International Journal of Remote Sensing
Vol. 26, No. 3, 10 February 2005, 579–593

Satellite image classification using genetically guided fuzzy clustering with spatial information

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(*Received 11 February 2003; in final form 30 June 2004*)

Land-cover classification of satellite images is an important task in analysis of remote sensing imagery. Segmentation is one of the widely used techniques in this regard. One of the important approaches for segmentation of an image is by clustering the pixels in the spectral domain, where pixels that share some common spectral property are put in the same group, or cluster. However, such spectral clustering completely ignores the spatial information contained in the pixels, which is often an important consideration for good segmentation of images. Moreover, the clustering algorithms often provide locally optimal solutions. In this paper, we propose to perform image segmentation by a genetically guided unsupervised fuzzy clustering technique where some spatial information of the pixels is incorporated. Two ways of incorporating spatial information are suggested. The characteristic of this technique is that it is able to determine automatically the appropriate number of clusters without making any assumptions regarding the dataset, while attempting to provide globally near-optimal solutions. In order to evolve the appropriate number of clusters, the chromosome encoding scheme is enhanced to incorporate the don't care symbol (#). Real-coded genetic algorithm with appropriately defined operators is used. A cluster validity index is used as a measure of the fitness value of the chromosomes. Results, both quantitative and qualitative, are demonstrated for several images, including a satellite image of a part of the city of Mumbai.

1. Introduction

Classification of satellite images into different land-cover regions is considered to be one of the fundamental operations in the domain of remote sensing image analysis. When no prior information about the pixels is available, then unsupervised segmentation, which is a critical component of any image processing and analysis system (Rosenfeld and Kak 1982, Gonzalez and Woods 1992) has traditionally been considered as an important approach for land-cover classification. Errors in segmentation often significantly affect the subsequent tasks of feature extraction, classification and interpretation of images. The problem of image segmentation can be formally stated as follows: Partition a given image into regions or segments such that pixels belonging to a region are more similar to each other than pixels belonging to different regions.

The primary approaches for segmenting an image (Jain and Dubes 1988) are based on (i) thresholding or clustering, (ii) boundary detection, and (iii) region growing. In this paper we concentrate on the clustering-based approach to image segmentation (Wharton 1983, Gowda 1984, Theiler and Gisler 1997), where pixels that share some common property are clustered into the same class. The spectral property of the pixels is an obvious choice on which the clustering may be performed. However, since the pixels inherently contain some spatial information, taking this into consideration as well appears to be a natural choice in the domain of image segmentation.

Uncertainty and ambiguity are inherent in the domain of image processing. Several types of ambiguities often faced in this domain are spectral ambiguity (e.g. due to the possible multivalues levels of intensity), geometrical ambiguity (e.g. in the boundary of segments, location of edges) and interpretational ambiguity (e.g. location of certain objects in the image). Thus incorporation of the flexibility and advantages of fuzzy information processing (Zadeh 1965), which is a way to represent vagueness in everyday life, to deal with possible uncertainty in images appears to be appropriate (Bezdek and Pal 1992, Bezdek *et al.* 1999, Kerre and Nachtegael 2000). As a result, in this paper we deal only with fuzzy clustering of the dataset, which is capable of providing fuzzy segments.

In fuzzy clustering of a dataset $X=\{x_1, x_2, \ldots, x_n\}$ in IR^N, the set of fuzzy partition matrices M_{fcn} may be represented as

$$\begin{aligned} M_{fcn} = \Big\{ U \in IR^N \mid U = [u_{ik}]_{c\times n},\ & 0 \le u_{ik} \le 1 \quad \forall i, k \\ & \forall k,\ u_{ik} > 0\ \exists\ i;\ 0 < \sum\nolimits_{k=1}^{n} u_{ik} < n \quad \forall i \\ & \sum\nolimits_{i=1}^{c} u_{ik} = 1\ \forall k \Big\} \end{aligned} \tag{1}$$

where u_{ik} denotes the membership of the pattern x_k, $1 \leqslant k \leqslant n$, to cluster i, $1 \leqslant i \leqslant c$.

