REGIONS MATCHING ALGORITHM FOR STEREO PAIRS

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ABSTRACT

The aim of this work is to match regions of a pair of stereoscopic images. The main idea is to use the relative position of regions. The matching hypothesis which don't violate the relative position constraint of regions will be given more confidence. To achieve this the following principle is followed: the relative position of two regions in one image will be the same as the relative position of their corresponding ones in the other image. The process of matching is achieved in two stages. The first one finds possible candidate matches on the basis of the relative position constraint. The second one selects the best match according to the criterion which we define. Experimental results demonstrate the effectiveness of the method.

Keywords: Stereo vision, regions matching,
segmentation.

1. INTRODUCTION

The key problem in stereo vision is a search problem which finds the corresponding 2D projected object points in a binocular image pair that are cast by the same physical point in a 3D scene.

The correspondence problem has been solved previously using correlation techniques [8], and by matching low level entities or features extracted from the images separately [2][14][13][10][7]. In this paper, we investigate region based matching as we feel that many of the shortcomings inherent in other approaches can be ovecome by taking more developed entities [4][5][9][12][16][17].

For regions matching in a stereo pair, algorithms usually use geometric and photometric caracteristics of the regions. But most of these are not homogenous by projection [16]. To overcome this, the constraint of adjacency between regions have been used [16][17]. Obviously, this constraint fails in occluded images areas, i.e., in the parts of the scene that are seen by one camera but not by the other. Therefore, there remain miss-correspondences in the final results, which are difficult to identify. In this paper, we propose a new solution to circumvent this problem. The main idea is to use the relative position of regions. The matching hypothesis which don't violate the relative position constraint of regions will be given more confidence. To achieve this the following principle is followed: the relative position of regions in one image will be the same as the relative position of their corresponding ones in the other image. This approach provides good results when compared to the former ones using the adjacency constraint.

The matching process is achieved in two stages. The first stage finds the possible candidate matches based upon the relative position constraint. The second stage selects the correct matchings, among all the candidate matches, according to the cost function which we propose. This function is defined on the basis of local property at the vicinity of region contours, which ensure a great similarity between regions.

The matching process is extended to the neighbouring regions by using the property of adjacency [12]. Starting with the couples of homologous basic regions [17], the adjacent regions are searched first and matched if possible. The process is gradually extended to all the regions on the image.

The remainder of this paper is organized as follows: The matching algorithm is described brievely in section 2. Experimental results are presented in section 3. The paper closes with a conclusion in section 4.

2. MATCHING ALGORITHM

2.1. Selection of possible candidate matches

In order to lower the combinatorial complexity of the matching problem, the possible homologous regions must meet two requirements. The filters in use eliminate a great number of regions while keeping the real homologous one.

2.1.1. The epipolar constraint on the inertia centers

Due to the parallel axis camera's geometry [1][2][3], the location of the inertia center of the right region will be displaced by a disparity value in the left image. Ideally, the disparity value is simply a horizontal shift, i.e., the inertia centers should be on the same epipolar line. However, due to geometrical distortion, imperfections in the extracting of regions, and partial occlusion, the inertia centers of the corresponding regions may not be exactly on the same epipolar line. However, for most of the corresponding regions, their inertia centers will fall within a few scan lines of each other.

2.1.2. The relative position constraint

Let R a given region, we define successively the following sets: $A(R) = Neigh(R)$: the set of adjacent regions of R. Then $A(R)$ is splitted in two subsets $UA(R)$ and $MA(R)$

such as:

$$\begin{aligned} UA(R) = \{R_i \quad / \quad & R_i \in A(R)\ and \\ R_i \quad & is\ an\ unmatched\ region\} \end{aligned} \tag{1}$$

$$\begin{aligned} MA(R) = \{R_i \quad / \quad & R_i \in A(R)\ and \\ R_i \quad & is\ a\ matched\ region\} \end{aligned} \tag{2}$$

If $MA(R)$ is not empty, we define the set of the homologous regions of $MA(R)$ by

$$HMA(R) = \bigcup_{R_i \in MA(R)} Homologous(R_i) \tag{3}$$

We define also the set $S(R)$ of unmatched regions, which belong to the neighborhood of the set $HMA(R)$ by

$$S(R) = \bigcup_{R_i \in HMA(R)} UA(R_i) \tag{4}$$

Finally, a region $R^* \in S(R)$ is possible homologous of the region R if the relative position of R and $R_i \in MA(R)$ is similar to the relative position of R^* and $Homologous(R_i)$ for all $R_i \in MA(R)$.

