

# A Specific Encoding Scheme for Genetic Stereo Correspondence Searching: Application to Obstacle Detection

Hazem ISSA<sup>1</sup>, Yassine RUICHEK<sup>2</sup>, Jack-Gérard POSTAIRE<sup>1</sup>

<sup>1</sup>Laboratoire d'Automatique I3D

Université des Sciences et Technologies de Lille  
Bâtiment P2, 59655 Villeneuve d'Ascq Cedex, France

[Jack-Gerard.Postaire@univ-lille1.fr](mailto:Jack-Gerard.Postaire@univ-lille1.fr)

<sup>2</sup>Laboratoire Systèmes et Transports

Université de Technologie de Belfort-Montbéliard

90010 Belfort Cedex, France

[Yassine.Ruichek@utbm.fr](mailto:Yassine.Ruichek@utbm.fr)

## ABSTRACT

Stereo correspondence is one of the most active research areas in computer vision. It consists in identifying features in two or more stereo images that are generated by the same physical feature in the three-dimensional space. In our approach, the matching problem is first turned into an optimization task where a fitness function, representing the constraints on the solution, is to be minimized. The optimization process is then performed by means of a genetic algorithm with a new encoding scheme. Experimental results are presented to demonstrate the robustness and the reliability of the proposed approach for obstacle detection in front of a vehicle using linear stereo vision.

**Keywords:** Genetic Algorithms, Linear Stereo Vision, Obstacle detection, Optimization, Stereo Matching.

## 1. INTRODUCTION

In the computer vision field, passive stereo vision is a well known approach for obtaining depth information of objects seen by two or more video cameras from different viewpoints [1-2]. The difference of the viewpoint positions in the stereo vision system causes a relative displacement, called disparity, of the corresponding features in the stereo images. This relative displacement encodes the depth information, which is lost when the three dimensional structure is projected on a retinal plane. The key problem is hence the stereo matching task, which consists in comparing each feature extracted from one image with a number, generally large, of features extracted from the other image in order to find the corresponding one, if any. Once the matching is established and the stereo vision system parameters are known, the depth computation is reduced to a simple triangulation technique.

According to the considered application, the existing stereo techniques are roughly grouped into two categories: the feature-based methods and the intensity- or area-based methods [3]. The feature-based methods use zero-crossing points, edges, line segments, etc. and are generally applied when only 3D information are required, as for obstacle detection. Intensity-based methods use dense low-level features and intensity. This type of approaches is considered for 3D scene reconstruction applications.

The problem addressed in this paper concerns the matching of features extracted from stereo linear images. Many approaches have been proposed to solve the stereo matching problem. A classical approach is to use correlation techniques [4]. In order to improve this basic approach, it has been proposed to explore the features of the two linear images sequentially, from one end to the other. A majority of candidate features can be matched without ambiguities by means of this scheme, performed forward and backward [5]. However, this sequential procedure can leave some unmatched features, and may lead to false matches, which are difficult to identify. To circumvent these difficulties, many authors have proposed to turn the matching problem into an optimization task where an objective function, representing the constraints on the solution, is to be minimized using a Hopfield neural network [6]. This neural approach provides good results when compared to the former ones using correlation. However, the Hopfield optimization process does not guarantee to reach the global minimum.

Genetic Algorithms (GAs) are randomized searching and optimization techniques guided by the principles of evolution and natural genetics [7]. They are efficient, adaptive and robust search processes, and they are not affected by the presence of spurious local extrema in the solution space. Indeed, GAs span the solution space and can concentrate on a set of promising solutions that reach the global extrema or converge near the optimal solution.

They have been applied successfully in many fields such as image processing, pattern recognition, machine learning, etc. [7]. Many genetic approaches have been proposed for the stereo matching problem [8-9]. To obtain a disparity map, these methods use fitness functions defined from similarity and disparity smoothness constraints.

Previously, the authors have proposed a genetic algorithm for matching features extracted from stereo linear images [10]. After generating a population of chromosomes representing possible matches with respect to two local constraints, a genetic searching is applied to find a solution for which the matches are as compatible as possible with respect to three competing global constraints. The genetic algorithm provides good matching results, but its major limitation is the computational effort necessary to reach an acceptable solution. This disadvantage comes from the fact that the genetic algorithm manipulates binary chromosomes, which introduce many matching ambiguities. Furthermore, the genetic algorithm requires much computing time to process these binary chromosomes, which have an important size. To overcome these limitations, we propose a new encoding scheme, which produces compact chromosomes with less matching ambiguities. With this new encoding scheme, the genetic searching algorithm explores more efficiently the solution space and requires less computing time to process the new compact chromosomes. Thus, the convergence time is considerably improved.

The outline of this paper is as follows. Section 2 presents the basic principles of linear stereo vision and the method used to extract prominent features from linear images. Section 3 shows how the stereo correspondence problem is achieved using a genetic approach with a new encoding scheme. Before concluding, experimental results are presented in section 4.

## 2. LINEAR STEREO VISION

A linear stereo system is built with two line-scan cameras, so that their optical axes are parallel and separated by a distance  $E$  (Fig. 1). Their lenses have identical focal lengths  $f$ .

