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

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Abstract

A new robust estimator based on an evolutionary optimization technique is proposed. The general hypothesize-and-verify strategy accelerates the parameter estimation substantially by systematic trial and parallel evaluation without the use of prior information.

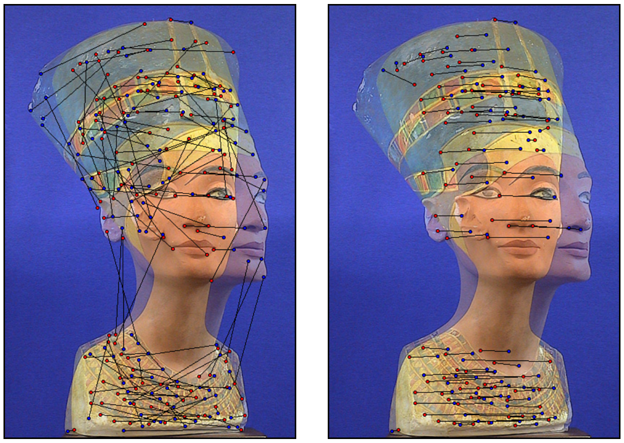
The method is evaluated by estimation of multi-view relations, i.e. the fundamental matrix. Additionally, some results for the trifocal geometry are presented. However, the general methodology could be used for any problem in which relations can be determined from a minimum number of points.

1. Introduction

This paper describes a new approach GASAC for robust parameter estimation. Here, the general method is applied to problems in computer vision, i.e. the estimation of *projective transformations*, such as homographies, fundamental-, essential- and projection matrices as well as the trifocal tensor [7]. These geometric relations are used for camera calibration, narrow and wide-baseline stereo matching, structure and motion estimation as well as in object recognition tasks.

A challenging step consists in automatically finding *reliable correspondences* in two or more images. Incorrect matches cannot be avoided at the beginning of the matching process, if only the correlation of local image descriptors is available. Due to their frequent occurrence, mismatches must be detected and removed by robust methods, which search for subsets of matches consistent with a global constraint (see Figure 1).

It is assumed that we have a data set consisting of putative feature correspondences. A subset is consistent with some projective transformation, of which the parameters are unknown. The task is to estimate these parameters, along with the set of consistent correspondences (*inliers*).



a.) Tentative matches using local image descriptors

b.) Robust estimated matches satisfying the epipolar constraint

Figure 1: Overlaid stereo images of the Nofretete bust. Matches are marked by a line joining the corresponding points.

In order to render the computation robust, two different types of measurement errors must be considered:

- **Small errors (*Noise*)**
  The localization accuracy of the coordinates may not be perfect. For such small deviations, a Gaussian error distribution can generally be assumed, and therefore a *non-linear optimization* can be used.
- **Blunders (*Outlier*)**
  A serious problem are blunders (i.e. wrong correspondences), which arise particularly in automatic measurements. For robust parameter estimation, the influence of errors can be limited using *M-Estimators* (see section 2.1).

  Hypothesize-and-verify approaches are more successful, which identify a minimal solution by *random trials*, supported by as much data as possible (see section 2.3). These simple and powerful methods are particularly insensitive to outliers, but significant in computational cost.

1.1. Related Work

An early example of a robust estimation algorithm is the *RANdom SAmple Consensus* (RANSAC) introduced by Fishler and Bolles in 1981 [6], which has become a standard choice for outlier removal in many computer vision problems [7, 20]. Recently, a variety of modifications to the basic RANSAC algorithm have been proposed to improve its efficiency.

Torr and Zisserman [21] established the *MLESAC* (Maximum Likelihood Estimation SAmple Consensus) as a generalization of the RANSAC method to estimate image geometry. It uses the same sampling strategy to generate putative solutions, but maximizes the likelihood rather than the number of inliers.

Torr [19] extended MLESAC to the Bayesian case with *MAPSAC* (Maximum A Posteriori SAmple Consensus) by replacing the likelihood with posterior probability. Tordoff and Murray [18] proposed a *Guided-MLESAC* estimation by adding prior information. They achieved faster image transform estimations by use of prior probabilities from the matching process. However, in most cases, the absence of meaningful prior information reduces it back to likelihood.

