

GENETIC ALGORITHMS FOR MULTI-SPECTRAL IMAGE CLASSIFICATION*

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ABSTRACT:

In this paper we describe the application of genetic algorithms (GA) to unsupervised multi-spectral image classification. We shortly review the principles of GA and discuss its iterative nature. One of the main advantages of GA is that the number of relevant clusters is derived during the computations rather than having to be determined prior to the classification, as is e. g. the case in the well known ISODATA algorithm. So called fitness functions are introduced and serve as criteria for controlling the iterations. In particular, we study the Davies-Bouldin, the Xie-Beni, and the K-Means Index. We illustrate our work with the help of examples. A multi-spectral satellite image is classified into several classes using both, various versions of GA and – as a reference – the ISODATA algorithm. The results demonstrate the feasibility of using GA for multi-spectral classification.

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- dedicated to Prof. Manfred Ehlers at the occasion of his 60th birthday
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1. INTRODUCTION

Multi-spectral image classification, including supervised and unsupervised classification, is a major analytical procedure in remote sensing. Supervised classification requires a human analyst to provide training areas in order to derive associated statistical descriptions. In comparison, unsupervised classification proceeds with only minimal input. An unsupervised classification divides all pixels within an image into a corresponding cluster pixel by pixel. Providing class labels to the clusters done by a human analyst in a separate step after clustering. Typically, the only input an unsupervised classification needs is the number of clusters of the scene. However, this value is usually not known a priori. Moreover, the spectral properties of specific classes within the images can change frequently and the relationships between the object classes and the spectral information are not always constant, and once defined for one image cannot necessarily be extended to others. Supervised and unsupervised classification suffers from these drawbacks.

Heuristic unsupervised classification works by establishing some mathematical model and then optimizing a predefined index to determine the number and centroids of the clusters in feature space automatically. Heuristic optimization processes, therefore, are seen as a repeatable, accurate, and time-effective method to classify remote sensing imagery automatically, which is the main objective of this research.

Genetic algorithms (GA) constitute one possibility for heuristic unsupervised classification. They are numerical optimization algorithms inspired by the nature evolution process and directed random search techniques and were introduced by John Holland in 1975 (Holland 1975). GA have been widely and successfully applied to optimization problems, such as the analysis of time series, water networks, work scheduling, and facial recognition (Coley, 1999; Rothlauf, 2006), which confirm the potential of GA to deliver high quality results especially when applied without any ground truth (Coley, 1999). Starting from multiple initial solutions selected randomly, GA preserve the appropriate solution based

on a so called fitness function (evaluating index). In this way, GA can avoid problems associated with inhomogeneous data distributions and automatically select the best solution through employing its three standard building blocks: selection, crossover, and mutation.

The research described in this paper focuses mainly on integrating GA with different fitness functions and on comparing the different results. A software program was developed in MATLAB and the GA unsupervised classifier was tested on an IKONOS satellite image, using ground truth information derived from a topographic map for the estimation of classification accuracy. The error matrix (confusion matrix) and K-HAT (kappa) statistics were adopted together with visual inspection to evaluate the results. Finally, the obtained results were compared with those from the traditional ISODATA analysis.

2. METHODOLOGY

In our work we concentrate on using GA for unsupervised classification. In GA the number of clusters does not have to be determined a priori, but can be determined during an iterative computational scheme. So called indices or fitness functions are used to determine whether convergence has been reached.

It is known that the choice of the index has a major impact on the results. Previous research used different indices, such as cluster distance, separation index, Fuzzy C-Means, K-means (KMI), Davies-Bouldin Index (DBI), and Xie-Beni Index (XBI) (Ross, 1995; Bandyopadhyay and Maulik, 2002). In our work, the DBI, XBI, and KMI were adopted. All three of them assign a pixel to one cluster only rather than using the concept of fuzzy membership. In this sense they form a group of related indices, and we believe there is value in comparing them prior to possibly extending the study to other indices and/or to a fuzzy framework. We also used the ISODATA algorithm to validate the effect of GA.

The following sections describe genetic algorithms and the way they can be applied to unsupervised image classification.

3. GENETIC ALGORITHMS

3.1 Chromosome representation

In GA applications, the unknown parameters are encoded in the form of strings, so-called chromosomes. A chromosome is encoded with binary, integer or real numbers. Since multi-spectral image data are usually represented by positive integers, in this research a chromosome is encoded with units (tuples) of positive integer numbers. Each unit represents a combination of brightness values, one for each band, and thus a potential cluster centroid.

The length of the chromosome, K , is equivalent to the number of units and thus of potential clusters in the classification problem. K is selected from the range $[K_{min}, K_{max}]$, where K_{min} is usually assigned to 2 unless special cases are considered (Bandyopadhyay and Maulik, 2002), and K_{max} describes the maximum chromosome length, which means the maximum number of possible cluster centroids. K_{max} must be selected according to experience.

Without assigning the number of clusters in advance, a variable string length is used. Invalid (non-existing) clusters are represented with negative integer "-1". The values of the different chromosomes are then changed in an iterative process involving different rules (called crossover and mutation) to determine the correct number of clusters (the number of valid units in the chromosomes) and the cluster centroids for a given classification problem.

