Genetic Algorithm SAmple Consensus (GASAC) -
A Parallel Strategy for Robust Parameter Estimation

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25 Years of RANSAC
Workshop in conjunction with CVPR

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Introduction

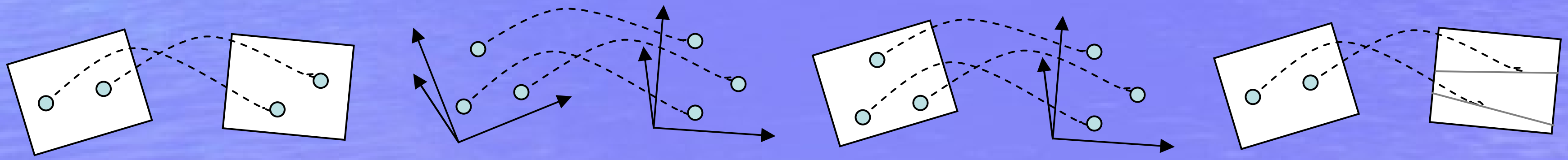
- New general approach GASAC for robust parameter estimation
- Based on the combination of **RANSAC-like** parameter estimation with an **evolutionary optimization** technique
- Applied to problems in **computer vision**
- Estimation of **geometric relations**
- **Applications:**
  - Camera calibration
  - Narrow and wide-baseline stereo matching
  - Structure and motion estimation
  - Object recognition tasks

Challenge

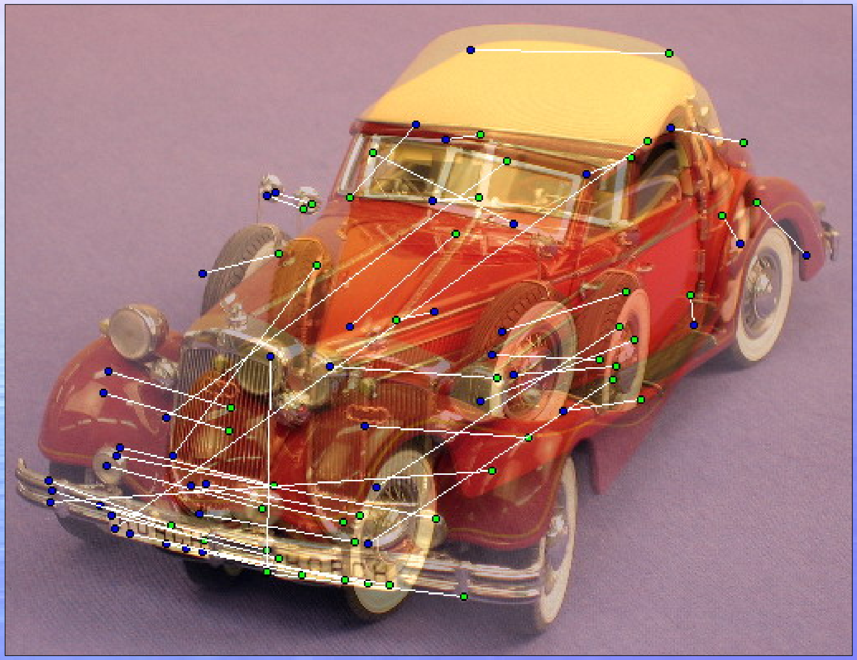
- **Automatically finding correspondences:**
  - At the beginning of an image matching process only the correlation of local descriptors is available
  - Mismatches (*outlier*) cannot be avoided and must be removed
- **Assumptions:**
  - We have a data set with putative feature correspondences
  - A subset is consistent with some geometric relation (*model*)
- **Task:**
  - Search for subsets of matches consistent with the model (*inlier*)
  - Estimate the transformation parameters

Projective Transformations

Transformations	**Parameter** p	**Minimum Points** m
2D-Homography $\mathbf{H}$	8	4
3D-Homography $\mathbf{H}$	15	5
Essential matrix $\mathbf{E}$	5	5
Projection matrix $\mathbf{P}$	11	6
Trifocal tensor $\mathcal{T}$	18	6
Fundamental matrix $\mathbf{F}$	7	7



Matches Consistent with Model



Tentative matches using local image descriptors (contain 42% outliers)

Robust estimated matches satisfying the epipolar constraint (F-Matrix)

Overview

- **Related Work**
- **Robust Parameter Estimation**
  - M-Estimators (Huber, Tukey)
  - Least Median of Squares
  - Monte-Carlo Method (RANSAC)
- **Genetic Algorithm GASAC**
  - Representation of the Gene Pool
  - Genetic Operators (Selection, Cross-over, Mutation)
  - Reproduction Plan
  - Adaptive Termination Criterion
- **Experimental Results**
  - Comparison of RANSAC with GASAC
- **Conclusions and Outlook**

RANSAC Related Work

- **RANSAC** *(RANdom SAmple Consensus)*
  by Fishler & Bolles, 1981
- **Various Improvements**
  - **MLESAC** (*Maximum Likelihood Estimation SAC*)
    by Torr & Zisserman, 2000
  - **MAPSAC** (*Maximum A Posteriori SAC*) by Torr, 2002
  - **Preemptive RANSAC** by Nistér, 2003
  - **Guided-MLESAC** by Tordoff & Murray, 2005
  - **PROSAC** (*PROgressive SAC*) by Chum & Matas, 2005
  - **R-RANSAC** (*Randomized RANSAC*) with **SPRT**
    (*Sequential Probability Ratio Test*) by Matas & Chum, 2005
  - **Bail-out Test** for RANSAC by Capel, 2005

GA Related Work

- **Evolutionary Strategy**
  - **Mutation selection strategy** by Rechenberg, 1973
  - **GA** (*Genetic algorithm*) by Holland, 1975
  - **GA** for geometric relations by Saito and Mori, 1995
  - **Adaptation** genetic operator by Chai and Ma, 1998
  - **sGA / mGA** (*Simple / Messy GA*) by Hu et al., 2002/4