Mathematically, the set $PH(R)$ is defined by

$$\begin{array}{rcl} PH(R) = \{R^* & / & R^* \in S(R) and \\ RP(R, R_i) & = & RP(R^*, Homologous(R_i)) \\ \forall \quad R_i \in MA(R) & \} & \end{array} \tag{5}$$

where $RP(R, R_i)$ (resp.$RP(R^*, Homologous(R_i))$) is the relative position of the regions R and R_i (resp. the regions R^* and $Homologous(R_i)$).

2.2. Cost functions

To select the best match from the set of possible homologous $PH(R)$, the cost function plays a crucial role. Then, we propose to use a criterion based on local property at the vicinity of region contours.

Let R a given region and ζ its contour. Then, ζ can be divided into three contour parts:

- The leftmost contour (LMC) which contains the points contour which are at the leftmost of the region R. It is defined by

$$LMC = \{(x^*, y^*) \in \zeta / x^* < x \; \forall (x, y^*) \in \zeta\} \tag{6}$$

- The rightmost contour (RMC) which contains the points contour which are at the rightmost of the region R. It is defined by

$$RMC = \{(x^*, y^*) \in \zeta / x^* > x \; \forall (x, y^*) \in \zeta\} \tag{7}$$

- The remaining contour (RM) which is defined by

$$RC = \zeta - (LMC + RMC) \tag{8}$$

Edge magnitudes along these contours can be used to measure the difference between the grey-level intensities at their sides. It can be enforced that two correctly matched contour points should have similar edge magnitudes. A higher cost function can be assigned to the candidate pair that has larger differences in their local properties.

Let R and R^* be two regions in the right and left images, respectively, such us the region R^* is a possible homologous of the region R ($R^* \in PH(R)$). For computing the cost functions, we use only the contours LMC and RMC of the matchable regions. Furthermore, the LMC of the region R will be matched with the LMC of the region R^* and the RMC of the region R will be matched with the RMC of the region R^*.

2.2.1. Cost function associated to the leftmost contours

Let α be the number of possible pairs of matching points on the leftmost contours LMC_l and LMC_r of the regions R^* and R respectively, and U_l^k and U_r^k be the edge magnitudes at the kth point. The cost function for measuring the difference of the local properties for contours LMC_l and LMC_r is defined as

$$C_1 = \frac{1}{\alpha} \sum_{k=1}^{\alpha} |U_l^k - U_r^k| \tag{9}$$

2.2.2. Cost function associated to the rightmost contours

Let β be the number of possible pairs of matching points on the rightmost contours RMC_l and RMC_r of the regions R^* and R respectively, and V_l^k and V_r^k be the edge magnitudes at the kth point. The cost function for measuring the difference of the local properties for contours RMC_l and RMC_r is defined as

$$C_2 = \frac{1}{\beta} \sum_{k=1}^{\beta} |V_l^k - V_r^k| \tag{10}$$

2.2.3. Choice of the homologous of a matchable region

For a given region R, we consider the associated set $PH(R)$ of possible homologous. Then, according to the above information, we can obtained the best candidate R^* as the solution of the following minimization problem:

$$\min_{R^* \in PH(R)} = \frac{1}{\alpha + \beta} (\alpha \, C_1 + \beta \, C_2) \tag{11}$$

Where α and β are the same defined before.

2.3. Propagation of the matching process

This process consists in propagating the matching to the other regions by using the dajacency relationship between the regions [6][11][12]. The process starts by choosing a couple of homologous basic regions [17]. An adjacent region is selected and its homologous region is searched on the other image. the homologous must meet the relative position constraint, the epipolar one, and must be similar to the region selected according to the local properties at the vicinity of the region contours. Further, the process is repeated until all the regions are exploited.