3.2 Chromosome representation

A population is the set of chromosomes. The typical population size can range from 20 to 1000 (Coley, 1999). The following example is given to explain the representation a the population: we assume to have a satellite image with three bands; K_{min} is set to 2 and K_{max} to 8. At the beginning, for each chromosome i ($i = 1, 2, \dots, P$, where P is the size of population) all values are chosen randomly from the data space (universal data set; here: positive integers with the appropriate radiometric resolution). Such a chromosome belongs to the

so-called parent generation. One (arbitrary) chromosome of the parent generation is given here (note that it contains only five valid centroids, since "-1" appears three times in this chromosome):

-1 (110,88,246) (150,78,226) -1 (11,104,8) (50,100,114) -1 (227,250 192)

3.3 Selection and crossover

The purpose of selection and crossover (the latter is also called recombination) is to create two new individual chromosomes from two existing chromosomes selected randomly from the crossover pool. The crossover pool contains a percentage (the so called crossover percentage) of the current population, which constitutes the best chromosomes according to the chosen index (see below). Typical crossover operations are one-point crossover, two-point crossover, cycle crossover and uniform crossover. The following example illustrates a one-point crossover operation (the point for crossover is situated after the 4th position):

Parent1:

-1 (110,88,246) (150,78,226) -1 (11,104,8) (50,100,114) -1 (227,250 192)

Parent 2:

(210, 188, 127) (110,88,246) -1 -1 (122,98,45) -1 (98,174,222) (125,101,233)

Child 1:

-1 (110,88,246) (150,78,226) -1 (122,98,45) -1 (98,174,222) (125,101,233)

Child 2:

(210, 188, 127) (110,88,246) -1 -1 (11,104,8) (50,100,114) -1 (227,250 192)

3.4 Mutation

Mutation follows crossover. During mutation, all the chromosomes in the population are checked unit by unit and according to a pre-defined probability all values of a specific unit may be randomly changed. An example explains this procedure; the bold-faced and italic units represent the result of the mutation.

Old string:

(210, 188, 127) (110,88,246) -1 -1 (122,98,45) -1 (98,174,222) (125,101,233)

New string:

(210, 188, 127) (97,22,143) -1 -1 (122,98,45) -1 (98,174,222) (125,101,233)

4. THE FITNESS FUNCTION (INDEX)

Based on crossover and mutation, the chromosomes, once initiated, iteratively evolve from one generation to the next. In each generation the fitness function (index) is used to measure the fitness or adaptability of each chromosome in the population. After calculating the index for each chromosome of a given population, the best chromosome is compared to the best one of the previous generation (iteration). The termination condition for the iterations is that the difference between these two values lies below a pre-defined threshold. In case this condition holds the best chromosome of the current generation is considered as the final result, it contains the number of clusters (number of units with values different from “-1”) and the cluster centroids (the values of the valid units). If the termination condition is not met, the best chromosomes are selected into the crossover pool (see above, the number of selected chromosomes is given by the crossover percentage) and after mutation a new iteration is started. The population thus evolves over generations in the attempt to maximize or stabilize the index. The computations are also stopped once a maximum number of generations is reached.

The different indices used in this research are described in the following.

4.1 Davies-Bouldin Index (DBI)

The Davies-Bouldin index (DBI) is one possibility to represent the fitness of a chromosome (see Eq. (1)~(7)) (Xie and Beni, 1991; Bezdek and Pal, 1998; Swanepoel, 1999; Martini and Schöbel, 2001; Yang and Wu, 2001; Groenen and Jajuga, 2001). First, each pixel of the whole image is assigned to the nearest cluster centroid of the given chromosome by setting the corresponding membership value μ to 1; μ is set to 0 for all other clusters, see Eq. (1). Next, the average and the standard deviation for each cluster are computed (Eq. (2) and (3)), followed by determining the Euclidian distance between the clusters (Eq. (4)). Subsequently, the value R for each cluster is computed as shown in Eq. (5). Then, the average R for all clusters in the chromosome is computed. For a chromosome to

survive this average should be as small as possible, thus the DBI is defined as the inverse of the average value for R , see Eq. (6), which is equivalent to the clustering with the smallest inner-cluster scatter (total variation) and the largest cluster separation.

$$\mu_{i,k} = \begin{cases} 1; & \|x_i - u_k\| \leq \|x_i - u_j\|, \\ 0 & \text{otherwise} \end{cases} \quad 1 \leq k, j \leq K; j \neq k; 1 \leq i \leq N \quad (1)$$

$$v_k = \frac{\sum_{i=1}^N (\mu_{i,k}) x_i}{\sum_{i=1}^N (\mu_{i,k})} = \frac{\sum_{x_i \in X_k} x_i}{M_k} \quad 1 \leq k \leq K \quad (2)$$

$$S_k = \left(\frac{1}{M_k} \sum_{x_i \in X_k} \|x_i - v_k\|^2 \right)^{1/2} \quad 1 \leq k \leq K \quad (3)$$

$$d_{kj} = \|v_k - v_j\| \quad 1 \leq k, j \leq K; j \neq k \quad (4)$$

$$R_k = \max_{j, j \neq k} \left\{ \frac{S_k + S_j}{d_{kj}} \right\} \quad 1 \leq k \leq K \quad (5)$$

$$DBI = 1 / \left(\frac{1}{K} \sum_{k=1}^K R_k \right) \quad (6)$$

where

x_i = pixel i with grey values x (one for each band)

u_k = grey values of k^{th} cluster centroid

$\mu_{i,k}$ = membership function of each pixel x_i belonging to the k^{th} cluster

