

# ON A NEW MIGRATION SCHEME FOR THE ISLAND MODEL PARALLEL GENETIC ALGORITHM TO THE CORRESPONDENCE PROBLEM

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**Abstract**— The island model parallel genetic algorithm is described to approach the correspondence problem in computer vision using contextual and structural features of a point, in which multiple points are simultaneously considered, under the structural coherence constraint. The correspondence is achieved by optimizing similarity measurements among the points' features and by satisfying the structural coherence constraint [4][13][14]. The Island Model Parallel Genetic Algorithm (GA) is used to search a large space by evolving different populations separately, using the Dempster-Shafer calculus for an individual's fitness evaluation. In order to try to introduce higher levels of diversity in the process, a new parameterization for the island model parallel GA model is proposed. The model was applied to a pair of real world indoor images to demonstrate the usefulness of the approach for the correspondence problem. The reported simulations were conducted using 9 virtual machines. Comparisons made with previous work show a higher accuracy for the island model parallel GA.

**Keywords**— Parallel Genetic Algorithm; Stereo Vision; Uncertainty-Reasoning; Correspondence Problem.

## 1 Introduction

This paper describes a parallel GA approach to the correspondence problem in stereo vision, which is a Computer Vision task that permits inferring 3D information from 2D data (images). The correspondence problem is the main problem related to such a task. It consists of establishing the correspondence among features in the images to assure they are images of the same scene [1][3].

In [1][3][5] several methods and algorithms are described that have been used to address the correspondence problem. New paradigms like neural networks, regularization, learning strategies, optimization techniques [7], and genetic algorithms [4][9][13][14][15] have also been tried, attempting to incorporate and exploit new aspects that may lead to more robust implementations that may cope with intrinsic problems in stereo vision like occlusion, that is, an object is blocked by others from one view to the other, due to the arrangement of the cameras (Figure 1).

The methods and algorithms for the correspondence problem are classified as area-based, token-based or hybrid approaches and they all must satisfy the constraints to the problem stated in [2]: point compatibility, uniqueness of correspondence, and map continuity. However, they usually fail due to problems in the images, such as illumination changes, occlusion, and the size and shape of the window used. A hybrid approach exploits the features and advantages of both area- and token-based methods and algorithms.

Exploiting new aspects is the main stream in research work on the correspondence problem that have tried to exploit new aspects as in [8] to better satisfy the constraints mentioned previously.

Whichever the approach is, the correspondence among images requires the choice of features in a reference image and the search for a similar features in the other images. Such search may result in a large number of possibilities, from which a unique correspondence has to be chosen due to the constraints to the problem.

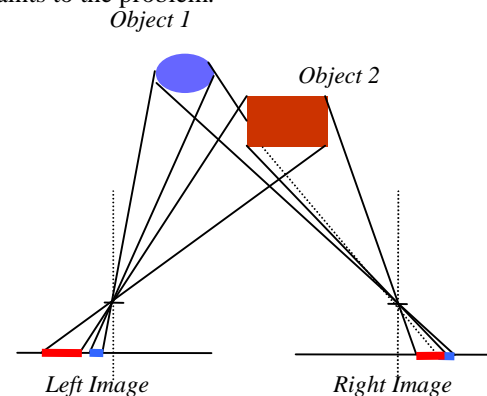


Figure 1 - The occlusion problem (object 1) in a parallel camera arrangement.

In [13][14][15] a point wise hybrid approach to the correspondence problem is proposed, based on contextual (area) and structural (token) features of a point and its neighborhood, taken as corresponding evidences. Similarities among corresponding points are measured by applying differences, correlation, and distance metrics. Multiple reference points ( $N$ ) are matched under the structural coherence constraint, related to the geometry of the polygonal regions emerged from the interconnection of the  $N$  points. The process is developed in a low-level point correspondence followed by a high-level correspondence among the polygonal regions. The complexity of the correspondence problem increases

with the number of simultaneous points to be corresponded, the number of candidate points for the reference points, the complexity of the geometric features of the polygonal regions, and the existence of occlusion in the images. A Genetic Algorithm is used to search the solution space, guided by a fitness function that considers the minimization of the sum of differences among the contextual, structural, and geometric evidences.

