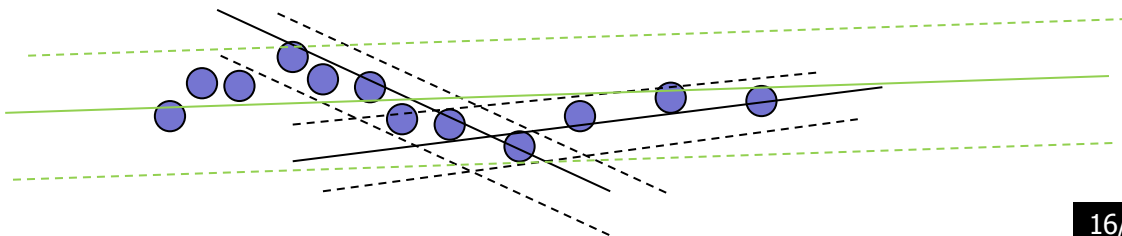
p^{out} = least square fit on the set of inliers to p^*

- The algorithm is extremely simple
- Can we stop the talk here?

- The algorithm is extremely simple, we stop the talk here?

NO!

- The (“gold”) standard algorithm often:
 - does not produce the correct model with the user-defined probability
 - outputs an inaccurate model
 - does not handle degeneracies
 - can be speeded up (by orders of magnitude)
 - does not guarantee maximum running time
 - needs information about the scale of the noise (this issue will not be discussed)
 - multiple models



Covered:
most practically important
developments, (most cited)

Not covered:

- scale selection
- maximum-likelihood link (MLE SAC, MSAC)
- methods guaranteeing optimal results:

Hongdong Li: Consensus set maximization with guaranteed global optimality for robust geometry estimation. ICCV 2009:

F Kahl - Computer Vision-ECCV 2008, 2008 - Robust Optimal Pose Estimation

1. Title: [RANSAC-based DARCES: A new approach to fast automatic registration of partially overlapping range images](#)
Author(s): Chen CS, Hung YP, Cheng JB
Source: **IEEE TRANSACTIONS ON PATTERN ANALYSIS AND MACHINE INTELLIGENCE**
Volume: 21 Issue: 11 Pages: 1229-1234 Published: NOV 1999
Times Cited: 78
2. Title: [Preemptive RANSAC for live structure and motion estimation](#)
Author(s): Nister D
Source: **MACHINE VISION AND APPLICATIONS** Volume: 16 Issue: 5 Pages: 321-329
Published: DEC 2005
Times Cited: 41
[Full Text](#)
3. Title: [Efficient RANSAC for point-cloud shape detection](#)
Author(s): Schnabel R, Wahl R, Klein R
Source: **COMPUTER GRAPHICS FORUM** Volume: 26 Issue: 2 Pages: 214-226 Published: 2007
Times Cited: 31
4. Title: [Locally optimized RANSAC](#)
Author(s): Chum O, Matas J, Kittler J
Conference Information: 25th Pattern Recognition Symposium of the German-Association-for-Pattern-Recognition, SEP 10-12, 2003 MAGDEBURG, GERMANY
Source: **PATTERN RECOGNITION, PROCEEDINGS** Book Series: LECTURE NOTES IN COMPUTER SCIENCE Volume: 2781 Pages: 236-243 Published: 2003
Times Cited: 30
5. Title: [Randomized RANSAC with T-d,T-d test](#)
Author(s): Matas J, Chum O
Source: **IMAGE AND VISION COMPUTING** Volume: 22 Issue: 10 Pages: 837-842 Published: SEP 1 2004
Times Cited: 22
[Full Text](#)
6. Title: [Optimal Randomized RANSAC](#)
Author(s): Chum O, Matas J
Source: **IEEE TRANSACTIONS ON PATTERN ANALYSIS AND MACHINE INTELLIGENCE**
Volume: 30 Issue: 8 Pages: 1472-1482 Published: AUG 2008
Times Cited: 17

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[Matching with PROSAC-progressive sample consensus](#)

O Chum... - ... 2005: CVPR 2005. IEEE Computer Society ..., 2005 - [ieeexplore.ieee.org](#)
A new robust matching method is proposed. The Pro- gressive Sample Consensus (PROSAC) algorithm exploits the linear ordering defined on the set of correspondences by a similarity function used in establishing tentative cor- respondences. Unlike RANSAC, ...
[Cited by 155](#) - [Related articles](#) - [BL Direct](#) - [All 12 versions](#)

M.A. Fischler and R.C. Bolles: Random sample consensus: A paradigm for model fitting with applications to image analysis and automated cartography. *CACM* 1981.

P. J. Rousseeuw and A. M. Leroy: *Robust Regression and Outlier Detection*. 1987.

Charles V. Stewart: MINPRAN: a new robust estimator for computer vision. *PAMI* 1995.

P. H. S. Torr and A. Zisserman: MLESAC: A new robust estimator with application to estimating image geometry. *CVIU* 2000.

C. F. Olson: A General Method for Geometric Feature Matching and Model Extraction. *IJCV* 2001.

B. Tordoff and D.W. Murray: Guided sampling and consensus for motion estimation. *ECCV* 2002.

D.R. Myatt, et al: Napsac: High noise, high dimensional robust estimation - it's in the bag. *BMVC* 2002.

D. Nistér: Preemptive RANSAC for live structure and motion estimation. *ICCV* 2003

RANSAC since 2006 (variants)

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A comparative analysis of **RANSAC** techniques leading to adaptive real-time random sample consensus

[\[PDF\] from psu.edu](#)

R Raguram, JM Frahm... - Computer Vision—ECCV 2008, 2008 - Springer

Abstract. The Random Sample Consensus (**RANSAC**) algorithm is a popular tool for robust estimation problems in computer vision, primarily due to its ability to tolerate a tremendous fraction of outliers. There have been a number of recent efforts that aim to increase the efficiency of ...

[Cited by 40](#) - [Related articles](#) - [All 16 versions](#)

[Optimal randomized **RANSAC**](#)

O Chum... - IEEE transactions on pattern analysis and ..., 2008 - computer.org

Abstract—A randomized model verification strategy for **ransac** is presented. The proposed method finds, like **ransac**, a solution that is optimal with user-specified probability. The solution is found in time that is close to the shortest possible and superior to any deterministic verification ...

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[Improved **RANSAC** performance using simple, iterative minimal-set solvers](#)

[\[PDF\] from arxiv.org](#)

E Rosten, G Reitmayr... - Arxiv preprint arXiv:1007.1432, 2010 - arxiv.org

Abstract **RANSAC** is a popular technique for estimating model parameters in the presence of outliers. The best speed is achieved when the minimum possible number of points is used to estimate hypotheses for the model. Many useful problems can be represented using ...

[Cited by 1](#) - [Related articles](#) - [All 3 versions](#)

[\[PDF\] Optimal Randomized **RANSAC**](#)

[\[PDF\] from cvut.cz](#)

O rej Chum... - IEEE TRANSACTIONS ON PATTERN ..., 2008 - cmp.felk.cvut.cz

Abstract—A randomized model verification strategy for **RANSAC** is presented. The proposed method finds, like **RANSAC**, a solution that is optimal with user-specified probability. The solution is found in time that is close to the shortest possible and superior to any deterministic ...

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[\[PDF\] New conditional sampling strategies for speeded-up **RANSAC**](#)

[\[PDF\] from free.fr](#)

T Betterill, S Mills... - Proceedings of the British Machine... 2009 - ohuissan.free.fr

RANSAC since 2006 (used)

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since 2006

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[Virtual mitochondrion: towards an integrated model of oxidative phosphorylation complexes and beyond.](#)

..., M Heiske, C Nazaret, S Ransac - Biochemical Society ..., 2010 - ncbi.nlm.nih.gov

The modelling of OXPHOS (oxidative phosphorylation) in order to integrate all kinetic and thermodynamic aspects of chemiosmotic theory has a long history. We briefly review this history and show how new ways of modelling are required to integrate a local model of the individual respiratory ...

[All 5 versions](#)

[The flitting of electrons in complex I: A stochastic approach](#)

S Ransac, C Arnarez... - Biochimica et Biophysica Acta (BBA)- ..., 2010 - Elsevier

A stochastic approach based on the Gillespie algorithm is particularly well adapted to describe the time course of the redox reactions that occur inside the respiratory chain complexes because they involve the motion of single electrons between the individual unique redox centres of ...

[Related articles](#) - [All 3 versions](#)

[How does antimycin inhibit the bc1 complex? A part-time twin](#)

S Ransac... - Biochimica et Biophysica Acta (BBA)-Bioenergetics, 2010 - Elsevier

Using a stochastic simulation without any other hypotheses, we recently demonstrated the natural emergence of the modified Mitchell Q-cycle in the functioning of the bc 1 complex, with few short-circuits and a very low residence time of the reactive semiquinone species in the Q ...

[Related articles](#) - [All 3 versions](#)

[\[CITATION\] A stochastic approach of the electron transport in the mitochondrial respiratory chain](#)

..., S Ransac - Biochimica et Biophysica Acta (BBA)-Bioenergetics, 2010 - Elsevier

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[\[CITATION\] S15. 14 Stochastic approach of bc1 complex functioning](#)

S Ransac... - Biochimica et Biophysica Acta (BBA)-Bioenergetics, 2008 - Elsevier

[Structural basis of phospholipase activity of Staphylococcus hyicus lipase](#)

..., G Pouderoyen, M Nardini, S Ransac... - Journal of molecular ..., 2007 - Elsevier

Staphylococcus hyicus lipase differs from other bacterial lipases in its high phospholipase A₁ activity. Here, we present the crystal structure of the S. hyicus lipase at 2.86 Å resolution. The lipase is in an open conformation, with the active site partly covered by a neighbouring ...

Locally optimised RANSAC

Chum, Matas, Kittler:

Locally Optimized RANSAC, *DAGM*, 2003

Chum, Matas, Obdržálek:

Enhancing RANSAC by Generalized Model Optimization, *ACCV*, 2004

It was observed experimentally, that RANSAC takes several times longer than theoretically expected. This is due to the noise on inlier measurement – not every all-inlier sample generates a good hypothesis.