Chum and Matas [5] demonstrate the *PROSAC* (PROgressive SAmple Consensus) on the wide-baseline matching problem. Instead of random guessing, they exploit the linear ordering defined on the set of correspondences by a similarity function to achieve computational savings.

Matas and Chum [12] presented a statistically optimal strategy for randomized evaluation (*R-RANSAC*) with a Sequential Probability Ratio Test (*SPRT*), which was shown to be ten times faster than RANSAC. Nistér [13] derived a framework for real-time ego-motion estimation using *Preemptive RANSAC* by scoring multiple motion hypotheses in parallel. Capel [2] proposed a statistical bail-out test for RANSAC that permits the scoring process be terminated early and reduces the computational costs.

In this paper an evolutionary strategy is used to improve RANSAC with a heuristic search optimization technique. Saito and Mori [16] already used genetic algorithms in the context of stereo matching to select the optimal disparity at each pixel position. Chai and Ma [3] introduced a new genetic operator *adaptation* to incorporate the epipolar geometry constraint into the matching process. In [4] they formulate the epipolar geometry estimation as a global optimization problem and present a genetic algorithm for parameter searching.

Hu et al. [9] compute the fundamental matrix based on a simple genetic algorithm (*sGA*) using different strategies according to the variable length of the chromosomes. In [10] an iterative optimization using messy genetic algorithm (*mGA*) was shown to be more robust, especially when the data contain a great number of outliers.

In the following, a new general hypothesize-and-verify method is introduced, that accelerates the robust parameter estimation substantially by systematic trial and parallel evaluation without the use of prior information.

The paper is organized as follows: In section 2, some common cost functions are summarized for clarity. The new contribution, a parallel strategy using the genetic algorithm GASAC, is described in section 3 and its performance is compared with RANSAC. Finally, results on real images are presented in section 5.

2. Robust Parameter Estimation

During automated parameter estimation the measured values can be distorted due to blunders. Special problems are *lever points*, which are located far from the mass of the data and exert a substantial influence on the parameter estimation [11]. By use of robust statistics, such outliers can be identified and their negative influence on the solution be excluded.

2.1. M-Estimators

Robust maximum likelihood estimators (M-Estimators) are frequently used in order to accomplish parameter estimation insensitive to outliers. If the error of the *i*-th observation is e_i, then the least squares method usually minimizes the sum of the squared residues e_i^2. The goal of the M-Estimators now consists in replacing this sensitive measure by a suitable cost function

$$C = \sum_i \rho\left(e_i\right), \tag{1}$$

for which many proposals exist in the literature. A comprehensive overview of the different methods is given e.g. in Zhang [22]. For the evaluation of GASAC (see section 5) the influence functions of Huber and Tukey were selected.

2.1.1 Min-Max-Function of Huber

A very popular and simple method is the robust min-max-function of Huber

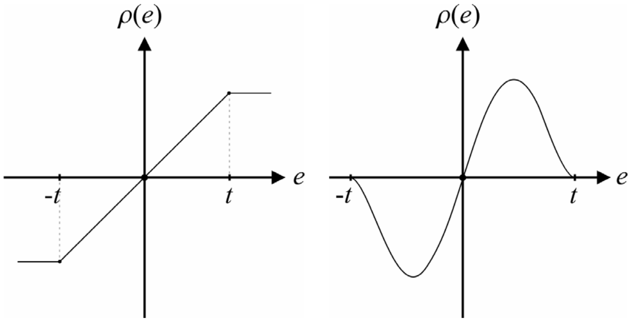
$$\rho\left(e\right) = \min\left(t, \max(e, -t)\right), \tag{2}$$

which excludes the residues *e* with large error from the estimation, as the influence is limited to a constant value starting from a user defined threshold *t* (see Figure 2.a).

2.1.2 Function of Tukey

With the function of Tukey the influence is not bounded above, but reduces again after a certain value:

$$\rho\left(e\right) = \begin{cases} e(t^2 - e^2)^2, & \left|e\right| < t \\ 0, & \text{otherwise} \end{cases} \tag{3}$$



a.) Min-max-function of Huber b.) Function of Tukey

Figure 2: Influence functions for M-Estimators

The influence of the described function is illustrated in Figure 2.b. The threshold t can be determined either empirically or estimated with the help of the χ^2 distribution. On the common assumption that the probability for a correct data selection is 95 percent, some thresholds are specified in Table 1. In order to reduce the influence of outliers on the computation of the standard deviation σ, Rousseeuw [15] suggests a robust method. Instead of the average deviation of the residues e from the mean, the following *robust standard deviation* was used

$$\sigma = 1.4826 \cdot \left(1 + \frac{5}{n-p}\right) \cdot \operatorname*{median}_i |e_i|, \tag{4}$$

where n denotes the number of the observations and p is the dimension of the parameter space. The median indicates the error of the middle element from the sorted list of residues.

