

A NICHE BASED GENETIC ALGORITHM FOR IMAGE REGISTRATION

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Abstract: Image registration aims to find the unknown set of transformations able to reduce two or more images to a common reference frame. Image registration can be regarded as an optimization problem, where the goal is to maximize a measure of image similarity. The measure of similarity on the overall image can be computationally expensive, leading to measure the similarity of smaller subimages. However, the reduction of subimage size results into a higher multi-modality for the optimizing function. Recent investigations have shown that genetic algorithms can address this problem. However, the simple scheme of genetic algorithms can still fall in local optima. In this paper, we explore the application of niche-oriented genetic algorithms, showing their strengths in providing a more effective image registration algorithm.

1 INTRODUCTION

Image registration is the process of overlaying one or more images to a reference image of the same scene taken at different times, from different viewpoints, and/or by different sensors. It geometrically aligns two images, namely the reference and the input image. Differences between images are introduced due to the different imaging conditions, such as a different sensor position. In this case, image registration entails with considering geometric transformations able to compensate the sensor misalignment (Figure 1).

The registration process mainly consists in determining the unknown transformation parameters required to map the input image to the reference image. The task of determining the best spatial transformation for the image registration can be characterized by four main components (Brown, 1992): (i) the feature space, (ii) the search space, (iii) the similarity measure, and (iv) the search strategy. The feature space represents the image content used to compare the input and the reference images. The search space is made by allowed transformations. The similarity measure provides a quality index of each solution. The normalized cross-correlation function is one of the most used similarity measure and can be written

as

$$CC = \frac{\sum_{i=0}^{N-1} \sum_{j=0}^{N-1} ((R_{ij} - R) \times (I_{ij} - I))}{\sqrt{\sum_{i=0}^{N-1} \sum_{j=0}^{N-1} (R_{ij} - R)^2 \times \sum_{i=0}^{N-1} \sum_{j=0}^{N-1} (I_{ij} - I)^2}} \quad (1)$$

where N is the number of pixels, R_{ij} (I_{ij}) is the pixel of the reference (input) image at position i, j , and R (I) is the pixel average value of the reference (input) image. The time complexity of the normalized cross-

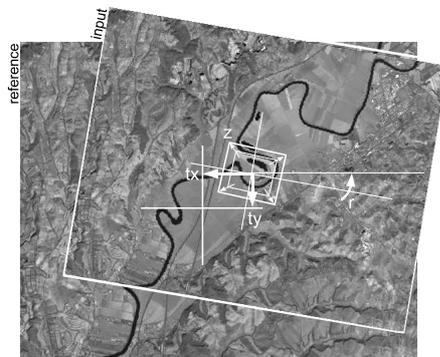


Figure 1: Image registration of satellite images considering translations (tx,ty), rotation (r) and zoom (z).

correlation is $O(N^2)$. Although expensive, it is ranked as one of most effective similarity measures. Because it is computationally expensive, cross-correlation is restricted to a subimage of input and reference images. The search strategy drives the exploration of the search space. Which strategy to adopt depends on characteristics of the similarity measure, the search space and the feature space. Indeed, these three elements determine the computational complexity and shape the search space landscape.

Key issues in image registration techniques regard accuracy and performances; in some applications registration accuracy is a key factor. For instance a study presented by Townshend et al. (Townshend et al., 1992) regarding the variation of land surfaces (measured using Normalized Difference Vegetation Index) shows that a misregistration by only 1 pixel can introduce error up to values higher than 50%.

This work focuses on image registration of two satellite or airborne images, subject to small affine transformations, using a niche based Genetic Algorithms (GA). We consider the set of image pixels as feature space and affine transformations as search space. In order to evaluate the solution quality we use a normalized cross-correlation similarity function. Genetic Algorithms help to explore the search space efficiently and avoiding to be trapped in local optima. The landscape multi-modality is emphasized by the smaller sub-image size. This effect is depicted by Figures 2 and 3. Although they only consider translations, the landscape roughness becomes more and more evident by reducing the image size. If we consider these transformations jointly to others, such as rotations and zooming, it appears evident that the problem cannot be addressed effectively by linear optimizing techniques.

Several researchers applied GAs to image registration (Brown, 1992; Zitová and Flusser, 2003). Most of them applied problem specific implementations of genetic operators in Simple-GA. However, this algorithm tends to converge to a single optimum, despite of the landscape multi-modality. In order to cope with this problem, niche oriented approaches have been proposed in literature. Niche based GA represents a more robust approach to search a multi-modal domain than traditional GA, since it provides a parallel exploitation of search space portions. Moreover the algorithm addresses the computational efficiency as it is able to reach an optimal solution by fewer iterations. Nevertheless, they have ever not been applied to image registration. This paper aims to investigate their application to this problem.