By applying local optimization (LO) to the-best-so-far hypotheses:

- (i) a better agreement with theoretical (i.e. optimal) performance
- (ii) lower sensitivity to noise and poor conditioning.

Note: the claim in Chum et al. 2003:

The LO is shown to be executed so rarely that it has minimal impact on the execution time.

not always true !

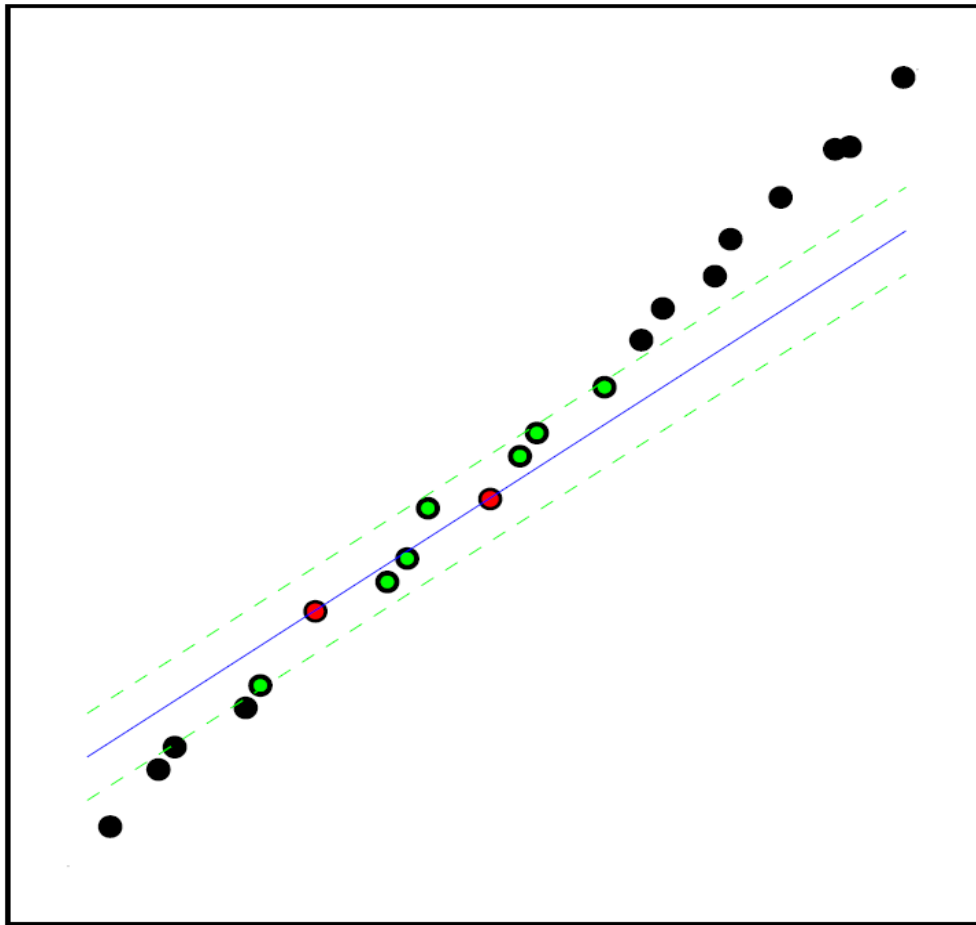
- Observation: often, the solution is found later than predicted, i.e. after on average k steps

$$k = \left(\frac{1}{\varepsilon} \right)^m$$

where ε is the fraction of inliers, m the sample size

- RANSAC stopping criterion makes a (hidden) assumption that *any* all-inlier sample leads to the solution.

.... Makes an Invalid Assumption



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
















































































































Lower number of inliers
is detected



RANSAC runs longer

full
data

slide
credit:
Karel
Lebeda

Solver→ Detectors→ Descriptors→			STD		STD,LSQ		STD,LO		STD,LO	
			MSER+ MSER-SIFT		MSER+ MSER-SIFT		MSER+ MSER-SIFT		MSER+ MSER-SIFT	
			(1000 runs)		(1000 runs)		(1000 runs)		(1000 runs)	
Image	Qty↓									
booksh		I	28.1 ±2.2 (24-33)		8.1 ±11.0 (0-32)		28.3 ±2.2 (24-33)		28.6 ±2.1 (24-33)	
		I (%)	65.4 ±5.2 (56-77)		18.8 ±25.5 (0-74)		65.9 ±5.1 (56-77)		66.6 ±4.8 (56-77)	
		Samp	90.9 ±45.2 (17-272)		90.9 ±45.2 (17-272)		90.9 ±45.2 (17-272)		80.3 ±38.9 (17-261)	
		Time _(ms)	1.0 (NA)		1.2 (NA)		3.9 (NA)		7.2 (NA)	
		Error	2.13 ±2.85 (0.3-20.4)		15.09 ±8.46 (0.7-70.7)		2.54 ±4.59 (0.3-81.5)		2.27 ±3.86 (0.3-54.3)	
		LO count	0.0 ±0.0 (0-0)		0.0 ±0.0 (0-0)		1.0 ±0.0 (1-1)		1.3 ±0.6 (1-4)	
box		I	190.3 ±5.8 (173-205)		194.5 ±5.0 (167-206)		198.4 ±2.6 (184-210)		199.4 ±1.2 (198-210)	
		I (%)	79.3 ±2.4 (72-85)		81.1 ±2.1 (70-86)		82.7 ±1.1 (77-88)		83.1 ±0.5 (82-88)	
		Samp	15.3 ±3.9 (8-30)		15.3 ±3.9 (8-30)		15.3 ±3.9 (8-30)		15.3 ±3.9 (8-30)	
		Time _(ms)	0.6 (NA)		0.7 (NA)		9.1 (NA)		9.1 (NA)	
		Error	39.40 ±17.82 (0.7-86.5)		42.47 ±15.93 (0.8-86.4)		44.23 ±13.52 (0.8-86.1)		46.02 ±12.30 (0.9-77.2)	
		LO count	0.0 ±0.0 (0-0)		0.0 ±0.0 (0-0)		1.0 ±0.0 (1-1)		1.0 ±0.0 (1-1)	
castle		I	98.2 ±6.8 (82-115)		102.9 ±14.9 (0-115)		108.6 ±6.3 (83-116)		111.4 ±2.9 (98-117)	
		I (%)	62.2 ±4.3 (52-73)		65.1 ±9.4 (0-73)		68.8 ±4.0 (53-73)		70.5 ±1.8 (62-74)	
		Samp	110.1 ±44.5 (28-307)		110.1 ±44.5 (28-307)		110.1 ±44.5 (28-307)		58.0 ±23.8 (28-224)	
		Time _(ms)	2.2 (NA)		2.3 (NA)		8.5 (NA)		7.4 (NA)	
		Error	4.36 ±6.35 (0.2-44.4)		5.09 ±12.66 (0.2-141.1)		3.98 ±7.69 (0.2-103.2)		1.08 ±2.08 (0.2-12.3)	
		LO count	0.0 ±0.0 (0-0)		0.0 ±0.0 (0-0)		1.0 ±0.0 (1-1)		1.0 ±0.1 (1-2)	
corr		I	62.9 ±4.1 (52-75)		1.6 ±4.0 (0-60)		62.9 ±4.1 (52-75)		62.9 ±4.1 (52-75)	
		I (%)	68.4 ±4.5 (57-82)		1.8 ±4.4 (0-65)		68.4 ±4.5 (57-82)		68.4 ±4.5 (57-82)	
		Samp	55.0 ±21.7 (11-169)		55.0 ±21.7 (11-169)		55.0 ±21.7 (11-169)		54.9 ±21.6 (11-169)	
		Time _(ms)	1.0 (NA)		1.2 (NA)		1.4 (NA)		3.9 (NA)	
		Error	0.37 ±0.24 (0.1-1.6)		36.47 ±19.05 (0.3-76.0)		0.37 ±0.24 (0.1-1.6)		0.39 ±0.65 (0.1-19.5)	
		LO count	0.0 ±0.0 (0-0)		0.0 ±0.0 (0-0)		1.0 ±0.0 (1-1)		1.3 ±0.5 (1-5)	
graff		I	79.9 ±3.9 (71-93)		83.5 ±4.9 (62-94)		89.0 ±3.9 (74-94)		91.3 ±1.1 (82-94)	
		I (%)	66.6 ±3.3 (59-78)		69.6 ±4.1 (52-78)		74.1 ±3.3 (62-78)		76.1 ±1.0 (68-78)	
		Samp	59.9 ±20.3 (21-134)		59.9 ±20.3 (21-134)		59.9 ±20.3 (21-134)		52.5 ±14.7 (21-120)	
		Time _(ms)	0.9 (NA)		1.0 (NA)		6.9 (NA)		6.6 (NA)	
		Error	2.10 ±1.27 (0.3-5.1)		2.07 ±1.32 (0.3-4.7)		2.17 ±1.74 (0.3-32.6)		2.44 ±1.30 (0.3-4.0)	
		LO count	0.0 ±0.0 (0-0)		0.0 ±0.0 (0-0)		1.0 ±0.0 (1-1)		1.0 ±0.0 (1-1)	
head		I	69.1 ±4.4 (57-79)		74.2 ±2.9 (60-78)		76.8 ±1.2 (69-79)		76.9 ±0.9 (75-79)	
		I (%)	78.5 ±5.0 (65-90)		84.3 ±3.3 (68-89)		87.3 ±1.3 (78-90)		87.4 ±1.0 (85-90)	
		Samp	20.7 ±9.5 (6-62)		20.7 ±9.5 (6-62)		20.7 ±9.5 (6-62)		20.6 ±9.3 (6-55)	
		Time _(ms)	0.4 (NA)		0.5 (NA)		5.4 (NA)		5.3 (NA)	
		Error	0.54 ±0.27 (0.2-1.9)		0.29 ±0.08 (0.2-1.0)		0.28 ±0.12 (0.2-2.8)		0.28 ±0.04 (0.2-0.7)	
		LO count	0.0 ±0.0 (0-0)		0.0 ±0.0 (0-0)		1.0 ±0.0 (1-1)		1.0 ±0.0 (1-1)	
kampe		I	46.0 ±2.5 (41-56)		46.0 ±4.4 (1-58)		49.4 ±3.6 (41-58)		51.3 ±2.8 (43-58)	
		I (%)	52.9 ±2.9 (47-64)		52.9 ±5.0 (1-67)		56.8 ±4.2 (47-67)		59.0 ±3.2 (49-67)	
		Samp	327.1 ±108.4 (85-682)		327.1 ±108.4 (85-682)		327.1 ±108.4 (85-682)		165.3 ±81.4 (50-682)	
		Time _(ms)	4.1 (NA)		4.2 (NA)		8.9 (NA)		9.2 (NA)	
		Error	12.29 ±10.26 (0.5-34.4)		12.05 ±10.19 (0.4-41.6)		15.97 ±15.10 (0.4-138.0)		8.55 ±9.47 (0.4-118.3)	
		LO count	0.0 ±0.0 (0-0)		0.0 ±0.0 (0-0)		1.0 ±0.0 (1-1)		1.7 ±0.9 (1-7)	
leafs		I	49.8 ±3.1 (41-60)		51.5 ±7.0 (1-59)		56.9 ±2.5 (44-60)		58.0 ±0.8 (49-60)	
		I (%)	59.3 ±3.7 (49-71)		61.3 ±8.3 (1-70)		67.7 ±3.0 (52-71)		69.0 ±1.0 (58-71)	
		Samp	159.1 ±71.6 (39-525)		159.1 ±71.6 (39-525)		159.1 ±71.6 (39-525)		76.3 ±46.2 (39-334)	
		Time _(ms)	1.8 (NA)		2.0 (NA)		9.9 (NA)		8.4 (NA)	

