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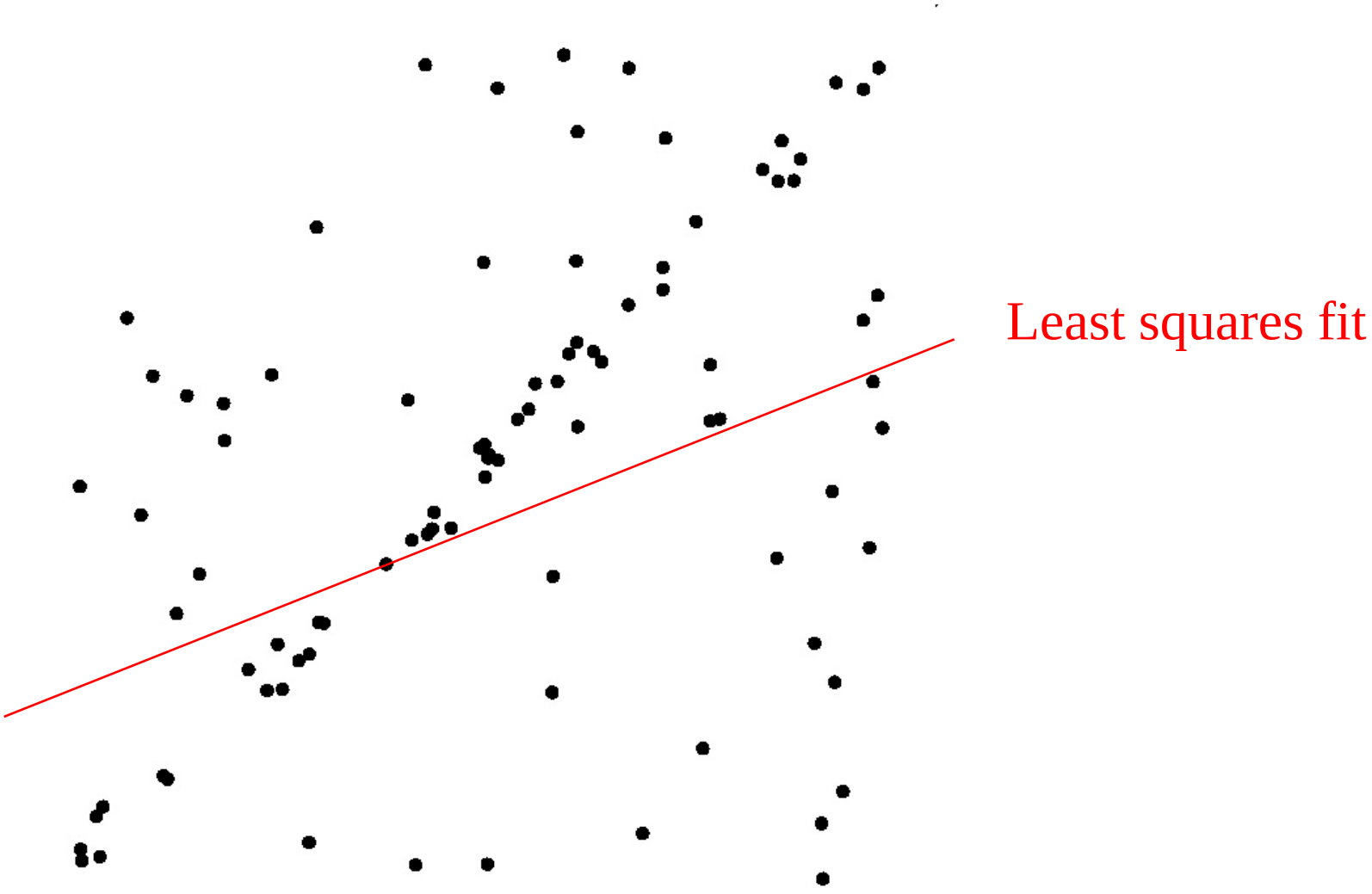
RANSAC

