

# A Genetic Algorithm for Motion Estimation

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## RÉSUMÉ

*Dans le contexte du codage vidéo comme dans celui de l'analyse de séquences d'images, l'estimation du mouvement présent dans la scène est primordial. Parmi l'ensemble de techniques d'estimation de mouvement, la technique d'appariement s'est montrée la plus performante. Néanmoins, elle est très demandante en du point de vue de calcul. Dans cet article, une technique pour l'estimation de mouvement par appariement est présentée. Elle est basée sur un algorithme génétique appliqué à un espace continu. Faisant partie de la classe de techniques d'optimisation stochastiques, elle est caractérisée par sa robustesse aux minima locaux, sa capacité de convergence et son implantation facile. Tant en termes d'efficacité machine qu'en ceux d'obtention de la solution optimale, les résultats expérimentaux démontrent que la technique proposée est plus performante que les techniques usuelles de recherche rapide.*

## ABSTRACT

*In video coding as well as in image sequence analysis, the estimation of the motion existing in the scene is fundamental. Compared to other motion estimation techniques, matching motion estimation has been shown to have the best performances. However, it implies a heavy computational load. In this paper, a Genetic Algorithm in the Continuous Space for matching motion estimation is proposed. Belonging to the class of stochastic optimization techniques, it is characterized by a resilience to local minima, convergence capability and ease of implementation. Considering computational load as well as obtaining the optimal solution, experimental results show that the proposed technique achieves better performances than fast search techniques such as hierarchical matching motion estimation.*

## 1 Introduction

In video coding as well as in image sequence analysis, the estimation of the motion existing in the scene is fundamental. In the framework of video coding, such an information permits to dramatically reduce the temporal redundancy. As far as image sequence analysis is concerned, the estimation of the motion information allows for a precise characterization of the moving objects present in the scene. Spatio-temporal segmentation [1] as well as tracking of the object of interest can then be carried out.

The motion existing in a scene has to be characterized by a model. The latter can be chosen to be either non-parametric, quasi-parametric or fully parametric [2]. The parametric model tries to define the motion of a whole region by a set of parameters while the other approaches lead to a dense motion field. Due to its natural application in the framework of object-based motion estimation, this paper assumes a parametric motion model.

In order to estimate the parameters of the motion model, two approaches have been investigated. The first techniques rely on a dense motion field computed with a non-parametric method. The motion parameters are then estimated by linear regression [3]. As the motion para-

eters are not computed from the luminance signal itself, these techniques can be referred to as indirect. The second techniques directly estimate the parameters of the motion model. Since the estimation is carried out on the luminance signal itself, these techniques can be seen as direct. However, the estimation problem turns out to be non-linear. So as to linearize the latter, a first class of direct techniques assume a model of the luminance signal. They are referred to as differential techniques [2]. The alternative approach is to use the matching technique which directly solves the non-linear estimation problem without any assumption on the luminance signal. The latter has been shown to outperform both differential and regression techniques when estimating the camera motion [4].

The motion estimation can be seen as an optimization problem. The aim is indeed to find the set of parameters which best captures the motion and hereby, minimizes an evaluation function. In the case of matching motion estimation techniques, the search for the parameters can either be carried out stochastically or deterministically. A global optimization is guaranteed only by an exhaustive deterministic search in the motion parameters space. The latter being continuous, such an exhaustive search is unrealistic.



In order to robustly estimate the motion parameters by matching motion estimation, the deterministic optimization methods arbitrarily quantize the motion parameters space in series of discrete tentative parameters values within a maximum displacement range. So as to reach precise estimates, the quantization should be quite fine leading to a heavy computational load. However fine, the quantization process renders the obtaining of the optimal motion parameters highly uncertain. To decrease the computational complexity, fast search techniques have been proposed [5]. Amongst the latter, fast search techniques based on a hierarchical representation of the image have been developed. Such hierarchical methods are very robust to local minima. They nevertheless require fine tuning to achieve good performances within a tolerable computational load.

In this paper, a Genetic Algorithm in the Continuous Space for matching motion estimation is proposed. Belonging to the class of stochastic optimization procedures, such optimization algorithms do not require any quantization of the search space. They are moreover characterized by a robustness to local minima and rapid convergence to the optimal solution. The latter characteristics make them perfectly suited to solve the optimization problem posed by matching motion estimation. They allow for a better motion estimation while requiring less than half of the computational load of usual fast search methods. Furthermore, little tuning is required.

The paper is structured as follows. In Sec. 2, the general description of the Genetic Algorithms is given. The proposed Genetic Algorithm in the Continuous Space for matching motion estimation is presented in Sec. 3. Experimental results are shown in Sec. 4 and Sec. 5 draws conclusions.