2.2. Least Median of Squares Method

A further robust method for parameter estimation is given by the *least median of squares* (LMedS), whose cost function is defined as follows:

$$C = \operatorname*{median}_i e_i^2 \tag{5}$$

The use of the extremely stable median operator, instead of a sum, tolerates outliers up to 50 percent, without degrading the estimation. In addition, no threshold must be defined.

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

Table 1: Thresholds for a confidence of 95 percent

2.3. Monte-Carlo Method (RANSAC)

In principle, the classical smoothing methods use as much data as possible in the initial estimation, in order to recognize and eliminate outliers afterwards. In contrast, the method of Fischler and Bolles [6] uses as few as possible data for a first estimation and then maximizes the quantity of the data consistent to this model.

The algorithm first generates a model hypothesis from the existing data set S with n points by selecting a subset of m points randomly. After finding the minimal solution, the number of data consistent with the estimated model can be determined with

$$\rho(e) = \begin{cases} 1, & |e| < t \\ 0, & \text{otherwise} \end{cases} \tag{6}$$

over all points in S and maximized iteratively. Therefore, the random selection of a minimal data set is repeated until a suitable termination criterion is fulfilled. If several solutions are applicable, then the data set with the smallest standard deviation σ is selected. After the estimation process, the outliers are eliminated and the model is computed again with all inliers.

Alternatively, a robust cost function (e.g. the M-Estimators or the LMedS) can be used to verify the model hypothesis concerning all points in S. In contrast to the maximization of consistent data, the robust error function must be minimized.

However, the RANSAC method requires a lot of computation, since for n observations with k unknown parameters, a combination of $\binom{n}{k} = \frac{n!}{k!\,(n-k)!}$ possibilities must be considered. Due to restrictions on the computation costs, only a representative subset can be selected.

3. Genetic Algorithm (GASAC)

A biologically motivated approach for the solution of optimization problems is the genetic algorithm, which imitates the successful principles of the evolution. Already in 1973 Rechenberg [14] developed a simple procedure for evolutionary optimization using the *mutation selection strategy*.

The philosophy of the *genetic algorithm* comes from Holland [8] and is based on the realization, that parameters of a problem can be considered as a construction plan of an organism (chromosome). Under the given environmental condition, survivability (fitness) in combination with evolutionary changes in the construction plan yield a better adapted generation.

In the following, the new combination of RANSAC-like parameter estimation with an evolutionary optimization technique is designated with GASAC (Genetic Algorithm SAmpling Consensus).

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

Table 2: Examples for projective transformations

3.1. Representation of the Gene Pool

A *population* $\mathbf{G}$ consists of several individuals, who are characterized by an individual chromosome. Such chromosome $\mathbf{g}=\left(g_1,\ldots,g_m\right)$ corresponds to a tuple of m elements, which are called *genes*. The representation of the existing problem by a chromosome is trivial, if for n homologous points $\mathbf{x}_i \leftrightarrow \mathbf{x}'_i$ or $\mathbf{x}_i \leftrightarrow \mathbf{x}'_i \leftrightarrow \mathbf{x}''_i$ the index i is directly defined as gene

$$g_k \in \{1,\ldots,n\} \quad \text{for} \quad k=1,\ldots,m\,, \tag{7}$$

where a gene may occur only once within the chromosome. Using the minimal number of points, the length of a chromosome remains constant (see Table 2).

The *fitness* of a chromosome decides on its ability to prevail within the gene pool. The computation requires a linear method for the appropriate projective transformation with minimal parameters (e.g. 7-point-algorithm for the epipolar and 6-point-algorithm for the trifocal geometry [7]). Then, the geometrical image error is determined for all points and a robust cost function (see Eqns. 1 or 5) is used to measure the fitness. Thus a small value corresponds to a large ability to prevail.