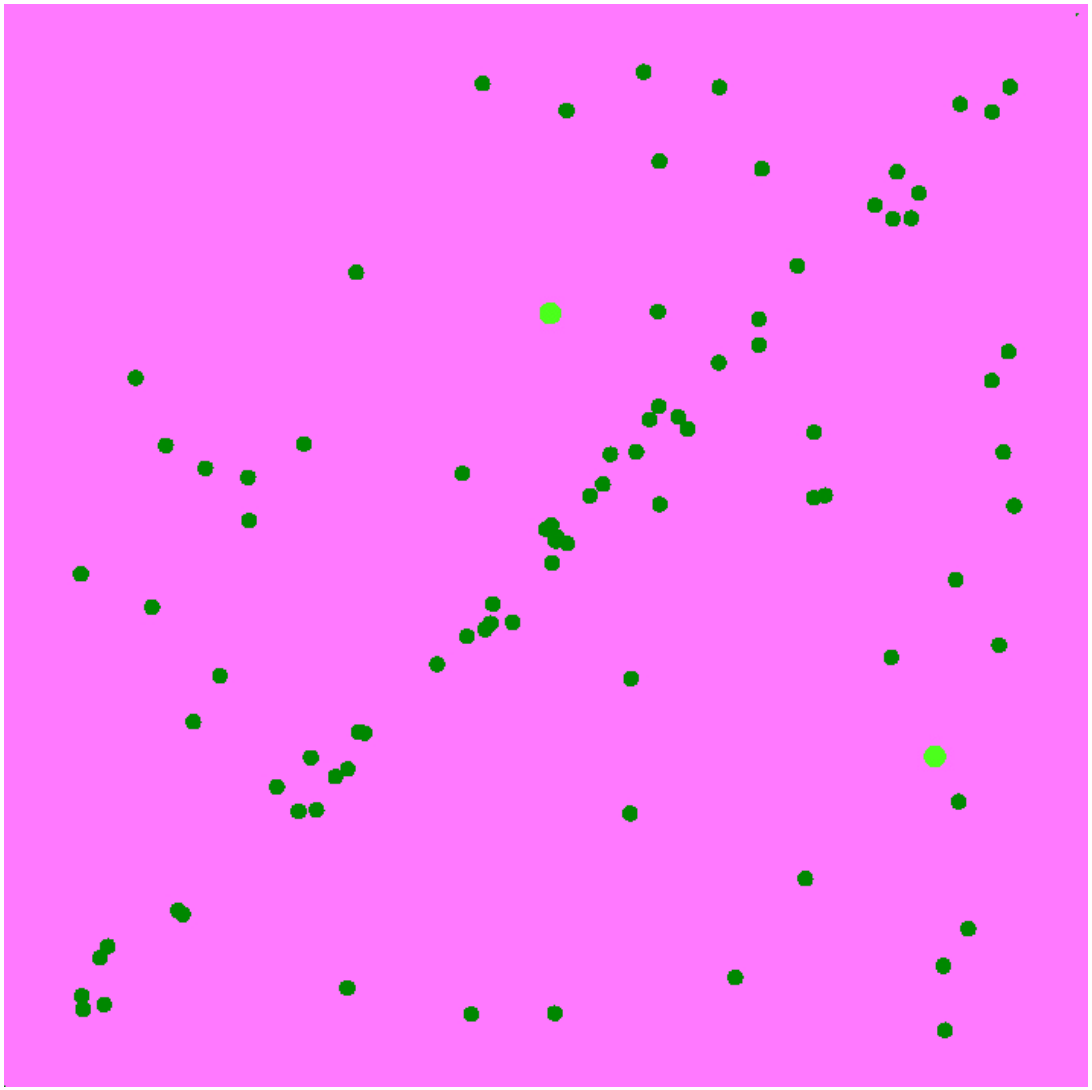
Robust model estimation from data contaminated by outliers