Solution: Local Optimisation Step

Repeat k times

1. Hypothesis generation
2. Model verification
 - 2b. If model best-so-far Execute (Local) Optimisation

Inner RANSAC + Re-weighted least squares:

- Samples are drawn from the set of data points consistent with the best-so-far hypothesis
- New models are verified on all data points
- Samples can contain more than minimal number of data points since consistent points include almost entirely inliers

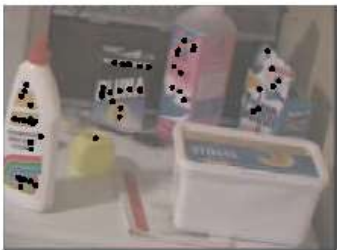
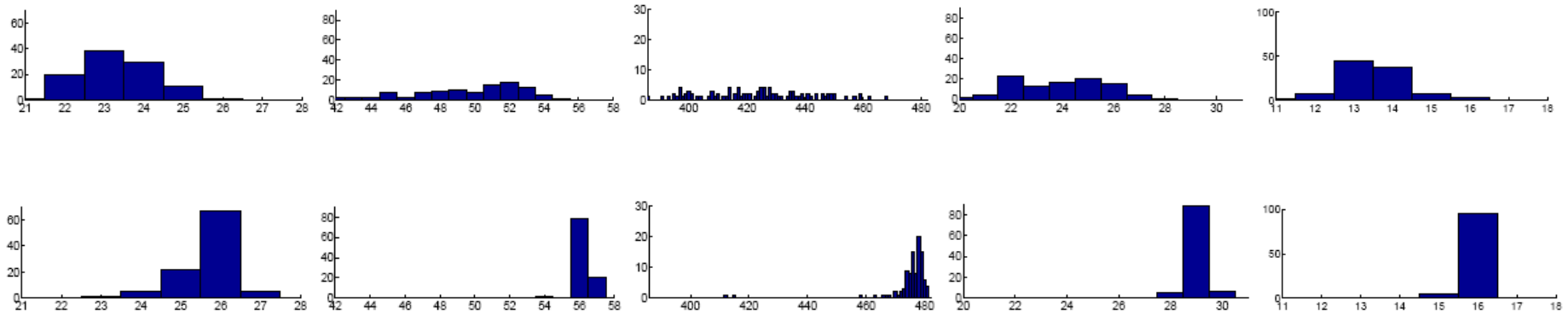
How often?

$$\sum_{l=1}^k P_l = \sum_{l=1}^k \frac{1}{l} \leq \int_1^k \frac{1}{x} dx + 1 = \log k + 1$$

Conclusion: the LO step 2b is executed rarely, does not influence running time significantly

Validation: Two-view Geometry Estimation

Histograms of the number of inliers returned over 100 executions of RANSAC (top) and LO-RANSAC (bottom)



Result:

- (i) variation of the number of inliers significantly reduced
- (ii) speed-up up to 3 times (for 7pt EG and 4pt homography est.)

A model from a random sample need not be required to be the solution. Any model that is consistent with a large proportion of inliers moves us closer to a solution, since its inliers can be sampled.

Idea:

1. Estimate approximate models with lower complexity (less data points in the sample) with loose thresholds
2. Followed by LO step estimating full model

Epipolar geometry and radial distortion

Standard:

9 point correspondences define the model

$$\mathbf{p} = \frac{1}{1 + \lambda |\mathbf{x}|^2} \mathbf{x}$$

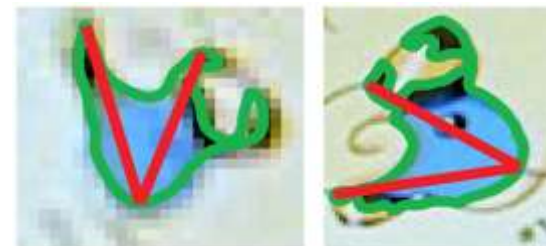
LO Ransac:

1. Approximated by EG with no radial distortion
2. In LO step (2b), estimate the full model from 9 (or more!) points

Division model
Fitzgibbon CVPR'01

EG from 3 local affine frame (LAF) correspondences

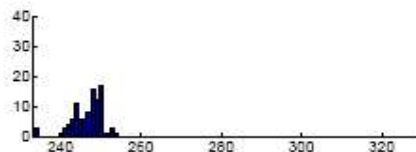
- each region provides 3 points
- 3 LAFs determine EG
- points close to each other (low precision)



Chum, Matas, Obdržálek: Enhancing RANSAC by Generalized Model Optimization, ACCV 2004

Distribution of inliers over 100 runs

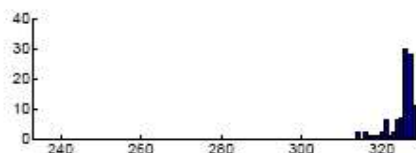
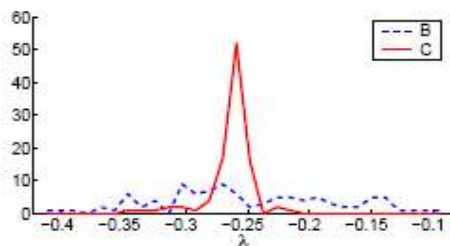
A: 7pt LO-RANSAC



B: 9pt RANSAC



C: LO-RANSAC-RD

Distribution of λ parameter

The number of samples

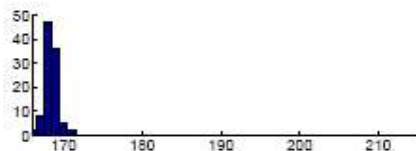
A	B	C
5 528	31 456	790

Orange house (45% of inliers)

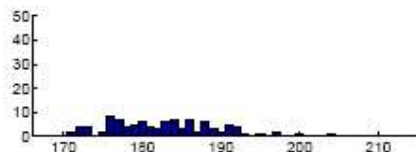


Distribution of inliers over 100 runs

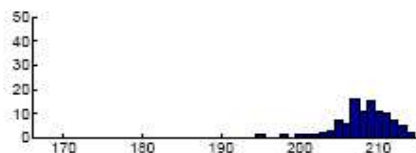
A: 7pt LO-RANSAC



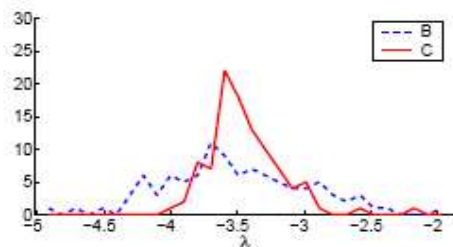
B: 9pt RANSAC



C: LO-RANSAC-RD



Distribution of λ parameter



The number of samples

A	B	C
1 861	6 863	432

Courtyard QY (48% of inliers)



EG from Three Correspondences

518 tentative correspondences, **7%** of inliers



Method	EG consistent	iterations
7pt LO-RANSAC	N/A	$\approx 684\,000\,000$
3LAF RANSAC	25	47 668
3LAF LO-RANSAC	36	14 880