N = total number of pixels

K = total number of clusters

v_k = average value of k^{th} cluster in the current iteration

X_k = set of pixels assigned to cluster k

M_k = the number of pixels belonging to the k^{th} cluster

S_k = standard deviation of the pixels in the k^{th} cluster

d_{kj} = Euclidian distance between the k^{th} and j^{th} centroid

4.2 Xie-Beni's separation Index (XBI)

The XB separation index (XBI) was proposed by Xie and Beni in 1991 (Xie and Beni, 1991; Yang and Wu, 2001). The XBI is computed similarly to the DBI. Again, each pixel is first

assigned to the nearest cluster centroid of the given chromosome according to Eq. (1). Then, the minimum distance d_{min} of all distances $d_{k,j}$ between two clusters of the chromosome is calculated, see Eq. (7). Finally, the XBI which expresses the ratio between the total variation and N times the minimum separation of the clusters, is computed, the inverse of which is the XBI, see Eq. (8).

$$d_{min} = \min_{\substack{k, j=1 \dots K \\ \text{and } k \neq j}} \{d_{k,j}\} \quad (7)$$

$$XBI = 1 / \left(\frac{\sum_{k=1}^K \sum_{i=1}^N \mu_{ik} \|x_i - v_k\|^2}{N * (d_{min})^2} \right) \quad (8)$$

4.3 K-Means Index (KMI)

K-Means is a simple and common clustering algorithm which can also be used in the GA framework (see e. g. Bandyopadhyay and Maulik, 2002). Compared to the XBI the minimum separation is omitted from the computations, the rest is identical. Thus, KMI represents the total variation

disregarding the distance between different clusters. KMI is computed according to the Eq. (9) as follows:

$$KMI = 1 / \left(\sum_{k=1}^K \sum_{i=1}^N \mu_{ik} \|x_i - v_k\|^2 \right) \quad (9)$$

5. GROUND TRUTH DATA

For our research we used a multi-spectral IKONOS image. The image depicts Chandlers Ford in the U.K. and was taken on 2000/08/25 with 4 meters pixel size and 11 bits per pixel (see Figure 1. (a), (b)). We selected a small test image with a total of about 15,000 pixels for our experiments. A higher resolution map served as a reference for obtaining ground truth information.

In the test image, there are three object classes. They are *farmland*, *grove*, and *irrigation canal*, respectively, see also Figure 1(c)-(e). It should be noted that the *farmland* area in the left part of the test image is significantly darker than the *farmland* in the other parts and is spectrally closer to *grove*. Thus, we expect some mixture between *farmland* and *grove* in this area. Also, the *irrigation canal* visually has a certain

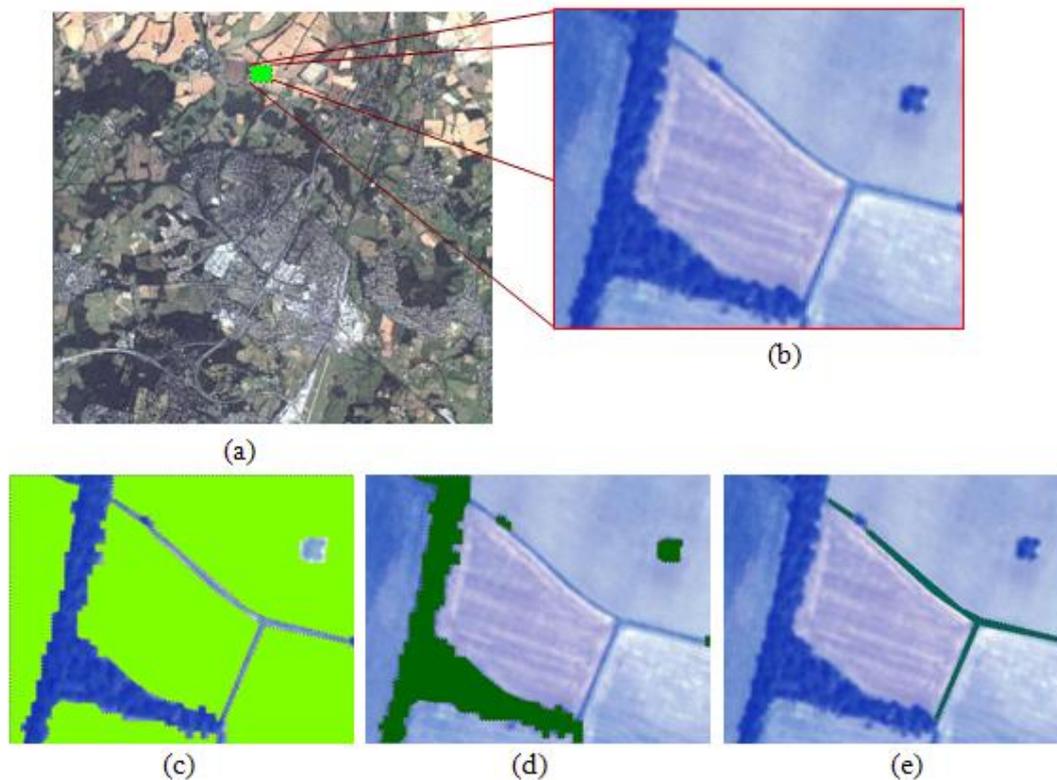


Figure 1. (a) The original IKONOS image; (b) The test image; (c)-(e) Masks for the three classes : (c) *farmland* (81% of the total amount of pixels in the subset image); (d) *grove* (16%); (e) *irrigation canal* (3%).

spectral similarity to *grove*; in addition it only covers a relatively small amount of the test image. It is for these aspects that we have selected the test image, as it presents a rather difficult case for classification.