Ondřej Chum and Jiří Matas

Fitting a Line

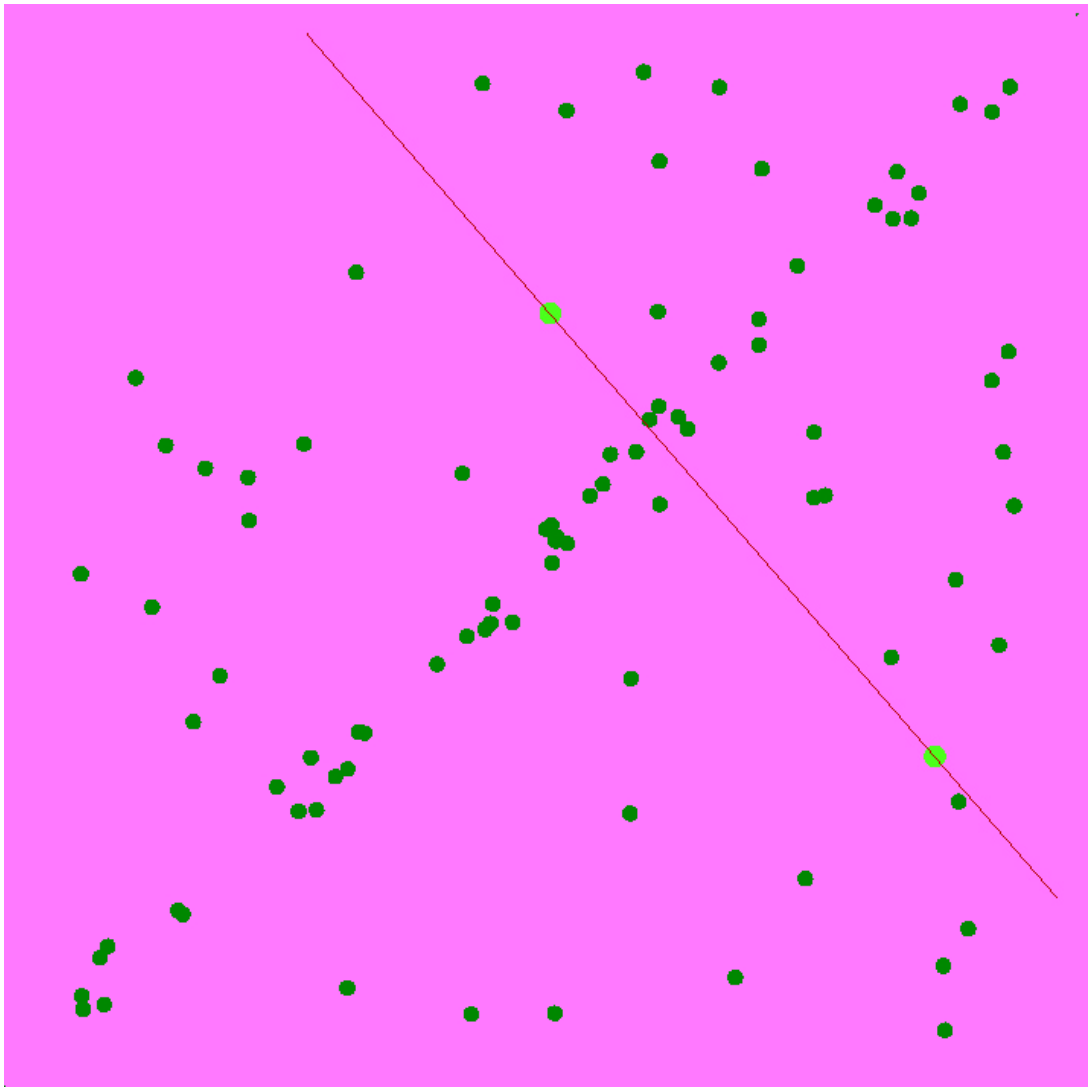


RANSAC



- **Select sample of m points at random**

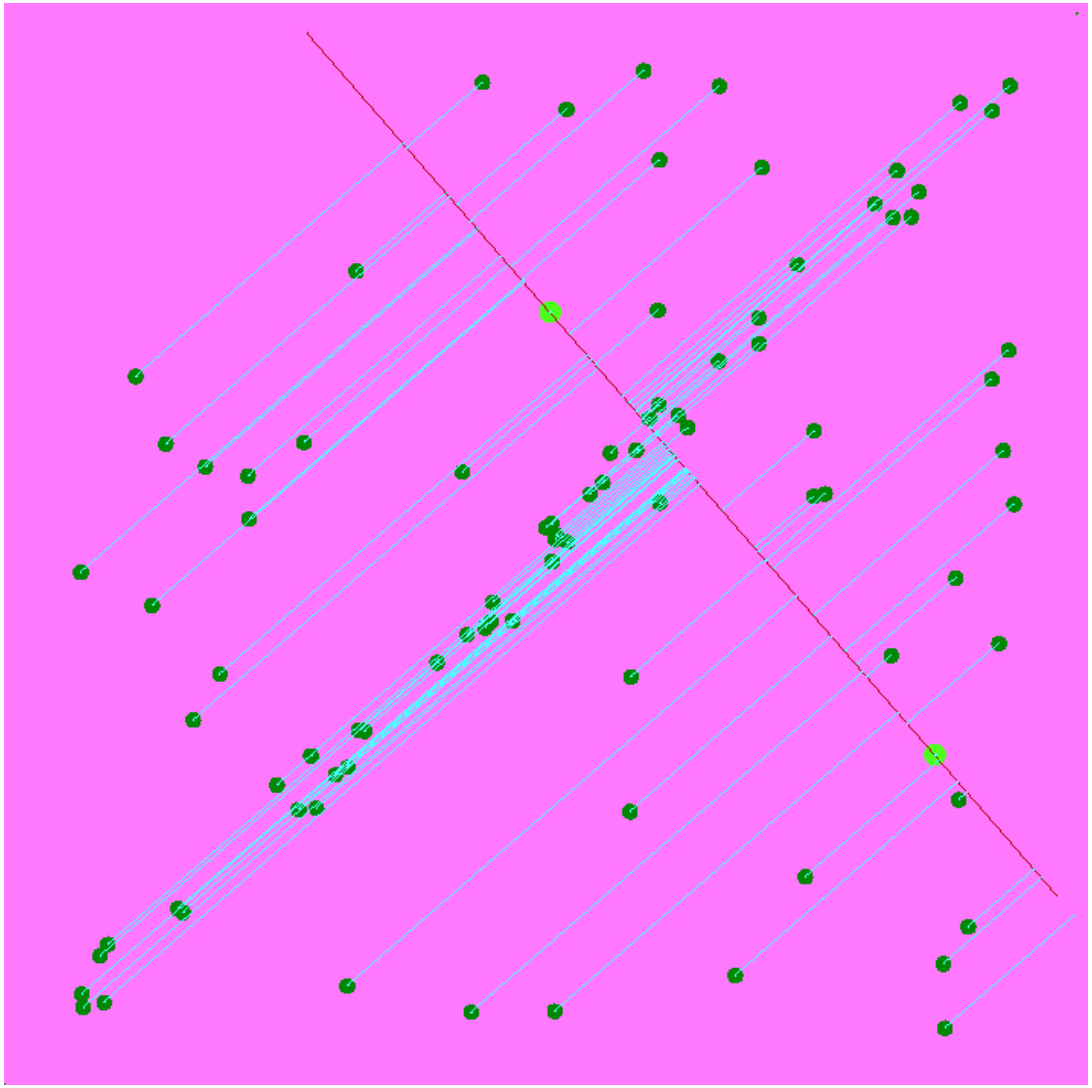
RANSAC



• Select sample of m points at random

• **Calculate model parameters that fit the data in the sample**