More than
10000-fold
speed-up

EG from Three Correspondences

518 tentat

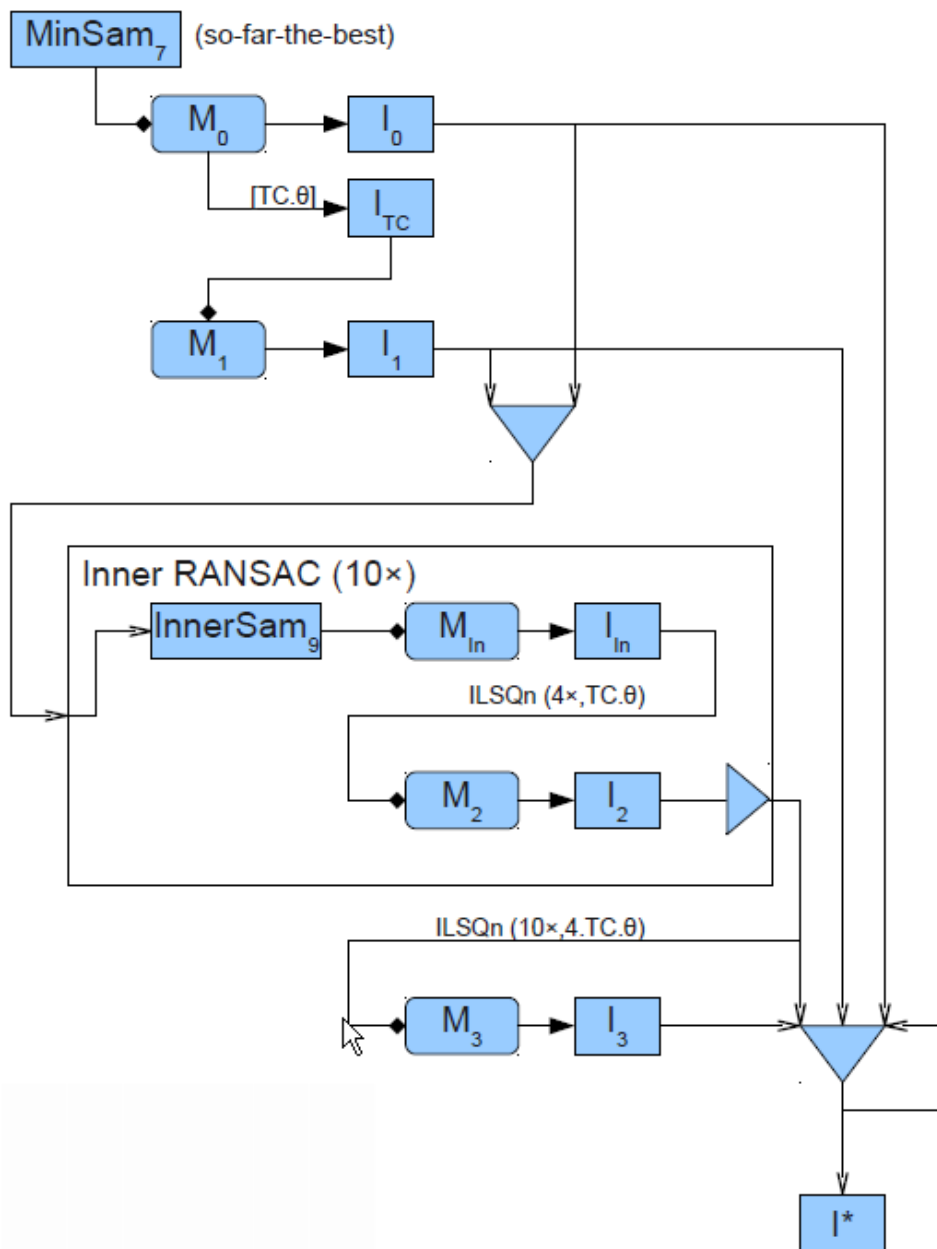


SUMMARY

- Not every all-inlier sample generates model consistent with all inliers due to noise
- Local data driven search initialised by the best-so-far solution saves computational effort
- Using hierarchical estimation (starting with approximate models) speeds up the estimation

iterations
84 000 000
47 668
14 880

LO RANSAC algorithm



$$TC = \sqrt{2}$$

ILSQn = Iterated
reweighted LSQ with
threshold narrowing

—◆ generate model

—► find inliers

▼ select biggest set

It must be possible to
simplify this and put
it on sound footing!

Degenerate Configurations

Chum, Werner, Matas: EG Estimation unaffected by dominant plane, *CVPR'05*

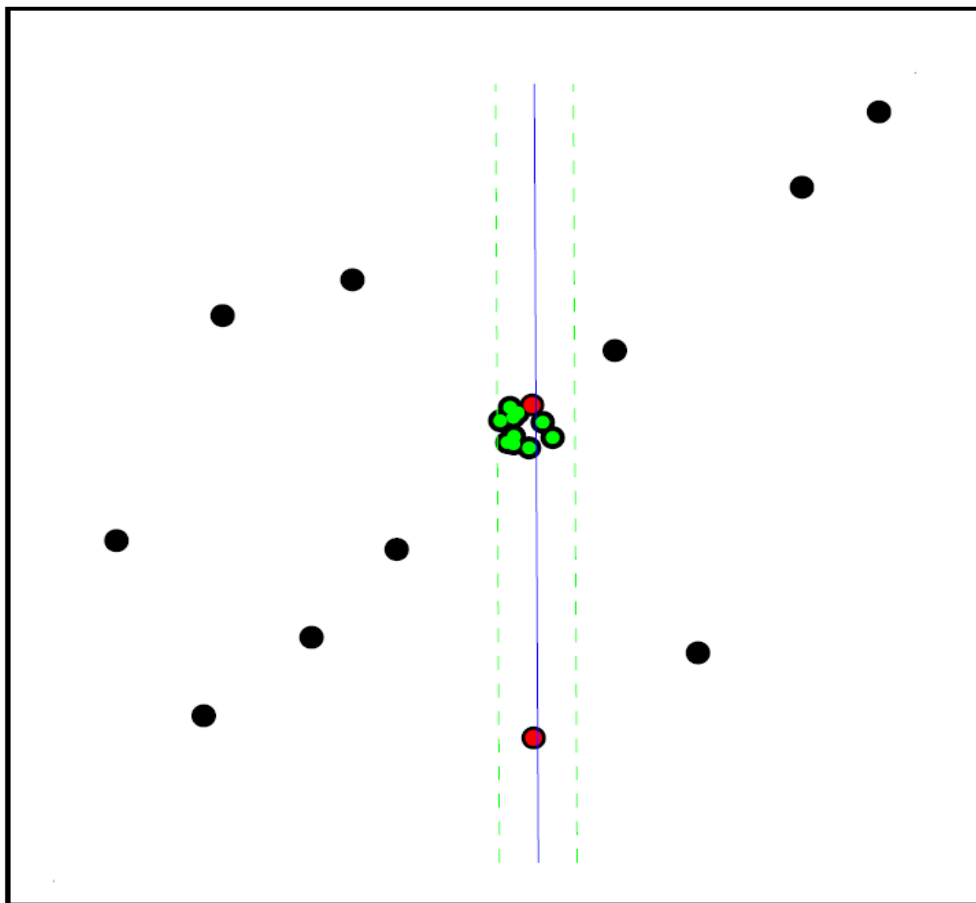
The presence of degenerate configuration causes RANSAC to fail in estimating a correct model, instead a model consistent with the degenerate configuration and some outliers is found.

The DEGENSAC algorithm handles scenes with:

- all points in a single plane
- majority of the points in a single plane and the rest off the plane
- no dominant plane present

No a-priori knowledge of the type of the scene is required





- Infinite number of models passes through a degenerate configuration
- Sample with points from both the degenerate configuration and outlier(s) is a problem – it has higher than random support

Robust fitting of a plane to 3D points

Algorithm:

- Draw samples of three points & fit a plane to them
- Calculate the support of the plane

Problem:

- High number of points lie on a line
- A sample containing two points from the line and one outlier has large support (the whole line)
- Such sample is not degenerate, the problem does not show as a singularity in the model estimation step
- Algorithm may return incorrect plane (that contains the line)

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

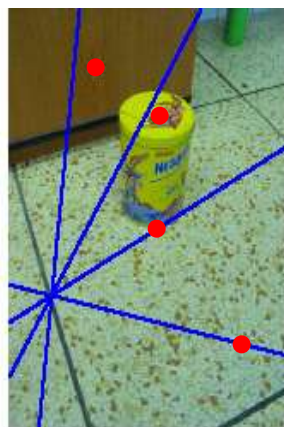
- RANSAC draws minimal samples of 7 correspondences to hypothesize the epipolar geometry
- When dominant plane is present, samples with more than 4 coplanar correspondences often appear
- 7 or 6 coplanar correspondences: the sample is consistent with a family of fundamental matrices. This case is easily detected.
- Chum et al. CVPR'05 show 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.

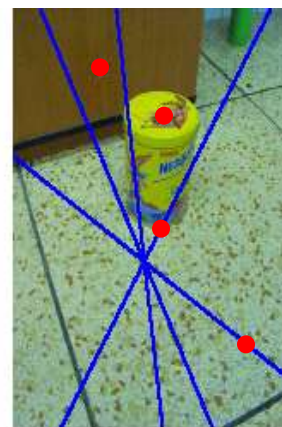
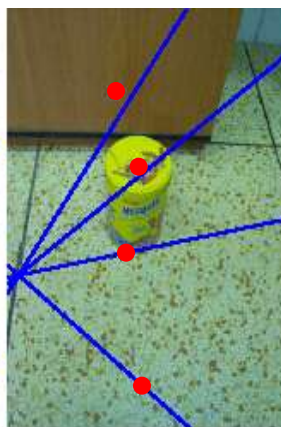
Different Solutions Returned by RANSAC



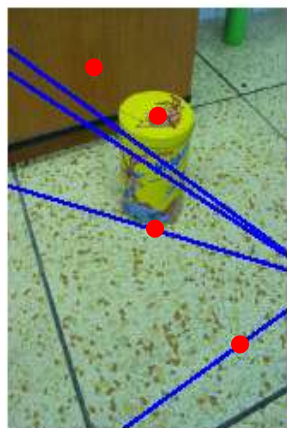
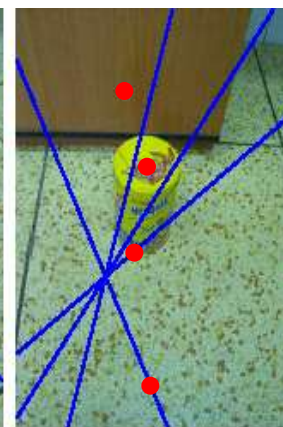
(a) 643 inliers ($\varepsilon = 0.67$)



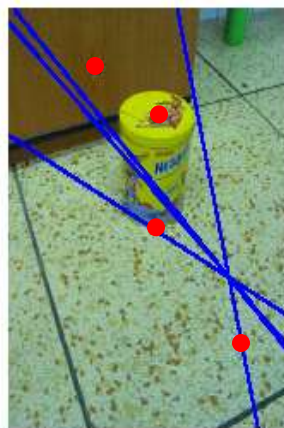
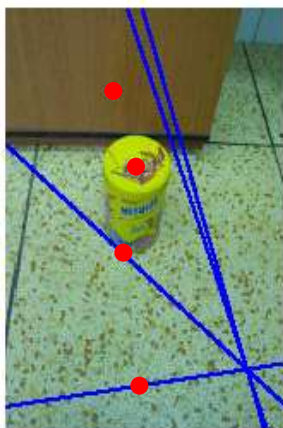
(b) 621 inliers ($\varepsilon = 0.65$)



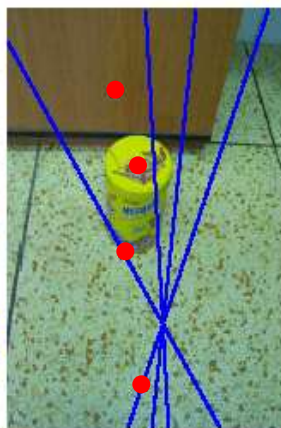
(c) 615 inliers ($\varepsilon = 0.64$)



(d) 614 inliers ($\varepsilon = 0.64$)



(e) 616 inliers ($\varepsilon = 0.64$)



(f) 615 inliers ($\varepsilon = 0.64$)

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 [Irani&Anadan ECCV'97].