Fuzzy C-Means (FCM) (Bezdek 1981) clustering is one of the widely used techniques for evolving the appropriate partition matrix $U \in M_{fcn}$ such that a criterion based on the squared error of the clusters is minimized. However, there are two primary drawbacks of the FCM method that limit its applicability: it requires an *a priori* knowledge of the number of clusters, and it often gets stuck at local optima.

In this paper we describe an approach to image segmentation using a genetically guided fuzzy clustering technique that can overcome the above-mentioned limitations of the FCM, while considering some additional characteristics over a window centred around each pixel in order to incorporate spatial information. The power of genetic algorithms (GAs) (Goldberg 1989, Davis 1991, Michalewicz 1992, Mitchell 1996, Maulik and Bandyopadhyay 2000), a well-known optimization tool that performs search in large, complex and multimodal spaces while providing near optimal solutions, is utilized for evolving an appropriate set of cluster centres such that the local optimum is avoided. In order to evolve the number of clusters automatically, the chromosome encoding incorporates a don't care (#) symbol. Real-coded GAs with modified versions of mutation operators are defined, which can alter, increase and decrease the string length. The *Fukuyama–Sugeno index* (Fukuyama and Sugeno 1989) is used as a measure of the cluster validity of the resulting clusters in the multispectral space. Hence this index is used to compute the fitness of a chromosome, which indicates the degree of goodness of the encoded solution (fuzzy partitions). Experimental results are provided for several images, both simulated and real, including a satellite image of a part of the city of Mumbai.

2. Genetic fuzzy clustering

In this section we describe the fuzzy clustering technique that utilizes the searching capabilities of genetic algorithms for automatically partitioning a dataset into an appropriate number of clusters. The basic steps in a conventional genetic algorithm are as follows.

Begin

1. t=0
2. initialize population P(t)
3. compute fitness P(t)
4. t=t+1
5. if termination criterion achieved go to step 10
6. select P(t) from P(t-1)
7. crossover P(t)
8. mutate P(t)
9. go to step 3
10. Output best solution

End

2.1 *String representation*

In the genetic fuzzy clustering technique, the chromosomes are made up of real numbers (representing the coordinates of the clusters centres) as well as the don't care symbol #. The value of c is assumed to lie in the range $[c_{\min}, c_{\max}]$, where $c_{\min}$ is chosen to be 2 and $c_{\max}$ is taken to be $\sqrt{n}$ (n is the size of the dataset) unless specified otherwise. The length of a string is taken to be $c_{\max}$ where each individual gene position represents either an actual centre or a don't care symbol.

2.2 *Population initialization*

For each string i in the population (i=1, …, P, where P is the size of the population), a random integer c_i in the range $[c_{\min}, c_{\max}]$ is generated. This string is assumed to encode the centres of c_i clusters. For initializing these centres, c_i distinct points are chosen randomly from the dataset. These points are distributed randomly in the chromosome. The other $(c_{\max}-c_i)$ positions of the chromosome are filled with #.

2.3 *Fitness computation*

As mentioned in section 1, the fitness of a chromosome is computed using the Fukuyama–Sugeno (FS) fuzzy cluster validity index. Given a partition matrix $U=[u_{ik}]_{c\times n}$, set of cluster centres $V=\{v_1, v_2, \ldots, v_i, \ldots, v_c\}$, and the centre of the data v^* computed as $v^*=\sum_{x\in X}\frac{x}{n}$, the FS index is defined as follows:

$$\mathrm{FS}(U, V; X)=\sum_{i=1}^{c}\sum_{k=1}^{n}u_{ik}^{m}\left(\|x_k-v_i\|^2-\|v_i-v^*\|^2\right) \tag{2}$$

Here m is the weighting coefficient. Note that $1<m<\infty$, and the membership value of the kth point to the i cluster, u_{ik}, is computed as (Bezdek 1981)

$$u_{ik} = \frac{1}{\sum_{j=1}^{c} \left(\frac{D_{ik}(v_i, x_k)}{D_{jk}(v_j, x_k)} \right)^{\frac{2}{m-1}}}, \text{ for } 1 \le i \le c;\ 1 \le k \le n \tag{3}$$

where $D_{ik}(v_i, x_k)$ is the distance from x_k to the ith cluster centre, v_i.