RANSAC

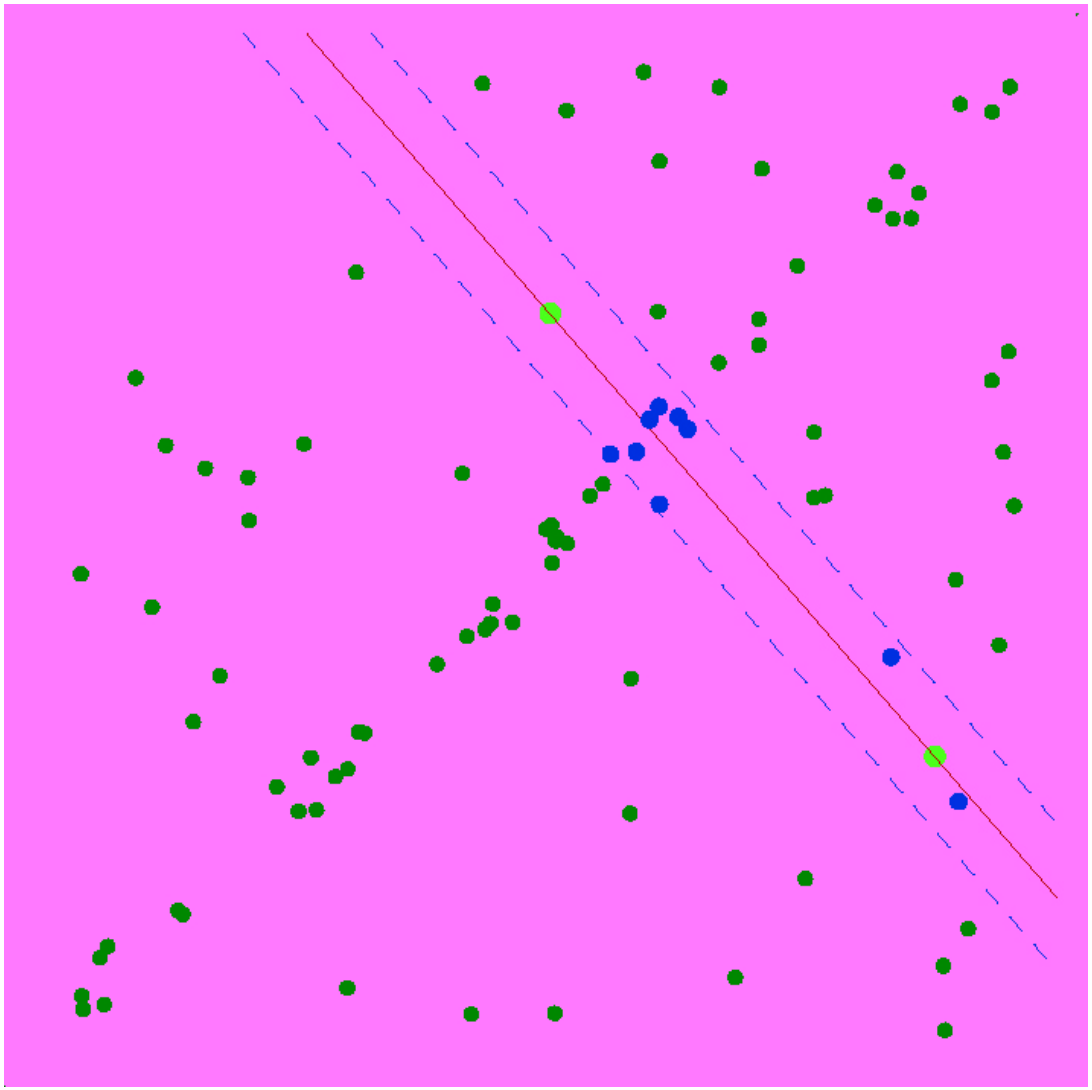


- Select sample of m points at random

- Calculate model parameters that fit the data in the sample

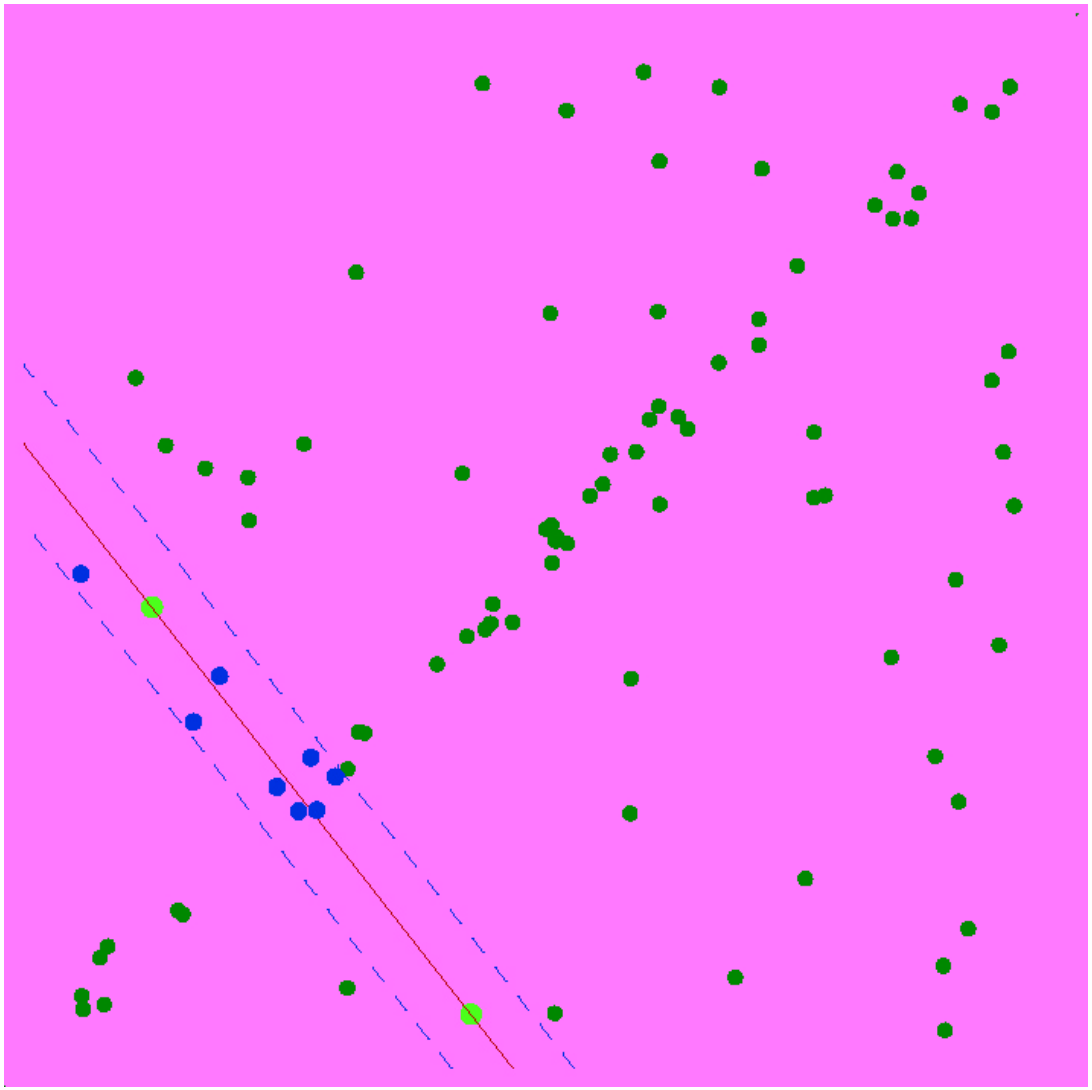
- **Calculate error function for each data point**