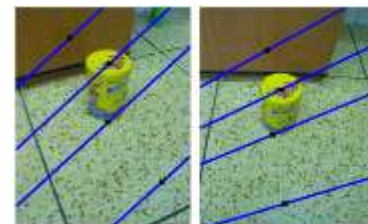
Note: the plane-and-parallax needs to draw samples of only 2 correspondences to hypothesize EG, therefore its complexity is negligible compared to RANSAC where 7 correspondences are drawn into a sample

Alternative to step 2: execute RANSAC detecting degenerate configuration on inliers:

Frahm, Pollefeys: RANSAC for (Quasi-)Degenerate Data (QDEGSAC),
CVPR'06

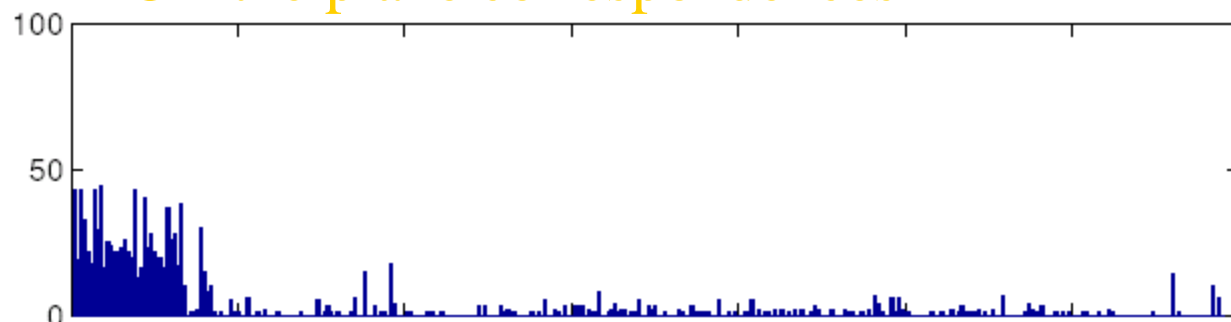
(and later improvements and generalization)

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

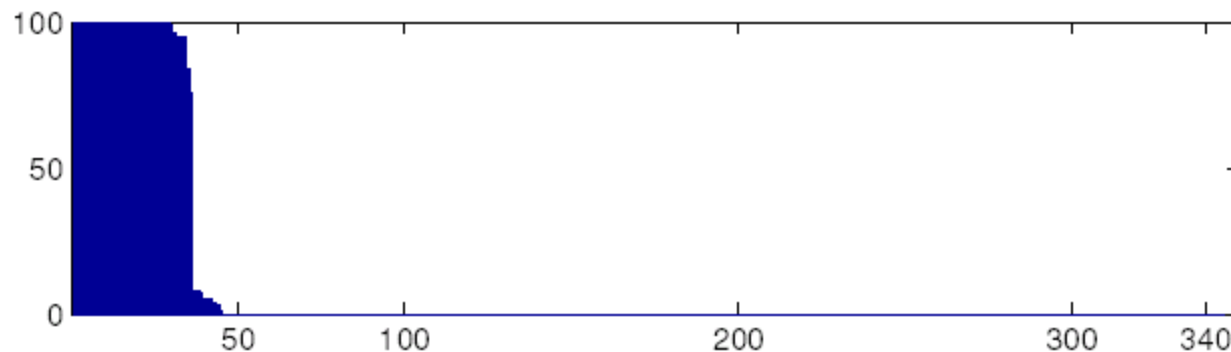


Off the plane correspondences

RANSAC



DEGENSAC

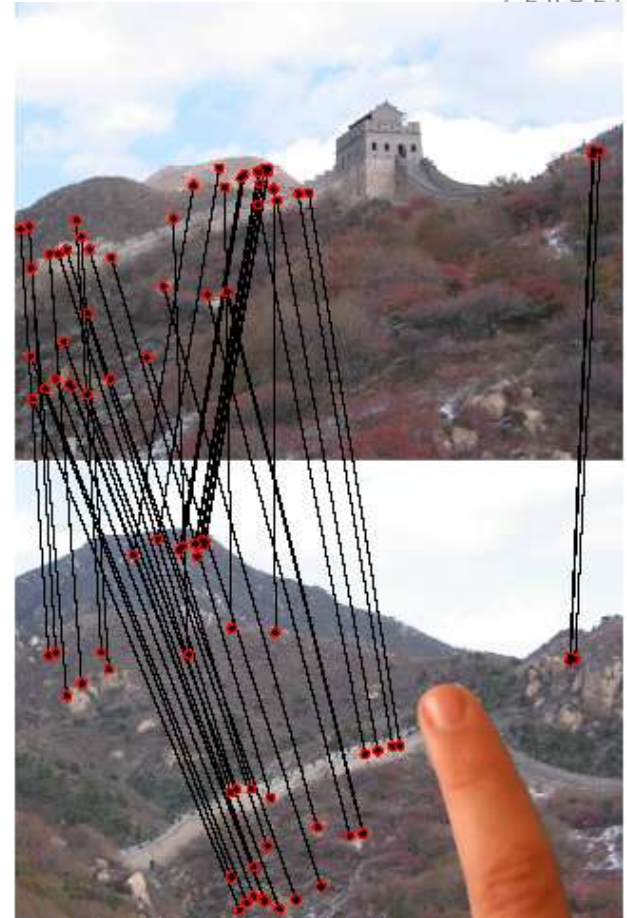


Correspondence number

PROSAC - Progressive Sampling and Consensus

O. Chum and J. Matas. Matching with PROSAC-progressive sampling consensus. CVPR, 2005.

Instead of drawing samples randomly, samples containing tentative correspondences are drawn preferably. The sampling procedure gradually progresses towards uniform sampling of standard RANSAC.



RANSAC tested 106,534 samples,
PROSAC tested only 9 samples

Idea: exploit the fact that all correspondences are not created equal.

In all (?) multi-view problems, the correspondences are from a totally ordered set (they are selected by thresholding of a similarity function)

Challenge:

- organize computation in a way that exploits ordering, and yet is equally robust as RANSAC

PROSAC properties:

- selection of correspondences and RANSAC integrated (no need for threshold on local similarity).
- Same guarantees about the solution as RANSAC
- Depending on the data, can be orders of magnitude faster

Idea:

1. Generate the maximal number of T_N RANSAC samples.
2. Evaluate the samples in order of decreasing quality of the samples. The quality of the sample is given by the lowest quality of correspondence in the sample.

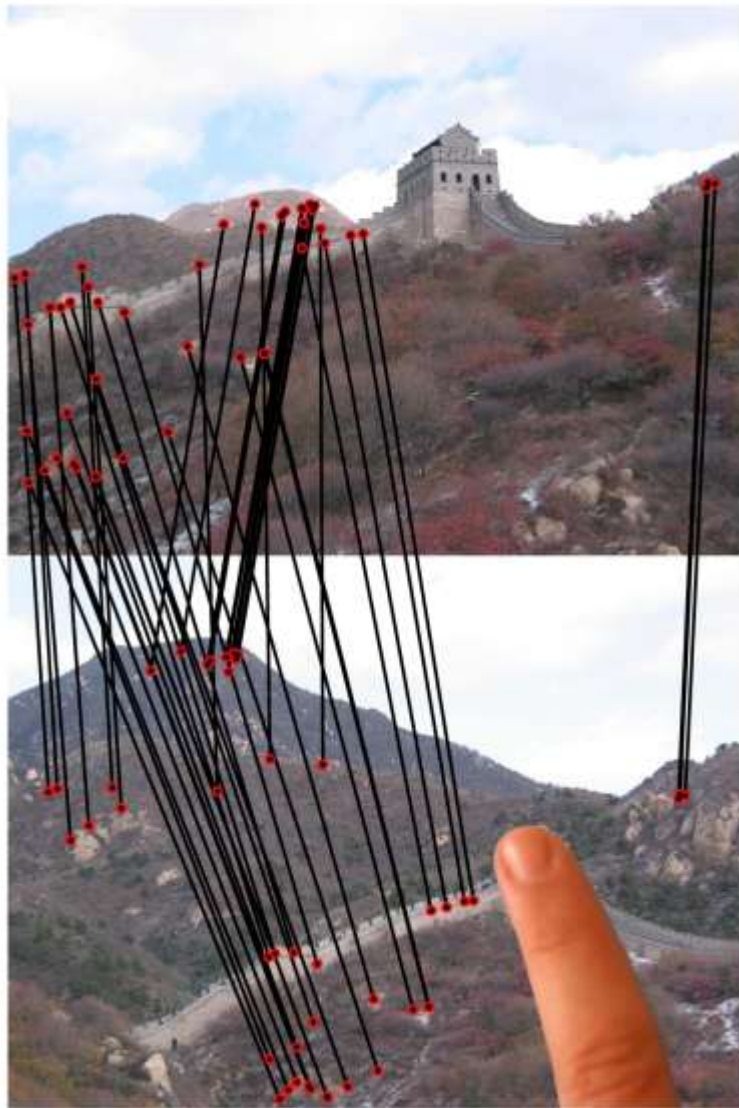
An efficient way (without generating all T_N samples beforehand) how to generate ordered samples of an 'average' RANSAC follows. RANSAC, on average, draws

$$T_n = T_N \frac{\binom{n}{m}}{\binom{N}{m}} = T_N \prod_{i=0}^{m-1} \frac{n-i}{N-i}$$