Influence Functions

- Over-determined homogeneous equation system

  $$\mathbf{A}\mathbf{x} = \mathbf{e}, \quad \mathbf{e} \neq \mathbf{0}$$

  Error of the i-th observation: e_i

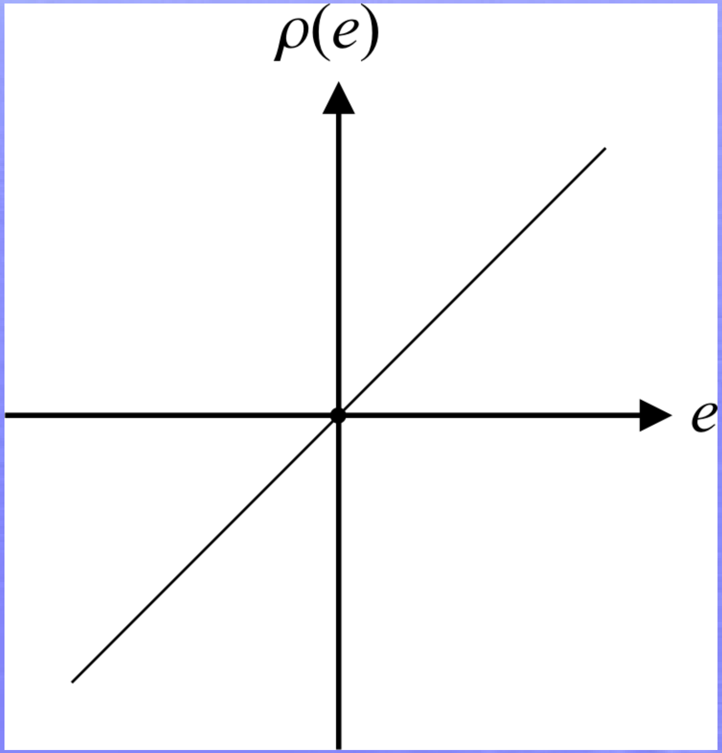
- **Least-Squares-Method:**

  $$C = \sum_i e_i^2$$

- **Problem:** The sum of squared errors e_i is a sensitive measure

- **Objective:** Find a suitable influence function

  $$C = \sum_i \rho\left(e_i\right)$$

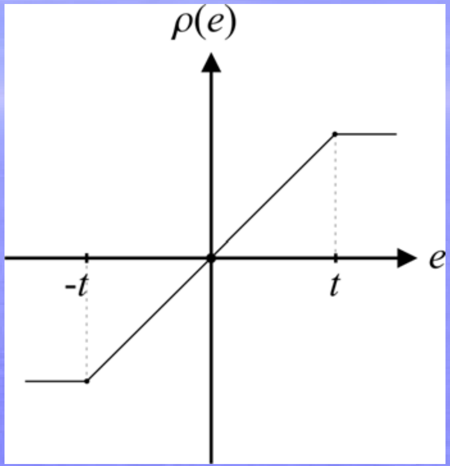


M(aximum-Likelihood)-Estimators

- Min-Max-Function of **Huber**

  the influence is limited to a **constant** value:

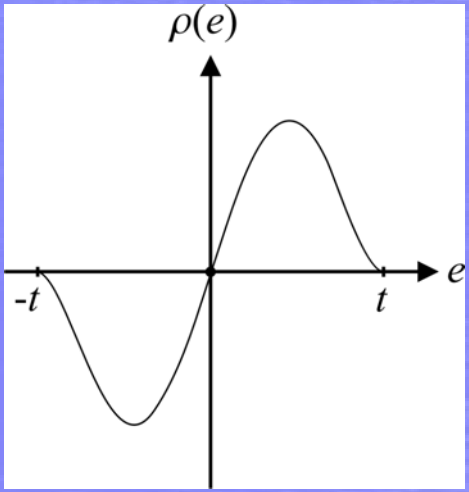
$$\rho\left(e\right) = \min\left(t, \max(e, -t)\right)$$



- Function of **Tukey**

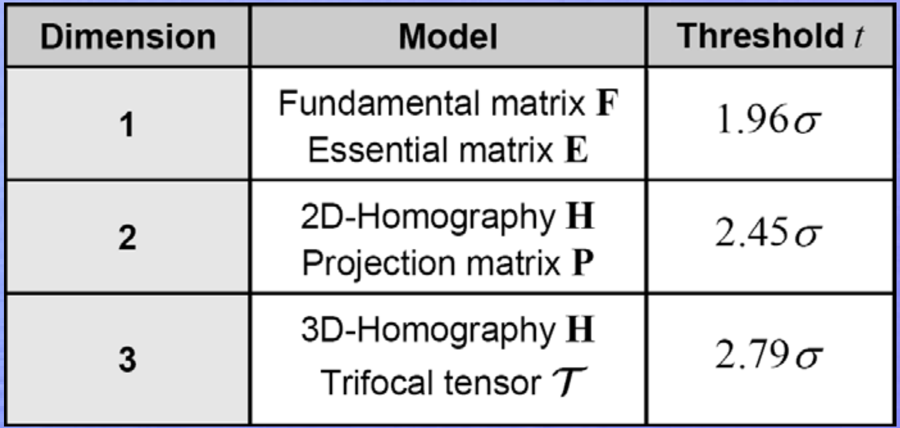
  the influence **reduces** again
  after a certain value:

$$\rho\left(e\right) = \begin{cases} e(t^2 - e^2)^2, & \left|e\right| < t \\ 0, & \text{otherwise} \end{cases}$$



Automatic Threshold

- **Thresholds** of the χ^2 distribution (confidence 95%)



Dimension	Model	Threshold t
1	Fundamental matrix $\mathbf{F}$ Essential matrix $\mathbf{E}$	1.96σ
2	2D-Homography $\mathbf{H}$ Projection matrix $\mathbf{P}$	2.45σ
3	3D-Homography $\mathbf{H}$ Trifocal tensor $\mathcal{T}$	2.79σ

- **Robust Standard Deviation**

$$\sigma = 1.4826 \cdot \left(1 + \frac{5}{n-p}\right) \cdot \operatorname*{median}_{i} \left| e_i \right|$$

With n **observations** and parameter space **dimension** p

Other Robust Methods

- **Least-Median-of-Squares Method** (LMedS)

$$C = \underset{i}{\operatorname{median}}\, e_i^2 \qquad e_1^2 \le e_i^2 \le e_n^2 \quad \text{for} \quad i = \frac{n}{2}$$

- Tolerates up to 50% outliers

- No threshold must be defined

- **Monte-Carlo Method** (RANSAC)

$$\rho(e) = \begin{cases} 1, & |e| < t \\ 0, & \text{otherwise} \end{cases}$$

Maximize the number of data, which is consistent to the minimal solution

Statistic Termination Criterion

- It is not feasible to test **all possible** combinations $\binom{n}{k} = \frac{n!}{k!\,(n-k)!}$ for n observations with k unknown parameters
- **Fraction of outliers** in the data set S with n elements:

$$\varepsilon = 1 - \frac{C}{n}$$

- **Confidence**, that at least **one minimal selection** with m elements out of R data sets contains **no outlier:**