6. EXPERIMENTAL TESTS AND ANALYSIS OF RESULTS

6.1 Criteria of evaluation

In order to evaluate the different results we compared the ground truth data to the individual classification results. For this purpose we computed the error matrix (confusion matrix) and the well-known criteria *producer's accuracy* or completeness (the number of pixels that are correctly assigned to a certain class divided by the total number of pixels of that class in the reference data), *user's accuracy* or correctness (the number of pixels correctly assigned to a certain class divided by the total numbers of pixels automatically assigned to that class), the overall accuracy and the K-HAT statistics (see Lillesand and Kiefer, 2000 for a quantitative definition).

6.2 Test description

For GA algorithms used as classifiers there are basically seven parameters which influence the result. These are the maximum length of the chromosome, the way to encode the chromosome units (binary, real number and so on), the population size, the crossover type and probability, the mutation probability, and the employed fitness function (Pham and Karaboga, 2000).

In our research a maximum chromosome length of $K_{max}=8$ was chosen, which is well above the maximum number of clusters in the test image. As explained above, coding was done using positive integers. To simplify our investigations and in accordance with many of the investigations on GA, only one-point crossover operations were considered. The other four parameters were systematically varied in order to study their influence on the result. For selecting the actual parameter values we took advice from general GA references (e. g. Coley, 1999). More specifically, the population size was set to 30, 60,

and 90 chromosomes, respectively, the crossover percentage was defined as 40%, 60%, and 80%, and for the mutation probability we selected values of 0.05, 0.25, and 0.5. One set of parameters, namely a population size of 90 with a crossover percentage of 80% and a mutation probability of 0.05 was considered as the baseline set, against which the other parameters were varied. Iterations were terminated as soon as the best chromosome (the one with the largest index) did not change any more from one iteration to the next. In this way, the three presented indices, DBI, XBI, and KIM were investigated, resulting in a total of nine results of each index.

7. RESULTS AND DISCUSSION

Figure 2 displays the visual results with respect to the variation of population size. The colors indicate the different classes: light green stands for *farmland*, dark green for *grove*, and bright for *irrigation canal*. The first row (Figure 2 (a)-(c)) contains the DBI results, the second one (Figure 2 (d)-(f)) the XBI results, and the third one (Figure 2 (g)-(i)) the KMI results. In the left column the results for a population size of 30 are presented, in the centre for a size of 60, and to the right for a size of 90. The Figures 3 and 4 contain similar results for the variation of crossover percentage (the chosen values are 40%, 60% and 80%) and mutation probability (0.05, 0.25 and 0.5).

Tables 1 to 3 are structured in the same way and contain the numerical results of the study. For each case, the producer's accuracy (PA), the user's accuracy (UA) for both, *farmland* and *grove*, the overall accuracy (OA) and the K-HAT value are given. The PA and UA values for *irrigation canal* are not recorded, since in all cases they are very small. The reason is that (as mentioned above) the canal is very narrow, and is spectrally rather similar to *grove*. While this fact can be considered a shortcoming of the present study it can also be interpreted as a rather difficult case for unsupervised multi-spectral classification. It should be noted that the right columns of Figures 2 and 3 and the left column of Figure 4 and the related Tables entries show results of the same experiments. They have been duplicated for reasons of clarity.