For each chromosome, the set of encoded clustre centres is first extracted and the fuzzy partition matrix is computed as above. Using these values, and the centre v^* (computed at the start of the process) for the data points $X=\{x_1, x_2, \ldots, x_n\}$, the $\mathrm{FS}(U, V; X)$ index is computed using equation (1). The objective of the clustering process is to minimize the $\mathrm{FS}(U, V; X)$ index for evolving the proper partitioning. Therefore, the fitness function for chromosome j is defined as

$$\frac{1}{\mathrm{FS}(U, V; X)_j}$$

Subsequently, the set of new cluster centres is computed as

$$v_i = \frac{\sum_{k=1}^{n} (u_{ik})^m x_k}{\sum_{k=1}^{n} (u_{ik})^m}, \quad 1 \le i \le c \tag{4}$$

These cluster centres are introduced into the chromosome, replacing the old ones. This, in effect, constitutes one iteration of the FCM process (Bezdek 1981), and is incorporated into the GA process to improve its convergence to the best solution. Note that the following criterion is minimized in the classical FCM algorithm:

$$J_m(U, V) = \sum_{i=1}^{c} \sum_{k=1}^{n} (u_{ik})^m D_{ik}^2(v_i, x_k) \tag{5}$$

In case the number of clusters, c, is varied, this criterion will achieve its minimum value for the largest c, being equal to zero when $c=n$ in the limiting case. Hence J_m cannot be used for proper clustering when c is variable.

2.4 *Genetic operations*

The following genetic operations are performed on the population of strings for a number of generations.

2.4.1 Selection. A commonly used selection strategy is called the roulette wheel selection, where each string receives a number of copies that is proportional to its fitness in the population. This selection scheme requires the fitness values to be greater than or equal to zero. Since in our case, the FS index can, and often will, assume negative values, we consider another scheme of selection, namely the binary tournament selection. In this strategy, a pair of individuals is picked up at random, and the fitter of the two is selected for propagation to the next generation. This process is repeated until the mating pool fills up.

2.4.2 Crossover. During crossover each cluster centre is considered to be an indivisible gene. Single point crossover is applied on each pair of strings with probability μ_c. Here, a crossover point is randomly chosen, and the genetic materials (cluster centres, as well as #s) to the right of the crossover point are swapped in the strings to produce two offspring.

2.4.3 Mutation. The process of mutation is defined in such a way that it has the capability of perturbing one or more cluster centres, deleting an existing cluster centre as well as introducing a new cluster centre. Thus accordingly we define three types of mutation, *normal mutation*, *deletion mutation* and *insertion mutation*. The first and the second ones, i.e. normal and deletion mutation, are applied to actual cluster centres which are encoded as real numbers in the chromosomes. During normal mutation at a location, its value is allowed to change by atmost f%, where f is user specified. That is, if the value at a location is v, then after mutation it will lie between

$$\left[v - \frac{fv}{100}, v + \frac{fv}{100}\right].$$

During deletion mutation, the corresponding centre is deleted and is replaced by #. The insertion mutation is applied probabilistically only on the #s. In this case, the # is replaced by a randomly picked point from the dataset, which is then perturbed in the manner of normal mutation.

2.5 *Termination criterion*

In this paper the processes of fitness computation, selection, crossover and mutation are executed for a maximum number of iterations. The best string having the largest fitness value seen up to the last generation provides the solution to the clustering problem. We have implemented elitism at each generation by preserving the best string seen up to that generation in a location inside the population. Thus on termination, this location contains the centres of the final clusters.