RANSAC



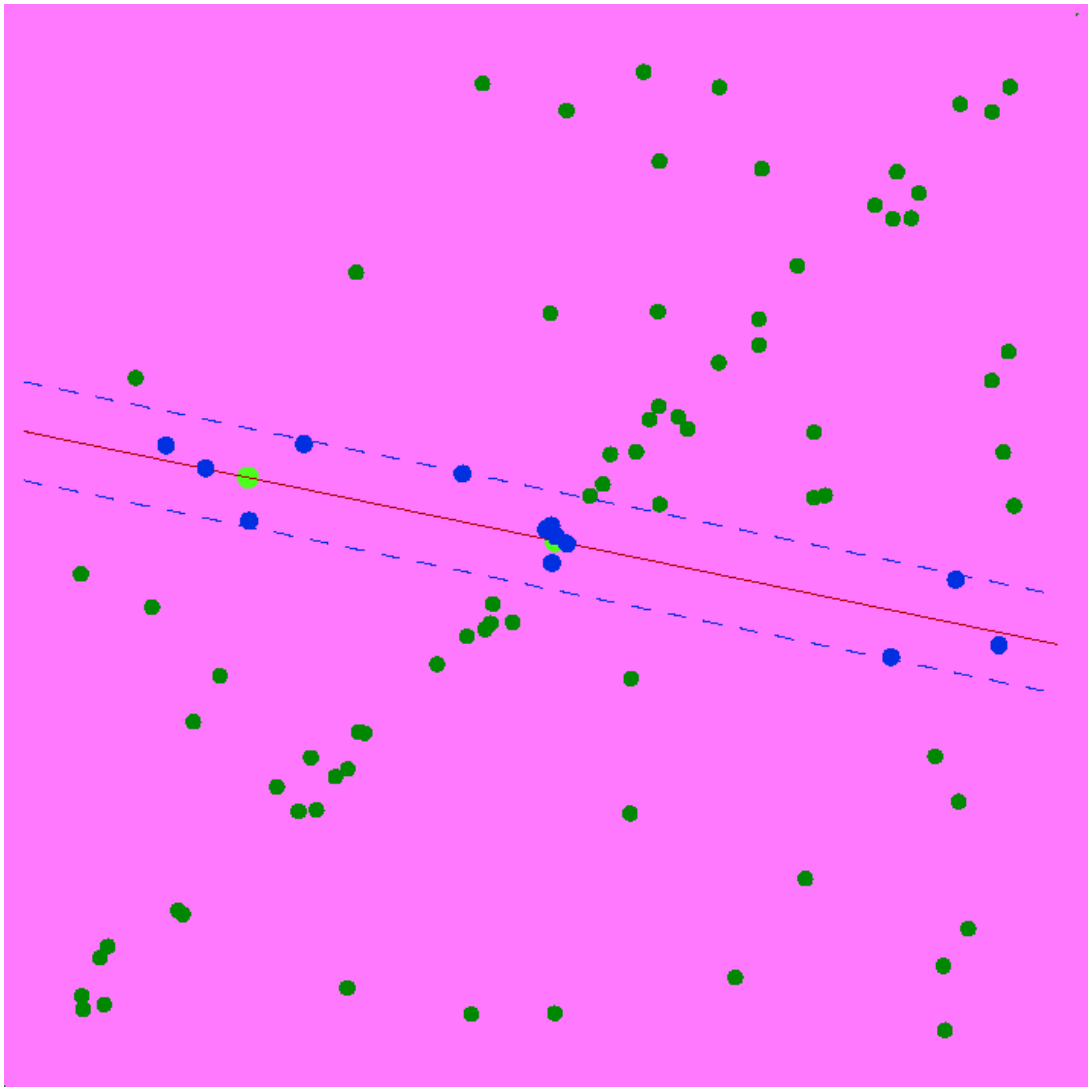
- Select sample of m points at random
- Calculate model parameters that fit the data in the sample
- Calculate error function for each data point
- **Select data that support current hypothesis**

RANSAC



- 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**

RANSAC



- 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**

How Many Samples?

On average

N … number of point
I … number of inliers
m … size of the sample

$$\text{P(good)} = \frac{\binom{I}{m}}{\binom{N}{m}} = \prod_{j=0}^{m-1} \frac{I-j}{N-j}$$

mean time before the success
E(k) = 1 / P(good)

How Many Samples?

With confidence p

How large k?

. . . to hit at least one pair of points on the line l with probability larger than p (0.95)

Equivalently

. . . the probability of not hitting any pair of points on l is $\leq 1 - p$

How Many Samples?

With confidence p

N … number of point
I … number of inliers
m … size of the sample

$$\text{P(good)} = \frac{\binom{I}{m}}{\binom{N}{m}} = \prod_{j=0}^{m-1} \frac{I-j}{N-j}$$

P(bad) = 1 – P(good)

P(bad k times) = $\big(1 - \text{P(good)}\big)^k$

How Many Samples?