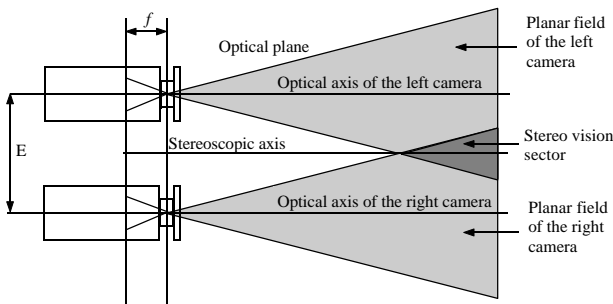


Fig. 1. Geometry of the cameras.

The fields of view of the two cameras are merged in the same plane, called the optical plane, so that the cameras shoot the same line in the scene [11]. If any object intersects the stereo vision sector, which is the common part of the two fields of view in the optical plane, it produces a disparity between the two linear images and, as a consequence, can be localized by means of triangulation.

### Depth reconstruction

Let us define the base-line joining the perspective centers  $O_l$  and  $O_r$  as the X-axis, and let the Z-axis lie in the optical plane, parallel to the optical axes of the cameras, so that the origin of the  $\{X,Z\}$  coordinate system stands midway between the lens centers (Fig. 2). Let us consider a point  $P(x_p, z_p)$  of coordinates  $x_p$  and  $z_p$  in the optical plane. The image coordinates  $x_l$  and  $x_r$  represent the projections of the point  $P$  in the left and right imaging sensors, respectively. This pair of points is referred to as a corresponding pair.

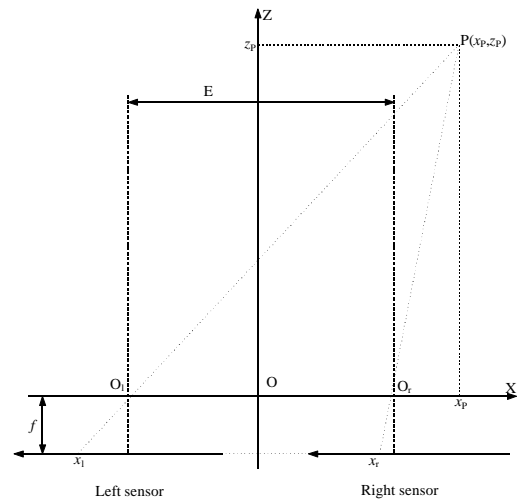


Fig. 2. Depth reconstruction with the pin-hole model.

Using the pin-hole lens model, the coordinates of the point  $P$  in the optical plane can be found as follows:

$$z_p = \frac{E \cdot f}{d}$$

$$x_p = \frac{x_l \cdot z_p}{f} - \frac{E}{2} = \frac{x_r \cdot z_p}{f} + \frac{E}{2}$$

where  $f$  is the focal length of the lenses,  $E$  is the base-line width and  $d = |x_l - x_r|$  is the disparity between the left and right projections of the point  $P$  on the two sensors.

### Feature extraction

Low-level processing of a couple of two stereo linear images yields the features required in the correspondence phase. Edges appearing in these simple images, which are

unidimensional signals, are valuable candidates for matching because large local variations in the gray-level function correspond to the boundaries of objects being observed in a scene.

Edge detection is performed by means of the recursive differential operator proposed by Deriche [12]. Before derivation, each linear image is first processed with a recursive smoothing filter, which removes noise while preserving edges.

For edge extraction, we use first a low threshold value  $t$  to remove only the very small responses of the differential operator lying in the range  $[-t, +t]$ . The adjustment of  $t$  is not crucial. Good results have been obtained with  $t$  adjusted at 10% of the greatest amplitude of the response of the differential operator. A procedure is then applied to select the pertinent local extrema among the remaining edges [5]. This is achieved by splitting the gradient magnitude signal into adjacent intervals where the sign of the response remains constant. In each interval of constant sign, the maximum amplitude indicates the position of a unique edge associated to this interval when, and only when, this amplitude is greater than  $t$ .

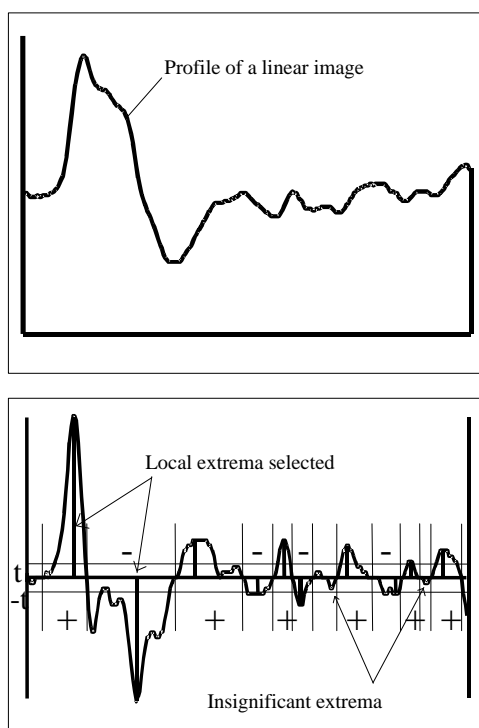


Fig. 3. Edge extraction.

