

# A NOVEL EVOLUTIONARY FRAMEWORK FOR FEATURE MATCHING\*

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**Abstract:** The paper presents a new feature matching scheme based on the Queen-bee Evolution for two uncalibrated images. Matching features needs an exhaustive search in a vast space, for which evolutionary algorithms are recommended recently. This paper propose a simple and effective algorithm. We intuitively encode a string of integer numbers assigned to the features as chromosomes and develop a novel crossover operator respectively which can preserve the position information without any disruption. We also tailor swap mutation operator to prevent from premature convergence and invalid solutions. As a result, the proposed algorithm can quickly achieve the global or near global optimal solution cooperating with the linear ranking selection and the elitist replacement. Meanwhile, it is a more general framework for matching various types of features. The experimental results illustrate the performance of the proposed approach.

## 1 INTRODUCTION

Matching features between two uncalibrated images constitutes a fundamental step in a variety of computer vision applications, including automatic robot navigation, target recognition, motion estimation, etc. Although solutions to the problem have been explored for many years, it remains of central interest because no general method can be proposed and the focus on the matching process has to vary with the requirements of different applications. We intent to estimate the pose of an aircraft in air by vision techniques and some classical matching algorithms, such as relaxation, cross-correlation, Least-Median-of-Squares were tested. Unfortunately all of them are not robust enough in our case. We make our first effort here although the result is not perfect now.

Feature matching is usually cast as a combinatorial optimization problem and the search strategy involved is one of the important parts to achieve optimal solutions. As a search strategy, Genetic Algorithms (GAs) take more attention recently due to its advantages: the global search ability, intrinsically parallel computing, the insensitivity to initial values, effective search on vast solution spaces, etc. (Chai and Ma, 1998) match corner points extracted from two

uncalibrated images using an evolutionary framework and propose a 2D chromosome structure with binary entries and an adaptation operator. (Ruichek et al., 2000) use the same chromosome structure and give the feature matching scheme for the images taken by linear stereo cameras. (Beveridge et al., 2000) compare three line matching techniques and recommend the method based on a Messy GA. Also, other evolutionary frameworks are used to search for corresponding features (Yuan et al., 2004).

This paper proposes a novel GA-based matching scheme based on the Queen-bee Evolution (QE) to establish correspondences between two uncalibrated images. Although in our specific implementation corners are used as features, it is indeed a relatively more general framework for matching various feature types, such as lines, edges, and so on. Benefiting from a novel chromosomal encoding with its proper crossover and mutation operators we developed, the proposed algorithm is simple and effective. Section 2 introduces the QE briefly. Section 3 describes our QE-based matching scheme in detail. Section 4 gives the experimental results to illustrate the performance of our approach. Section 5 concludes our work.

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## 2 QUEEN-BEE EVOLUTION

Queen-bee evolution is really a variation of classic GAs. It mimics the nature that the queen bee cross-breeds with drone bees and plays a major role in the reproduction process. Here, the queen is the fittest individual in a generation, and the drones are the individuals selected as parents to crossbreed with the queen. It is noticeable that all drones crossbreed only with the queen-bee but not with each other. This enhances the exploitation of genetic information in the queen, meanwhile leading to an increased probability of premature convergence. To solve the problem, some individuals in a population are strongly mutated so that the exploration of GAs is reinforced. Interested readers are referred to the reference (Jung, 2003) for detailed information.

## 3 MATCHING WITH QUEEN-BEE EVOLUTION

The purpose of feature matching is to establish correspondences between the features of two images taken by an uncalibrated camera system. We use corner points as features because they are easily found in man-made scenes. Assume that they have been extracted with an improved Harris corner detector (Harris and Stephens, 1988; Schmid et al., 2000) from the two images independently. The following will perform the matching task benefiting from QE.