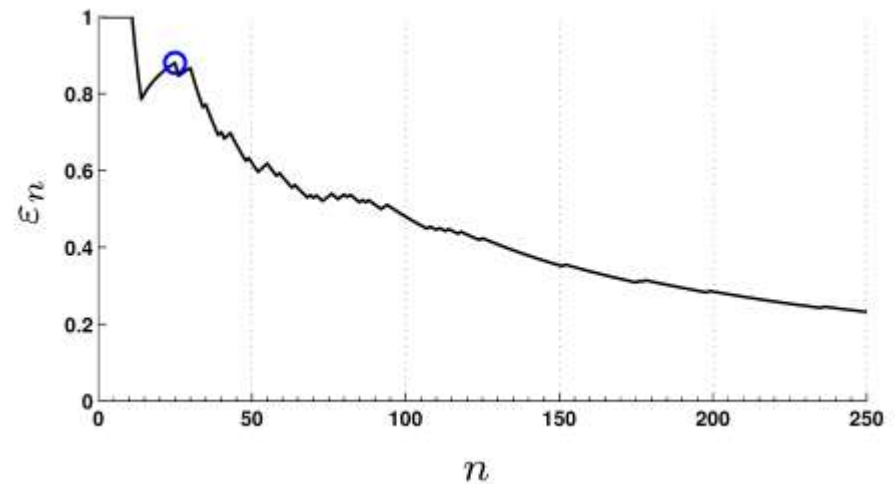
samples of size m that contain only data points from the set of n top quality data points \mathcal{U}_n . There are T_n samples containing only data points from \mathcal{U}_n and $T_{n+1} = \frac{n+1}{n+1-m} T_n$ samples containing only data points from \mathcal{U}_{n+1} . Since $\mathcal{U}_{n+1} = \mathcal{U}_n \cup \{\mathbf{u}_{n+1}\}$, there are $T_{n+1} - T_n$ samples that contain a data point \mathbf{u}_{n+1} and $m - 1$ data points drawn from \mathcal{U}_n .

Efficient algorithm:

```
for  $n = m \dots N$   
    Generate  $\lceil T_{n+1} - T_n \rceil$  samples consisting of a data point  $\mathbf{u}_{n+1}$   
    and  $m - 1$  data points drawn from  $\mathcal{U}_n$  at random.
```



- The fraction of inliers in top n correspondences:

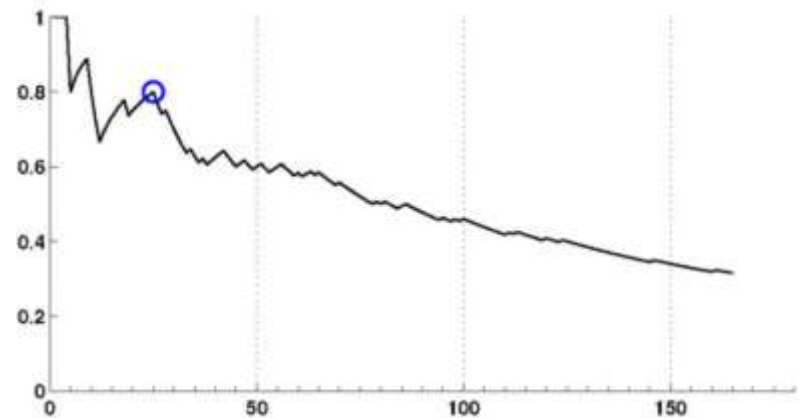
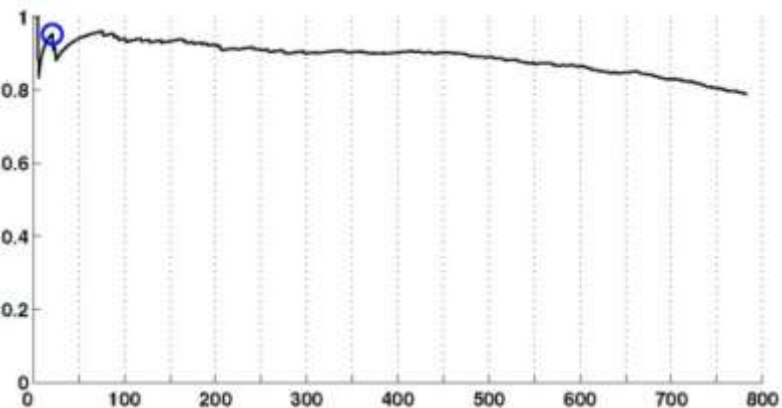
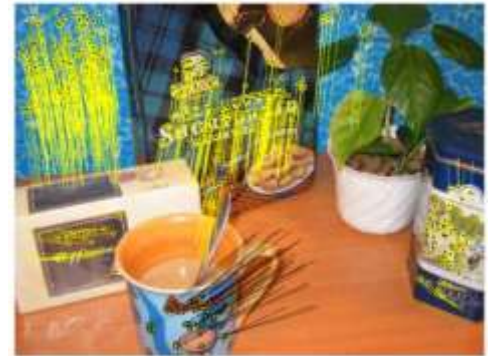


	k	min k	max k	time [sec]
PROSAC	9	5	29	0.06
RANSAC	106,534	97,702	126,069	10.76

Multiple motion experiment



Background	$N = 783, \varepsilon = 79\%$		
	I	k	time [sec]
PROSAC	617	1.0	0.33
RANSAC	617	15	1.10
Mug	$N = 166, \varepsilon = 31\%$		
	I	k	time [sec]
PROSAC	51.6	18	0.12
RANSAC	52.3	10,551	0.96



Note: What is an inlier does not depend on the on the similarity of appearance!

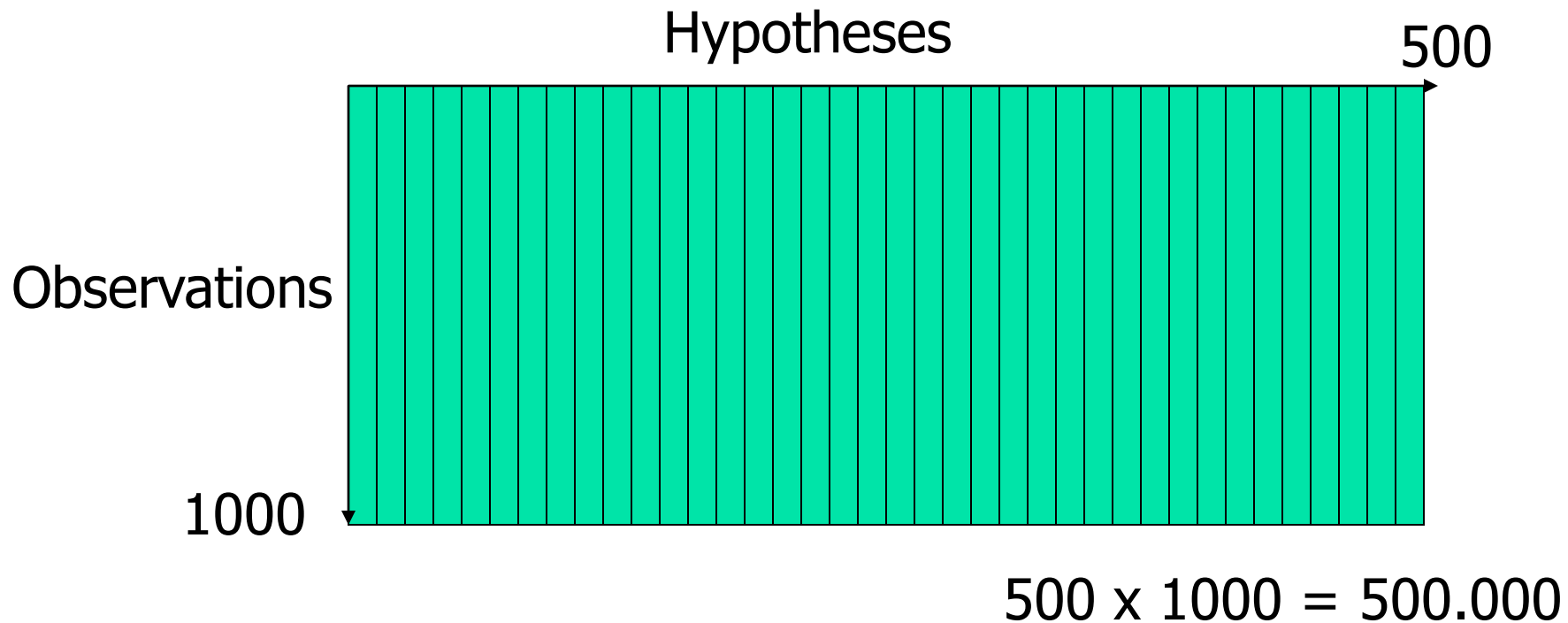
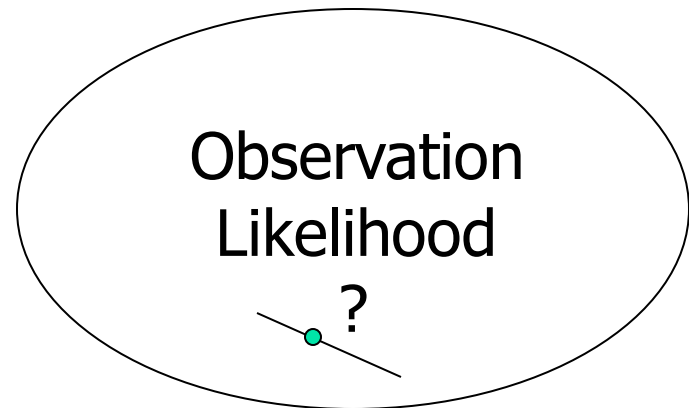
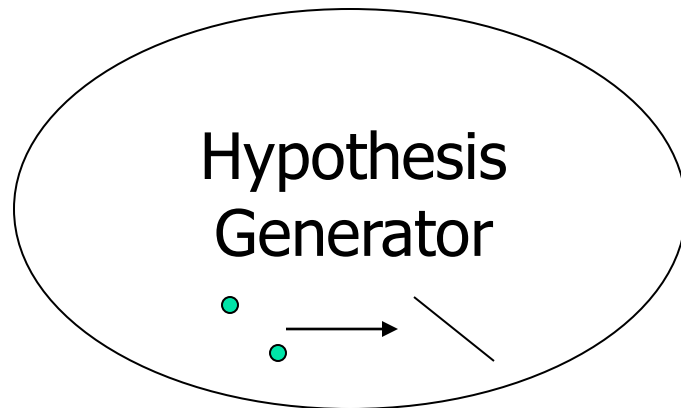
- In many cases, PROSAC draws only a few samples.
- The information needed to switch from RANSAC to PROSAC - ordering of features - is typically available
- Note that the set of data points that is sampled to hypothesise models and the set used in verification need not be the same.
- RANSAC needs protection against degenerate configurations and Local Optimisation (effectively we ran LO-DEGEN-PROSAC). This is important, since often top correspondences lie on the same plane.