### 3. GENETIC STEREO CORRESPONDENCE

The stereo correspondence can be viewed as a constraint satisfaction problem where the objective is to highlight a solution for which the matches are as compatible as possible with respect to the imposed constraints. In our

approach, the stereo correspondence problem is characterized by two types of constraints: local and global ones.

The two following local constraints are used to discard impossible matches and to consider only potentially acceptable pairs of edges as candidates. Resulting from the sensor geometry, the first constraint, named geometric constraint, assumes that a couple of edges  $i$  and  $j$  appearing in the left and right linear images, respectively, represents a possible match if the constraint  $x_i > x_j$  is satisfied, where  $x$  denotes the position of the edge in the image. The second local constraint, named slope constraint, means that only the pairs of edges with the same sign of the gradient are considered as possible matches.

Three global constraints are used in the searching process of best matches by evaluating the compatibility between the possible pairs. The first one is the uniqueness constraint, which assumes that one edge in the left image matches only one edge in the right image (and vice-versa). The second constraint is the smoothness constraint, which supposes that neighboring edges have similar disparities. The third constraint is the ordering constraint, which tends to preserve the order between the edges of possible pairs. This means that two possible pairs  $(i,j)$  and  $(k,l)$  are compatible with respect to the ordering constraint if one of the two following conditions is satisfied:

$$x_i < x_k \text{ and } x_j < x_l$$

or

$$x_i > x_k \text{ and } x_j > x_l$$

#### New encoding scheme

To solve the stereo correspondence problem by means of a genetic algorithm, one must find a chromosome representation in order to code the solution of the problem. Let  $L$  and  $R$  be the lists of the edges extracted from the left and right linear images, respectively. Let  $N_L$  and  $N_R$  be the numbers of edges in  $L$  and  $R$ , respectively. A classical encoding strategy is to use a  $N_L \times N_R$  binary matrix representation where each element  $E_{ij}$  explores the hypothesis that the edge  $i$  in the left image matches or not the edge  $j$  in the right image (Fig. 4): if  $E_{ij} = 1$ , then the edges are matched; otherwise, they are not matched [10]. Note that the matrix chromosome codes only possible matches with respect to the local constraints.

This binary encoding strategy introduces matching ambiguities simultaneously on the lines and columns of the matrix chromosome. Therefore, a genetic algorithm based on this encoding strategy does not explore the whole solution space in the best way. Furthermore, the genetic algorithm requires much computing time to process these binary chromosomes, which have a large

size. As a consequence, the convergence time of the genetic algorithm toward a good solution is long.

To overcome these limitations, we propose a new encoding scheme, referred hereafter as an integer encoding scheme, which produces compact chromosomes with less matching ambiguities. This will allow a genetic algorithm to explore more efficiently the solution space and to reduce the computing time required for the chromosome processing. Thus, the convergence time of the genetic algorithm will be considerably improved.

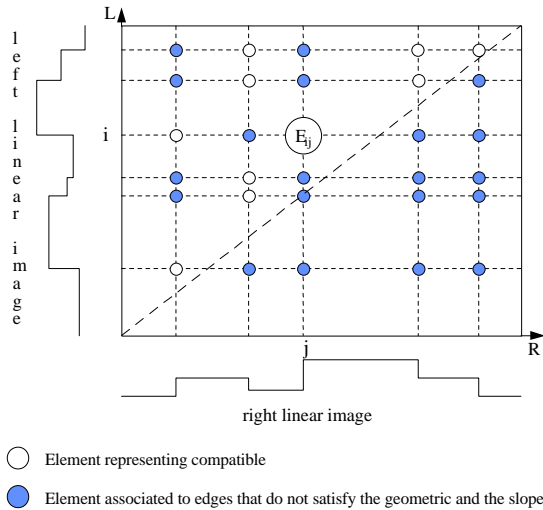


Fig. 4. Binary encoding strategy.

Let  $T_{max} = \{1, 2, \dots, N_{max}\}$  and  $T_{min} = \{1, 2, \dots, N_{min}\}$  be the edge lists of sizes  $N_{max} = \max(N_L, N_R)$  and  $N_{min} = \min(N_L, N_R)$ , respectively. This means that if  $N_{max} = N_L$ , then  $T_{max} = L$  and  $T_{min} = R$  (and vice-versa). The integer encoding scheme consists in representing a solution as a chain  $C$  indexed by the elements of the list  $T_{max}$  and which takes its values in the list  $\{0\} \cup T_{min}$ . The interpretation of the new encoding scheme is as follows: if  $C_i = 0$ , then the edge  $i$  in  $T_{max}$  has no corresponding edge. Otherwise, the edges  $i$  in  $T_{max}$  and  $C_i$  in  $T_{min}$  are matched. As in the binary representation, an integer chromosome codes only possible matches with respect to the local constraints. Figure 5 gives an example of a chromosome, which represents a matching possibility between the edges of figure 4 using the integer encoding scheme. In this example,  $T_{max} = \{1, 2, 3, 4, 5, 6\}$  and  $T_{min} = \{1, 2, 3, 4, 5\}$  represent the lists of the edges appearing in the left and right images, respectively.