Section 2 describes the genetic algorithms considered by this paper, in particular the Simple-GA, and

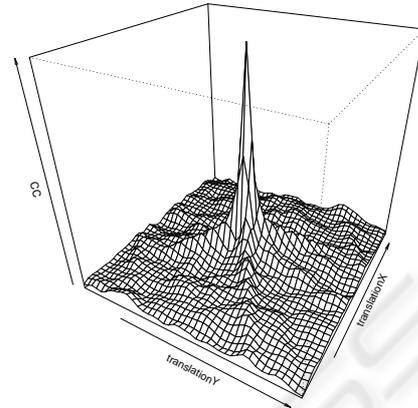


Figure 2: Landscape of cross-correlation function using a 128×128 sub-image - Translation along X and Y axes are the only considered.

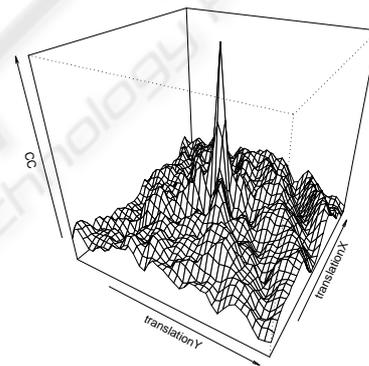


Figure 3: Landscape of cross-correlation function using a 32×32 sub-image - Translation along X and Y axes are the only considered.

two niche-oriented algorithms, i.e. Crowding-GA and Sharing-GA. Section 3 presents some experimental results. Conclusions and future work are outlined in Section 4.

2 GENETIC ALGORITHMS

In this work we aim to compare niche oriented GA algorithms to Simple-GA. In particular, two algorithms are considered: (Deterministic) Crowding-GA and Sharing-GA. Both are inspired by the niche exploitation in nature, so that only similar individuals mate and reproduce. Despite of the approach, the chromosome is always represented as a bit string. Each trans-

formation is coded by a fixed-length bit sub-string, as depicted in Figure 4.

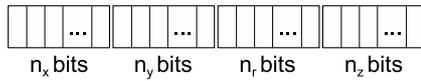


Figure 4: The chromosome structure.

The number of bits representing each transformation depends on the transformation range, given the precision (0.01 in our experimentation). Therefore each substring represents a fixed floating point real number. The first bit is used for coding the sign, whilst the remaining bits represent the magnitude of the transformation parameter.

The Simple-GA (Goldberg, 1989) is able to explore effectively a multimodal search space. However it tends to find one single optimum, thus it can still be trapped in local optima. This problem is the result of *genetic drift* (De Jong, 1975), which is the genetic algorithm's tendency to select a population with similar chromosomes, thus to converge towards one solution. One strategy to overcome this problem consists in maintaining population diversity, so that different sub-populations are able to explore different portions of the search space, in order to identify and converge towards different multiple optima. Niche based GAs represent an elegant and nature inspired solution to address the issue of keeping the population diversity. In a multimodal search space, each peak can be thought of as a niche explored by a subpopulation, similarly to nature where there are environments (niches) that can support different types of life (Goldberg, 1989), as depicted in Figure 5.

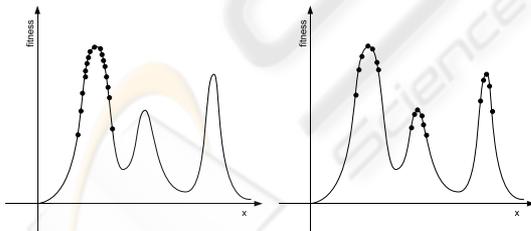


Figure 5: The convergence of Simple-GA versus Niche-GA.

In nature, a niche is able to support a certain number of individuals depending on the niche fertility and the individual capacity of exploiting this fertility. If there are too many individuals, the niche will not be able to support all of them, and less competitive individuals are likely to die. Differently, if there are too few individuals, they will start to reproduce quickly in order to exploit the niche. Two of most success-

ful mechanisms are the *fitness sharing* (Goldberg and Richardson, 1987) and *deterministic crowding* (Mahfoud, 1995).