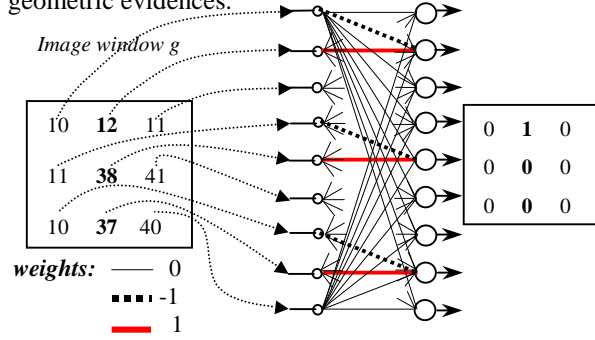


Figure 2 - The vertical line structure in a 3 x 3 window. Weights are inserted as shown.

This paper describes a point wise approach to the correspondence problem as a continuation of previous work [13][14][15]. The correspondence among the images is established by combining evidences of correspondences, that is, the similarity measurements among the contextual and structural features of the points and the geometric features of the polygonal regions.

Degrees of beliefs are assigned to the similarity measurements. The Dempster-Shafer Theory for uncertainty reasoning is used to perform the combination of the evidences resulting in a combined evidence with a degree of belief. Such measurement guides the Island Model Parallel Genetic Algorithm in the search for the best solution. The parameterization used in the parallel GA implementation is modified to increase diversity in the search and reduce the convergence time.

Section 2 briefly describes the extraction of area and token features used as corresponding evidences. Section 3 introduces the Dempster-Shafer theory concepts. Section 4 describes the Island Model Parallel Genetic Algorithm. Section 5 presents some results of applying the proposed methodology on indoor images. Finally, section 6 brings the conclusions and comments.

## 2 Corresponding Evidences

The methodology described in this paper uses a point-wise hybrid approach to the correspondence problem in which contextual features of a point provide local and global information of the context of the a point, within a certain neighborhood (area). The contextual features are the micro area (determined by a predefined window size) and the macro area (within a window  $n$  times bigger than the micro area) of the

point. Such features are first established in the reference image and search in the other image. The similarities are computed by correlating the features.

Structural features consist of binary tokens computed by operating on the image pixels within a window with the size of the micro area. The results in this paper consider 8 such features: the vertical and horizontal lines, the principal and secondary diagonals, and the bottom right, top right, top left, and bottom left corners. Perceptron neural networks are used to extract such features (Figure 2), thus avoiding gradient operations for edge detection and a token description phase, which are time consuming tasks. The weights of the Perceptrons are inserted and represent prior knowledge of each different desired binary structure. As an example, Figure 2 shows a Perceptron neural network architecture for extracting the vertical line structure in a 3 x 3 window. Similar networks are used for the other binary features. It is to be noticed that bigger windows will require redefinition of these neural network architectures for such structures.

Two additional binary structures are the *pattern of differences* among the central pixel and its connected neighbors, and the *predominant structure*, computed within a connected neighborhood. The pattern of differences gives the directions of differences among the point and its neighbors. The predominant structure shows the spatial distribution of the pixels that lead to high levels of energy for certain predefined orientations. Both features require a definition of connectivity to fit windows which are greater than 3 x 3.

**Definition 1.** The *main neighborhood* of a point  $P$  is defined by the points on the same line coordinate or on the same pixel coordinate of point  $P$  (Figure 3a).

**Definition 2.** The main neighborhood and every point in the vicinity of  $P$ , limited to the window size (Figure 3b), define the *secondary neighborhood* of a point  $P$ .

**Definition 3.** A  $\left(\frac{n-1}{2}\right) \mapsto 4$  *connected*

neighborhood of a point  $P$  includes the points of its main neighborhood up to the  $\left(\frac{n-1}{2}\right)$  level of connectivity, where  $n$  is the window size (Figure 3a).

**Definition 4.** A  $\left(\frac{n-1}{2}\right) \mapsto 8$  *connected*

neighborhood of point  $P$  includes the points in its secondary neighborhood up to the  $\left(\frac{n-1}{2}\right)$  level of connectivity, where  $n$  is the window size (Figure 3b).