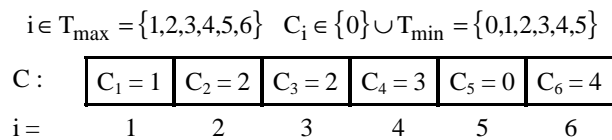


Fig. 5. A chromosome based on the integer encoding scheme.

Note that it is easy to transform an integer chromosome  $C$  into a binary matrix representation  $E$ . Indeed, for  $i \in T_{max}$  and  $j \in T_{min}$ ,  $E_{ij} = 1$  if  $C_i = j$ , otherwise  $E_{ij} = 0$ . We can see that the matrix representation of figure 6 obtained from the integer chromosome of figure 5 presents less ambiguities than the binary representation of figure 4 obtained directly from the binary encoding strategy. There are no ambiguities on the lines of the binary matrix obtained from the integer encoding scheme. Therefore, a genetic algorithm manipulating integer chromosomes will explore more efficiently the solution space and hence will reduce considerably the time computation necessary to converge toward a good solution.

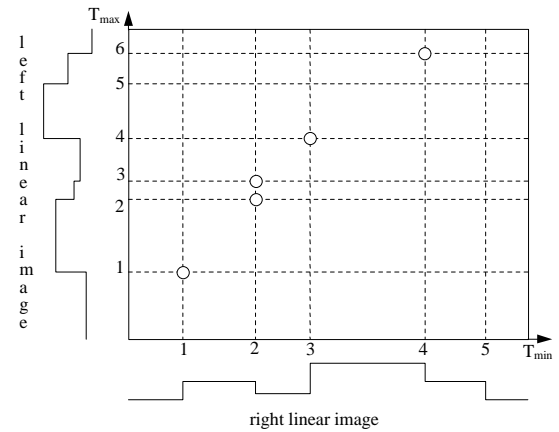


Fig. 6. From an integer chromosome to a binary one.

### Integer chromosome evaluation

A genetic algorithm needs a fitness function for evaluating the chromosomes. As one can pass from the integer encoding scheme to the binary one, the evaluation of an integer chromosome  $C$  is achieved through the evaluation of its matrix representation  $E$  (Fig. 6). Thus, the fitness function can be expressed as:

$$F = K_u \sum_{j \in T_{min}} \left( 1 - \sum_{i \in T_{max} / (i,j) \in \mathcal{D}} E_{ij} \right)^2 + K_m \left( N_{min} - \sum_{(i,j) \in \mathcal{D}} E_{ij} \right)^2 + K_o \sum_{(i,j) \in \mathcal{D}} \sum_{(k,l) \in \mathcal{D}} O_{ijkl} E_{ij} E_{kl} - K_s \sum_{(i,j) \in \mathcal{D}} \sum_{(k,l) \in \mathcal{D}} S_{ijkl} E_{ij} E_{kl}$$

where  $K_u$ ,  $K_m$ ,  $K_o$  and  $K_s$  are weighting positive constants.  $\mathcal{D}$  is the set of all possible matches between the edges in the lists  $T_{max}$  and  $T_{min}$ , i.e., the set of all pairs of edges  $(i, j)$  that satisfy the local constraints:

$$\mathcal{D} = \{(i, j) \in T_{max} \times T_{min}, (i, j) \text{ satisfying the local constraints}\}$$

The first term of the fitness function corresponds to the uniqueness constraint. This term tends to a minimum when the sum of the elements of the matrix chromosome in each column is equal to 1. The second term is used to enforce the chromosomes that encode a maximum

number of matches. This term tends to a minimum when the number of matches is equal to  $N_{min}$ . The third term allows to respect the ordering constraint. The coefficient  $O_{ijkl}$  indicates if the order between the two possible pairs  $(i,j)$  and  $(k,l)$  is respected. It is computed as:

$$O_{ijkl} = \left| \text{signe}(x_i - x_k) - \text{signe}(x_j - x_l) \right|$$

with:

$$\text{signe}(a) = \begin{cases} 1 & \text{if } a > 0 \\ 0 & \text{otherwise} \end{cases}$$

The fourth term is used to enforce the smoothness constraint. The coefficient  $S_{ijkl}$  indicates how compatible are the two possible pairs  $(i,j)$  and  $(k,l)$ . This compatibility measure is computed as follows:

$$S_{ijkl} = S(X_{ijkl}) = \frac{2}{1 + e^{(X_{ijkl} - q)}} - 1$$

where  $X_{ijkl}$  is the absolute value of the difference of the disparities of the possible pairs  $(i,j)$  and  $(k,l)$ , expressed in pixels.

The nonlinear function  $S(X)$  scales the compatibility measure smoothly between  $-1$  and  $1$  (Fig. 7). The parameter  $q$ , which controls the position where the nonlinear function crosses the X-axis, is adjusted so as to allow some tolerance with respect to noise and distortion. It is chosen such that a high compatibility is reached for a good match when  $X$  is close to  $0$ , while a low compatibility corresponds to a bad match when  $X$  is very large. A satisfying value of this parameter is experimentally selected as  $q = 20$ .