The idea behind the sharing method is to reduce the fitness of individuals that are very similar in their chromosome. By this way, individuals that uniquely exploit portions of the search space are privileged for reproduction, while discouraging redundant individuals in the same area. The method is based on the determination of the shared fitness of the individual i as

$$f'(i) = \frac{f(i)}{m_i} \quad (2)$$

where $f(i)$ is the individual's raw fitness, and m_i is the niche count, that is defined as

$$m_i = \sum_{j=1}^n sh(d(i, j)) \quad (3)$$

The sharing function sh depends on the distance (dissimilarity) $d(i, j)$ between the individual i and the individual j . It is a monotonically decreasing function, so that the niche count is reduced if individuals are closer. In particular, it returns 1 if the elements are identical, and 0 if they exceed some threshold of dissimilarity. The function originally proposed by Goldberg (Goldberg and Richardson, 1987) is defined as

$$sh(d) = \begin{cases} 1 - (\frac{d}{\sigma_{share}})^\alpha & \text{if } d < \sigma_{share} \\ 0 & \text{otherwise} \end{cases} \quad (4)$$

where d is the distance, α is a constant used to regulate the shape of the sharing function, and σ_{share} the dissimilarity threshold. When $\alpha = 1$, the function is triangular.

The chromosome similarity can be measured by different metrics, aimed to measure the genotype or phenotype similarity. A genotype similarity metric is domain independent, as it considers the distance between string coding of chromosomes, such as the Hamming distance. A phenotype similarity is related to the chromosome structure in genes and to their semantic, thus it is domain specific. The main drawback of the sharing approach is in estimating proper values for the sharing function parameters, moreover the complexity for the fitness evaluation becomes $O(N^2)$, since a pairwise similarity measure is required at each evaluation step.

The other mechanism for maintaining population diversity is the *determinist crowding* (Mahfoud, 1992), that is an evolution of De Jong's crowding schema (De Jong, 1975). In De Jong's schema, at each generation only a portion of the population, called population gap is selected for reproduction

(crossover and mutation). After reproduction, generated offsprings take the place of old individuals following this strategy: for each offspring a certain number of individuals are randomly selected from the population, and the most similar is the replaced by the offspring. Similarity measures can be both genotypic or phenotypic. The De Jong’s mechanism is thought to reduce convergence of population to a single local optimum. The drawback is that this algorithm slows down the search space exploration.

In attempting to improve the De Jong’s schema, Mahfoud suggests a new crowding schema called Deterministic Crowding. In Mahfoud’s crowding schema, members are randomly chosen for reproduction, then an offspring replaces a parent only in case of higher fitness. To determine which of the possible parent-offspring pairing ($\{\text{parent1-offspring1, parent2-offspring2}\}$ OR $\{\text{parent1-offspring2, parent2-offspring1}\}$) should be used in comparing the parents to the offsprings, the total of the parent-offspring similarities for each of the two possible combinations is determined. The parent-offspring pair that has the highest total similarity is used to determine if the offspring should replace the parent. This allows to keep population diversity and to efficiently explore the search space, as different individuals do not influence each other. Mahfoud also discourages the use of genotypic similarity, in favor of phenotypic similarity measure, as domain-specific knowledge is able to better measure the similarity between individuals. Both assumptions result into better performances.

3 EXPERIMENTATION

Although, niche based GAs promise to overpass Simple-GA limitations, the successful application of them depends on the problem characteristics. In this section we report a summary of an experimentation aimed to verify if the niche approach provides effective advantages to image registration.

Experimentation has been conducted applying

Table 1: Algorithm configurations.

Parameter	Simple-GA	Crowding-GA	Sharing-GA
population	100	100	100
$P_{crossover}$	1.0	1.0	1.0
$P_{mutation}$	0.05	0.05	0.05
Elitism	yes	yes	yes
coding	binary MS	binary MS	binary MS
σ	-	-	2.0
α	-	-	1
distance	-	Phenotypic	Phenotypic

Simple-GA, Crowding-GA and Sharing-GA to a 20 high resolution images. These are satellite or airborne images of European cities acquired by different sensors (see Table 2 for more details). Algorithms end after 100 generations. Algorithm configurations are summarized in Table 1. For each image 50 runs have been performed, obtaining 1000 data points for analysis. The data flow followed at each run is described by Figure 6.