3. EXPERIMENTAL RESULTS

This section discusses the results obtained when we applied our stereo algorithm to synthesized and real stereo images.

The regions detector used is a region growing algorithm which is based on the split-and-merge algorithm [15]. The first step of the algorithm splits the image until obtaining a partition P such as all the regions satisfy a homogeneity criterion. The second step merges adjacent regions by considering new homogeneity criterions. Then, the very small regions are grouped with the nearest adjacent large one. The algorithm is detailed in [4].

We first applied the stereo algorithm to the synthesized stereo images shown in Figure 1 (obtained from INRIA). The stereo images have a size 256x256 with an intensity resolution 256. Figure 2 shows the results provided by the segmentation algorithm and the matching process. The process of matching is performed from right-to-left. Two matched regions are labeled with the same number on the left and right images. The number of matched pairs is twelve. All the pairs are correctly matched.

The stereo algorithm has also been applied to the indoor scene stereo images shown in Figure 3. The stereo images have a size 165x340 with an intensity resolution of 256. Figure 4 shows the results of both segmentation and matching algorithms. The number of matched pairs is ten. All the pairs are correctly matched.

4. CONCLUSION

In this paper an algorithm, which match the regions of a pair of stereoscopic images, is presented. It uses the relative position of regions, which allow the reduction of the combinatorial complexity and eliminate unreliable matching. The results are very satisfying since the most reliable matching are done first and extended to the other regions by exploiting the previous results.

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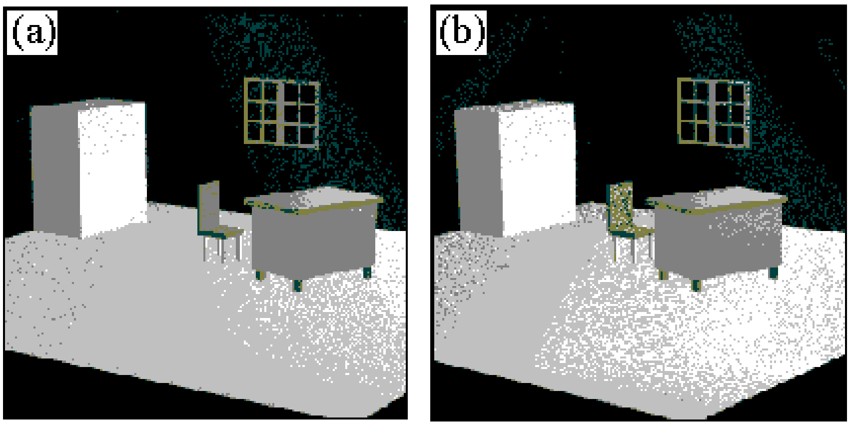