3. Segmentation using genetic fuzzy clustering

In order to segment images using the above technique, the natural choice of the data to be clustered is the intensity values of the pixels. Note that in this case the dimension of the feature space, N, is equal to the number of available spectral bands of the image. For example, $N=1$ for grey-level images, $N=3$ for colour images. However, as already mentioned, clustering in only the spectral domain effectively ignores the spatial information that is inherent in the pixels. On the contrary, while segmenting images, it seems natural that we take into account not only the spectral properties of the pixels, but also their spatial information. For example, if we consider a 3×3 neighbourhood, then while deciding on the clustering of two pixels (i, j) and (i', j') such that $|i-i'|$ and $|j-j'| \leqslant 1$, the fact that the two pixels are neighbours should also be taken into account.

There are two approaches in which spatial information can be incorporated in the clustering process. The first approach is by modifying the optimizing criterion such that it takes into account the contiguity of the segments in some form. Some such attempts may be found in Theiler and Gisler (1997) and Dulyakarn and Rangsanseri (2001). Note that, in the former this has been done for the well-known k-Means algorithm (Tou and Gonzalez 1974) while in the latter, the authors have used partial supervision in fuzzy clustering (Pedrycz 1997) with a local spatial information. Both these methods require *a priori* specification of the number of clusters, and provide locally optimal solutions. Also note that the basic clustering algorithm needs to be altered in these techniques.

The other approach of incorporating spatial information in the clustering process is by including the spatial information in the data representation itself. This would involve an increase in the dimensionality of the data, while keeping the clustering technique unaltered. The approach adopted in this paper belongs to this category. A general procedure for doing this is by adding the intensity values of all the neighbouring pixels as components of the pixel of interest. For example, if the intensity value of a pixel at location (*i*, *j*) is $p_{i,j}$, and we are considering a 3×3 neighbourhood, then the pattern in the extended feature space will be

$$\left(p_{i-1,j-1}\ p_{i-1,j}\ p_{i-1,j+1} \quad p_{i,j-1}\ p_{i,j}\ p_{i,j+1} \quad p_{i+1,j-1}\ p_{i+1,j}\ p_{i+1,j+1} \right)$$

It can be easily noted that this approach will be computationally very expensive, and therefore infeasible in practice. If we consider the same example but with say five bands of the image, then the increase in dimensionality of the dataset used for clustering is from five to $3 \times 3 \times 5 = 45$. Note that, with the increase in the size of the window, the dimensionality of the data will increase further (the relationship being quadratic in nature).

In order to overcome this problem, while still extending the feature space with spatial information, we consider two approaches. In the first one (referred to as WinAvg), the average intensity value over a specified neighbourhood across the pixel of interest is considered. In other words, if the intensity value of a pixel at location (*i*, *j*) is $p_{i,j}$, and we are considering a 3×3 neighbourhood, then the average intensity is computed as

$$\overline{p_{i,j}} = 1/9 \sum_{r=-1}^{1} \sum_{c=-1}^{1} p_{i+r,j+c}$$

The pattern in the extended space becomes

$$\left(p_{i,j}\ \overline{p_{i,j}} \right)$$

In the other approach (referred to as WinTopDown), the difference between the intensity values of the pixels above and below the pixel under consideration is taken as the first additional feature, while the difference between the intensity values of the pixels to the left and right of the pixel under consideration is taken as the second additional feature. Thus the pattern in the extended space becomes

$$\left(p_{i,j}\ \left(p_{i-1,j} - p_{i+1,j} \right)\ \left(p_{i,j-1} - p_{i,j+1} \right) \right)$$

Note that if the image has N spectral bands, the above computation is done in each band; thereby resulting in an increase in dimensionality of the data from N to $2N$ in the first approach, and from N to $3N$ in the second approach. The genetic fuzzy clustering is performed for the data in this extended feature space in order to segment the given image.

4. Implementation

The effectiveness of the genetic clustering technique is demonstrated on two images, namely, the *Spanner* image and a satellite image of a part of the city of Mumbai. Results comparing the performance of the clustering method both with and without the spatial information is provided, both pictorially as well as in terms of a quantitative index. The parameters of GAs are taken as follows. The population size is taken to be 20, μ_c=0.8, probabilities of normal, insertion and deletion mutations are set to 0.1, value of the maximum perturbation during mutation f=20%, maximum number of iterations of GA=100 and weighting coefficient m=2.0.