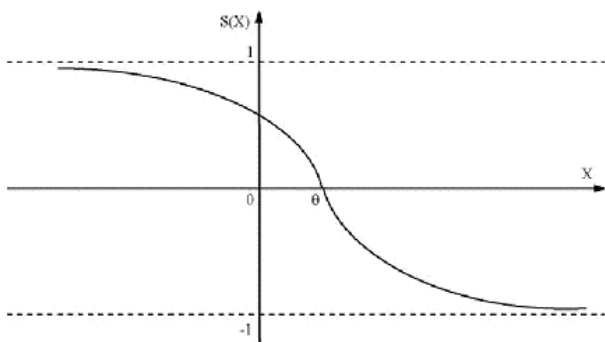


Fig. 7. Graph of the nonlinear function  $S(X)$ .

### Genetic matching algorithm

The genetic algorithm for solving the stereo correspondence problem consists first in generating randomly an initial population of chromosomes representing possible matches that satisfy the local stereo constraints. The evolution process is then performed during some generations thanks to reproduction and selection operations in order to extract the best

chromosome, which minimizes the fitness function. The whole genetic algorithm is summarized in figure 8.

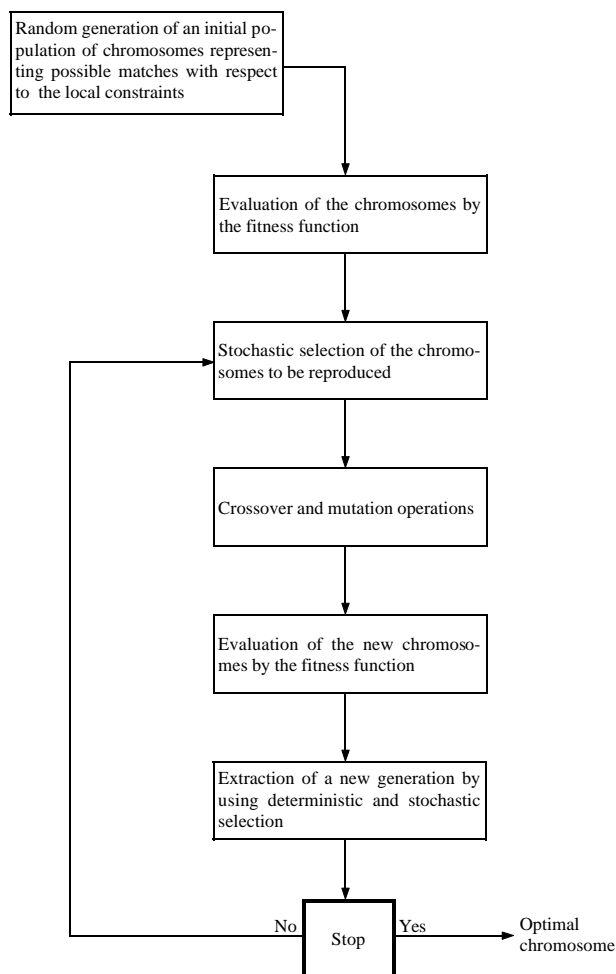


Fig. 8. The genetic algorithm.

Starting from a current population in which each chromosome is evaluated, particular chromosomes are chosen with a selection probability proportional to the fitness value. These selected chromosomes are first reproduced using a single point crossover operation, i.e., two chromosomes are divided at a random position, and a portion of each chromosome is swapped with each other. The whole of the chromosomes are then processed by a mutation procedure, which is randomly performed for each gene.

After the crossover and mutation phases, a new generation is obtained thanks to two selection procedures: deterministic and stochastic ones. The deterministic selection is performed by means of an elitist strategy and used to select 10% of the size of the population. The stochastic selection is based on the same principle as that used to select chromosomes to be reproduced.

The algorithm is iterated until a pre-specified number of generations is reached. Once the evolution process is

completed, the optimal chromosome, which corresponds to the minimum value of the fitness function, indicates the pairs of matched edges.

#### 4. APPLICATION TO OBSTACLE DETECTION

The performance of the proposed genetic matching algorithm has been evaluated for obstacle detection in front of a vehicle using linear stereo vision. A stereo set-up, built with two line-scan cameras, is installed on top of a car for periodically acquiring stereo pairs of linear images as the car travels (Fig. 9). The tilt angle is adjusted so that the optical plane intersects the pavement at a given distance  $D_{max}$  in front of the car.

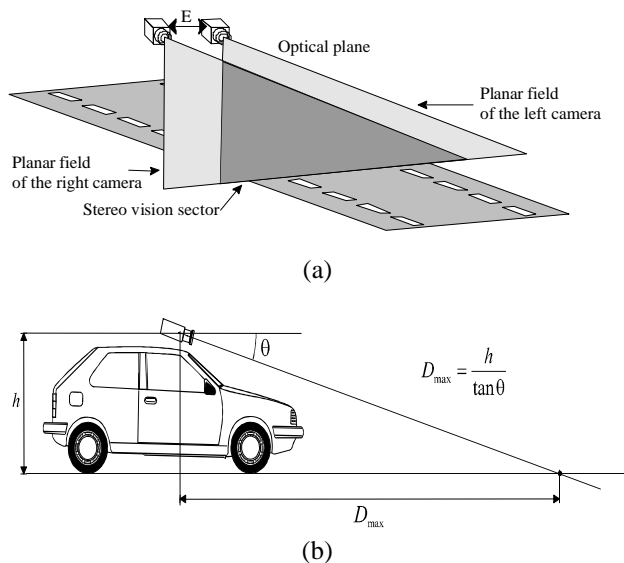


Fig. 9. Stereo set-up: (a) top view, (b) side view.