Figure 1: Synthesized stereo images. (a) left image. (b) right image

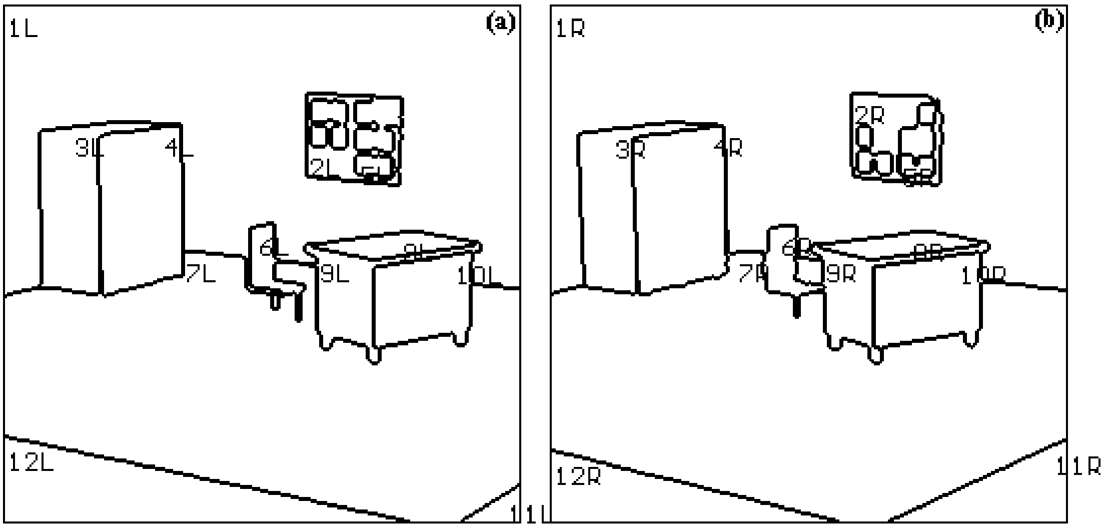

Figure 2: Results of the segmentation and the matching process. (a) left image. (b) right image

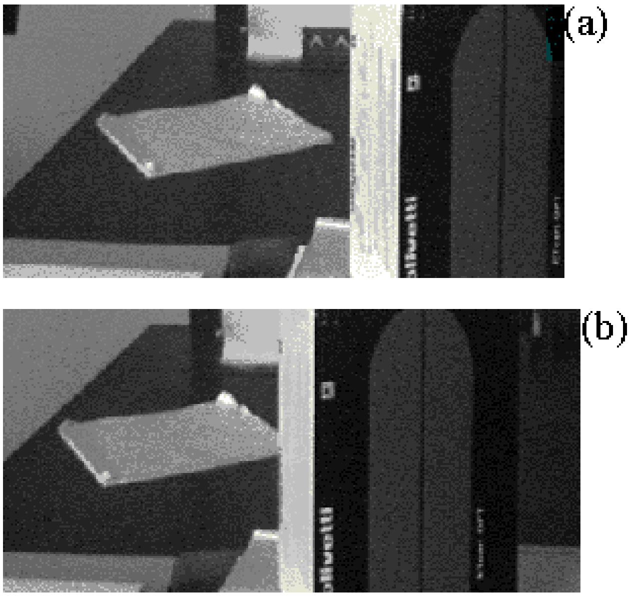

Figure 3: Real stereo images. (a) left image. (b) right image

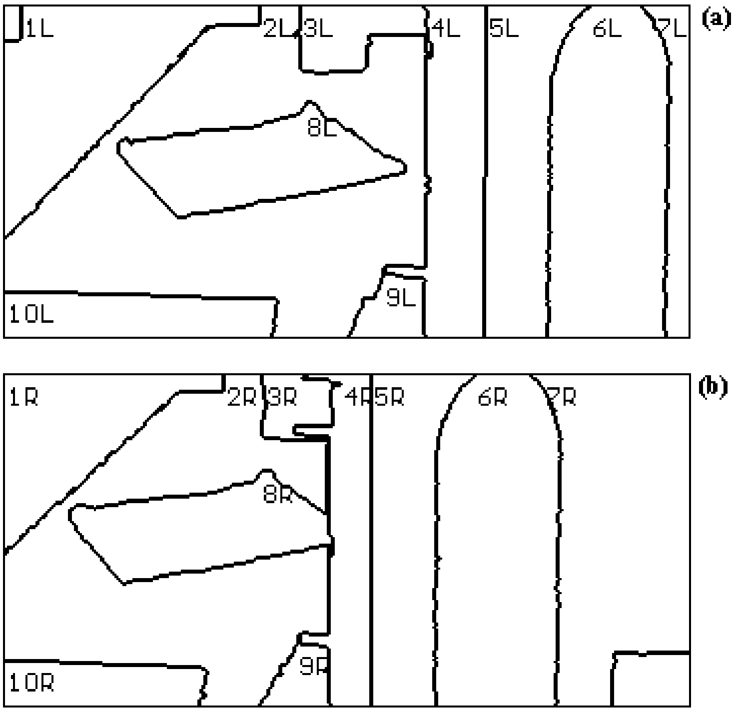

Figure 4: Results of the segmentation and the matching process. (a) left image. (b) right image