It is to be noted that for  $n=3$ , definitions 3 and 4 reduce to the classical definition of 4 connectivity and 8 connectivity, respectively. In Figure 3, each  $d_i$  represents the difference between the central pixel and its  $\left(\frac{5-1}{2}\right) \mapsto 4$  and  $\left(\frac{5-1}{2}\right) \mapsto 8$  connected neighbors.

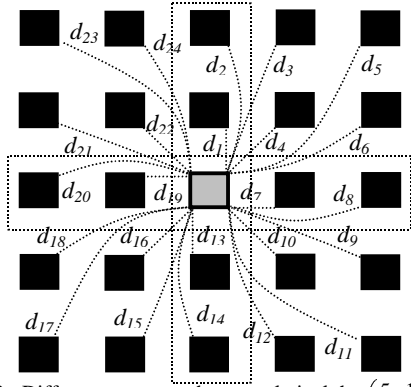


Figure 3 - Differences among the central pixel the  $\left(\frac{5-1}{2}\right) \mapsto 4^-$  and the  $\left(\frac{5-1}{2}\right) \mapsto 8^-$  - connected neighbors within a  $5 \times 5$  window.

The pattern of differences is defined as an ordered binary vector  $D$  with  $n^2-1$  components given by the threshold function.

$$T(d_i) = \begin{cases} 1 & d_i \geq 0 \\ 0 & d_i < 0 \end{cases} \quad D = [T(d_1), T(d_2), \dots, T(d_{n^2-1})]$$

A Perceptron neural network, with weight insertion, as in Figure 2, computes the pattern of differences within a window. As an example, for the  $3 \times 3$  image window in Figure 2, the pattern of differences is given by:

$$D = [T(12-38), T(11-38), T(41-38), T(40-38), T(37-38), T(10-38), T(11-38), T(10-38)] \Rightarrow D = [0, 0, 1, 1, 0, 0, 0, 0]$$

The *predominant structure* is computed by the convolution of the image window with predefined morphological kernels, as in Figure 4 (for  $3 \times 3$  window) defined by equation (1), where:  $C_K$  is the computed correlation for kernel  $K$ ;  $n$  is the window size;  $l$  and  $p$  are the line and pixel coordinates of each pixel in the image;  $f^K(i, j)$  is the kernel  $K$  value at position  $(i, j)$ . Equation (1) computes the correlation between the normalized image window and a kernel.

$$C_K = \sum_{i=-\frac{n}{2}}^{\frac{n}{2}} \sum_{j=-\frac{n}{2}}^{\frac{n}{2}} g(l+i, p+j) \times f^K(i, j) \quad (1)$$

0 0 0	0 1 0	0 1 0	0 0 0	0 0 0	0 1 0	1 0 0	0 0 1	1 0 0	0 0 1
1 1 1	0 1 0	0 1 1	0 1 1	1 1 0	1 1 0	0 1 0	0 1 0	0 1 0	0 1 0
1 0 1	0 0 0	0 1 0	0 1 0	0 0 1	1 0 0	0 0 0	0 0 1	0 0 0	1 0 0
0 1 0	0 1 0	0 1 0	0 1 0	0 1 0	0 1 0	1 1 0	1 1 0	0 1 1	0 1 1

Figure 4 - Basic binary morphological structures within a  $3 \times 3$  window.

The kernel with highest convolution value is chosen as the *predominant structure* within the window. This process can be thought of as an energy analysis given by the convolution. Figure 4 shows examples of 20 binary morphological kernels for a  $3 \times 3$  window. Bigger windows lead to a larger number

of kernels to be defined. The bigger the window size and the larger the number of structural features, the more complex the binary structures are, thereby increasing the likelihood of the uniqueness constraint to be satisfied.