$$p = 1 - \left(1 - (1 - \varepsilon)^m\right)^R$$

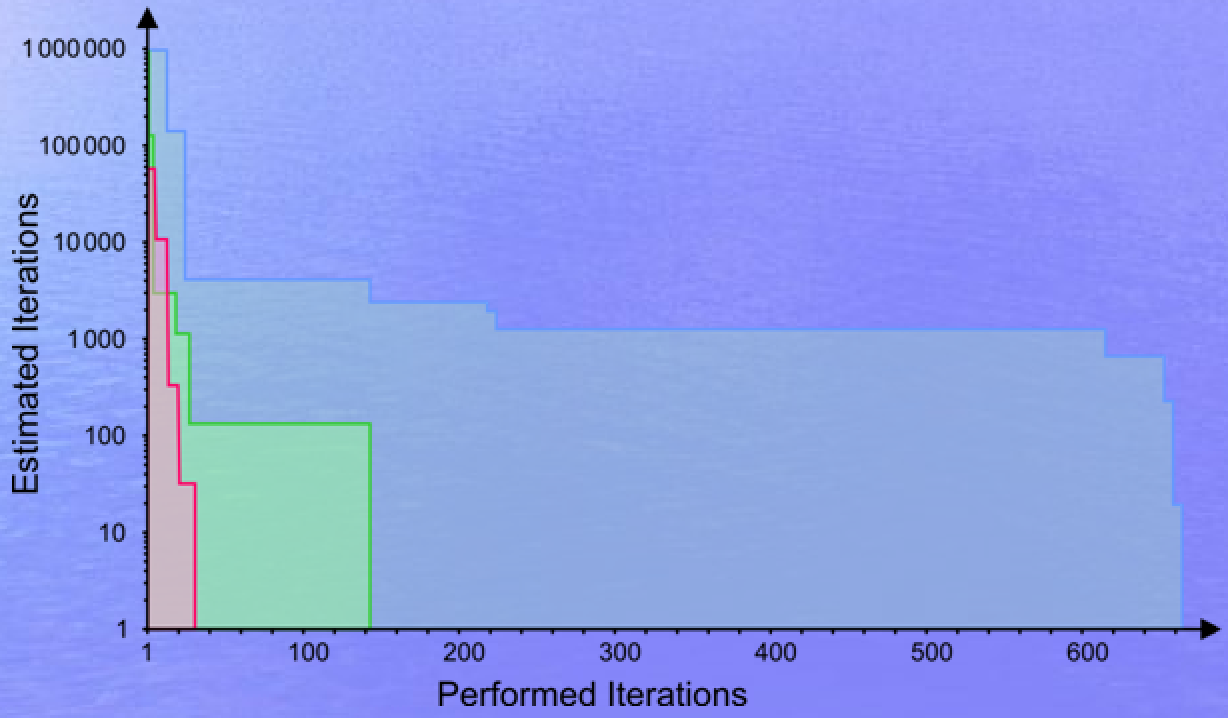
- **Minimal number** of the tries: $R = \dfrac{\ln(1-p)}{\ln\left(1-(1-\varepsilon)^m\right)}$

Termination Criterion Example

- Linear computation of the fundamental matrix (m = 8) using n = 25 image correspondences
- All possible attempts: $\binom{25}{8} = 1\,081\,575$
- Tolerating 45% outliers (ε = 0.45)
- Confidence of an error-free selection 99% (p = 0.99)
- Estimated attempts R = 548

Adaptive Termination Criterion

- **Idea:** Update the number of required samples R each iteration using the actual fraction of outliers ε_i



- **Problem:** With strongly disturbed data the number is too small !

Genetic Algorithm

- **Biologically motivated** approach for the solution of optimization problems
- Imitates the successful principles of the evolution
- **Philosophy:**
  - Parameters of a problem can be considered as a construction plan of an organism (chromosome)
  - Under the given environmental condition
    - Survivability (fitness)
    - Evolutionary changes

yield a better adapted generation

Gene Pool Representation

- **Population $\mathbf{G}$:** Consists of several individuals
- **Individual**: Is characterized by a chromosome

$$\mathbf{g} = \left(g_1, \ldots, g_m \right)$$

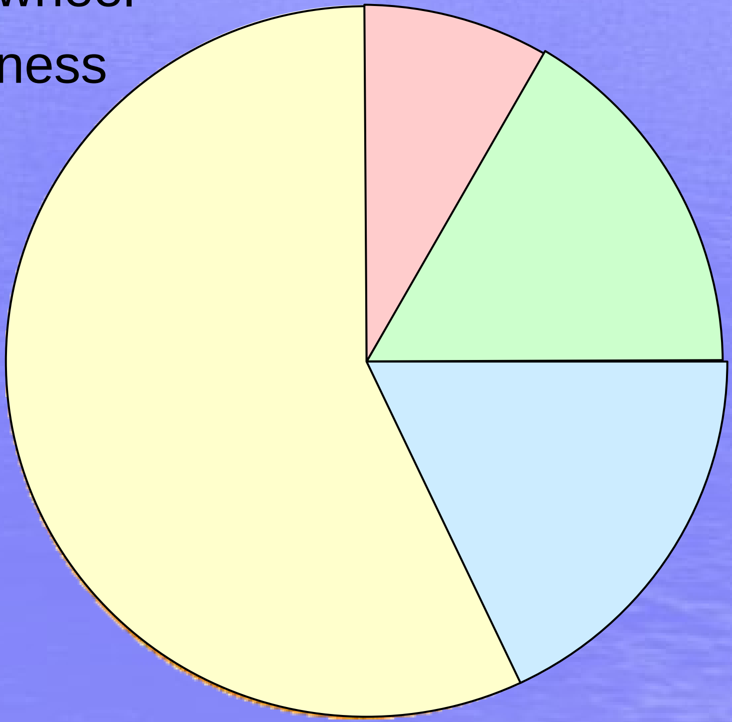
- **Chromosome**: Consist of m elements, which are called genes
- **Gene**: For n corresponding points $\mathbf{x}_i \leftrightarrow \mathbf{x}'_i$ the **index** i is used

$$g_k \in \left\{ 1, \ldots, n \right\} \quad \text{for} \quad k = 1, \ldots, m$$

  which may occur **only once** within one chromosome
- **Fitness:** Ability to prevail within the gene pool
  - **Geometrical error** for all points using a **robust cost function**
  - A small value corresponds to a large fitness

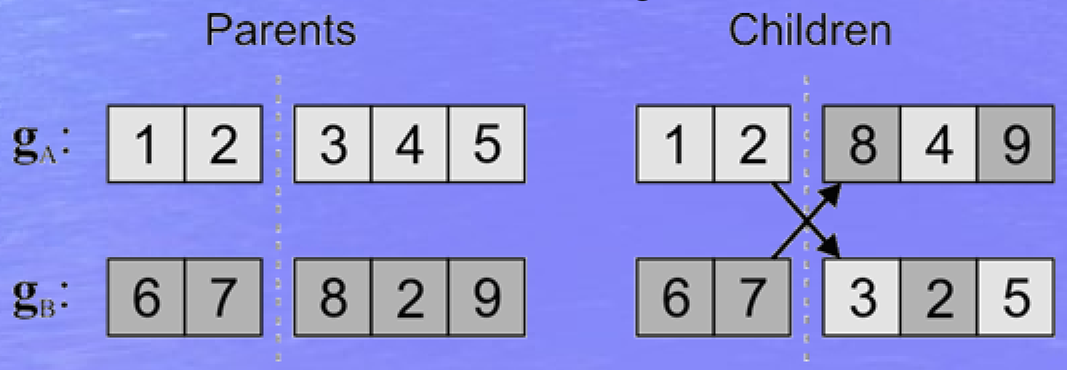
Selection Operator

- Select parents for reproduction
- Roulette wheel:
  - Each individual get a sector on the wheel
  - The sector size in related to their fitness
  - The position is chosen randomly