crossover percentage = 80%; mutation probability = 0.05

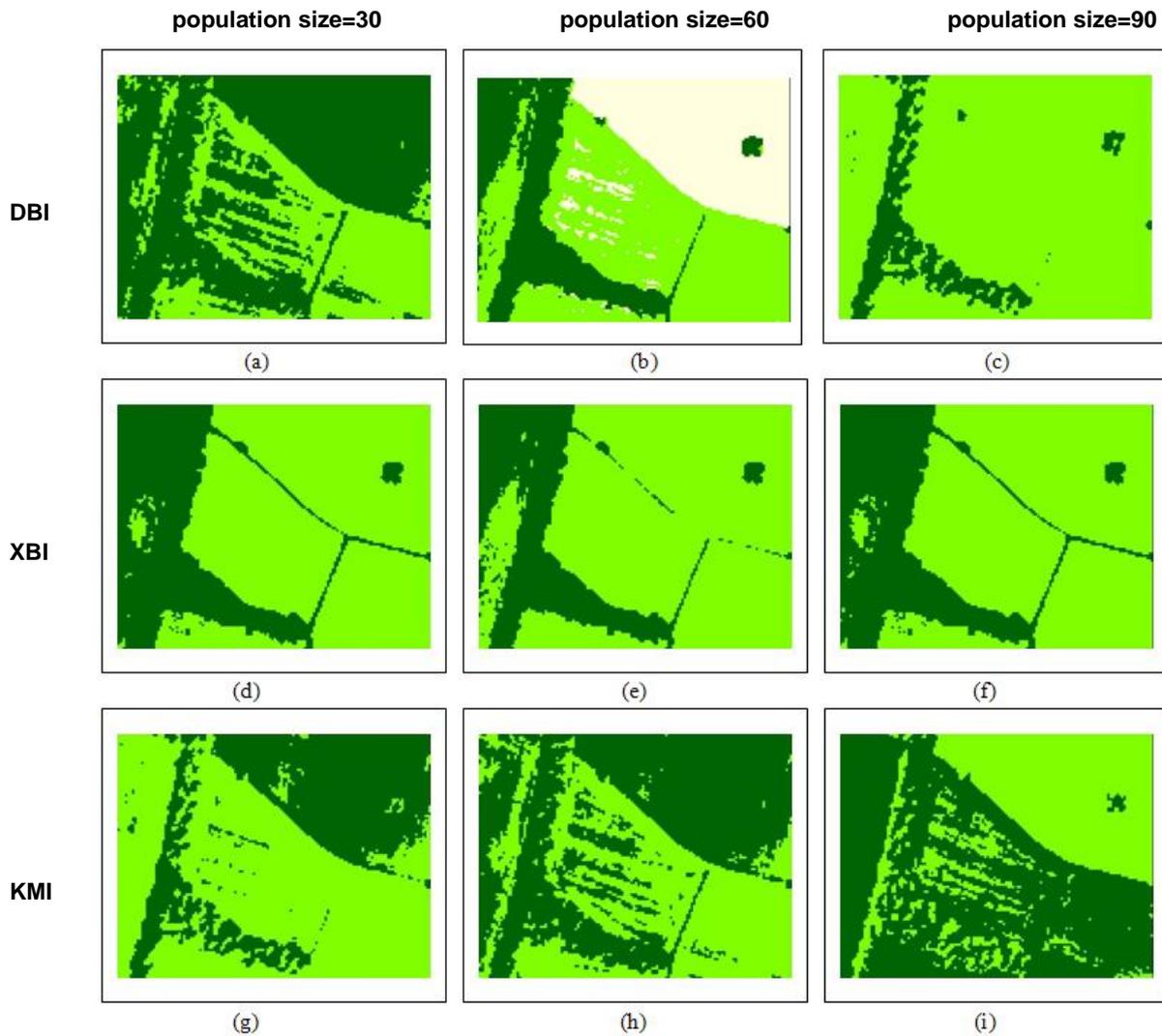


Figure 2. Visual results for variation of population size

From the provided results the following conclusions can be drawn:

- Most results only show two clusters, which can be associated with *farmland* and *grove*. The class *irrigation canal* is only visible in Figures 2(b), 3(a) and 4(b). The areas classified as *irrigation canal* in these cases are, however, wrong.

- As far as a comparison of the different indices is concerned, the XBI clearly performs best. This is true when comparing the visual results to the reference image (Figure 1), and also when studying the numerical results. For XBI the overall accuracy lies consistently above 80% and reaches up to 89.7 % in the best case. Also the producer's accuracy is very good; only the

user's accuracy for *grove* is a little low, because part of the *farmland* in the left part of the test image is classified as *grove* (see also discussion about ground truth). Furthermore, XBI is rather insensitive to the variation of parameters, which is obviously an additional advantage.

- The DBI must be rated second. Acceptable results are obtained for the case depicted in Figure 2 (c), which is identical to the one shown in Figure 3(c) and the one shown in Figure 4(a), see above. For the other cases the quality of the results quickly degenerates. Thus, the DBI is much less robust than the XBI. Problems occur mainly for the user's accuracy for *grove*, but the other indicators are also effected in a number of cases.