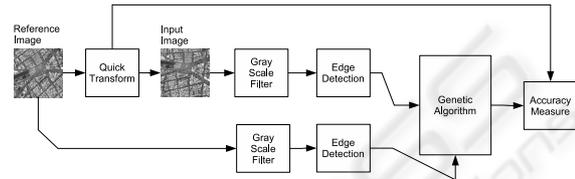


Figure 6: Experimentation steps.

The Quick Transform generates a misaligned input image applying a random affine transformation to the reference image (linear interpolation is used). Transformation components are generated assuming a normal gaussian distribution ($\mu = 0, \sigma = 2.551$), in order to simulate a realistic sensor misalignment. The range of misalignments are rotation = $\pm 5^\circ$, and translation = ± 5 px. As scaling is particularly annoying for image registration algorithms, we focused our attention on it. We considered different scaling ranges from $[0.9, 1.1]$ to $[0.6, 1.5]$. A gray scale filter converts the reference and input images to gray scale, in order to make the registration more robust. An edge detection filter (e.g. Sobel’s filter) is also applied. The two images are passed to the registration algorithm. Finally the registration solution is compared to the original misaligning transformation in order to measure accuracy, computed as the Pearson’s correlation coefficient between the actual parameters a_{act} and the estimated parameters a_{est} . This is akin to computing the cosine of the angle between the parameters vectors associated with the source and the target images.

$$\rho = \frac{(a_{act} \cdot a_{est}^T)}{\|a_{act}\| \cdot \|a_{est}\|} \quad (5)$$

Correlation coefficient is in $[-1, 1]$. Close to one correlation coefficients mean a small error between the actual and the estimated parameters.

For practical purposes, a registration can be considered successfully executed, if the accuracy is over a given threshold (0.8 in our experimentation.) The percentage of tests providing an accuracy higher of the threshold provides the algorithm *success rate*.

Figures 7 and 8 represent the success rate of the three GA compared. The success rate analysis shows

Table 2: Images characteristics.

Image	Acquisition	Dimension	Entropy(normalized)
Rome 1	Landsat 7 data (ETM+ bands 3, 2, and 1)	512 × 512	0.622
Rome 2	ASTER (Terra)	512 × 509	0.563
Venice	Ikonos	512 × 607	0.595
Naples	Shuttle, Hasselblad camera with a 250 mm lens.	512 × 512	0.508
London	ASTER (Terra)	512 × 366	0.503
Berlin	ASTER (Terra)	512 × 458	0.550
London	Space photograph, Kodak 760C with 800 mm lens.	512 × 384	0.554
Madrid	ASTER (Terra)	512 × 471	0.622
Athens	Astronaut photograph, Kodak K60C with 400 mm lens	512 × 471	0.616
Athens olympics	Ikonos	512 × 776	0.597
Bilbao	ASTER (Infrared image)	512 × 512	0.580
Madrid	Photo Satellite Quickbird, Digital globe	1123 × 512	0.641
Paris	Infrared image from ASTER (Terra)	512 × 443	0.543
Copenhagen	Photo Satellite Quickbird, Digital globe	512 × 512	0.626
Hamburg	Photo Satellite Quickbird, Digital globe	512 × 509	0.581
Brussels	Photo Satellite Quickbird, Digital globe	512 × 458	0.538
Paris	Photo Satellite Quickbird, Digital globe	512 × 512	0.559

that Crowding-GA is more accurate than Simple-GA, as the related success rate is always higher. The better performances are due to the capacity of crowding of exploiting different niches, without being trapped in any local optimum. Simple-GA instead tends to converge to a single local optima, despite of multimodality of the search space.

The experimentation results provide also evidence that the Crowding-GA is more robust than the Simple-GA approach. Indeed using 64×64 subimages, then increasing landscape multimodality, the Crowding-GA success rate is subject to small reductions (3-4% lesser than 128×128 case), whilst Simple-GA performances are significantly affected. Comparing performances of algorithms with different subimage sizes make this evident (Figure 9). Computationally, the two algorithms are comparable.

The performance of Sharing-GA are intermediate

between Simple-GA and Crowding-GA. Similarly to the Simple-GA, the Sharing-GA is less accurate and robust than the Crowding-GA. However, it performs slightly better than the Simple-GA. This is in accordance with the benefits expected by a niche based algorithm. Weaker performances can be imputed to sensitivity of the algorithms to parameters. Selecting proper values for the Sharing-GA parameters is not a trivial process. Therefore, the need of a precise calibration can be considered as weakness of the algorithm itself.