Preemptive RANSAC

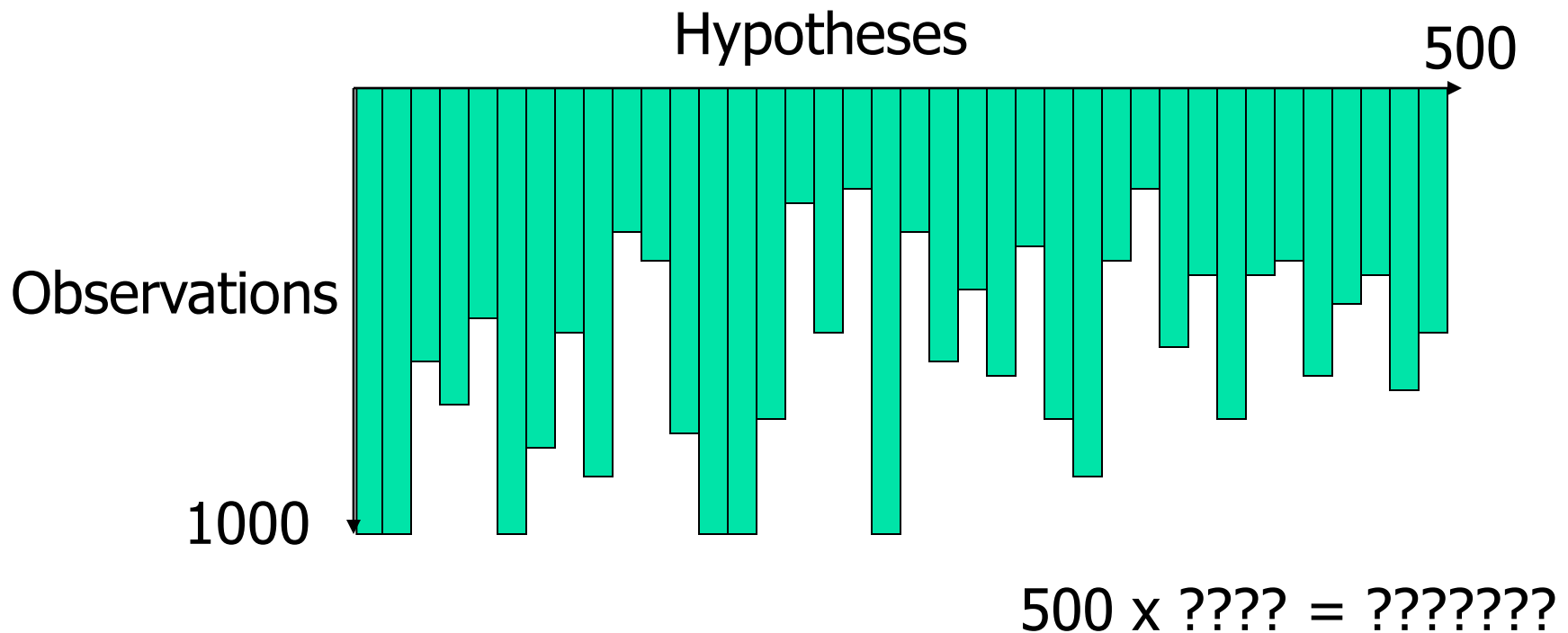
D. Nistér:

Preemptive RANSAC for live structure and motion estimation.

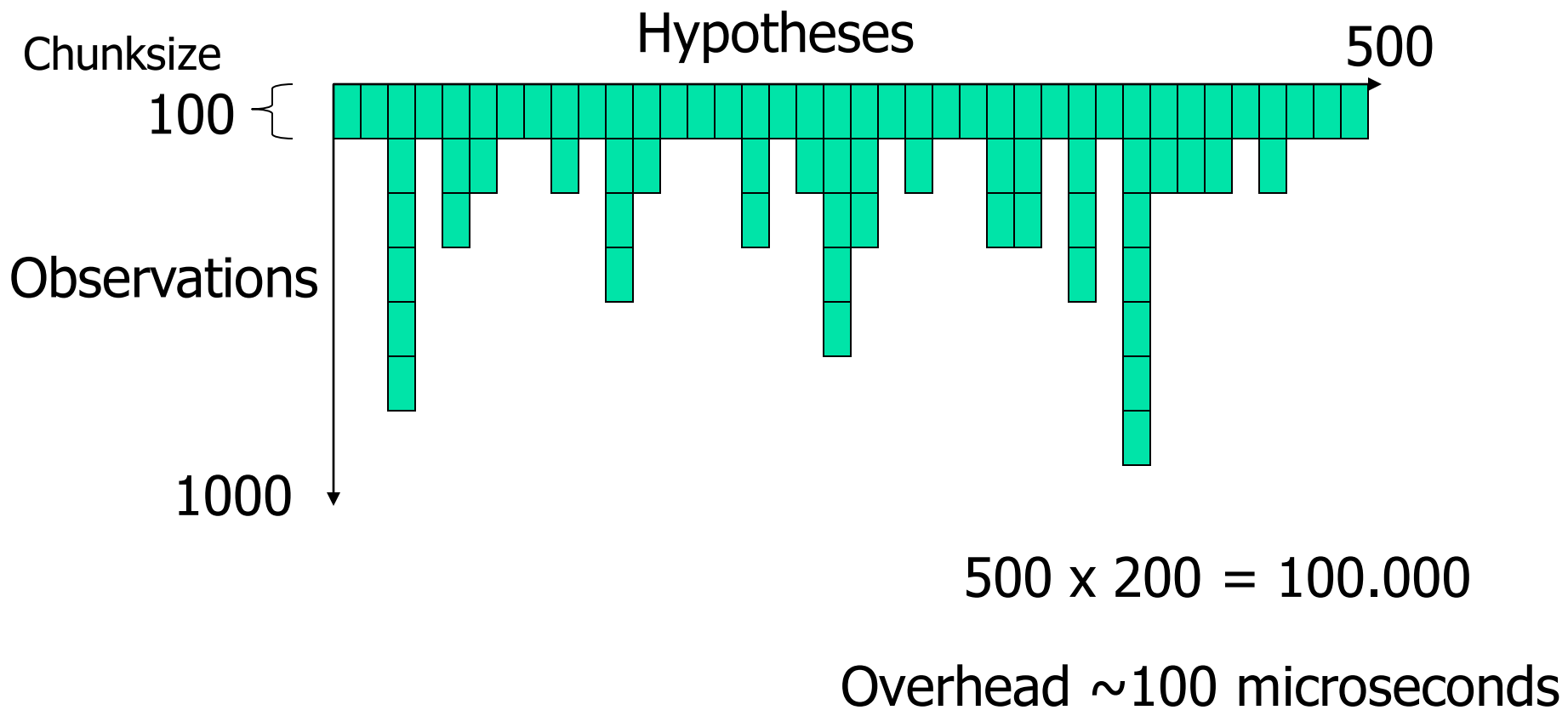
ICCV 2003

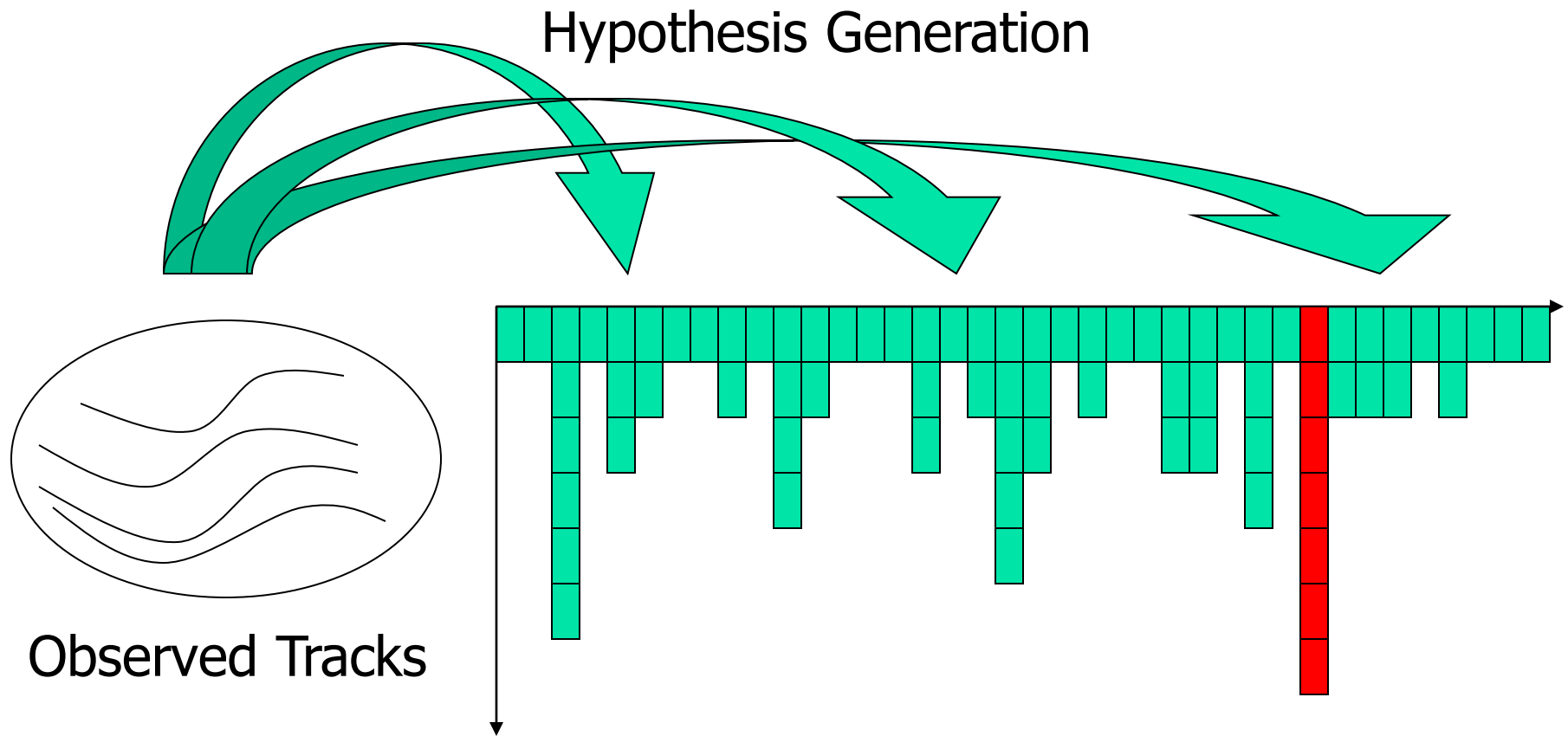


Depth-first Preemption



Breadth-first Preemption





WaldSAC – Optimal Randomised RANSAC

Chum, Matas: Randomized RANSAC with Td,d test,
British Machine Vision Conference, Cardiff, 2002.