4.1 *Image datasets*

In this section we describe the datasets used for the experiments. The first is the Spanner image shown in figure 1. This is a 256×256 grey-scale image. (The corresponding genetically segmented images obtained without using spatial information and with WinAvg approach are shown in figures 2 and 3, respectively, as discussed in section 4.2.)

The Mumbai image, shown in figure 4, was obtained from Indian Remote Sensing Satellite (IRS-1A). Data used for this work were captured using the LISS-II sensor,

Figure 1. Input Spanner image.

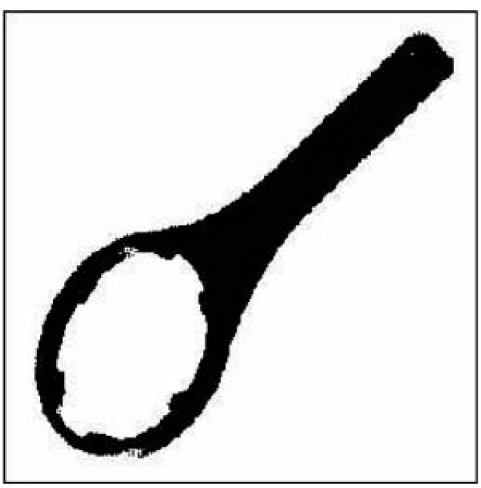

Figure 2. Segmented Spanner image without using spatial information.

Figure 3. Segmented Spanner image with spatial information using WinAvg approach.

which has a focal length of 324.4 m, radiometric resolution of 128 and spatial resolution of $36.25\,\mathrm{m} \times 36.25\,\mathrm{m}$. We have considered here two bands, namely green band of wavelength 0.52–0.59 μm, and near-infrared band of wavelength 0.77–0.86 μm.

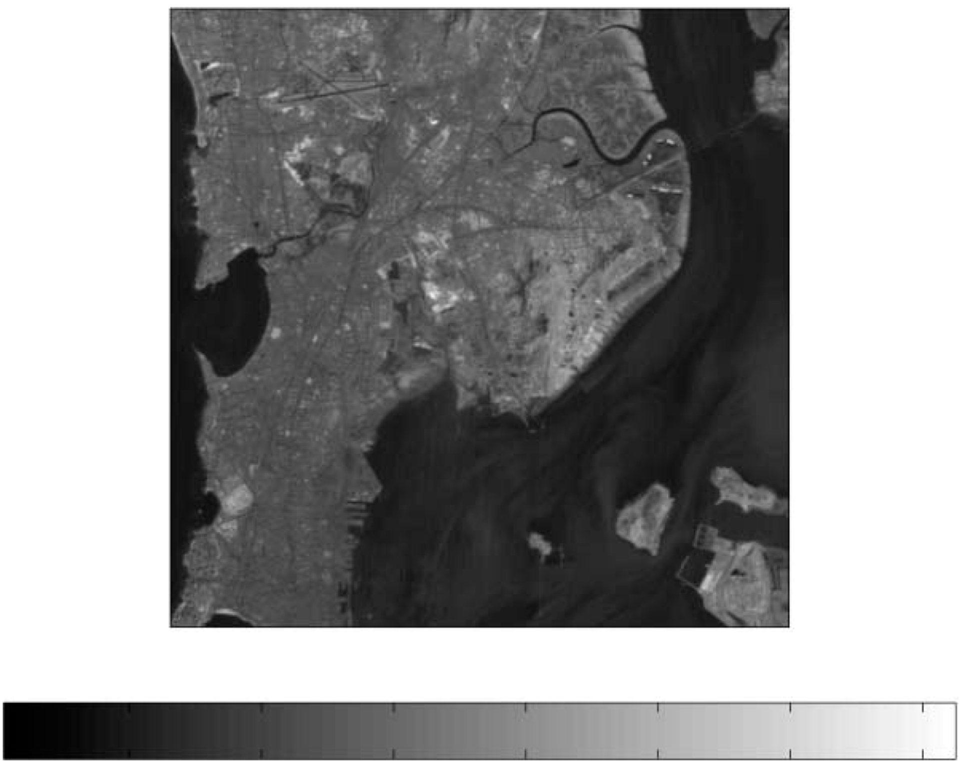

Figure 4. Near-infrared band of the Mumbai image with histogram equalization.