3.2. Genetic Operators

In order to optimize an existing population, biologically motivated change mechanisms can be used.

3.2.1 Cross-over Operator

Mixing the genes of successful individuals is realized with the so-called *crossover* operation. Two chromosomes are cut apart and built up over cross again (see Figure 3).

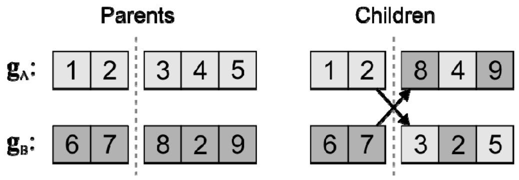


Figure 3: Exchange of chromosome parts using cross-over

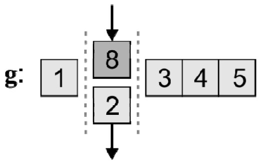


Figure 4: Modification of genes by mutation

The execution of the operation and the section point are selected randomly. It must be ensured that by exchanging chromosome parts no double genes result. Starting from the section point, only those pairs of genes which ensure an individual occurrence are considered. For the implementation the probability of a crossover P_C was set to 0.5, so that approximately each second chromosome is changed on average.

3.2.2 Mutation Operator

In order to prevent convergence in a suboptimal local minimum, it must be possible to supply new gene material. This is achieved by randomly changing genes, where it must also be ensured that no double genes result (see Figure 4). The probability P_M for the mutation of a gene was set to $\frac{1}{2m}$, so that a gene is changed in approximately every second chromosome on average. Beside these two important operators also *inverting* and *recombination* are commonly used [1]. Since, for the chosen representation, the sequence of the genes is not important and the length of the chromosomes remains constant, these additional operators were neglected.

3.3. Reproduction Plan

The strategy for a successful evolutionary development is fixed in the reproduction plan. Initially, a population $\mathbf{G}$ with N individuals is created, where the minimal subsets of m genes are selected randomly. Degenerated configurations (e.g. collinear points) should be recognized and, to avoid extrapolation problems, a good spatial distribution should be strived.

Then, for each individual in $\mathbf{G}$**,** a model hypothesis is generated. This model is verified by finding support from consistent data points. The error e for each datum is calculated and the appropriate fitness is determined using a robust cost function C (Eq. 1 or 5).

From this initial population, pairs of parents must be chosen for reproduction. The selection is performed randomly in with respect to their fitness. This can be achieved by sampling only the half of the population with the best fitness. Subsequently, children are created with the help of genetic operators (see section 3.2). This procedure is continued until M new individuals are generated.

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GASAC Algorithm
Prerequisites:
  • a set $S$ of $n$ feature correspondences
  • a function for model parameter estimation
  • a robust cost function $C$