By considering the contextual and structural features of a point, the correspondence takes place under the continuity map constraint, which requires that a reference point and a candidate corresponding point must lie within similar macro and micro contexts, and must belong to similar structures within the images. For this purpose 14 similarity criteria are adopted for the correspondence of a candidate point to a reference point:

- The non-normalized Euclidean distance between the micro areas ( $ES$ )
- The Correlation index between the micro ( $C_{micro}$ ) areas
- The Correlation index between the macro ( $C_{macro}$ ) areas
- The Hamming distance between the 10 different binary structures ( $N_1 N_2 N_3 N_4 N_5 N_6 N_7 N_8 N_9 N_{10}$ )
- The Absolute difference between the gray levels ( $G$ )

Following feature extraction, each candidate point  $i$  is assigned a vector with similarity measurements for the 14 different matching criteria, together with the point line and pixel coordinates ( $l_i, p_i$ ).

$$Q_i = [l_i p_i ES C_{macro} N_1 N_2 N_3 N_4 N_5 N_6 N_7 N_8 N_9 N_{10} G C_{micro}]$$

## 2.1 Geometric Features

Three geometric features deal with the structural coherence constraint between the polygonal regions:

- Sum of the angles formed by the sides of the polygonal region in relation to the horizontal line;
- Area of the polygonal region;
- Sum of the Euclidean distances among the incenter of the polygonal region and its vertices.

The geometric features must be computed for both the reference and candidates polygonal regions and the similarity among them are computed by absolute differences.

The use of contextual and structural features of each point (vertex), as well as geometric properties of the polygonal regions characterizes the methodology described in this paper as a hierarchical approach to the correspondence problem, in which point correspondence happens in a low level by analyzing local properties of a point, and a high level correspondence occurs globally across the image, while matching the polygonal regions. Thus, for a given reference polygonal region, the correspondence is a process of finding a polygonal region in the other image, among a large number of candidate regions (or search space), that may match the reference.

### 3 Uncertainty Reasoning in the Correspondence Evaluation

#### 3.1 The Dempster-Shafer Theory

The Dempster-Shafer (DS) Theory assumes a *Universe of Discourse*  $U$  or *Frame of Discernment*, which is a set of mutually exclusive alternatives that may correspond to an attribute value domain [10]. Then, if one is trying to determine the disease of a patient, for instance, the set  $U$  may consist of all possible diseases. In DS theory each subset  $S$  of  $U$  has associated to it: a basic probability  $m(S)$  (or the strength of some evidence), a belief  $Bel(S)$  (Belief), and a plausible belief  $Pls(S)$  (Plausibility) for which the values must belong to the interval  $[0,1]$ , and  $Bel(S)$  cannot be greater than  $Pls(S)$ .

In applying a rule, for instance,  $m$  may represent the effect of that rule.  $Bel(S)$  summarizes all the reasons to believe  $S$ .  $Pls(S)$  expresses how much one should believe in  $S$  if all currently unknown facts were to support  $S$ . Thus, the true belief in  $S$  will be somewhere in the belief interval  $[Bel(S), Pls(S)]$ .

The basic Probability Assignment  $m$  is defined as:

$$m : 2^U \rightarrow [0,1]$$

where  $m(\emptyset) = 0$  ( $\emptyset$  is the empty set), and the sum of  $m$  over all subsets of  $U$  is 1 ( $\sum_{S \subseteq U} m(S) = 1$ ).

It can be shown that for a given basic probability assignment  $m$ , the belief ( $Bel$ ) of a subset  $A$  of  $U$  is the sum of  $m(B)$  for all subsets  $B$  of  $A$ , and that the plausibility ( $Pls$ ) of a subset  $A$  of  $U$  is  $1 - Bel(A')$ , where  $A'$  is the complement of  $A$  in  $U$ .

Two basic probability assignments  $m_1$  and  $m_2$  are combined into a third basic probability assignment by the orthogonal sum  $m_1 \oplus m_2$  (Dempster rule of combination) defined as

$$m_1 \oplus m_2(A) = \frac{\sum_{X \cap Y = A} m_1(X)m_2(Y)}{1 - k}, \quad k = \sum_{X \cap Y = \emptyset} m_1(X)m_2(Y) \quad (2)$$

Equation (2) is the original formula for basic probabilities combination; however it is time consuming. A faster alternative to the combination of evidences is given in [12], which is equivalent to the orthogonal sum of equation (2). Equations (3) and (4) directly combine beliefs and plausibilities.

$$Bel(S) = 1 - \frac{(1 - Bel_1(S))(1 - Bel_2(S))}{1 - [Bel_1(S)(1 - Pls_2(S)) + (1 - Pls_1(S))Bel_2(S)]} \quad (3)$$

$$Pls(S) = \frac{Pls_1(S)Pls_2(S)}{1 - [Bel_1(S)(1 - Pls_2(S)) + (1 - Pls_1(S))Bel_2(S)]} \quad (4)$$