Figure 10 shows a stereo sequence shot by the set-up where the linear images are represented as horizontal lines, time running from top to bottom. In this simple sequence, a pedestrian travels in front of the car according to the trajectory shown in figure 11. The pedestrian first moves toward his starting point, located slightly beyond the intersection between the optical plane and the pavement (A). When he leaves the plane of vision of the stereoscope (B), he disappears from the images. A few seconds later, he starts moving toward the stereoscope. He reappears in the vision plane, while he moves toward the left camera (C), before walking toward the right camera (D). Finally, he runs toward its left and leaves the vision plane of the stereoscope (E).

On the images of the sequence, we can clearly see the white lines of the pavement. The shadow of a car, located out of the vision plane of the stereoscope, is visible on the right of the images as a black area.

This stereo sequence has been processed using the proposed genetic matching algorithm. For each stereo pair, the disparities of all matched edges are used to

compute the positions and distances of the edges of the objects seen in the stereo vision sector. The results are shown in figure 12 in which the distances are represented as gray levels, the darker the closer, whereas positions are represented along the horizontal axis. As in figure 10, time runs from top to bottom. The results are obtained with the following genetic parameters. The size of the population is equal to 100, the number of generations is set to 300, the crossover probability is 0.6 and the mutation probability is equal to the inverse of the number of genes in a chromosome. The weighting positive constants  $K_u$ ,  $K_m$ ,  $K_o$  and  $K_s$  are set to 5, 5, 5, 1, respectively.

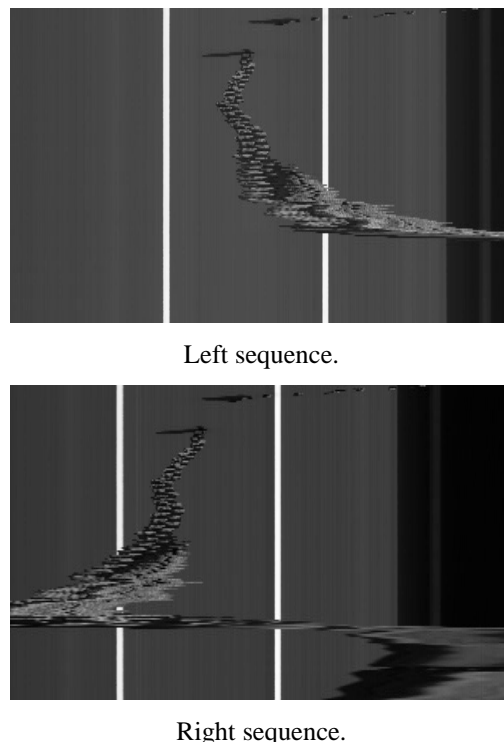


Fig. 10. Pedestrian stereo sequence.

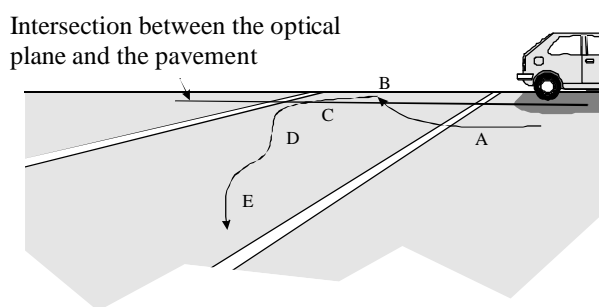
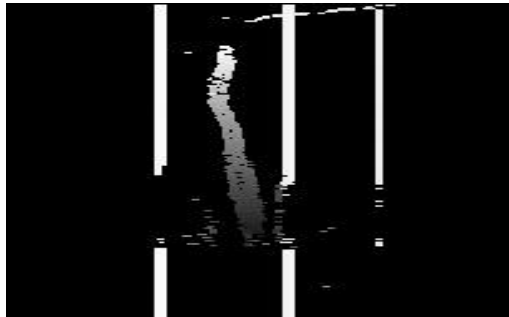


Fig. 11. Trajectory of the pedestrian during the sequence.

Figure 12 shows that the genetic approach provides good matching results. The edges of the two white lines have been correctly matched and their detection is stable along the sequence. Indeed, the positions and distances remain constant from line to line. The pedestrian is well detected

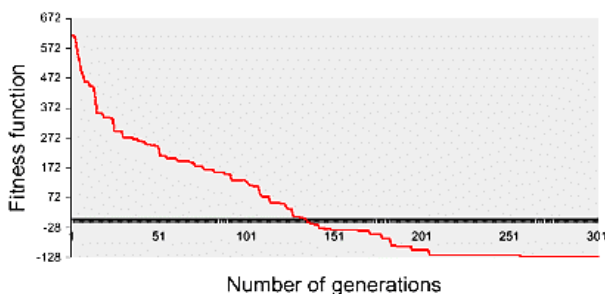
as he comes closer and closer to the car. The transition between the pavement and the area of shadow is also well detected. The presence of a few bad matches is noticed when occlusions occur, i.e., when the pedestrian hides one of the white lines to the left or right camera. These errors are caused by matching the edges of the white line, seen by one of the cameras, with those representing the pedestrian.



