Genetic Algorithms applied to Binocular Stereovision

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Abstract. This paper describes an original approach to the problem of edge-based binocular stereovision. The tokens to be matched are sub-chains of the chains of connected pixels. Local constraints of the stereovision problem are first used in associating to each token a set of potential matches. Global constraints are embedded in a cost function and we look for the minimum of this cost function. The optimisation search is conducted using genetic algorithms.

1 Introduction

In this work, we propose an original approach to the problem of edge-based binocular stereovision. Classical solutions are: feature point based approaches ([Gri85], [PMF85], [OK85]), line segment based approaches ([MN85]), curve based approaches ([BB89], [RF91]). An extensive survey of the literature is done in [DA89].

Here, we propose to use chains of connected edge points as tokens to be matched. The number of such features is relatively small (less than 300 in typical images). The matching process is implemented by first reducing the set of potential matches for each chain by using local constraints (epipolar constraint, disparity constraint, disparity gradient constraint and orientation of the gradient intensity constraint). In a following step, the solution of the matching problem is searched by using more global constraints. These constraints are embedded in a cost function and we look for a minimum of this cost function. This optimisation problem is solved using a genetic algorithm. The cost function evaluates the mapping from the set of features of the first image to the set of features of the second image and NIL. This problem reveals itself well adapted to the philosophy of the genetic algorithms. Using genetic algorithms, the optimisation of this function is done through a competition between different possible solutions to the problem of matching. This competition is assessed using the cost function. The different mappings are combined to form a new one using the cross-over operator. For example, in the ideal case of two mappings, one which is good for the upper part of the image but introduces errors for the lower part and the other which is only good for the lower part of the image are combined in such a way that the two good parts are joined in one new solution.

2 Binocular Stereovision

The problem of binocular stereovision is the reconstruction of the 3D coordinates of a number of points in a scene given two images obtained by cameras of

known relative position and orientation. In this paper, we are more specifically interested by the correspondence problem. This problem has been widely studied and various constraints have been proposed.

The first and most important is the epipolar constraint (see [Fau93]). We simplify its use by first rectifying the images (see [HAL88]).

The edges of the images are extracted by classical techniques ([Der87]) and we form a set of chains of connected pixels for each image. We propose to divide each chains of pixels in sub-chains such that, in the rectified image, the ordinates of the pixels change monotically when we move from the beginning of the sub-chain to its end. Consequently, the intersection between an epipolar line and each sub-chains contains at most one point.

Individual constraints We now introduced a set of individual constraints. These constraints have to be verified for a match of a token of the first image with a token of the second image. By using them, we associate to each sub-chain ch_1 of the first image, a subset of the sub-chains of the second image which are potential matches for ch_1. These individual constraints are: the epipolar constraint, the disparity constraint, the disparity gradient constraint and orientation of the gradient of intensity. Details on the integration of these constraints are in [VG93].

Global Constraints The global constraints apply for the major part of the tokens of the scene. These constraints are the uniqueness constraint, the order constraint and the continuity constraint. These last two constraints are not always verified and it is not possible to build an algorithm which enforces them for all the tokens. So, we choose to impose these constraints to a solution of the matching problem globally and to look for the solutions among the mimima of a cost function. This function increases whenever some pair of matches violates one of the constraints. The cost function is a mapping σ from the set of valid solutions to $\mathbb{R}$. We call valid solutions the ones which respect the uniqueness constraint.

$$f(\sigma) = -\lambda_{match}f_{match}(\sigma) + \lambda_{order}f_{order}(\sigma) + \lambda_{dist}f_{dist}(\sigma) + \lambda_{angle}f_{angle}(\sigma)$$

- $f_{match}(\sigma)$ is the sum of the length of the matched sub-chains.
- $f_{order}(\sigma)$ is the sum of the length of the common part of the couples of matched chains which violate the order constraint.
- $f_{dist}(\sigma)$ and $f_{angle}(\sigma)$ evaluates the local continuity.

λ_{match}, λ_{order}, λ_{dist} and λ_{angle} are appropriate weighting coefficients.