### 3.1 Chromosomal Encoding of Solutions

Feature matching can be cast as such a combinatorial optimization problem that the  $M$  features in the first image match to the  $N$  features in the second image. That is, a candidate solution of the problem is a specific mapping between the two feature sets. According to the uniqueness assumption that any feature in one image can be assigned to at most one feature in the other, permutation is preferable to encode the feasible solutions since it has been widely used to solve similar problems, such as TSP, JSP, and QAP (Bierwirth et al., 1996). However, two main differences need be considered: feature matching focuses on the mapping between the elements of two feature sets but not on the order of the elements in one set; and usually some features in one image may not match to any feature in the other, hence a correct solution often contains only a portion of all extracted features.

We define the chromosome as an integer string

with length  $M$ , each position corresponding to a feature in the first image (Fig. 1). The integer values ranging from 1 to  $N$  on those positions are the label numbers uniquely assigned to the features in the second image. They are named *talking genes* against the value 0's, so called *dummy genes*, which means no match in the second image. In a specific chromosome, each talking gene is unique whereas a dummy gene often duplicates several times because multiple features in the first image usually don't match to any feature in the second. Inversely, multiple features in the second image usually don't match to any feature in the first, so the genes in a chromosome constitute only a  $k$ -subset of all available talking genes  $\{1, 2, \dots, N\}$ . That is, the encoding is not a true permutation, so called partial permutation.

Position	1	2	3	4	5	6
Gene	2	0	1	0	4	3

Figure 1: A chromosome with the partial permutation encoding.

### 3.2 Matching Constraints and Fitness Function

On the view of optimization, our solution scheme is to find the permutation of the feature labels in the second image that maximizes a given fitness function. We define the fitness of chromosomes as follows.

First, the normalized cross-correlation is computed for the neighborhood of every point in the first image to the ones in the second. Combining with special similarity of features, we threshold the correlation score to reduce the search space, which is also employed in the initialization and the mutation phases of our evolution process.

Second, the neighbor features are found for every candidate match containing in a chromosome. If its neighbors are also candidate matches in the chromosome, they give support for each other and have higher matching strength. Detailed computing is referred to (Zhang et al., 1994). Differently, the rotation limitation is not used here. Furthermore, the uniqueness assumption has been embedded in our encoding process so that the computing symmetry problem does not exist here.

Third, the fitness function summarizes the strengths of all candidate matches in the chromosome.

### 3.3 Selection and Replacement

Selection is applied to population of each generation so that fitter chromosomes, i.e. those satisfy the matching constraints better, will have more breeding

chances to have offspring by crossover. Linear ranking selection (Zhang and Kim, 2000) is proved to be efficient in our proceeding experiments. Different from simple GAs, it only operates on the drone bees and the queen-bee in QE must be one of the two parents to crossover (Fig. 2).

Replacement is a process that chooses survivors from offspring to form the next generation. A widely used scheme replaces the current population with its offspring no matter whether they are fitter than their parents. Slightly different, we mix the old queen with the offspring first. Then, a new queen is picked out and other offspring is preserved as drones for the next generation. Hence, the old queen may survive without crossover and the fittest chromosome will never be kicked out of population during evolution, so called Elitist Replacement.

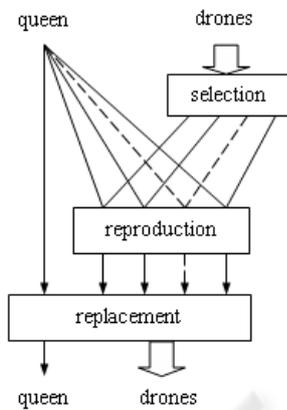


Figure 2: Selection and replacement.

### 3.4 Crossover Operator

The basic idea of the crossover is that several characteristics of some genotypes in parents are recombined into their offspring. With permutation encoding, a gene in a chromosome contains the information of position, order, and/or adjacency (Starkweather et al., 1991). Various crossover operators have been developed intending to preserve respective favorable information depending on problems. In our problem, we expect the position to be of particular interest because it directly expresses corresponding relations between two feature sets. Cycle Crossover is such an operator that always preserves the absolute position of genes from one parent or the other without any disruption. Unfortunately, the partial permutation may present multiple dummy genes in one chromosome, and all genes in the chromosome usually constitute only a subset of all available genes so that the cycle crossover doesn't respect the semantic properties of

the representation.