#### 3.2 Correspondence Associations

The correspondence evidences found are mapped into basic probabilities, in which only the available information is considered, that is, no probability is assigned to evidences that contradicts the hypothesis. Then, each candidate polygonal region will have 14 beliefs and plausibilities associated to the structural and contextual information of the points, and three beliefs and

plausibilities associated to the geometric evidences. The Dempster-Shafer calculus combines such beliefs and plausibilities resulting in a belief and a plausibility of the combined evidence that represent a consensus on the correspondence. Figure 5 shows the result of applying the Dempster-Shafer Theory to correspond one point in a pair of images. The aim of the method presented in this paper to maximize the belief in the combined evidences.

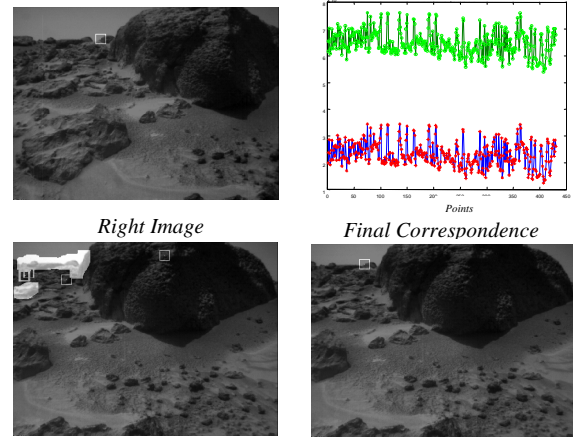


Figure 5 - Results of applying the Dempster-Shafer Theory to establish the correspondence of one point. The graphics show the degrees of belief and plausibility for each candidate point.

### 4 The Island Model Parallel GA

The idea behind the island model parallel GA is the independent (parallel) evolution of separated subpopulations, based on the fact that distributed multiple subpopulations, with local rules and interactions form a more realistic model of species in nature [6][11]. A fundamental characteristic of the island model parallel GA is the migration of highly fitted individuals across the subpopulations, which increases the selective pressure since highly fitted individuals will mean new reproduction attempts in the receiving subpopulation. The highly fitted individuals will help to maintain the genetic diversity of the local subpopulation.

The island model parallel GA implementation requires parameter specification to be used in the various GAs. The required parameters are the type of GA to be used in each processor, the number of migrating individuals, the migration frequency, and the policy for choosing the migrating and the substituted individuals. Such scheme results in a more realistic model of species in nature [6]. Figure 6 shows the algorithm to implement the island model GA.

```

Island_Model_GA()
begin
    t=0; initialize P(t); evaluate P(t);
    while ( NOT Stop condition ) do
        begin
            t=t+1;
            select P(t) from P(t-1);
            recombine P(t);
        end
    end

```

```

send(migrating_individual)
if ( migration_generation )
    mig_ind = receive_migrating( )
    rep_ind = chose_individual_for_change( )
    change_individuals(P(t), mig_ind, rep_ind)
end
evaluate P(t);
end
end

```

Figure 6 - The Island Model Genetic Algorithm.

The migration scheme is predetermined, that is, the sub-populations know in advance the destination where to send its migrating individual. However, a sub-population should have the opportunity to send its migrating individual to any other sub-population, so that, each sub-population could have the same probability to bring in new diversity a migrating individual might be able to.

This paper proposes a migration scheme for the island model GA, in which all the sub-populations have the same probability of receiving a high fitted individual. The migrating individuals are all sent to a repository with identification tags. At its migrating generation the sub-population requests randomly chosen individual from the repository. It then continues the evolution process.

## 5 Results

The present approach was applied to several real world image pairs with different sizes and gray levels, aiming at establishing the correspondence among  $N$  ( $N=6$ ) simultaneous points as in [13][14].

Initially,  $N$  ( $N=6$ ) reference points are chosen in the left image ( $L$ ) (Figure 7.a). The candidate corresponding points are then selected in the right image ( $R$ ) (Figure 7.b), based on contextual features of the points. The similarities among the features of the points are computed and arranged in a vector that is assigned to the candidate point.