**Fig. 12.** Depth reconstruction of the pedestrian sequence.

When compared to the binary encoding strategy, the integer encoding scheme reduces drastically the convergence time of the genetic algorithm. With a *PC Intel-Pentium IV* running at *2 GHz*, the pedestrian stereo sequence is processed in about *20 minutes* thanks to the integer encoding scheme instead of about *4 hours* with the classical binary encoding strategy.

To show the abilities of the new encoding scheme, a couple of stereo images is extracted from the pedestrian stereo sequence in order to analyze the evolution of the fitness function during the genetic process. Figure 13 illustrates this evolution using the new encoding scheme. With a population of *100 chromosomes* and *300 generations*, the fitness function reaches a minimum value of *-128*.

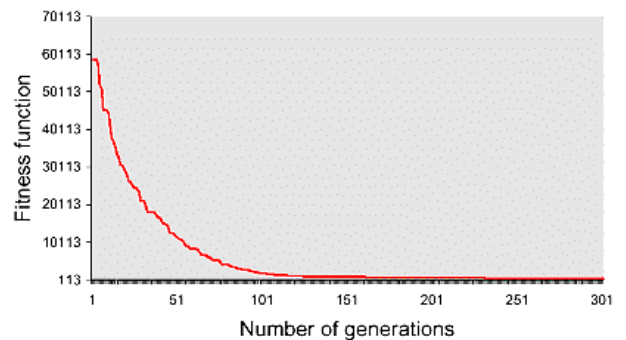


**Fig. 13.** Convergence with the integer encoding scheme.

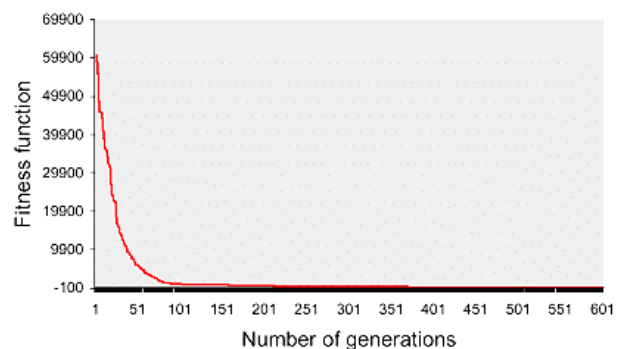
When using the binary encoding strategy with the same values for the population size and the number of generations, the fitness function reaches a minimum value of *112* (Fig. 14). To allow the genetic algorithm to converge toward a solution close to the one obtained when using the integer encoding scheme, it is necessary to increase the population size and the number of generations. When these parameters are set to *300* and

*600*, respectively, the fitness function reaches a minimum value of *-99* (Fig. 14).

These experiments show that the integer encoding scheme allows the genetic algorithm to converge toward a good solution rapidly by exploring efficiently the solution space.



(a): with 100 chromosomes and 300 generations.



(b): 300 chromosomes and 600 generations.

**Fig. 14.** Convergence with the binary encoding scheme.

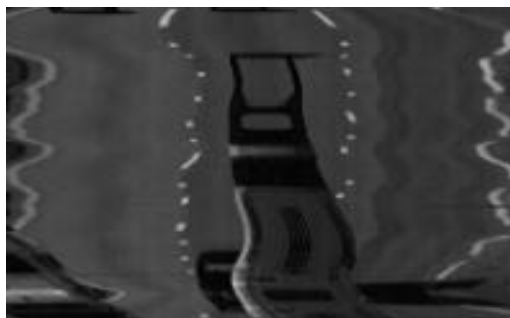
To achieve blind evaluation, the proposed genetic matching algorithm has been applied to process complex stereo sequences acquired in real traffic conditions. One of the complex sequences shot by the linear stereo set-up is shown in figure 15. In this sequence, the prototype car travels in the central lane of the road and follows another car. The optical plane intersects gradually the shadow of the preceding car, then the whole car from the bottom to the top, as the prototype car comes near to it. A third car pulls back into the central lane after overtaking the preceding car. The prototype car is itself overtaken by another one, which is traveling in the third lane of the road. The trajectories of the different vehicles during the sequence are shown in figure 16.

We can see on the pictures of figure 15 the white lines, which delimit the pavement of the road and, between these lines, the two dashed white lines and the preceding car. At the bottom of the pictures, we can see on the left most lane the car, which is overtaking the prototype car and, in the middle, the shadow of the vehicle, which pulls back in front of the preceding car. The curvilinear aspect of the lines is due to the changes in the stereoscope tilt

because of the uneven road surface. Note that the depth reconstruction is not affected by these oscillations of the car.

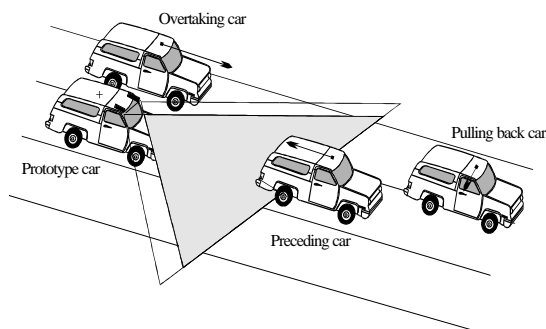


Left sequence.