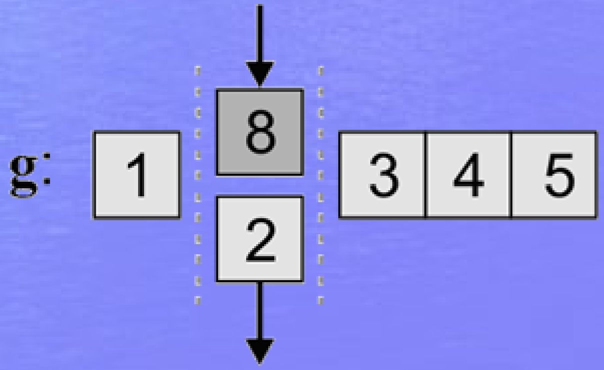
Crossover Operator

- Two chromosomes are cut apart and built up over cross again
- The **execution** of the operation and the **section point** are selected randomly
- Only those pairs of genes are considered, which ensure an **individual occurrence**
- The **crossover probability** P_C is 0.5



Mutation Operator

- **Prevent** convergence in a suboptimal **local minimum**
- Randomly **changing of genes** supply new gene material
- It must also be ensured that **no double genes** result
- The **mutation probability** P_M of a gene is $\frac{1}{2m}$



Technical Modifications

- **Change Mechanisms**
  - The **sequence** of the genes is **not important**
  - The **length** of the chromosomes remains **constant**
  - **Inverting** & **recombination** operators are neglected
- **Convergence Criterion**
  - **Removing double individuals** from the gene pool accelerates the optimization process
  - A solution reached cannot worsen again, if the **chromosome with best fitness stays unmodified** in the gene pool

Reproduction Plan (Algorithm)

Prerequisites:

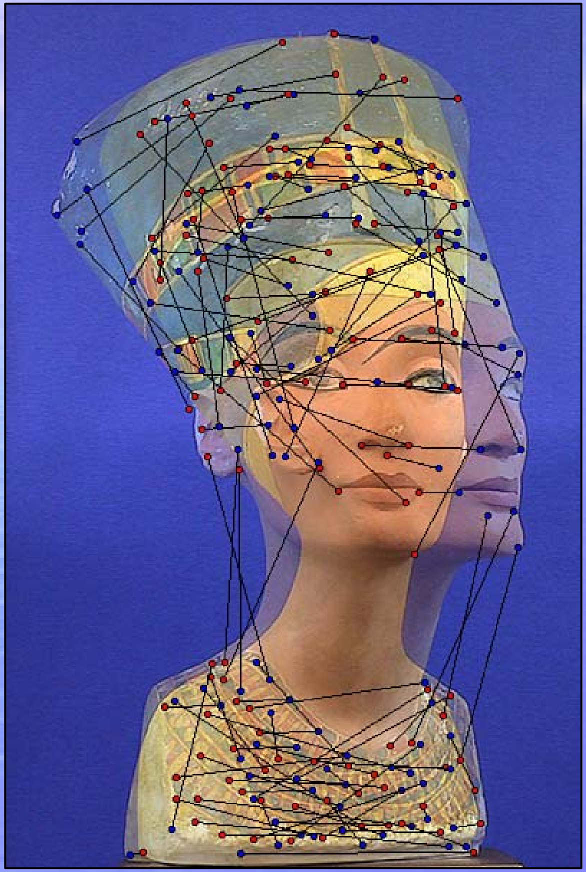
- a set *S* of *n* correspondences (*e.g. Matched image coordinates*)
- a function for model parameter estimation (*e.g. F-Matrix, Trifokal-Tensor*)
- a robust cost function *C* (*e.g. Huber, Tukey, LMedS*)

```
for $i$=1 to $N$ initial individuals do
    $\mathbf{G}_i$ = Sample randomly a subset of $m$ genes from $S$
    Generate model hypothesis from this minimal set
    Evaluate consensus score using robust $C$
end

for $i$=1 to $R$ cycles do
    for $j$=1 to $M/2$ new individuals do
        Select two parents from $\mathbf{G}$ in relation to their fitness
        Apply crossover operator with probability $P_C$
        for child$_1$ and child$_2$ do
            Apply mutation operator with probability $P_M$
            Generate model hypothesis
            Evaluate model using robust $C$
        end
    end
    Clone best individual in $\mathbf{G}$ unmodified
    Reduce $\mathbf{G}$ to the best $N$ individuals
end

Return model of that individual in $\mathbf{G}$ with best fitness $C_{min}$
```

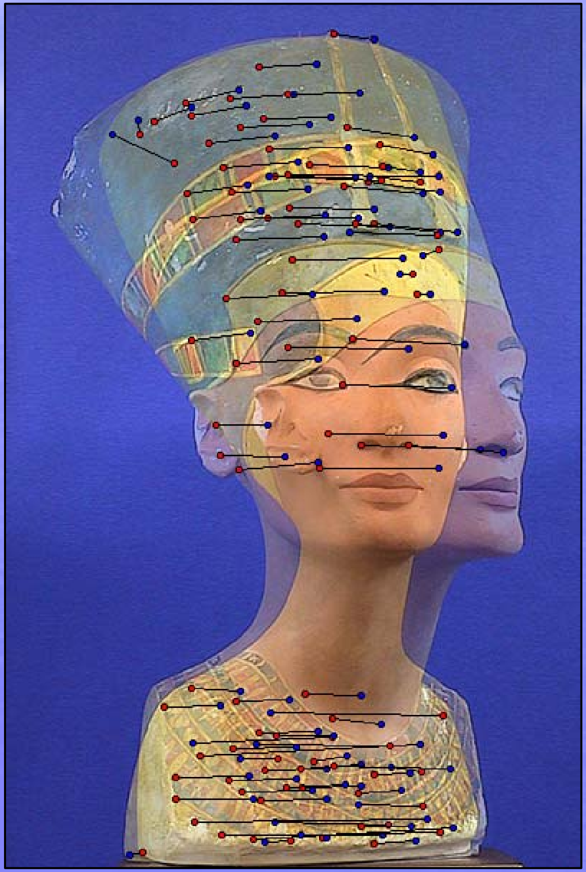
Comparison RANSAC/GASAC

- 25 image pairs of the Nofretete bust were prepared with 50 strongly disturbed point correspondences
- Computation of the fundamental matrix with the **7-point-algorithm** using **LMedS** minimization of the symmetrical epipolar distance
- Exactly **5000 model hypotheses** were evaluated (N = 200 and M = 400 in 12 cycles)
- All image pairs were evaluated 100 times