With confidence p

$$\text{P(bad } k \text{ times)} = \big(1 - \text{P(good)}\big)^k \leq 1 - p$$

$$k \log \big(1 - \text{P(good)}\big) \leq \log(1 - p)$$

$$k \geq \log(1 - p) \,/\, \log \big(1 - \text{P(good)}\big)$$

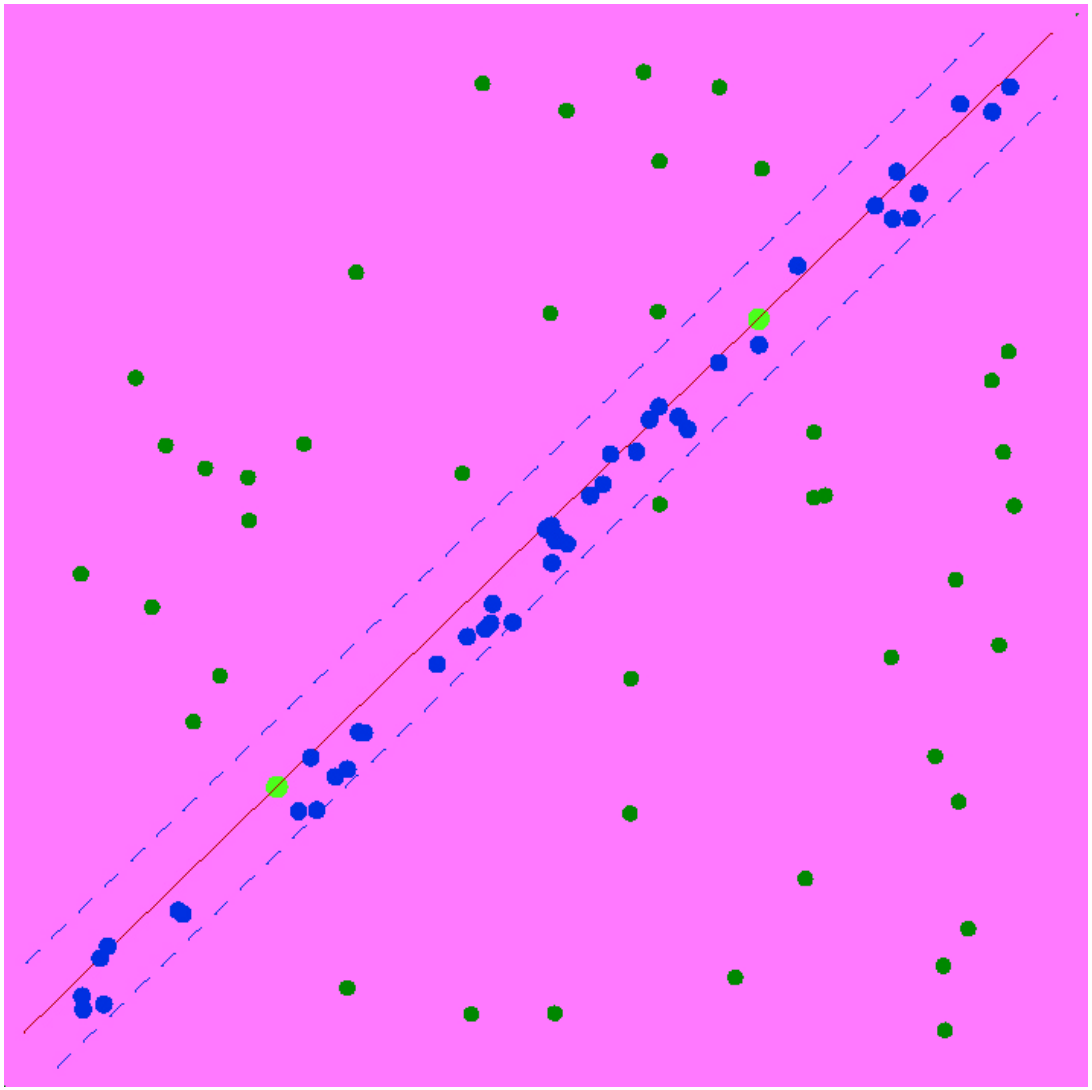
How Many Samples

I / N [%]

Size of the sample m

	15%	20%	30%	40%	50%	70%
2	132	73	32	17	10	4
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
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	∞	∞	∞	$2.70 \cdot 10^{16}$	$3.29 \cdot 10^{12}$	$4.71 \cdot 10^6$

RANSAC



$$k = \frac{\log(1-p)}{\log\left(1-\frac{I}{N}\frac{I\text{-}1}{N\text{-}1}\right)}$$

k … number of samples drawn

N … number of data points

I … time to compute a single model

p … confidence in the solution (.95)

RANSAC [Fischler, Bolles '81]

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{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

(III. Is the solution valid?)

RANSAC Issues:

RANSAC is a very general robust estimation method, any problems?

- **Correctness of the results. Degeneracy.**
  Solution: DegenSAC.
- **Stopping criterion?**:

Repeat until

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

- **Cost function:**
  Solutions: Least median of Squares, MINPRAN
- **Accuracy** (model parameters are estimated from minimal samples):
  Solution: Locally Optimized RANSAC
- **Speed:**
  Running time grows with
  1. number of data points,
  2. number of iterations (polynomial in inlier ratio)

  Addressing the problem:
  RANSAC with SPRT (WaldSAC), PROSAC

RANSAC – Time Complexity

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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

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

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

Randomised RANSAC [Matas, Chum 02]

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Repeat k/(1-α) times

1. Hypothesis generation
2. Model pre-verification $T_{d,d}$ test
   - Verify $d << N$ 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

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Model Verification is Sequential Decision Making

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

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

$x_i = 1$ x_i is consistent with the model

where

H_g - hypothesis of a `good` model (≈ from an uncontaminated sample)

H_b - hypothesis of a `bad` model, (≈ 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]

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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 $V = C \log(A)$

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

SPRT properties

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

$$\lambda_i = \prod_{j=1}^{i} \frac{P(x_j|H_b)}{P(x_j|H_g)} = \frac{P(x|H_b)}{P(x|H_g)}, x = (x_1, \ldots, x_i)$$

If $\lambda_i > A$ then $P(x|H_g) < P(x|H_b)/A$, therefore

$$\alpha = \int_{\lambda_i > A} P(x|H_g)dx < \int_{\lambda_i > A} P(x|H_b)/A dx =$$

$$= \frac{1}{A} \int_{\lambda_i > A} P(x|H_b)dx \leq \frac{1}{A} \int P(x|H_b)dx = \frac{1}{A}$$

WaldSAC

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Repeat $k/(1\text{-}1/A)$ times
1. Hypothesis generation
2. Model verification
   use SPRT

Time
t_M

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

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

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

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.