3 Genetic Algorithms applied to Binocular Stereovision

The genetic algorithms mimic the mechanisms involved in natural selection to conduct a search through a given parameter space for the maximum/minimum of some objective function. Here, we will present the main features of the genetic algorithms. A detailed presentation can be found in [Gol89]. A point of the parameter space is called a chromosome. The algorithm maintains a population of N individuals which are represented by their chromosomes. It is rather different from the classical optimisation algorithms which maintains only one point in the

search space. Operators are applied to the population and successive generation of the population are derived. These operators rely on probabilistic rules. The search for an optimal solution starts with a randomly generated population of chromosomes. The objective function f is estimated for each individual of the population. A new set of individuals, obtained by the application of the different operators, is the next generation. A stop criterion is tested. If it is decided to continue, the process for computing new generations is iterated.

Encoding of the Solutions We denote Ch_1 (resp. Ch_2) the set of sub-chains of connected pixels of the first image (resp. the second image) which vary monotically (see section 2). A valid solution σ of the matching problem associates to each element of Ch_1 one or zero element of Ch_2. For each element ch_1 of Ch_1, $\sigma(ch_1)$ must belong to the set of potential matches of ch_1 or be NIL (i.e. no match). Each element ch_2 of Ch_2 must be associated to at most one element of ch_1. This is the uniqueness constraint for the elements of Ch_2.

The description of an individual is an array which gives the number of the element of Ch_2 (or NIL) associated with each element of Ch_1. The elements of Ch_1 are introduced in the table according to a precise order defined by the position of their highest point in the image.

Selection The operator of selection chooses, among the N individuals of the population of the current generation, the elements which will be present in the next generation. The selection is based on the cost function.

Cross-Over This operator is used for mixing two individuals and deriving from them two new viable individuals. In accordance with the basic principle set out in [Gol89], a cut site is randomly chosen. It defines two sections on each individual. Two new individuals are derived by combining the opposing sections from the two initial individuals. Of course, the uniqueness constraint for the elements of Ch_2 is no longer necessarily respected and both new individuals must be corrected. The correction is done by scanning each individual from the first element to the cross-over site. For each element ch_1 of Ch_1, we test if the uniqueness constraint is respected for the element of Ch_2 which is associated to it. If it is not, we associate to ch_1 a randomly chosen element among the potential matches of ch_1. We restrict this choice to the elements which are not already used in this individual. If, the set of such elements is empty, no element is associated to ch_1.

Mutation A random site, which represents a sub-chain ch_1^i of Ch_1 is replaced randomly by one of the other potential matches of ch_1^i which are still free. If none is free, no element of Ch_2 is associated to ch_1^i. Processing like this, the result of the mutation is viable (respect the uniqueness constraint).

The Algorithm

Normal Algorithm

1. Initialization of a random population of viable individuals. An individual is randomly constructed by choosing successively for each element ch_1 of Ch_1 its associated element among the potential matches of ch_1 that are not already used. If none exists, no element is associated to ch_1. For this process, the elements of Ch_1 are scanned in random order. In this way, the individuals

built cover correctly the set of possible viable individuals.

2. Computation of the cost function associated with each individual and application of the selection operator. Application of the cross-over and the mutation.

3. While a stop criterion is false, goto 2.

The stop criterion that we have used is the total number of generations.

A Coarse to Fine Approach The proposed algorithm does not make any distinction between the most important structures that are a priori described by the longest sub-chains and the details which are described by shorter sub-chains. A solution to this problem is to use only the longest sub-chains at the beginning and progressively to insert the others. The number of genes of the individuals is increased. This operation is done simultaneously for all the individuals of the population. The insertion operation is a variant of the selection.

4   Experimental results and conclusion

Experimental results In this section, we show the results obtained using our algorithm. Figure 1.(a) shows the original doublet of images. Figure 1.(b) shows the extracted edges before rectification[1]. Figure 1.(c) shows the edges that have been matched by the algorithm. Figure 1.(d) shows the erroneous matches[2]. These results have been obtained by using the coarse to fine approach: the sub-chains are inserted progressively in the chromosome.
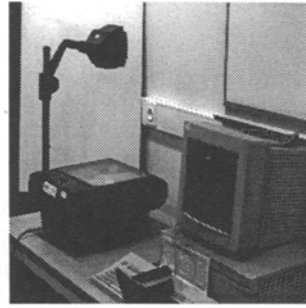
In these experiments, we have used the following parameters. number of individuals in the population: 100, probability of cross-over: 0.7, probability of mutation: 0.2, 2000 generations. The size of the population is increased by 20 every 200 generations. The computational time is directly proportional to the complexity of the cost function. In our case, the construction of a new generation needs several seconds.