## 2 Genetic Algorithm

Genetic Algorithms (GA) are a class of robust stochastic search and optimization procedures based on the Darwinian theory of evolution. Their basic principles were first described by Holland, and their mathematical framework as well as examples of application can be found in [6]. GAs have been employed with success in a variety of problems such as combinatorial optimization, system identification, image enhancement, to name but a few. The lure of GAs in these different contexts is that they do not require differentiability or even continuity of the search space. Furthermore, they are robust to local minima and very easy to implement.

A GA typically consists in a population of suitably encoded solutions to the problem at hand, together with an evaluation function. In order to create successive generations of solutions, there is a need for operators which generate new solutions starting from the previous ones. These operators mimic the biological phenomena of *crossover* and *mutation*. The choice of the solutions upon which they are used is dictated by the evolutionary principle of the *survi-*

*val of the fittest*. The selection is performed according to the evaluation function.

In order to work in the GA framework, the solutions have to be encoded in an appropriate manner. The most common approach is to quantize the parameter values forming a solution and to binarize them. The chain of all these binary representations form an unique bit string called for obvious reasons a *chromosome*. Crossover generally consists in building a new chromosome from two other ones referred to as the parents. The operation is carried out by concatenating randomly chosen parts of the parents. For instance, if the two parent chromosomes are 11110011 and 01011010 and position five is drawn at random, then the resulting chromosome will be 11110010. Mutation commonly consists in considering in turn each bit of a given chromosome and changing its value with a predefined low probability called the mutation rate. Although very widely used, the above approach to solutions encoding suffers from the following drawbacks:

1. The operators do not take into account any possible link between different solution parameters. As the crossover operation mixes these parameters in an arbitrary way, convergence speed may be slowed down.
2. Quantization implies that the parameters are restricted to some amplitude range.
3. The obtained solution is quantized. Improvement in the accuracy implies additional bits in the chromosomes and hence a decrease in convergence speed.

So as to overcome the above drawbacks and constraints of usual encoding, a GA working directly on the parameter space is needed. In other words, the chromosomes should no longer be series of bits but actual floating point vectors. As no quantization is needed, such type of GA will be referred to as Genetic Algorithms in the Continuous Space (GACS). The main idea consists in defining operators whose effects are similar to the ones of the operators of classical GAs while avoiding the need for a quantization and binarization of the solutions. Mutation must remain a way to explore the search space and crossover must allow to obtain chromosomes with better performances starting from available well performing ones. In consequence, the mutation operator is defined by:

$$\vec{b} = \vec{a} + \vec{g}$$

where  $\vec{a}$ ,  $\vec{b}$  and  $\vec{g}$  are respectively the chromosome, the mutated chromosome and a Gaussian distributed random vector. The components of the random vector  $\vec{g}$  must be uncorrelated so as not to favor any particular direction in the stochastic search. As far as their variances are concerned, they play the same role as the mutation rate of classical GAs. The crossover operator is given by:

$$\vec{b} = (1 - \lambda) \vec{a}_1 + \lambda \vec{a}_2$$

where  $\lambda$  is a random variable uniformly distributed on the unit interval. The resulting chromosome  $\vec{b}$  lies literally 'in-between' its parents  $\vec{a}_1$  and  $\vec{a}_2$ . In case constraints on the solution induce the convexity of the search space, the crossover operator generates a refined chromosome starting from acceptable parents.

### 3 Matching Motion estimation based on a GACS

Due to their intrinsic characteristics, GACSs are perfectly suited to solve the optimization problem represented by matching motion estimation. Moreover, the transcription of motion estimation in the framework of GACSs is readily performed. A chromosome can be identified with the vector formed by the parameters of the motion model. In case of an affine motion model, the chromosome is thus formed by the concatenation of the six continuous motion parameters. The evaluation function is simply chosen to be the Mean Square Error (MSE).

The GACSs property of not enforcing any discretization of the search parameters space allows a more thorough search. Not only does it allow for a better performance, but also entails decreased need for tuning as discretization steps are not to be provided.

With regard to GACSs resilience to local minima and convergence capabilities, they are closely linked to the way in which the algorithm mimics the Darwinian selection theory. In other words, the manner in which the evolutionary process is carried out influences greatly the performances. In [7], an evolution algorithm well adapted for GACSs is presented. It is very well suited to small populations of chromosomes and has attractive convergence capabilities. It features the use of local instead of global competitions for the crossover operator. Local competitions have the property of conserving the genetic diversity of the population. Such a strategy helps avoiding local minima and thus contributes to the robustness of GACSs. Moreover, the mutation operator corresponds to a random search relying on perturbations with an infinite-support distribution (i.e. Gaussian distribution). Combined with the fact that the best chromosome is kept for the next generation, convergence with probability one is assured.