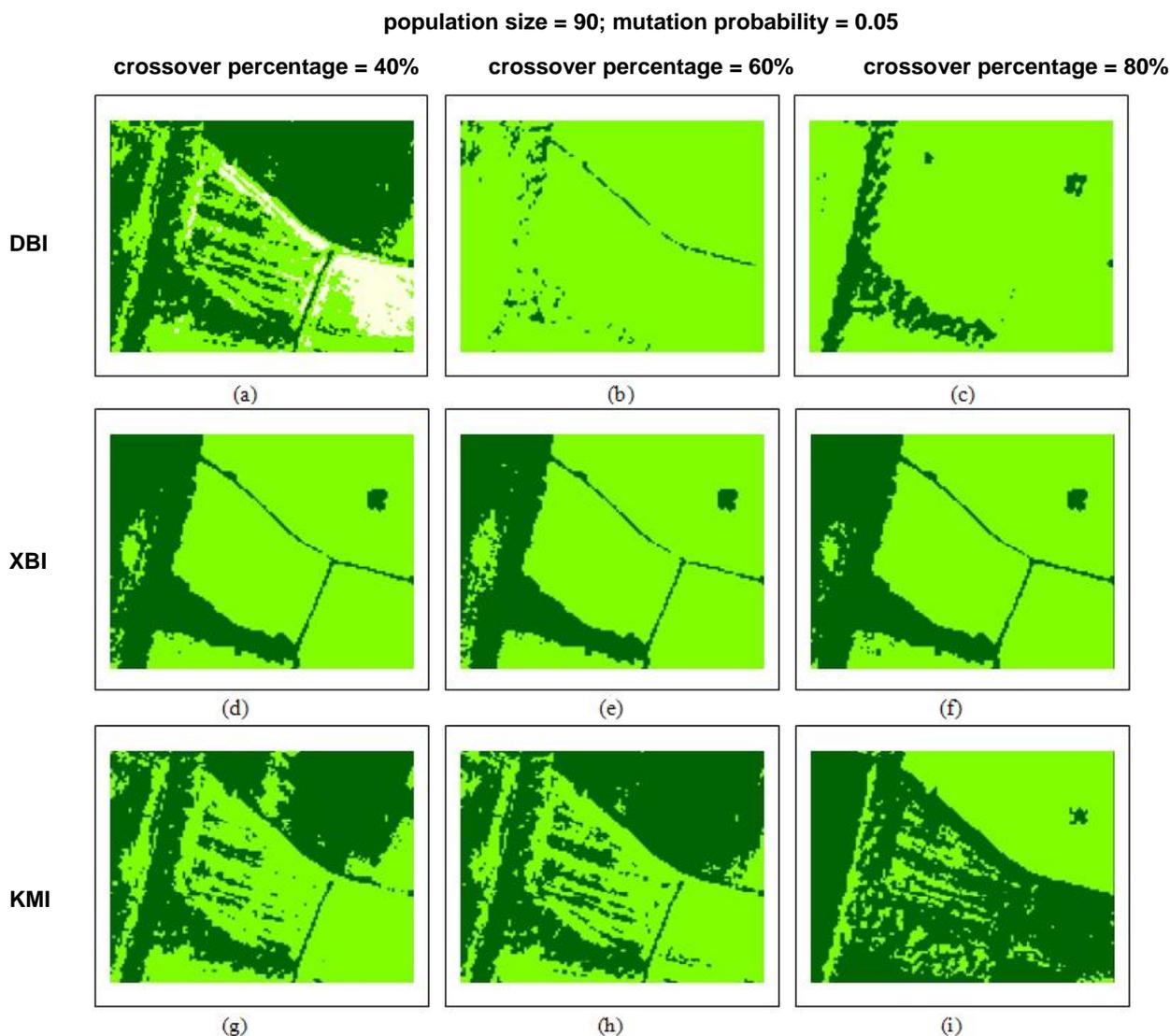


Figure 3. Visual results for variation of crossover percentage

- KMI yields unacceptable results. For the best case, the overall accuracy reaches only 65.3 %. There seems to be very little possibility to distinguish between *farmland* and *grove*. The user's accuracy for *grove* is again the largest problem, but the other values are not much better.

- In terms of computational resources, XBI also possesses advantages over DBI, because it can be computed with fewer steps (see also the equations given above). While it is true that KMI is even faster to compute, the results indicate that it is not a suitable index for the given task.

- In all presented cases, also for the good XBI results, the K-HAT value is rather low. This indicates a number of errors of omission and commission, which can also be observed

when investigating the full error matrices (due to space limitations, these matrices are not given in their complete form in this paper).

- The results do not consistently depend on the input parameters. For DBI a larger population size, a larger crossover percentage and a smaller mutation probability seems to be advantageous, XBI is rather robust with respect to changing the parameters, and for KMI no definite conclusions should be drawn, since the results are too poor.

In order to be able to better evaluate the overall quality of the results obtained with GA, we have also run the ISODATA algorithm to find clusters for our test image. We asked the