Right sequence.

**Fig. 15.** Road stereo sequence.

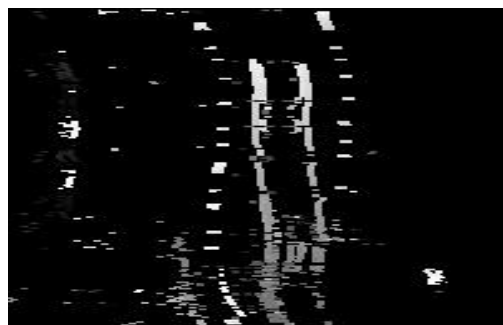


**Fig. 16.** Trajectories of the vehicles during the sequence.

This stereo sequence has been processed by the proposed genetic matching algorithm. The parameters are set to the same values as those used for the processing of the pedestrian stereo sequence. The results are shown in figure 17.

Good matching results are obtained. The edges of the two dashed lines have been correctly matched. The edges of the lines, which delimit the pavement, cannot be matched continuously because they do not always appear in the common part of the fields of the cameras. The preceding vehicle is well detected as it comes closer and closer to the prototype car as time runs. The shadow of the vehicle, which pulls back in front of the preceding vehicle, is identified as a white continuous line, at the bottom of the

reconstructed image. Finally, we can see the dark oblique line, which represents the vehicle overtaking the prototype car, at the bottom of this reconstructed image.



**Fig. 17.** Depth reconstruction of the road sequence.

As expected, the processing time is considerably reduced with the use of the new integer encoding scheme. The road stereo sequence is processed in about 6 minutes instead of 50 minutes when using the binary encoding strategy.

## 5. CONCLUSION

A genetic scheme for feature-based stereo matching is presented. The correspondence problem is first turned into an optimization task where a fitness function, which represents the constraints on the solution, is to be minimized. The optimization process is then performed thanks to a genetic algorithm for which a new encoding scheme is proposed. The performance of the genetic matching approach is evaluated for obstacle detection in front of a vehicle using linear stereo vision. The tests carried out with stereo sequences acquired on real traffic environment show the interest of the proposed approach in terms of robustness and reliability of depth computation. When compared to the classical binary encoding strategy, the new integer encoding scheme produces compact chromosomes with less matching ambiguities. This allows the genetic algorithm to explore much more efficiently the solution space and to reduce the computing time required for the chromosome processing. Thus, the convergence time toward the solution is considerably improved. The implementation of the genetic procedure on specific parallel architecture would improve the processing time for an effective exploitation.

## 6. REFERENCES

- [1] D.H. Ballard, C.M. Brown, Computer Vision, Prentice Hall, Englewood Cliffs, 1982.
- [2] B. Jähne, H. Haußecker, Computer Vision and Applications, Academic Press, 2000.
- [3] R.M. Haralick, L.G. Shapiro, Image Matching, Computer and Robot Vision, Part 2, Addison-Wesley, New York, 1992.



- [4] J.L. Bruyelle, J.G. Postaire, "Direct Range Measurement by Linear Stereo Vision for Real-Time Obstacle Detection in Road Traffic", *Robotics and Autonomous Systems*, No. 11, 1993, pp. 261-268.
- [5] J.C. Burie, J.L. Bruyelle, J.G. Postaire, "Detecting and Localising Obstacles in front of a Moving Vehicle using Linear Stereo Vision", *Mathematical and Computer Modelling*, Vol. 22, No. 4-7, 1995, pp. 235-246.
- [6] Y. Ruichek, J.G. Postaire, "A New Neural Real-Time Implementation for Obstacle detection using Linear Stereo Vision", *Real-Time Imaging*, No. 5, 1999, pp. 141-153.
- [7] D. Goldberg, *Genetic Algorithms in Search, Optimization and Machine Learning*, Addison-Wesley, Reading, MA, 1989.
- [8] K.P. Han, K.W. Song, E.Y. Chung, S.J. Cho, Y.H. Ha, "Stereo matching using genetic algorithm with adaptative chromosomes", *Pattern Recognition*, No.34, 2001, pp. 1729-1740.
- [9] H. Saito, M. Mori, "Application of genetic algorithms to stereo matching of images", *Pattern Recognition Letters*, No.16, 1995, pp. 815-821.
- [10] Y. Ruichek, H. Issa, J.G. Postaire, Genetic approach for obstacle detection using linear stereo vision, *IEEE Intelligent Vehicles Symposium*, 2000, pp. 261-266.
- [11] J.-L. Bruyelle, "Conception et Réalisation d'un Dispositif de Prise de Vue Stéréoscopique Linéaire - Application à la Détection d'Obstacles à l'Avant des Véhicules Routiers", PhD Thesis, Université des Sciences et Technologies de Lille, France, 1995.
- [12] R. Deriche, "Fast Algorithms for Low-Level Vision", *IEEE Trans. on Patt. Anal. Mach. Intel.*, Vol. 12, No. 1, 1990, pp. 78-87.