Bust of Nofretete

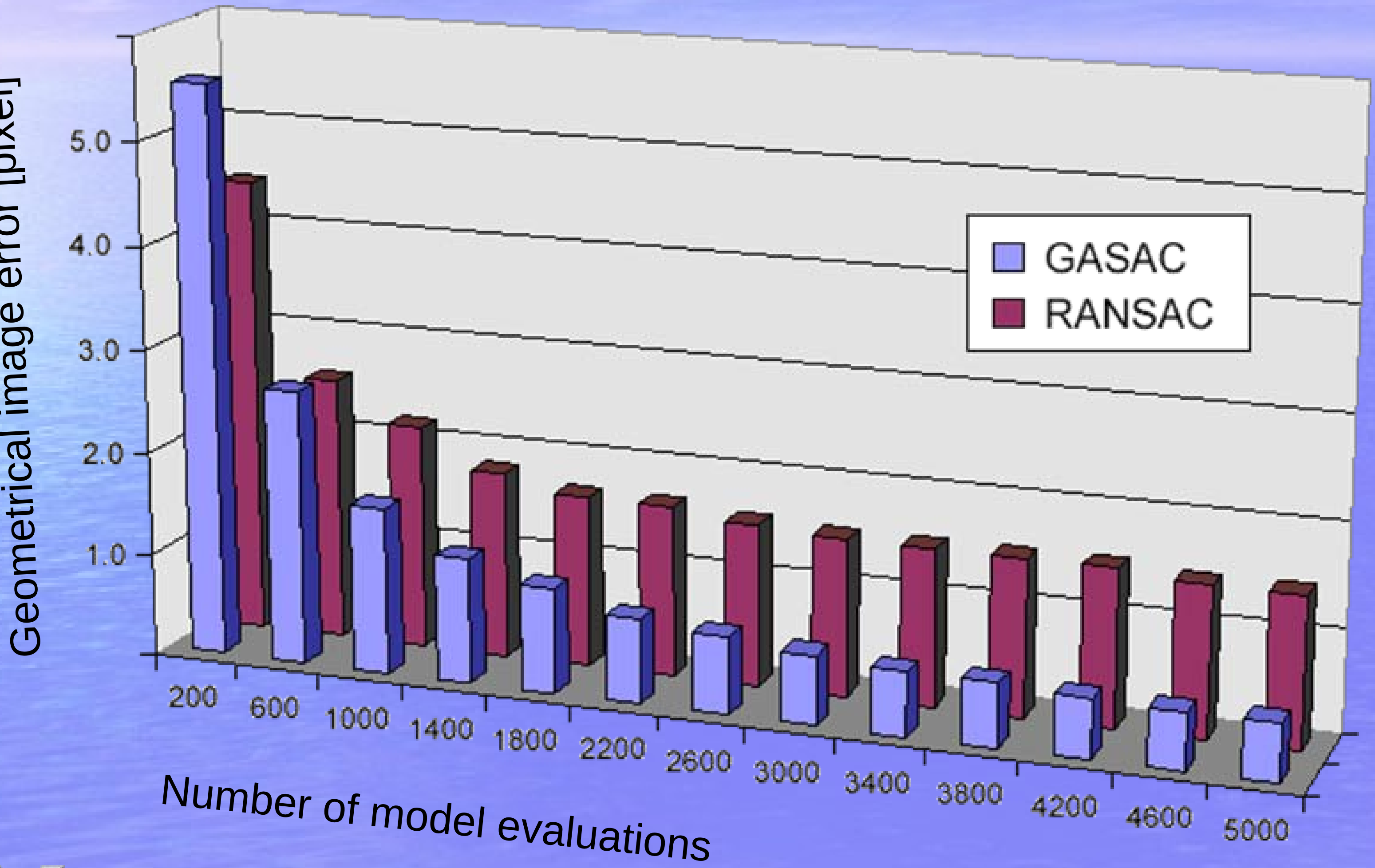


a.) Tentative matches using
local image descriptors



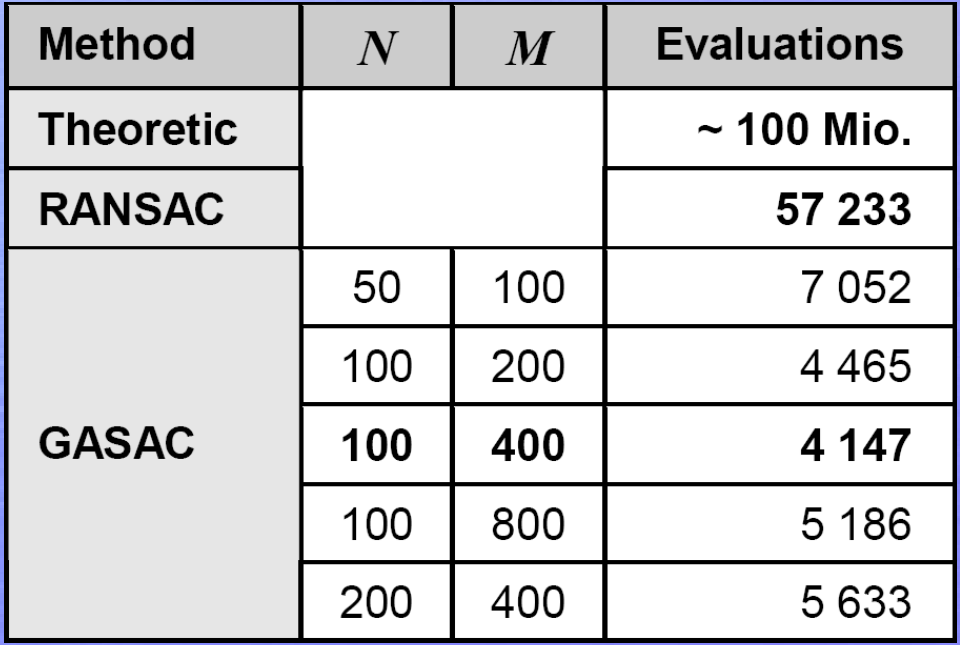
b.) Robust estimated matches
satisfying the epipolar constraint