population size = 90; crossover percentage = 80%

mutation probability = 0.05

mutation probability = 0.25

mutation probability = 0.5

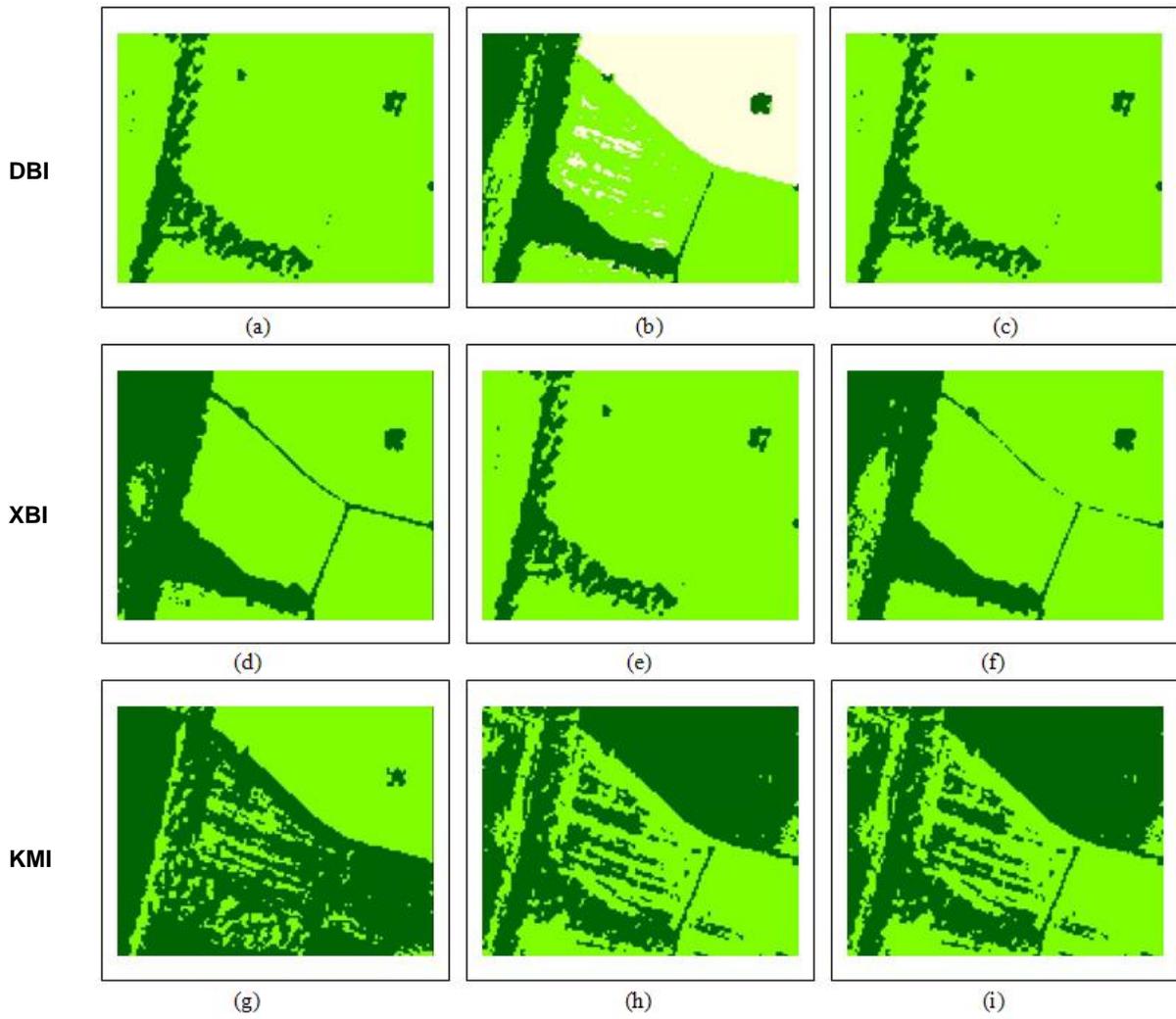


Figure 4. Visual results for variation of mutation probability

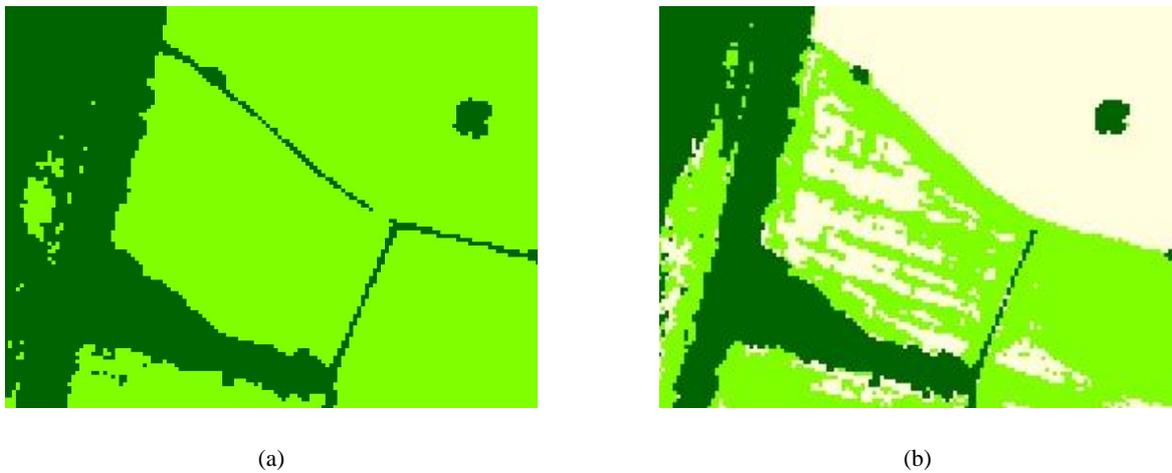


Figure 5. Visual results for ISODATA algorithm: (a) with two clusters, (b) with three clusters.

crossover percentage = 80%; mutation probability = 0.05												
	population size=30			population size=60			population size=90					
		PA [%]	UA [%]		PA [%]	UA [%]		PA [%]	UA [%]			
DBI	Farmland	49.5	91.3	Farmland	54.0	91.9	Farmland	97.7	90.4			
	Grove	90.1	26.3	Grove	89.7	61.6	Grove	67.1	85.3			
	OA = 54.7 %		K-HAT = 10.2 %		OA = 58.4 %		K-HAT = 16.3 %		OA = 89.8%		K-HAT = 17.5 %	
	(a)			(b)			(c)					
XBI		PA [%]	UA [%]		PA [%]	UA [%]		PA [%]	UA [%]			
	Farmland	81.4	96.7	Farmland	87.0	95.6	Farmland	81.6	96.6			
	Grove	95.2	48.6	Grove	94.0	57.9	Grove	95.0	48.9			
	OA = 81.2%		K-HAT = 21.2 %		OA = 85.6 %		K-HAT = 22.1 %		OA = 81.4 %		K-HAT = 21.3 %	
	(d)			(e)			(f)					
KMI		PA [%]	UA [%]		PA [%]	UA [%]		PA [%]	UA [%]			
	Farmland	67.9	86.4	Farmland	49.3	89.8	Farmland	41.6	85.4			
	Grove	64.6	28.9	Grove	86.8	25.5	Grove	35.7	17.8			
	OA = 65.3 %		K-HAT = 8.2 %		OA = 54.0%		K-HAT = 9.2 %		OA = 44.3 %		K-HAT = 2.7 %	
	(g)			(h)			(i)					
Table 1: Num. results for variation of population size (PA: producer's accuracy, UA: user's accuracy, OA: for overall accuracy)												

algorithm to find two or three clusters, respectively. The rationale for this selection is that the user would probably ask for three clusters based on the ground truth knowledge (there are three different object classes on the ground), while most GA results only reported two clusters. Thus ISODATA was also run with two clusters to enable a better comparison.

The results are shown in Figure 5(a) and (b) and in Tables 4 and 5. It can be seen that the ISODATA result with two clusters is very similar to the best XBI result, while the one with three clusters is far worse. In the latter case similar problems occur as in some of the GA cases (see Figures 2(b), 3(a) and 4(b)): in particular the *irrigation canal* poses a major obstacle to a correct classification, since much of the *farmland* in the upper right part of the test image is misclassified as *irrigation canal*. Also, the user' accuracy for *grove* is unacceptably low. Thus, while the results of both methods are similar, GA does not need the desired number of classes as additional input.

8. CONCLUSION

In this research we have described how to employ genetic algorithms (GA) for unsupervised multi-spectral classification. GA provides a possibility to compute the number of clusters present in a scene from the image data by using a particular fitness function (index). We have tested three different indices, namely the Davies-Bouldin Index (DBI), the Xie-Beni, Index (XBI) and the K-Means Index (KMI). Experimental data were obtained by classifying a part of a multi-spectral IKONOS scene depicting three different classes, namely *farmland*, *grove* and *irrigation canal* with the different indices while varying a number of parameters of the GA. We have also compared our results to those obtainable by employing the well known ISODATA algorithm. We have based our evaluation on visual inspection of the results, the error matrix and the K-HAT statistics, computed from independent reference data.