Algorithm:
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 $C_{min}$
```

Figure 5: Outline of the GASAC algorithm

Finally, the fitness of the children is determined and the best N individuals of all are selected, to prevent an increase in population size. This reproduction step is repeated until a suitable termination criterion is fulfilled. In order to improve the convergence of the genetic algorithm, some technical modifications, which are not supported by the evolutionary theory, are recommended:

- Starting with a small population, individuals with identical genes may evolve despite a balanced initialization. *Removing double individuals* from the gene pool accelerates the optimization process.
- Individuals created by genetic operations are not necessarily better than the original. In order to ensure that a solution reached cannot worsen again, the chromosome with *best fitness stays unmodified* in the gene pool.

At the end, the model of the individual with maximum fitness (the smallest LMedS error) defines the final solution. An outline of the algorithm is given in figure 5.

3.4. Adaptive Termination Criterion

Considering the computation costs, it is not feasible to test all possible data combinations. A global termination criterion indicates when enough samples have been taken. Using the maximization of consistent data, the number of iterations can be estimated as follows [7].

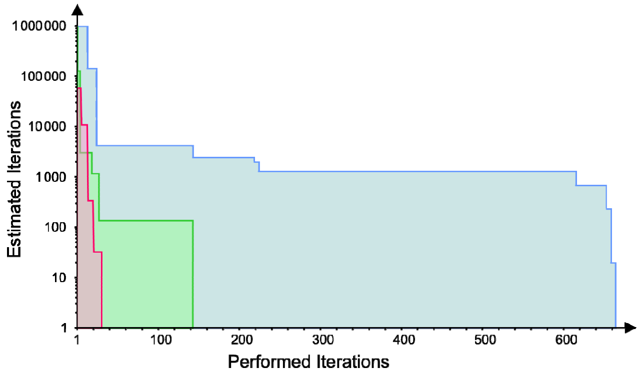

Figure 6: Dynamic adjustment of the estimated iterations for three runs of the Nofretete example

Let

$$\varepsilon = 1 - \frac{C}{n} \tag{8}$$

be the fraction of outliers in the data set S and

$$p = 1 - \left(1 - \left(1 - \varepsilon\right)^m\right)^R \tag{9}$$

the confidence, that at least one minimal selection with m elements out of R data sets contains no outlier. Then, the minimum number of the tries can be measured with:

$$R = \frac{\ln\left(1 - p\right)}{\ln\left(1 - \left(1 - \varepsilon\right)^m\right)} \tag{10}$$

For example, to linearly determine the fundamental matrix $(m = 8)$ tolerating 45 percent outliers $(\varepsilon = 0.45)$ with a confidence of 99 percent $(p = 0.99)$ only $R = 548$ samples should be sufficient, in contrast to the $\binom{25}{8} = 1\,081\,575$ possible attempts.

Using the adaptive procedure [7], the number of required iterations R is updated each iteration with the actual ε, so that R reduces in large steps. Figure 6 illustrates the dynamic adjustment of R for three typical examples. However, practical experiences with strongly disturbed data showed that the estimated minimum number is too small and more attempts are necessary. Future work should replace this optimistic criterion with a more realistic one, e.g. based on the idea of Capel [2] or Matas and Chum [12].

4. Comparison of the Methods

In order to demonstrate the difference between systematic and random trials, the GASAC is compared to the RANSAC approach. For the comparison, a test environment with 25 image pairs of the Nofretete bust was prepared (see Figure 1).

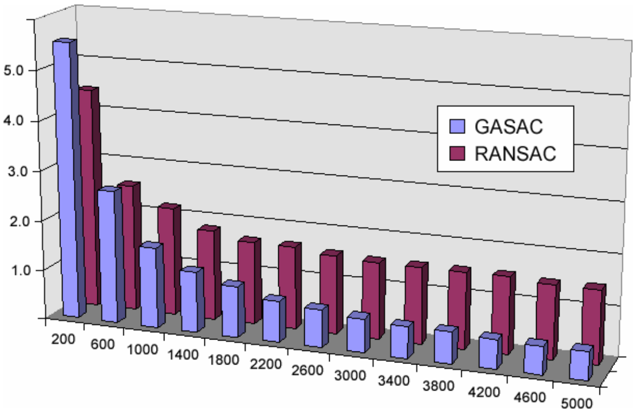

Figure 7: Improvement of the geometrical image error [in pixel] over 5000 attempts

Each of them was reduced in resolution and contains 50 strongly disturbed point correspondences. Both methods use for the computation of the fundamental matrix the 7-point-algorithm [7] and the LMedS minimization (Eqn. 5) of the symmetrical epipolar distance [22].

Figure 7 illustrate the improvement of the geometrical image error during the robust parameter estimation of **F** in relation to the number of attempts. For the RANSAC method and for GASAC, using $N = 200$ and $M = 400$ in 12 cycles, exactly 5000 model hypotheses were evaluated.

In order obtain a statistically representative result, all images were evaluated 100 times and the individual errors were arithmetically averaged. This experiment shows that the GASAC performs 2.5 times better than RANSAC.

The advantage of the GASAC method becomes clear if the number of required evaluations for reaching the optimal solution is taken into account (see Table 3). The computational cost can be reduced significantly by a factor around 13. The user defined sizes of the initial population N and the next generation M are not the crucial factor.