Geometrical Image Error



Number of Evaluations

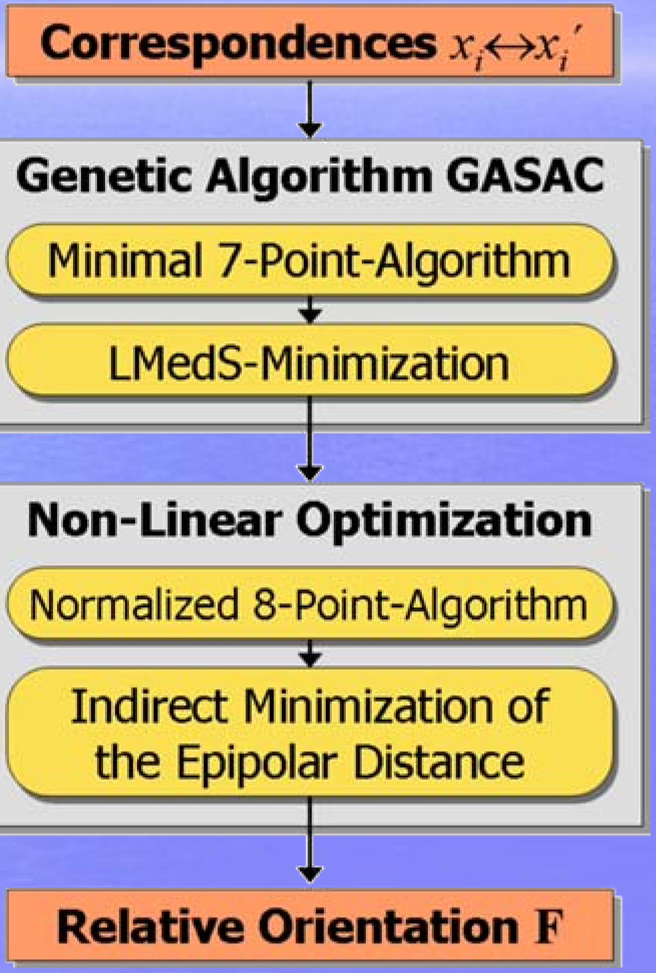
- Evaluations for reaching the **optimal solution**:



Method	***N***	***M***	**Evaluations**
Theoretic			**~ 100 Mio.**
RANSAC			**57 233**
GASAC	50	100	7 052
	100	200	4 465
	100	**400**	**4 147**
	100	800	5 186
	200	400	5 633

- The user defined sizes of the **initial population** N and the **next generation** M are not the crucial factor