We define a new crossover for the partial permutation encoding. Firstly, some positions are randomly selected in the parents to crossover, and the genes on those positions transfer to their two offspring at the same positions. The genes on the other positions in the offspring are inherited from the other parent at the same positions. Secondly, duplicate talking genes are detected. If two genes present identically in the same offspring, one of the genes cannot be inherited from its original parent but from the other. The second operation is repeated until no duplicate talking genes present in the offspring. Obviously, two different offspring can be obtained from the process above at the same time and they are of genetic complement, so called complementary crossover. Thus, position information is preserved without any disruption.

### 3.5 Mutation Operator

Mutation injects new genes into population to prevent GAs from premature convergence. (Brizuela and Aceves, 2003) compared three types of mutation operators for multi-objective flowshop optimization problems using permutation codes. They are all less effective to the partial permutation, even produce invalid solutions. We prefer to tailor the swap operator to our use.

Before mutation, a probability check for mutation is performed on every position in a chromosome. If the probability check is passed on a certain position, the gene on that position will be mutated to an alternative one randomly selected in the subset of potential genes for the position. Here, a potential gene means satisfied with intensity and spacial similarities between the two corresponding features. If the alternative gene isn't present in the same chromosome, a new gene is injected into the current chromosome. If the alternative gene is found on another position in the chromosome except for dummy genes and they are swappable, the two genes are swapped one time between the two positions; otherwise a dummy gene would be injected into the chromosome. As a result, the tailored swap mutation can add a new gene into a chromosome, swap two genes, or delete an existent talking gene from the chromosome.

It is worth noting that QE with normal mutation probability is prone to premature convergence because it exploits the genetic information of the queen too intensively during reproduction processes. To solve the problem, two mutation probabilities are employed in QE. Some chromosomes are normally mutated as in the simple GAs and the others are strongly mutated. The better values set for the normal mu-

tation rate, normal and strong mutation probabilities have to be determined in experiments.

## 4 EXPERIMENTAL RESULTS

As shown in Fig. 3, corners extracted independently from the two uncalibrated images are denoted by symbol "+" and "x", respectively. There are 34 points in the first image and 37 in the second. In either image, there are some corners without matches in the other.

The proposed GA is set as follows: population size 20, crossover probability 1.0, normal mutation probability 0.01, strong mutation probability 0.3, and normal mutation rate 0.5. Among them, the later two are the QE-specific parameters.

The generations needed for convergence are 50 averagely that means the speed of convergence is fast. Certainly, it varies with the different number of features, parameter settings, and so on. The resultant correspondences are shown in the same figure denoted by symbol "\*" assigned with a number. Observably, the percentage of matched points achieves nearly the maximum.

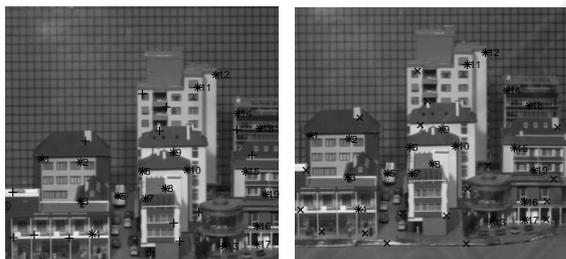


Figure 3: The resultant correspondences.

## 5 CONCLUSIONS

The paper has presented a novel feature-based matching scheme using queen-bee evolution. Intuitively, the candidate solutions to correspondences of two uncalibrated images are encoded with the label numbers of features. Respectively, a new crossover is developed to preserve the position information without any disruption, and the swap mutation is improved to respect the semantic properties of the genetic representation. The matching scheme uses the measure very similar in the form to that used in (Zhang et al., 1994), but a modified version. Comparing with the relaxation technique, our approach can obtain more correct correspondences and achieve the global or near global optimal solution more easily. The experiment shows that it gets convergence quickly and isn't sensitive to

the initial values with proper selection and replacement techniques.

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