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

Table 3: Number of evaluations as function of the population size N and the reproduction behavior

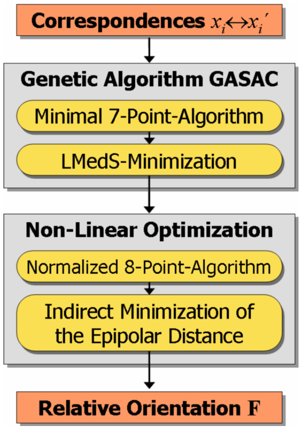

Figure 8: Orientation of an image pair from homologous points using the robust estimation of the fundamental matrix

4.1. Robust Orientation Procedure

This section summarizes an accelerated procedure for the robust computation of the fundamental matrix **F** using at least seven image point correspondences. First blunders from wrong correspondences are eliminated with the genetic algorithm GASAC (see Figure 5) using the LMedS minimization (Eqn. 5) of the symmetrical epipolar distance.

Small errors resulting from inaccurate measurements are reduced afterwards with the help of a *non-linear optimization method*. If, after the elimination of outliers, more than seven points remain, the application of the over-determined 8-point-algorithm [7] is recommended. An outline of the suggested method for the robust estimation of **F** is shown in Figure 8.

5. Experimental Results

To compare the different methods for computing the fundamental matrix **F**, 25 image pairs of the Nofretete were used in high resolution with $N = 350$ image point correspondences and approximately 45 percent outliers. For a statistically representative result, 100 test runs were evaluated on a Pentium 4 with 3GHz (see table 4). The non-linear optimization uses the *indirect* minimization of the geometrical image error by adjusting the elements of second projection matrix and the set of triangulated object point coordinates [7]. This minimal *bundle-adjustment* over $12 + 3N$ parameters is statistically optimal, but the computation cost is high. In addition to the geometrical image error, the difference $\Delta\mathbf{F} = \left\| \mathbf{F} - \mathbf{F}_{Calib} \right\|$ of the computed fundamental matrix to the matrix determined by classical calibration $\mathbf{F}_{Calib}$ is shown using the Frobenius norm:

$$\|\mathbf{F}\| = \sqrt{\sum f_{ij}^2} \qquad (11)$$

Method	N	Geometrical Error [pixel]		ΔF		CPU [sec.]
		Mean	Max	Mean	Max	
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

Table 4: Comparison of the different methods for computation of the fundamental matrix

Finally, to allow a visual verification of the results, epipolar lines were overlaid for two examples (see Figures 9 and 10). In addition, an example for the reduction of matching errors by optimizing the trifocal geometry using GASAC is illustrated in Figure 11. After the extraction of 500 interest points, 240 tentative matches were found. The robust GASAC eliminated 74 outliers (31%), and the guided matching enhanced the number of inliers to 241.

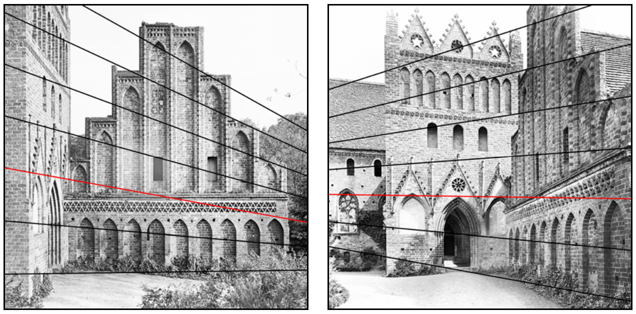

Figure 9: Computed epipolar geometry for a wide-baseline stereo image of the monastery in Chorin

Figure 10: Automatically estimated epipolar geometry for a rotated image pair of the church in Valbonne [17]

a.) Linked tentative matches

b.) Outliers found by GASAC

c.) Inliers consistent with the trifocal geometry

d.) Completed result using guided matching

Figure 11: Example for the reduction of matching errors by optimizing the trifocal geometry with GASAC. Three pictures of the Victoria statue are overlaid and corresponding points are connected with a line

6. Conclusions

A significant acceleration can be achieved when random trials are replaced by a systematic strategy. In this paper, a new robust parameter estimation method GASAC, using a genetic algorithm for evolutionary optimization, was proposed. While most optimization methods perform sequential improvements, the genetic algorithm exploits the fact that several evaluated solutions exists simultaneously. This parallel processing makes it possible to extract and combine the best parameter combinations to generate better solutions.

The methods examined show the best results in combination with the stable LMedS. Additionally, this criterion needs no pre-defined threshold contrary to the M-Estimators. Using a non-linear optimization of the algebraic solutions, small measurement inaccuracies can be eliminated. From a statistical point of view, this method is optimal but the computation cost is high.

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