Robust Orientation Procedure



Correspondences $x_i \leftrightarrow x_i'$

Genetic Algorithm GASAC

Minimal 7-Point-Algorithm

LMedS-Minimization

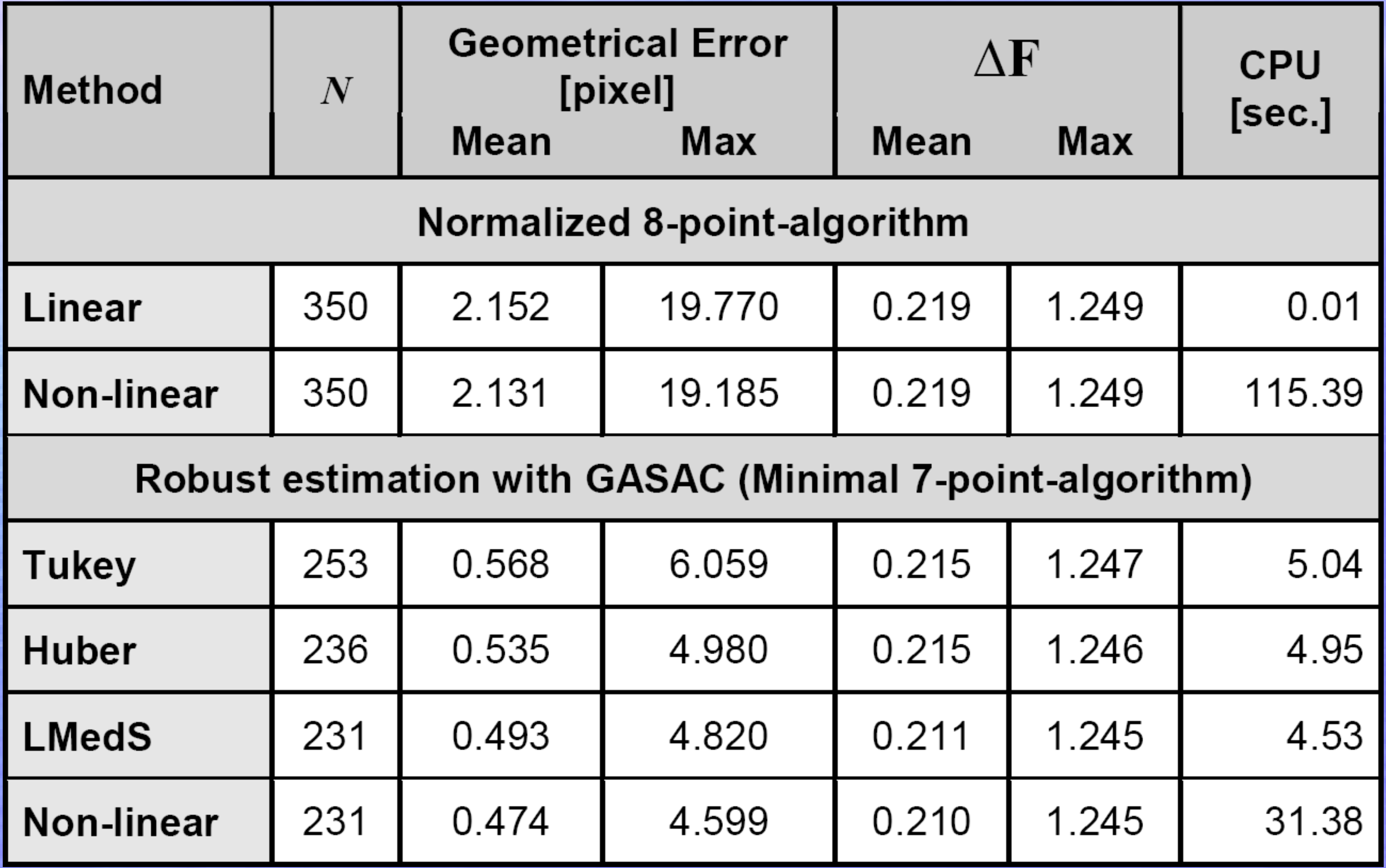
Non-Linear Optimization

Normalized 8-Point-Algorithm

Indirect Minimization of the Epipolar Distance

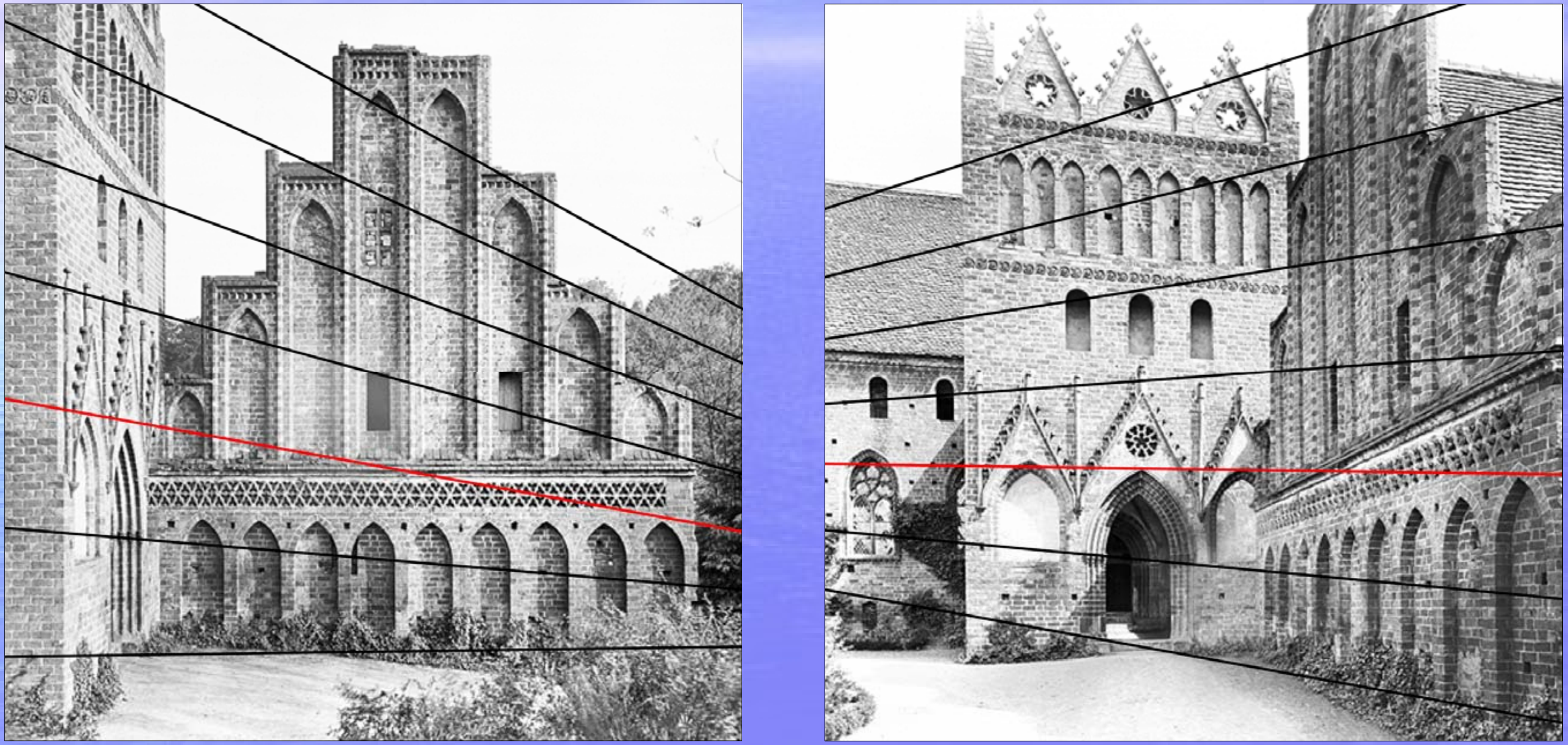
Relative Orientation $\mathbf{F}$

Computation of the F-Matrix



Method	N	Geometrical Error [pixel] Mean	Geometrical Error [pixel] Max	$\Delta\mathbf{F}$ Mean	$\Delta\mathbf{F}$ Max	CPU [sec.]
Normalized 8-point-algorithm						
Linear	350	2.152	19.770	0.219	1.249	0.01
Non-linear	350	2.131	19.185	0.219	1.249	115.39
Robust estimation with GASAC (Minimal 7-point-algorithm)						
Tukey	253	0.568	6.059	0.215	1.247	5.04
Huber	236	0.535	4.980	0.215	1.246	4.95
LMedS	231	0.493	4.820	0.211	1.245	4.53
Non-linear	231	0.474	4.599	0.210	1.245	31.38