Optimal test (optimal A) given ε and δ

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Optimal A^*

$$A^* = \arg\min_A t(A)$$

Optimal A^* found by solving

$$\frac{\partial t}{\partial A} = 0$$

$$A^* = \frac{t_M}{\overline{m}_s C} + 1 + \log A^*$$

$$A^* = \lim_{n \to \infty} A_n$$

$$A_0 = \frac{t_M}{\overline{m}_s C} + 1, \quad A_{n+1} = \frac{t_M}{\overline{m}_s C} + 1 + \log A_n$$

SPRT

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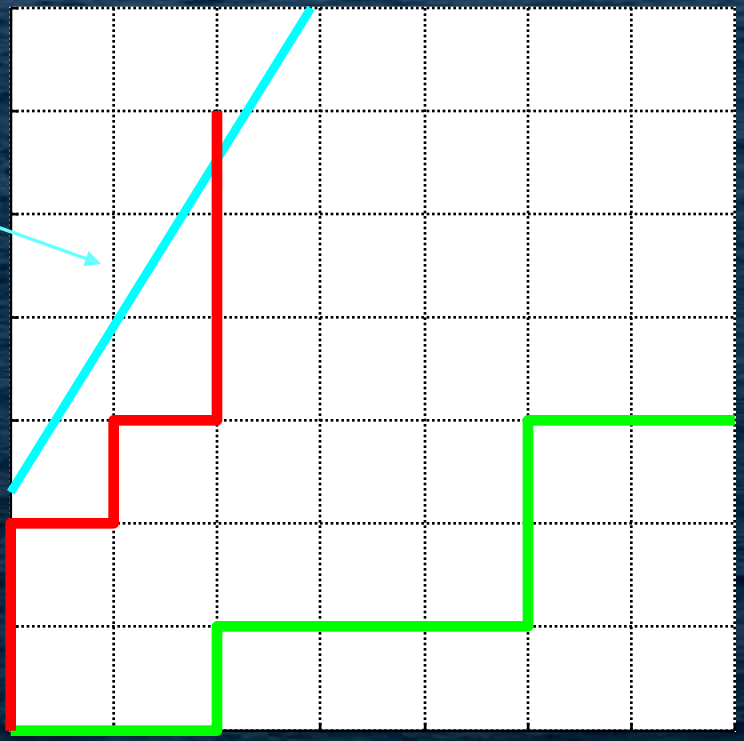

Note: the Wald's test is equivalent to series of $T(d, c)$, where $c = \lceil (\log A - d \log \lambda_1) / \log \lambda_0 \rceil$

Exp. 1: Wide-baseline matching

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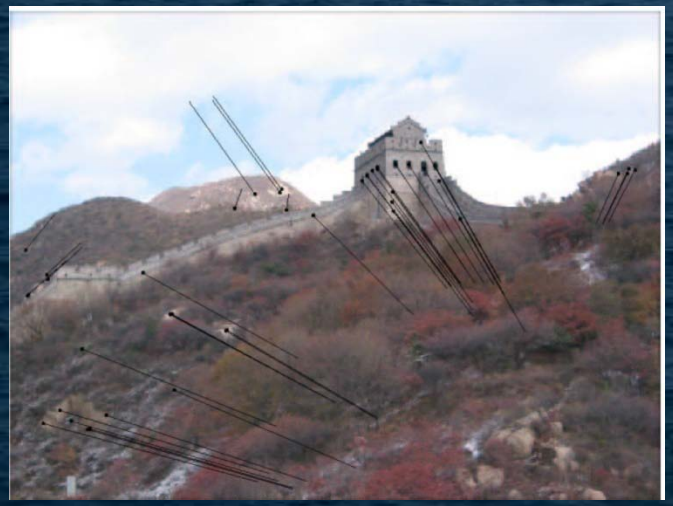

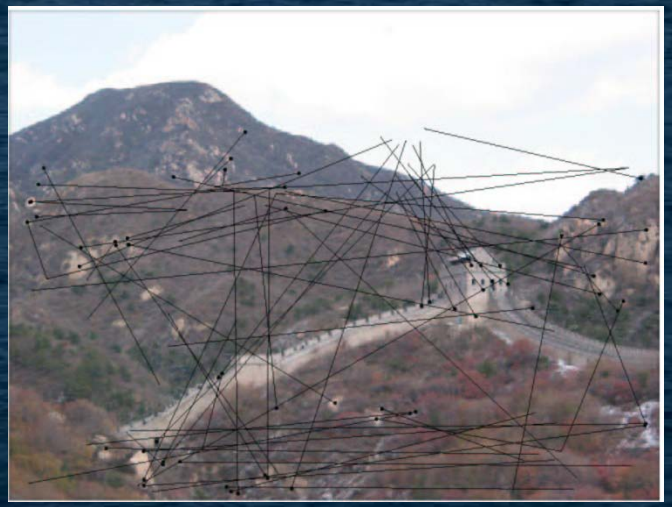

	samples	models	V	time	spd-up
R	2914	7347	110.0	1099504	1.0
R-R	7825	19737	3.0	841983	1.3
Wald	3426	8648	8.2	413227	2.7

Exp. 2 Narrow-baseline stereo

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	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

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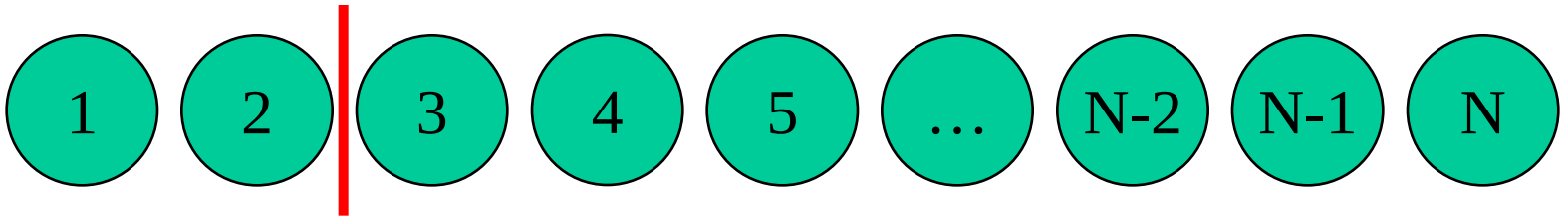
- The same confidence η in the solution reached faster (data dependent, $\approx$ 10x)
- No change in the character of the algorithm, it was randomised anyway.
- Optimal strategy derived using Wald`s theory for known ε and δ.
- Results with ε **and** δ estimated during the course of RANSAC are not significantly 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!