Matas, Chum: Optimal Randomised RANSAC,
International Conference on Computer Vision, Beijing, 2005

IEEE Trans. PAMI, 2008, 8, pages 1472-1482

Instead of verifying all data points in the verification phase, a statistical test is introduced. Only promising hypotheses are fully verified.

RANSAC time complexity

$$t = k(t_M + \overline{m}_s N)$$

R-RANSAC time complexity

$$t = \frac{k}{1 - \alpha} (t_M + \overline{m}_s V)$$

$$\alpha \ll 1 \quad \text{and} \quad V \ll N$$

RR with T(d,d) test – simple, mathematically tractable test

RR with SPRT – optimal test (minimises the total running time t)
based on Wald's Sequential Analysis [1947]

Chum, Matas: Randomized RANSAC with T(d,d) test, *BMVC* 2002

Matas, Chum: Randomized RANSAC with SPRT, *ICCV* 2005 (to appear)

RANSAC – Time Complexity

Repeat k times (k is a function of η, I, N)

1. Hypothesis generation

- Select a sample of m data points
- Calculate parameters of the model(s)

2. Model verification

- Find the support (consensus set) by
- verifying all N data points

Time

t_M

$\overline{m}_s \cdot N$

t_M – time needed to draw a sample

\overline{m}_s – average number of models per sample

Total running time:

$$t = k(t_M + \overline{m}_s N)$$

I – the number of inliers

N – the number of data points

η – confidence in the solution

RANSAC time complexity

$$t = k(t_M + \overline{m}_s N)$$

The number of samples $k \sim \frac{1}{P}$

where P is a probability of drawing an all-inlier sample

$$P = \frac{\binom{I}{m}}{\binom{N}{m}} \approx \varepsilon^m$$

where m is size of the sample

and ε is the fraction of inliers I/N

Repeat $k/(1-\alpha)$ times

1. Hypothesis generation
2. Model pre-verification $T_{d,d}$ test
 - Verify $d \ll N$ data points, reject
 - the model if not all d data points
 - are consistent with the model
3. Model verification
 - Verify the rest of the data points

Time
 t_M

$\overline{m}_s \cdot V$

V – average number of data points verified

α – probability that a good model is rejected by $T_{d,d}$ test

$$t = \frac{k}{1 - \alpha} (t_M + \overline{m}_s V)$$

Optimal Randomised Strategy

Model Verification is Sequential Decision Making

$$H_g: P(x_i = 1 | H_g) \geq \varepsilon$$

$$H_b: P(x_i = 1 | H_b) = \delta$$

$$x_i = 1 \quad x_i \text{ is consistent with the model}$$

where

H_g - hypothesis of a 'good' model (\approx from an uncontaminated sample)

H_b - hypothesis of a 'bad' model, (\approx from a contaminated sample)

δ - probability of a data point being consistent with an arbitrary model

Optimal (the fastest) test that ensures with probability α that that H_g is not incorrectly rejected is the

Sequential probability ratio test (SPRT) [Wald47]

SPRT

[simplified from Wald 47]

Compute the likelihood ratio $\lambda_i = \prod_{j=1}^i \frac{P(x_j|H_b)}{P(x_j|H_g)}$

if $\lambda_i > A$ reject the model

if $i = N$ accept model as 'good'

Two important properties of SPRT:

1. probability of rejecting a "good" model $\alpha < 1/A$
2. average number of verifications $V = C \log(A)$

$$C \approx \left(P(0|H_b) \log \frac{P(0|H_b)}{P(0|H_g)} + P(1|H_b) \log \frac{P(1|H_b)}{P(1|H_g)} \right)^{-1}$$

Repeat $k/(1-1/A)$ times

1. Hypothesis generation

2. Model verification

use SPRT

Time

t_M

$\bar{m}_s \cdot C \log A$

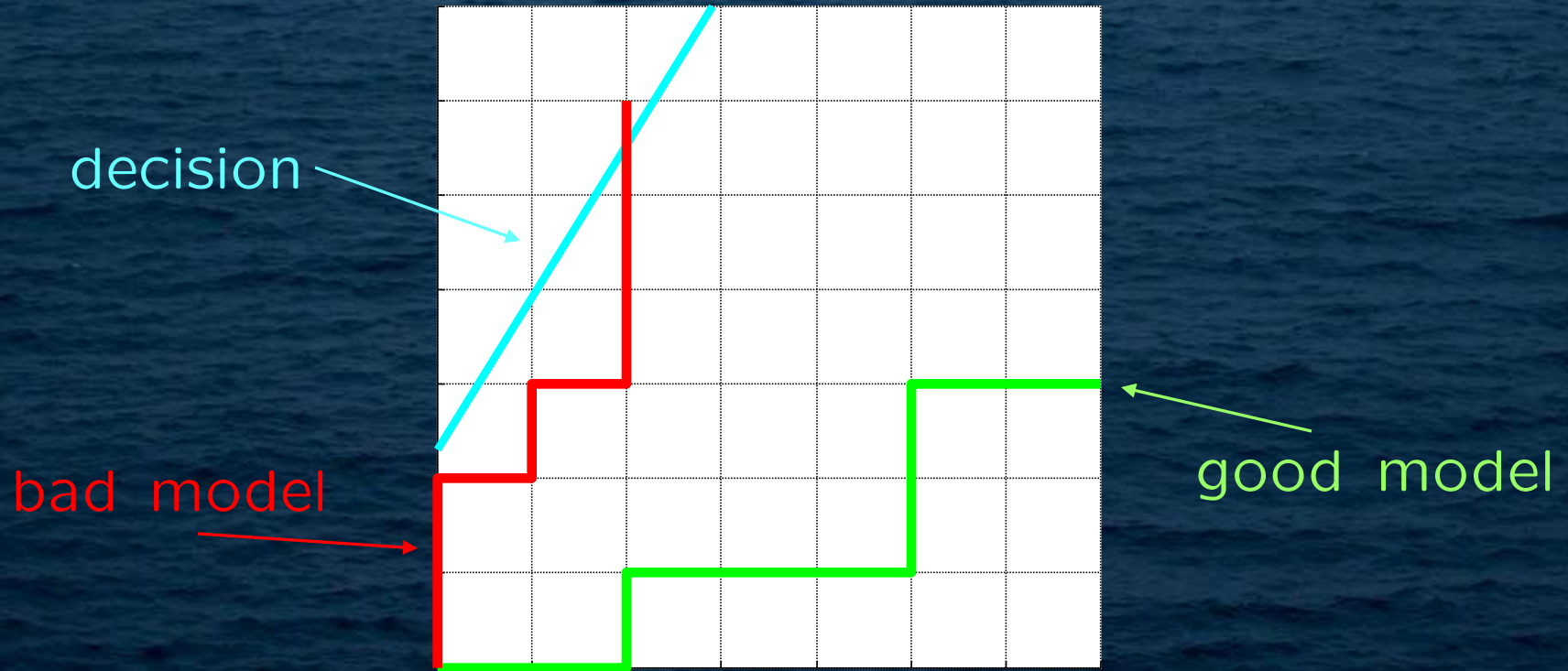
$$C \approx ((1 - \delta) \log \frac{1-\delta}{1-\varepsilon} + \delta \log \frac{\delta}{\varepsilon})^{-1}$$

$$t(A) = \frac{k}{(1 - 1/A)} (t_M + \bar{m}_s C \log A)$$

In sequential statistical decision problem decision errors are traded off for time. These are two incomparable quantities, hence the constrained optimization.

In WaldSAC, decision errors cost time (more samples) and there is a single minimised quantity, time $t(A)$, a function of a single parameter A .

SPRT



Note: the Wald's test is equivalent to series of $T(d, c)$, where $c = \lceil (\log A - d \log \lambda_1) / \log \lambda_0 \rceil$

Exp. 1: Wide-baseline matching



	samples	models	V	time	spd-up
R	2914	7347	110.0	1099504	1.0
R-R	7825	19737	3.0	841983	1.3
Wald	3426	8648	8.2	413227	2.7

Exp. 2 Narrow-baseline stereo



	samples	models	V	time	spd-up
R	155	367	600.0	235904	1.0
R-R	247	587	86.6	75539	3.1
Wald	162	384	23.1	25032	9.4

Randomised Verification in RANSAC:

Conclusions

- The same confidence η in the solution reached faster (data dependent, $\approx 10x$)
- No change in the character of the algorithm, it was randomised anyway.
- Optimal strategy derived using Wald's theory for known ε and δ .
- Results with ε and δ estimated during the course of RANSAC are not significantly different. Performance of SPRT is insensitive to errors in the estimate.
- δ can be learnt, an initial estimate can be obtained by geometric consideration
- Lower bound on ε is given by the best-so-far support
- Note that the properties of WaldSAC are quite different from preemptive RANSAC!

- RANSAC is in principle simple, but (as is often the case), a state-of-the-art implementation is not.
- A public version of RANSAC with PRO-sampling, LO-optimization, DEGENERACY protection and WALD-evaluation will be made public in (hopefully near) future.

Thank you.

Questions, please?