Genetic fuzzy stereo matching with new encoding scheme

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1 Introduction

This paper presents a genetic stereo matching algorithm with fuzzy evaluation function. The proposed algorithm presents a new encoding scheme in which a chromosome is represented by a disparity matrix. Evolution is controlled by a fuzzy fitness function able to deal with noise and uncertain camera measurements, and uses classical evolutionary operators. The result of the algorithm is accurate dense disparity maps obtained in a reasonable computational time suitable for realt-time applications.

2 New encoding scheme

State of-the-art genetic stereo algorithms provide good matching results, but their major limitation is the computational time. This comes from the fact that the genetic algorithm manipulates binary chromosomes, which introduce many matching ambiguities. To overcome this limitation, we propose a new encoding scheme, which produces compact chromosomes with less matching ambiguities. A chromosome is defined as a matrix C with the same size $(R \times C)$ as the input image. The value of the cell (r,c) of the chromosome matrix represents the disparity d between the pixel (r, c) in the reference image (the right image) and the correponding pixel in the target image.

3 Fuzzy fitness

We propose to model the similarity assumption by a fuzzy measure more robust to noise and illumination changes. This measure expresses the degree of membership of two pixels to a same grey class. We define a grey scale classication of pixels. Three classes are defined; *black*, *white* and *average*. Membership functions of these grey classes, given in Eq.1, are Gaussian centred in 0, 127.5 and 255.

$$\mu_{class}(m) = exp\left(-\frac{(I(m) - c_{class})^2}{2\sigma^2_{class}}\right) \tag{1}$$

I(m) is the intensity at the pixel m, c_{class} and σ_{class} are the center and the standard deviation of the class under consideration. Based on similarity assumption, we can assume that the pairing of two pixels m_1 and m_2 projections of the same physical point M on the stereo images, is *possible* if the two pixels belong to the same gray class. That means (m_1 is **black** AND m_2 is **black**) OR (m_1 is **white** AND m_2 is **white**) OR (m_1 is **average** AND m_2 is **average**). In a fuzzy semantic, this can be expressed by a fuzzy *matching possibility* metric: $\Pi(m_1, m_2)$ (given by Eq. 2). $\Pi(m_1, m_2)$ is a measure of co-membership to a same gray class. It reflects how much it is possible to have m_1 and m_2 as corresponding pixels. Therafter, we will use the notation $\Pi(r, c, d)$=$\Pi(m_1, m_2)$ with $m_1 = (r, c)$ and $m_2 = (r, c, d)$.

$$\Pi(m_1, m_2) = \max\begin{pmatrix} \min(\mu_{black}(m_1), \mu_{black}(m_2)), \\ \min(\mu_{average}(m_1), \mu_{average}(m_2)), \\ \min(\mu_{white}(m_1), \mu_{white}(m_2)) \end{pmatrix} \tag{2}$$

$$F(C) = \sum_{r,\,c} |\nabla(r, c)|\,|\nabla(r, c + C(r, c))| \sum_{(i,\,j)\,\in\,N} \Pi(r + i, c + j, C(r + i, c + j)) \tag{3}$$

As classical approaches, our fitness function uses intensity similarity and disparity smoothness. But instead of using the difference of intensity measurements, which can be easily affected by noise, we use the matching possibilties. That makes the proposed fuzzy fitness more robust to noise, change of view point, occlusions... The Fitness of an individual matrix C is given by Eq. 3.

$C(r, c)$ is the disparity value of the cell (r, c) within the chromosome matrix C. N is a neighbouring introduced to have a discriminating comparison between the projections. $|\nabla(r, c)|$ and $|\nabla(r, c + C(r, c))|$ are Sobel gradient norms respectively on reference pixel (r, c) and target pixel $(r, c + C(r, c))$. That is intended to penalise pixels which project onto uniform regions, i.e. less significant pixels.

4 Genetic operators

The crossover operation generates offspring from two chosen individuals in the population, by exchanging a part of the matrices in the two individuals (Figure 1). The offspring thus inherit some characteristics from each parent. The corossover line is chosen randomly in the interval $[1, R]$ for a $R \times C$ image. The mutation rate is set to 40% and affects matrix cells with lower matching possibilities. After the generation the initial population, the gene pool is filled with other chromosomes produced by crossover and mutation operators. All the chromosomes in a generation are evaluated by the proposed fuzzy fitness function, Some chromosomes that will serve as the parents of the next generation are then selected. Thereafter, the recursive process is continued until the stop condition is satisfied. Selection is elitist and deterministic. It ranks chromosomes according to their fitness values and retains the best individuals (around 40%). All individuals are evaluated by Eq. (3), and each fitness value is transformed into a survival probability for a selection. The selection is conducted using a random function that generates a random number between 0 and 1. An individual whose survival probability is greater than the random number will then survive and prepare to breed for the next generation. If the fittest individual of the current generation does not satisfy a stop condition, the recursive process will be continued from production to evaluation.

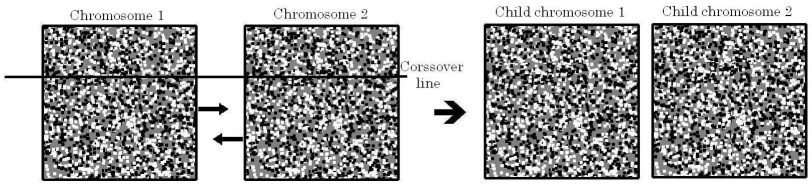

Fig. 1. Example of a crossover of two chromosomes in a random dot matrices

5 Experimental results

Table 1 shows the percentage of incorrect pixels obtained via the Middlebury evaluation site [1]. The execution time of our algorithm for a (217x190) *sawtooth* image after 12 generations of 50 individuals is 0.9 seconds.

	Tsukuba	Venus	Teddy	Cones
error rate	2,74%	2,5%	14,7%	7,78%

Table 1. Error rate, according to the Middlebury evaluation site for our approach

References

1. Middlebury stereo vision page (http://vision.middlebury.edu/stereo).