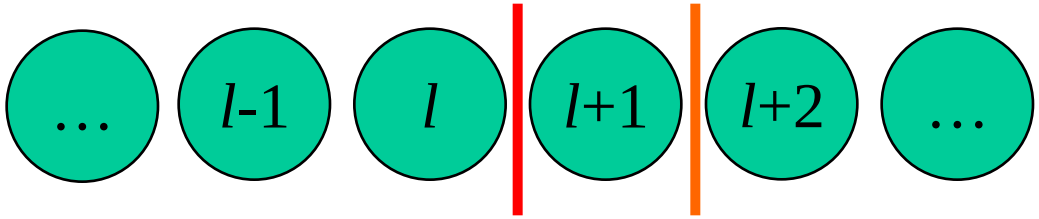
PROSAC – PROgressive SAmple Consensus

- Not all correspondences are created equally
- Some are better than others
- Sample from the best candidates first



Sample from here

PROSAC Samples



Draw T_l samples from (1 … l)
Draw T_{l+1} samples from (1 … l+1)

Samples from (1 … l) that are not from (1 … l+1) contain l+1

Draw T_{l+1} - T_l samples of size m-1 and add l+1

Locally Optimized RANSAC

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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 near perfect agreement with theoretical (i.e. optimal) performance

(ii) lower sensitivity to noise and poor conditioning.

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

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

Locally Optimized RANSAC

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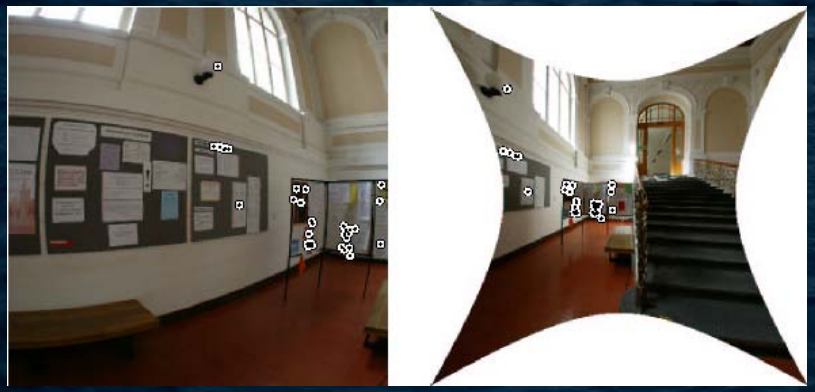
Estimation of (approximate) models with lower complexity (less data points in the sample) followed by LO step estimating the desired model speeds the estimation up significantly.

The estimation of epipolar geometry is up to 10000 times faster when using 3 region-to-region correspondences rather than 7 point-to-point correspondences.



Fish-eye images by Braňo Mičušík

Simultaneous estimation of radial distortion and epipolar geometry with LO is superior to the state-of the art in both speed a precision of the model.

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

Degenerate Configurations

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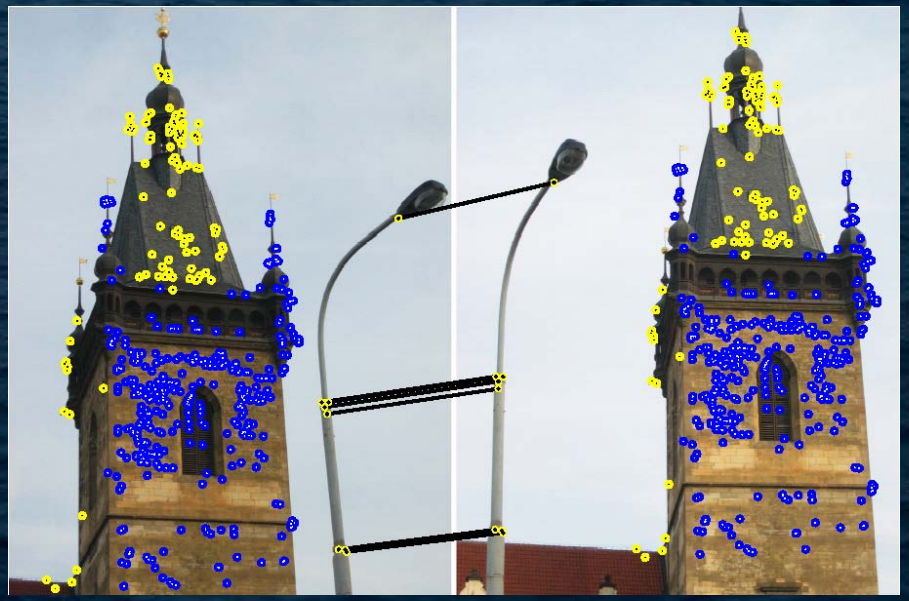
The presence of degenerate configuration causes RANSAC to fail in estimating a correct model, instead a model consistent with the degenerate configuration and some outliers is found.

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

Chum, Werner, Matas: Epipolar Geometry Estimation unaffected by dominant plane, *CVPR* 2005

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