Monastery in Chorin

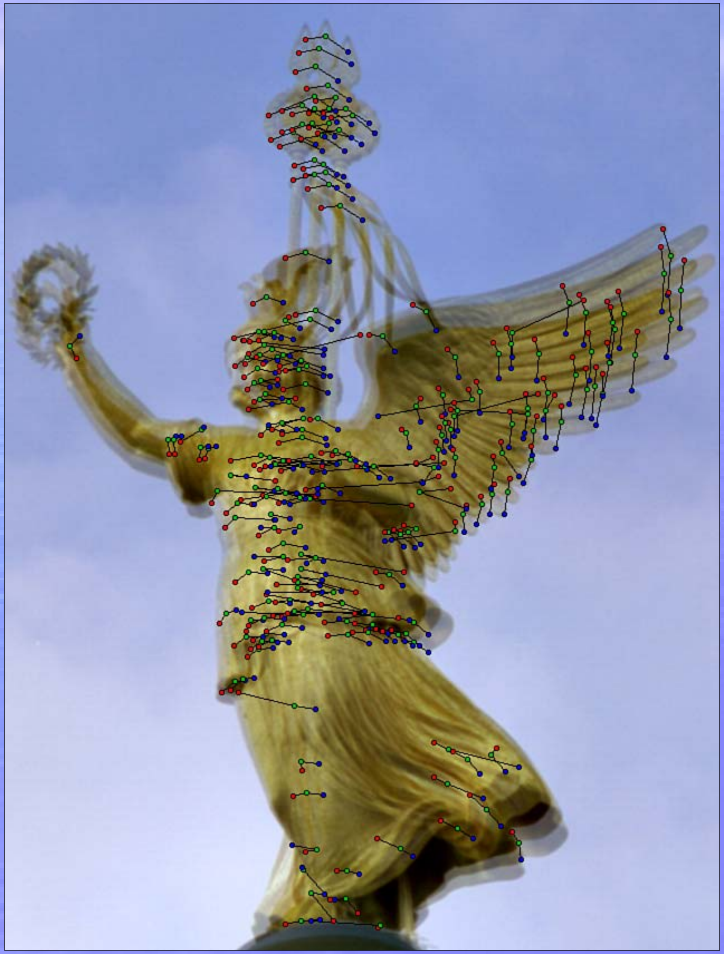


Computed epipolar geometry for a wide-baseline stereo image

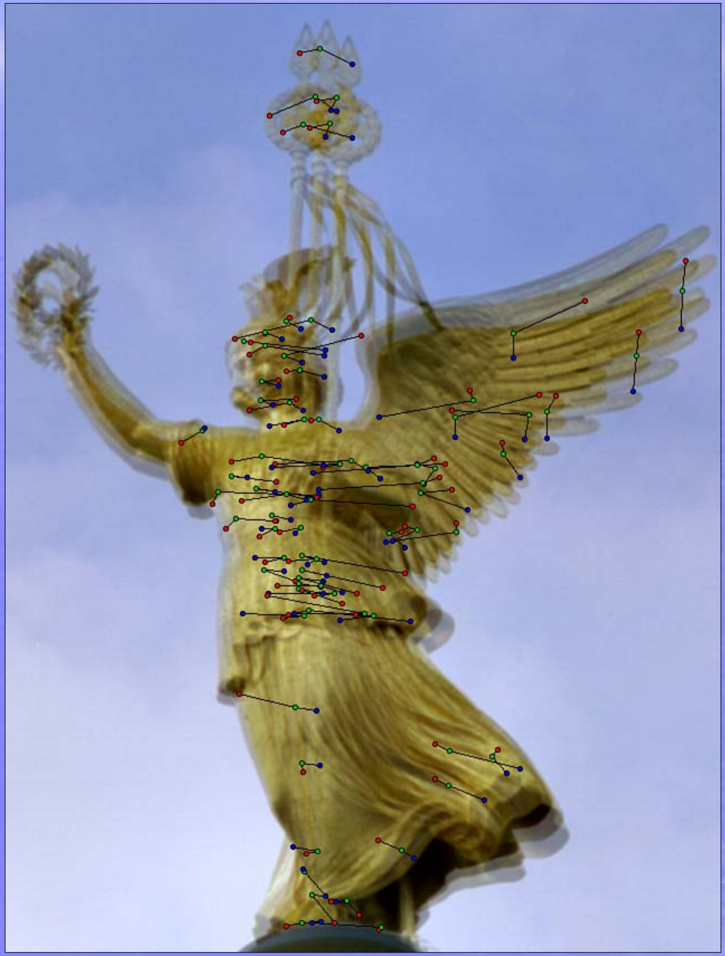
Church in Valbonne, France

Automatically estimated epipolar geometry for a rotated image pair (INRIA)

Robust Trifocal Geometry 1/2

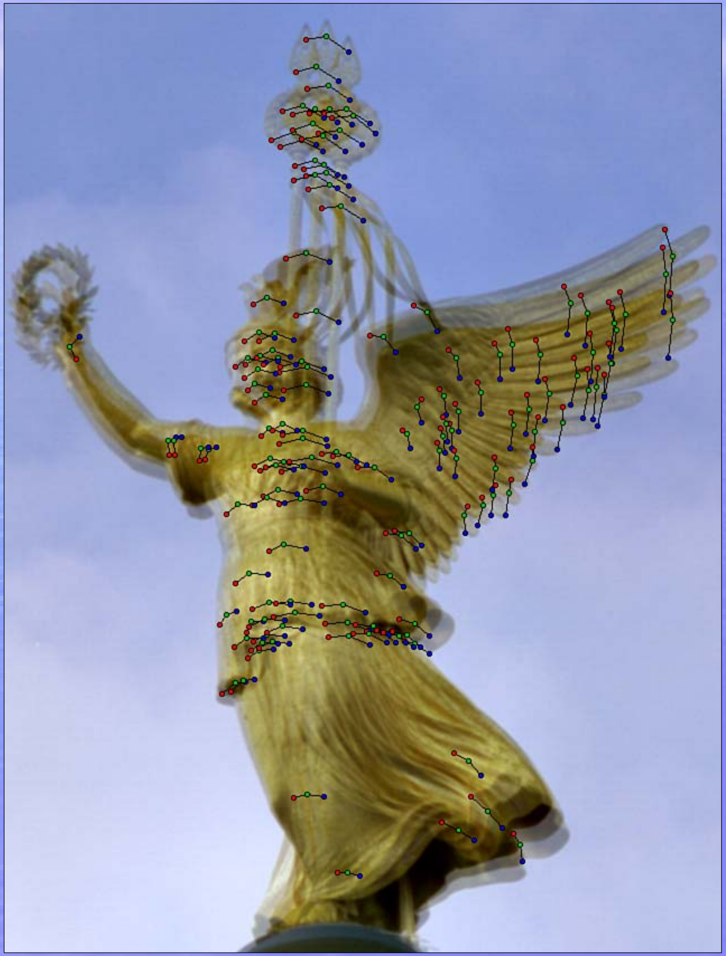


a.) Linked tentative matches

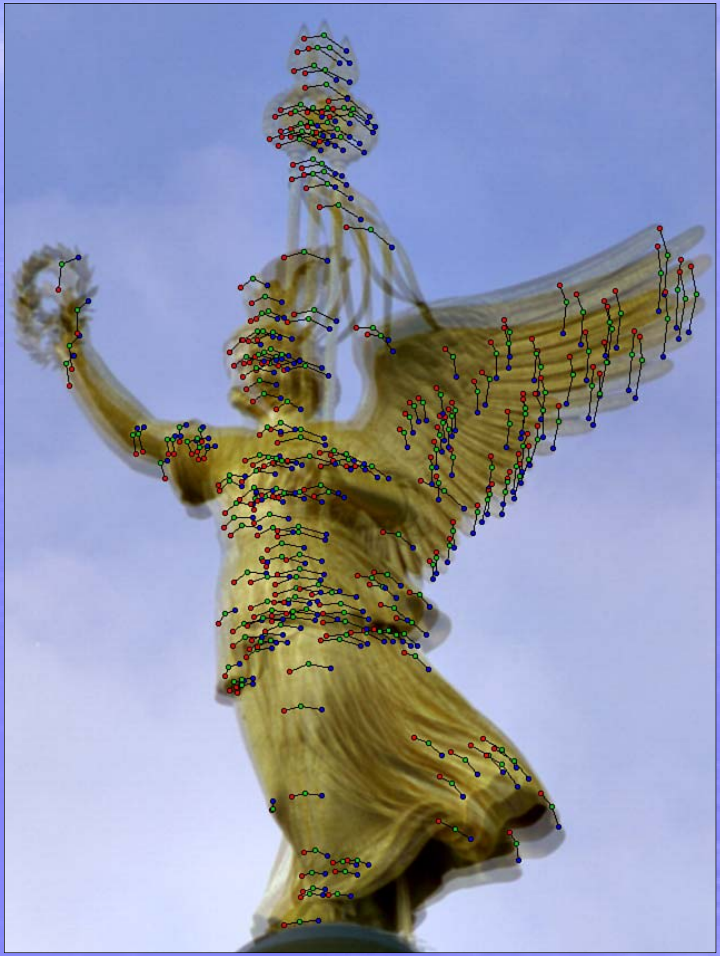


b.) Outliers found by GASAC

Robust Trifocal Geometry 2/2



c.) Consistent to trifocal geometry



d.) Guided matching

Conclusions and Outlook

- **GASAC:**
  - New robust estimator based on an evolutionary optimization technique
  - Best results in combination with the stable **LMedS**
- **General methodology:**
  - Could be used for **any problem** in which relations can be determined from a minimum number of points
  - **Without** the use of **prior information**
- **Significant acceleration:**
  - Can be achieved when random trials are replaced by a **systematic strategy**
  - **Parallel Evaluation:**
    - Several evaluated solutions exists simultaneously
    - The combination of the best parameters generates better solutions
- **Future work:**
  - Replace the optimistic **termination criterion** with a more realistic one (e.g. based on Capel or Matas & Chum)