The experimentation has been conducted making assumptions that could not be met in real applications. Indeed, input image can differ from the reference image due to morphological (e.g growth of vegetation) or radiometric (e.g. images taken at different hours of a day) changes. Also partial occlusions (e.g. clouds) can occur in real cases. Such differences can be mis-

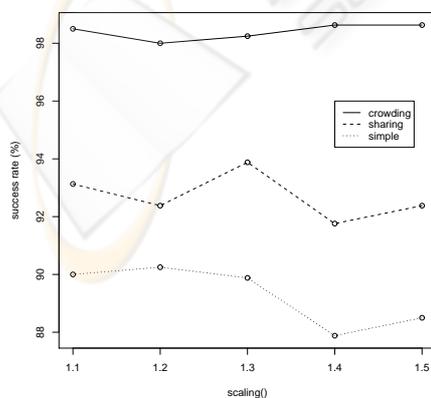


Figure 7: Algorithms success rates using a 128×128 sub-image.

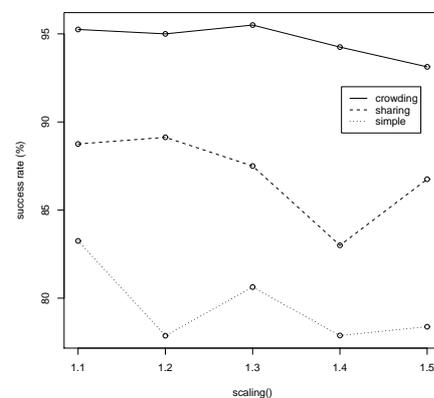


Figure 8: Algorithms success rates using a 64×64 sub-image.

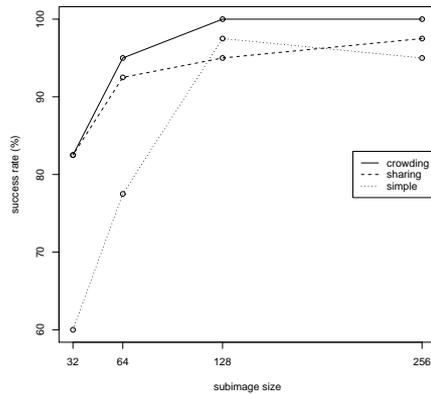


Figure 9: Success rates of the three algorithms for different sub-image sizes.

leading for a registration algorithm and should be considered in testing a registration algorithm. Another approximation is that we do not take into consideration perspective transformations. For satellite images, however, this transformation can be ignored because of the great distance. This effect is more relevant in airborne images.

The better results obtained by Crowding-GA and Sharing-GA are not due to the parameter configuration. Indeed, in Table 3 and Table 4 we report performances of Simple-GA with different parameter values.

Table 3: Success rate at different crossover rates.

	Crossover probability ($p_{mutation} = 0.05$)					
Zoom	1.00	0.95	0.90	0.85	0.80	0.75
1.1	90.0	92.0	93.0	90.1	88.7	90.0
1.5	88.5	88.0	88.0	87.9	88.9	88.6

Table 4: Success rate at different mutation rates.

	Mutation probability, ($p_{crossover} = 1.0$)					
Zoom	0.01	0.02	0.05	0.20	0.15	0.20
1.1	84.9	85.6	90.0	94.0	92.5	89.7
1.5	80.5	83.3	88.5	92.0	89.0	86.6

It results, that Sharing-GA and Crowding-GA outperform Simple-GA. Indeed success rate of Sharing-GA is between 92.4 (zoom = 1.5) and 93.1 (zoom=1.1), whilst Crowding-GA success rate is 98.6 (zoom = 1.5) and 98.5 (zoom=1.1). In both cases the result is better of Simple-GA performance. It worths to notice that comparison is made with 128×128 sub-image, thus entailing stronger landscape unimodality.

4 CONCLUSIONS AND FUTURE WORKS

In this paper we investigated the application of niche based genetic algorithms for image registration, as an effective way to improve algorithm precision, instead of adopting more complex genetic operators. In particular, the paper described the use of two niche based algorithms, namely the Sharing-GA and the Crowding-GA. Experimentation has shown that there is a real and consistent advantage in using the Crowding-GA. The Sharing-GA, although confirming the advantages provided by a niche approach, resulted in lower performances, due the higher algorithm sensitivity to parameter calibration.

Future work aims to extend the experimentation in order to include some of the image differences that can be encountered in real applications (i.e. photometric and morphologic differences, occlusions, etc.). Moreover some improvements can be obtained by properly selecting the realignment region, according to the entropy and other image characteristics.

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