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

Volker Rodehorst and Olaf Hellwich

Computer Vision & Remote Sensing
Berlin University of Technology, Germany

{vr, hellwich}@cs.tu-berlin.de

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

<table>
<thead>
<tr>
<th>Transformations</th>
<th>Parameter $p$</th>
<th>Minimum Points $m$</th>
</tr>
</thead>
<tbody>
<tr>
<td>2D-Homography $H$</td>
<td>8</td>
<td>4</td>
</tr>
<tr>
<td>3D-Homography $H$</td>
<td>15</td>
<td>5</td>
</tr>
<tr>
<td>Essential matrix $E$</td>
<td>5</td>
<td>5</td>
</tr>
<tr>
<td>Projection matrix $P$</td>
<td>11</td>
<td>6</td>
</tr>
<tr>
<td>Trifocal tensor $\mathcal{T}$</td>
<td>18</td>
<td>6</td>
</tr>
<tr>
<td>Fundamental matrix $F$</td>
<td>7</td>
<td>7</td>
</tr>
</tbody>
</table>
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
  \(Ax = e, \ e \neq 0\)
  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
  \[C = \sum_{i} \rho(e_i)\]
M(aximum-Likelihood)-Estimators

- Min-Max-Function of **Huber**
  
  the influence is limited to a **constant** value:
  \[ \rho(e) = \min(t, \max(e, -t)) \]

- Function of **Tukey**
  
  the influence **reduces** again after a certain value:
  \[
  \rho(e) = \begin{cases} 
  e(t^2 - e^2)^2, & |e| < t \\
  0, & \text{otherwise}
  \end{cases}
  \]
Automatic Threshold

- **Thresholds** of the $\chi^2$ distribution (confidence 95%)

<table>
<thead>
<tr>
<th>Dimension</th>
<th>Model</th>
<th>Threshold $t$</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Fundamental matrix $F$</td>
<td>$1.96 \sigma$</td>
</tr>
<tr>
<td>2</td>
<td>Essential matrix $E$</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>2D-Homography $H$</td>
<td>$2.45 \sigma$</td>
</tr>
<tr>
<td>2</td>
<td>Projection matrix $P$</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>3D-Homography $H$</td>
<td>$2.79 \sigma$</td>
</tr>
<tr>
<td>3</td>
<td>Trifocal tensor $T$</td>
<td></td>
</tr>
</tbody>
</table>

- **Robust Standard Deviation**

\[
\sigma = 1.4826 \cdot \left(1 + \frac{5}{n - p}\right) \cdot \text{median} \left| e_i \right|
\]

With $n$ observations and parameter space dimension $p$. 
Other Robust Methods

- **Least-Median-of-Squares Method** (LMedS)
  
  \[ C = \text{median}_i e_i^2 \]
  
  \[ e_1^2 \leq e_i^2 \leq e_n^2 \text{ for } i = \frac{n}{2} \]

  - 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:
  \[ R = \frac{\ln(1 - p)}{\ln\left(1 - (1 - \varepsilon)^m\right)} \]
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 \((\varepsilon = 0.45)\)
- 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 $\varepsilon_i$

- **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 G**: Consists of several individuals
- **Individual**: Is characterized by a chromosome
  \[ g = (g_1, \ldots, g_m) \]
- **Chromosome**: Consist of \( m \) elements, which are called genes
- **Gene**: For \( n \) corresponding points \( x_i \leftrightarrow x'_i \) the **index** \( i \) is used
  \[ g_k \in \{1, \ldots, n\} \quad \text{for} \quad k = 1, \ldots, m \]
  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

<table>
<thead>
<tr>
<th>Parents</th>
<th>Children</th>
</tr>
</thead>
<tbody>
<tr>
<td>$g_A$:</td>
<td>1 2 3 4 5</td>
</tr>
<tr>
<td>$g_B$:</td>
<td>6 7 8 2 9</td>
</tr>
</tbody>
</table>
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 $\frac{1}{2m}$

\[
g: \begin{array}{c}
1 \\
2 \\
3 \\
4 \\
5 \\
8
\end{array}
\]
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
  $G_i$ = 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 $G$ 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 $G$ unmodified
  Reduce $G$ to the best $N$ individuals
end

Return model of that individual in $G$ 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

![Bar graph showing Geometrical Image Error with different numbers of model evaluations for GASAC and RANSAC.]
Number of Evaluations

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

<table>
<thead>
<tr>
<th>Method</th>
<th>$N$</th>
<th>$M$</th>
<th>Evaluations</th>
</tr>
</thead>
<tbody>
<tr>
<td>Theoretic</td>
<td></td>
<td></td>
<td>~ 100 Mio.</td>
</tr>
<tr>
<td>RANSAC</td>
<td></td>
<td></td>
<td>57,233</td>
</tr>
<tr>
<td>GASAC</td>
<td>50</td>
<td>100</td>
<td>7,052</td>
</tr>
<tr>
<td></td>
<td>100</td>
<td>200</td>
<td>4,465</td>
</tr>
<tr>
<td></td>
<td>100</td>
<td>400</td>
<td>4,147</td>
</tr>
<tr>
<td></td>
<td>100</td>
<td>800</td>
<td>5,186</td>
</tr>
<tr>
<td></td>
<td>200</td>
<td>400</td>
<td>5,633</td>
</tr>
</tbody>
</table>

- The user defined sizes of the **initial population** $N$ and the **next generation** $M$ are not the crucial factor.
Robust Orientation Procedure

1. **Correspondences** $x_i \leftrightarrow x_i'$
2. **Genetic Algorithm GASAC**
   - Minimal 7-Point-Algorithm
   - LMedS-Minimization
3. **Non-Linear Optimization**
   - Normalized 8-Point-Algorithm
   - Indirect Minimization of the Epipolar Distance
4. **Relative Orientation** $F$
## Computation of the F-Matrix

<table>
<thead>
<tr>
<th>Method</th>
<th>$N$</th>
<th>Geometrical Error [pixel]</th>
<th>$\Delta F$</th>
<th>CPU [sec.]</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Mean</td>
<td>Max</td>
<td>Mean</td>
</tr>
<tr>
<td><strong>Normalized 8-point-algorithm</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Linear</td>
<td>350</td>
<td>2.152</td>
<td>19.770</td>
<td>0.219</td>
</tr>
<tr>
<td>Non-linear</td>
<td>350</td>
<td>2.131</td>
<td>19.185</td>
<td>0.219</td>
</tr>
<tr>
<td><strong>Robust estimation with GASAC (Minimal 7-point-algorithm)</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Tukey</td>
<td>253</td>
<td>0.568</td>
<td>6.059</td>
<td>0.215</td>
</tr>
<tr>
<td>Huber</td>
<td>236</td>
<td>0.535</td>
<td>4.980</td>
<td>0.215</td>
</tr>
<tr>
<td>LMedS</td>
<td>231</td>
<td>0.493</td>
<td>4.820</td>
<td>0.211</td>
</tr>
<tr>
<td>Non-linear</td>
<td>231</td>
<td>0.474</td>
<td>4.599</td>
<td>0.210</td>
</tr>
</tbody>
</table>
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

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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)