The similarity measurements are then mapped into beliefs and plausibilities. The sub-populations are randomly initialized with a fixed number of individuals (100 in the experiments). Each individual is an ordered sequence of randomly chosen vertices, forming a polygonal region,  $Q_1 Q_2 \dots Q_i \dots Q_N$  where  $Q_i$  belongs to a set  $SC_i$  of candidate points showing relative similarity with point  $i$ .

The experiments were conducted by using 9 processors evolving 9 sub-populations during 200 generations. Point evidences were combined by equations (3) and (4), thus resulting in a belief and plausibility on the combined point evidences. The geometric features of the polygonal regions were mapped into beliefs and plausibilities that were combined with the belief and plausibility of the combined evidence of the points, thus leading to a final belief and plausibility that represent a consensus on the correspondence. Among all the individuals in

the population, the process picks the one with highest belief on the combined evidences. Equation (3) is the fitness function that measures the performance of individuals in each subpopulation. Each genetic algorithm used a 50% crossover probability and a 25% mutation probability.

The uncertainty reasoning approach was applied to the same image pairs using one GA only, in order to compare it with the discussed parallel implementation in terms of computational time. Figure 8 shows a comparison of the evolution for one GA and for the parallel implementation. The parallel implementation quickly reaches a stable solution, when compared to the use of a single GA.

Table 1 shows the computed squared errors for the correspondences found by the parallel GA. The mean squared error between the set of references and the set of corresponding points has an accuracy of less than 1 pixel.

Table 1 – Computed squared errors for the correspondences in Figure 5.

	Reference points		Solution		Ground truth		Squared errors	
	Line	Pixel	Line	Pixel	Line	Pixel	Line	Pixel
1	56	150	55	136	55	136	0	0
2	34	91	34	77	34	77	0	0
3	88	69	89	27	88	27	1	0
4	173	90	172	46	172	46	0	0
5	168	226	169	187	169	187	0	0
6	137	241	137	223	137	223	0	0
Mean Squared Error :							0.166	0

An iterative process is used to overcome the occlusion problem. Such process consists of alternating the reference image from one iteration to the other. The process then chooses an initial set of reference points, searches for the correspondences in the other image, which become the references for the next iteration, and so on. In the experiments, the algorithm converges to sets of repeated points, from an iteration to the next.

## 6 Conclusion

This paper describes the use of a parallel GA to solve the correspondence problem in computer vision. Structural and contextual features of the points are used as correspondence evidences to which beliefs and plausibilities are assigned.

The beliefs and plausibilities are combined under the Dempster-Shafer uncertainty-reasoning paradigm. The correspondence problem is taken as a maximization problem, in which the combined evidences are maximized. Feature extraction follows [13] and [14]. The structural coherence of the polygonal regions is also considered, thus permitting simultaneous correspondence of multiple points.

The model aims at establishing control points in the image, before recovering a complete disparity map. Figure 9 shows a computed disparity map for the corresponded points in Figures 7a and 7b.

Increasing the number of multiple points, implies in more complex geometric features of the polygonal region and a larger number of simultaneous correspondences.

The experiments showed the effectiveness of the use of a parallel genetic search, in pursuing the best correspondence for multiple reference points, within a huge search space.



Figure 7 - a) Reference image with 6 points; b) Corresponding points.

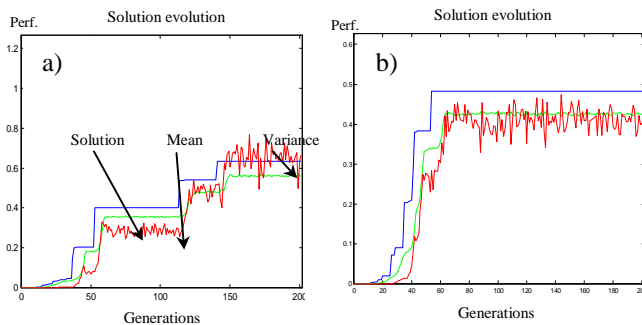


Figure 8 - Performance comparison between the use of a) one sequential GA and b) the island model parallel GA.



Figure 9. Disparity map generated from the 6 correspondences found in Figures 7a and 7b.

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