We could show that while all experiments somewhat suffer from the difficult test scene, the GA provides acceptable

population size = 90; mutation probability = 0.05											
crossover percentage = 40%			crossover percentage = 60%			crossover percentage = 80%					
	PA [%]	UA [%]		PA [%]	UA [%]		PA [%]	UA [%]			
DBI	Farmland	38.3	88.5	Farmland	98.5	82.4	Farmland	97.7	90.4		
	Grove	85.8	25.5	Grove	11.0	48.7	Grove	67.1	85.3		
	OA = 45.6 %		K-HAT = 8.4 %		OA = 81.2 %		K-HAT = 3.0 %		OA = 89.8%		K-HAT = 17.5 %
	(a)			(b)			(c)				
XBI	Farmland	82.8	96.4	Farmland	84.1	96.3	Farmland	81.6	96.6		
	Grove	94.8	50.6	Grove	94.8	52.6	Grove	95.0	48.9		
	OA = 82.3%		K-HAT = 21.5 %		OA = 83.4 %		K-HAT = 21.8 %		OA = 81.4 %		K-HAT = 21.3 %
	(d)			(e)			(f)				
KMI	Farmland	56.9	91.5	Farmland	55.0	85.2	Farmland	41.6	85.4		
	Grove	88.5	29.1	Grove	85.6	25.0	Grove	35.7	17.8		
	OA = 60.4 %		K-HAT = 11.8 %		OA = 55.0%		K-HAT = 9.2 %		OA = 44.3 %		K-HAT = 2.7 %
	(g)			(h)			(i)				

Table 2: Num. results for variation of crossover percentage (PA: producer's accuracy, UA: user's accuracy, OA: overall accuracy)

population size = 90; crossover percentage = 80%											
mutation probability = 0.05			mutation probability = 0.25			mutation probability = 0.5					
	PA [%]	UA [%]		PA [%]	UA [%]		PA [%]	UA [%]			
DBI	Farmland	97.7	90.4	Farmland	53.6	92.0	Farmland	34.6	58.0		
	Grove	67.1	85.3	Grove	90.1	61.0	Grove	54.0	12.6		
	OA = 89.8 %		K-HAT = 17.5 %		OA = 58.1 %		K-HAT = 16.2 %		OA = 30.5%		K-HAT = 14.7 %
	(a)			(b)			(c)				
XBI	Farmland	81.6	96.6	Farmland	97.8	90.3	Farmland	86.3	95.9		
	Grove	95.0	48.9	Grove	66.2	85.6	Grove	94.3	56.4		
	OA = 81.4%		K-HAT = 21.3 %		OA = 89.7 %		K-HAT = 17.2 %		OA = 85.0 %		K-HAT = 22.1 %
	(d)			(e)			(f)				
KMI	Farmland	41.6	85.4	Farmland	46.2	89.0	Farmland	34.5	56.4		
	Grove	35.7	17.8	Grove	53.8	24.3	Grove	53.6	13.6		
	OA = 44.3 %		K-HAT = 2.7 %		OA = 51.4%		K-HAT = 8.1 %		OA = 30.5 %		K-HAT = 5.7 %
	(g)			(h)			(i)				

Table 3: Num. results for variation of mutation probability (PA: producer's accuracy, UA: user's accuracy, OA: overall accuracy)

		Farmland	Grove	Irrigation canal
Classification	Farmland	81.8%	4.9%	53.7%
	Grove	18.2%	95.1%	46.3%
	Irrigation canal	0.0%	0.0%	0.0%

Producer's Accuracy		User's Accuracy	
Farmland = 81.8%		Farmland = 96.5%	
Grove = 95.1%		Grove = 49.4%	
Irrigation canal = 0.0%		Irrigation canal = 0.0%	
Overall accuracy = 81.6%		K-HAT = 21.3 %	

Table 4: Error matrix for ISODATA results, two clusters

		Farmland	Grove	Irrigation canal
Classification	Farmland	41.9%	5.3%	79.9%
	Grove	43.5%	91%	13%
	Irrigation canal	14.7%	3.7 %	7.2%

Producer's Accuracy		User's Accuracy	
Farmland = 41.9%		Farmland = 91.2%	
Grove = 91%		Grove = 29.7%	
Irrigation canal = 7.2%		Irrigation canal = 1.7%	
Overall accuracy = 48.9%		K-HAT = 10.8 %	

Table 5. Error matrix for ISODATA results, three clusters

results for a number of cases. The XBI turned out to be the most accurate and by far the most robust index. The overall accuracy was consistently above 80 %, with the best values reaching 90 %. The DBI is much more sensitive to parameter tuning, and the KMI seems to be unsuitable for the use in unsupervised classification. The GA results are similar to those obtained with the ISODATA algorithm, if results with the same number of clusters are compared. However, whereas GA determines this number automatically, it needs to pre-defined for ISODATA. Thus, GA algorithms seem to be more flexible and therefore advantageous to more traditional unsupervised classification techniques.

In the future we plan to extend our study to process more and larger scenes in order to confirm the results found so far. We

are also interested to experiment with different termination

conditions such as an absolute fitness level which needs to be reached and to study under which conditions our approach reaches the best solution. Finally, we want to integrate indices based on fuzzy theory into the investigations.

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