The values of these parameters have not been thoroughly optimised. Only a few experiments have been done with different values. These experiments have shown that the results are quite insensitive to the precise values of the parameters. However, we think that some of these parameters, especially the increment of the population size and the number of generations with a fixed size could be set to decrease the computational time.
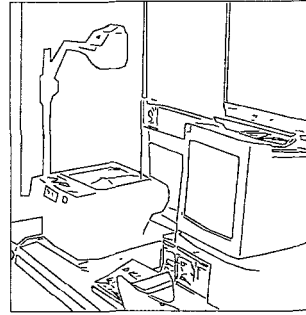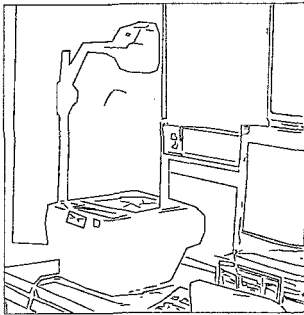
Conclusion In this article, we have presented an original approach to the edge-based stereovision problem. We propose to match sub-chains of connected edge pixels. The split of the chains in sub-chains is done using the epipolar constraint. This solution allowed us to operate on curved objects. We have first shown how we organized the specific constraints of the stereovision problem in such a way that finding a solution to the problem of matching is equivalent to a search for the minimum of a specific cost function. The cost function is

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[1] For each sub-chain, we have only drawn a polygonal approximation of the part of the sub-chain which corresponds exactly to its match. This part is defined using the epipolar constraint.
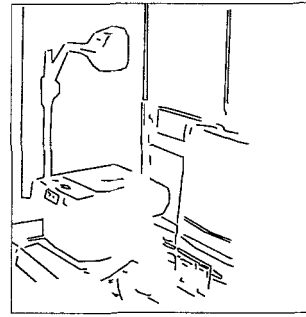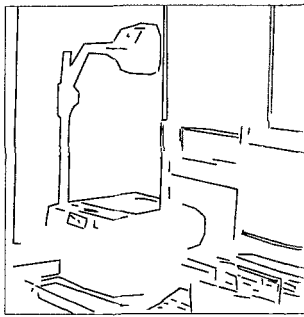
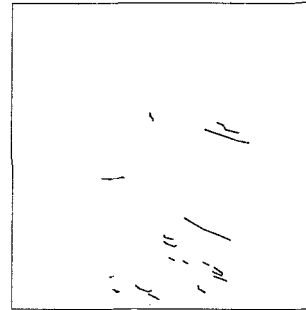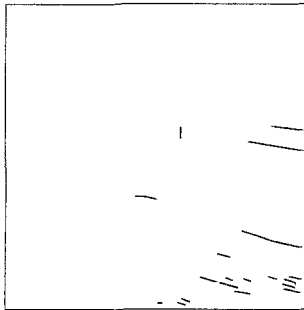[2] The classification between correct and incorrect matches has been made by hand.

Fig. 1. (a) the original doublet of images and (b) the extracted edges, (c) the matched edges and (d) the erroneous matches

minimized using genetic algorithms. It is remarkable to notice that only a few modifications have been given to the classical operators of genetic algorithms. The operator of cross-over appeared to be remarkably adapted to the problem of stereovision, as two solutions which are not correct in the same parts of the image, could be merged in such a way that their correct parts are joined.

It is straight forward to combine a coarse to fine strategy with the genetic algorithms approach. In this article, we have proposed to integrate first the main features of the image in the cost function and to add successively the less important ones. Other strategies could be devised. A possible idea is to divide the image in several horizontal strips (three for examples) and to run the genetic algorithm independently for each of these strips. Afterwards, the obtained results are merged using a variant of the selection operator and the genetic algorithm is run another time on the resulting population. We hope that, by using these strategies, the global computation time will be reduced.

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