In Sec. 4, it is shown that the proposed GACS-based matching motion estimation achieves better performances than the hierarchical fast search technique, while requiring less than half of the latter computational load. Furthermore, the presented algorithm demands much less tuning than usual techniques in order to reach good performances.

## 4 Experimental results

The proposed GACS-based matching motion estimation is tested against the hierarchical matching motion estimation used in [4]. The performances of both methods in

estimating the camera motion existing in a scene are compared. So as not to bias the estimation by the presence of outliers and avoid the phenomenon of "locking on" for the hierarchical approach [8], the support of estimation is restricted to the background [4]. The motion model is chosen to be affine.

Figures 1 and 2 compare the performances of the proposed GACS-based method with the hierarchical method for respectively the sequence "Table Tennis" and "Flower Garden" (CIF format). The former sequence is characterized by a strong zooming while the latter sequence undergoes a panning. The results for the GACS-based method were obtained by performing 100 evolutionary steps. Although this corresponds only to one third of the computational load of the hierarchical method, the proposed GACS-based method achieves better performances in terms of the evaluation function (i.e. MSE).

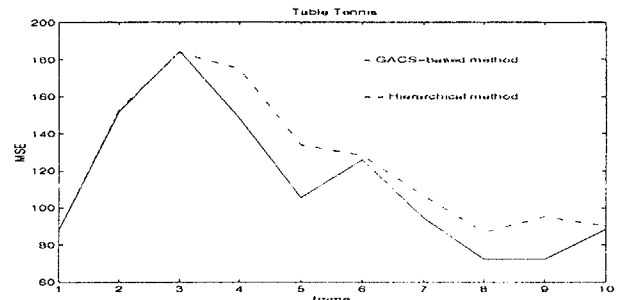


Figure 1: Performances of the proposed GACS-based method and the hierarchical method for the "Table Tennis" sequence.

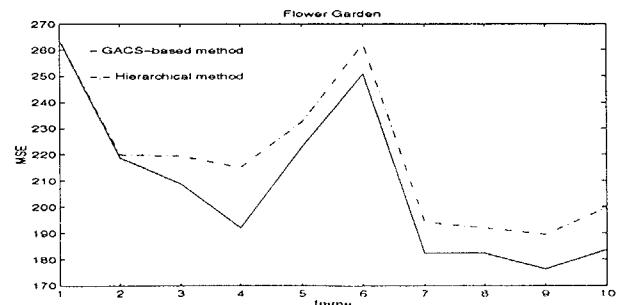


Figure 2: Performances of the proposed GACS-based method and the hierarchical method for the "Flower Garden" sequence.

As far as the optimization is concerned, the typical behavior of the proposed GACS-based method is highlighted by Fig. 3. In the first stage of the evolution, the best performing solutions are found by mutation. The latter allowing dramatic changes in the search space, it permits to enter the zone encompassing the optimal solution. At this stage, the refinement of the available solutions is carried out by crossover. By combining the information present in different well performing solutions, the optimal one can thus be reached.

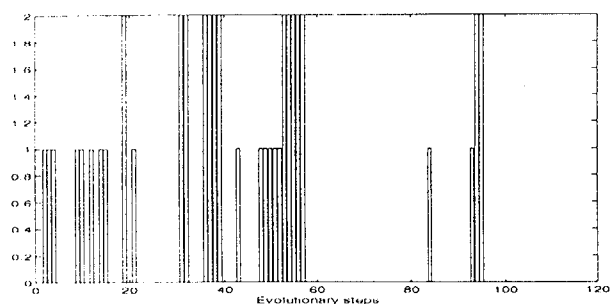


Figure 3: Typical optimization behavior of the GACS-based method (crossover = 2, mutation = 1 and no improvement = 0)

## 5 Conclusion

In this paper, a GACS-based method for matching motion estimation is proposed. Belonging to the class of stochastic optimization method, it tries to mimic the Darwinian evolutionary theory. Conversely to usual GAs, the proposed method does not require any binarization of the solutions. It is characterized by its robustness to local minima and good convergence capability. Furthermore, it does not require extensive tuning and is readily implementable.

Experimental results have shown that the proposed GACS-based method outperforms hierarchical matching motion estimation. Better optimization performances are achieved while reducing the computational load by two-third.

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