Some important land covers of Mumbai obtained from the ground data, and as seen more prominently from the near-infrared band (figure 4 shows the image with histogram equalization to make it more prominent) are as follows. The elongated city area is surrounded by the Arabian Sea. There is a concrete structure (on the right top corner) connecting Mumbai to New Mumbai. On the southern part of the city, there are several islands, including the well-known Elephanta islands. The dockyard is situated on the south-eastern part of Mumbai, which can be seen as a set of three finger-like structures. On the upper part of the image, towards the left, there is a distinct crisscrossed structure. This is Santa Cruz airport.

It may be noted that these data have been used earlier for classifying the pixels into different categories under the supervised framework (Bandyopadhyay and Pal 2001, Pal *et al.* 2001). From the ground data, five different land-cover types, namely, turbid water (TW), Concrete (Concr), Habitation (Hab), Vegetation (Veg) and Open Space (OS), were known to be present. Training points were extracted from the different land-cover regions, and the class labels were manually associated by an expert knowledgeable about the area. The classified image using the well-known k-NN rule (for $k=1$) and the Bayes maximum likelihood classifier (Tou and Gonzalez 1974) are provided in figures 5 and 6, respectively. Note that the utility of an unsupervised scheme, which does not require the *a priori* specification of the number of clusters (such as the one described in this paper), becomes evident if the manual intervention for extracting training points needs to be reduced or eliminated totally.

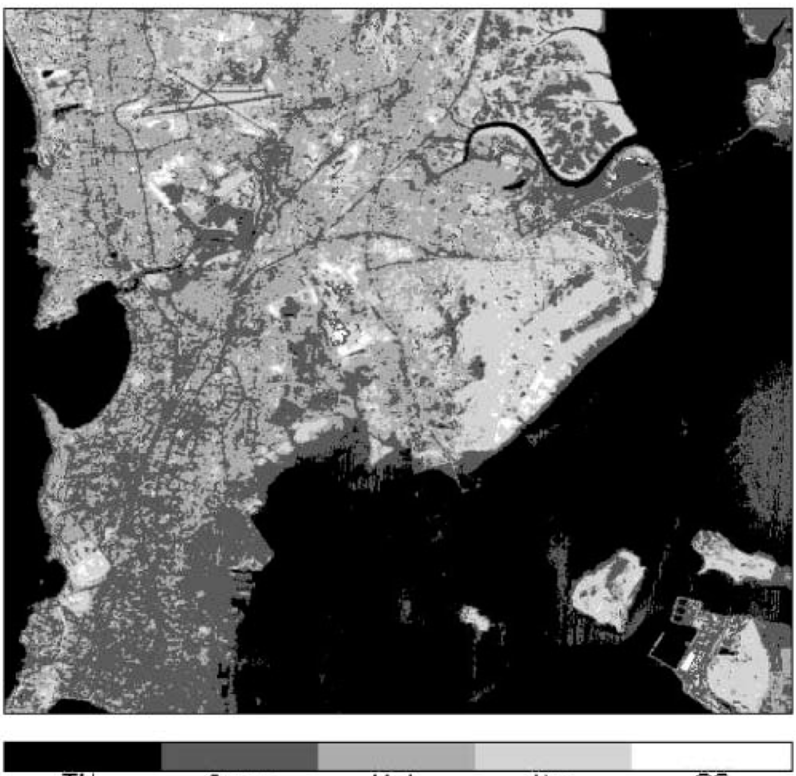

Figure 5. Classified Mumbai image using the k-NN classifier ($k=1$).

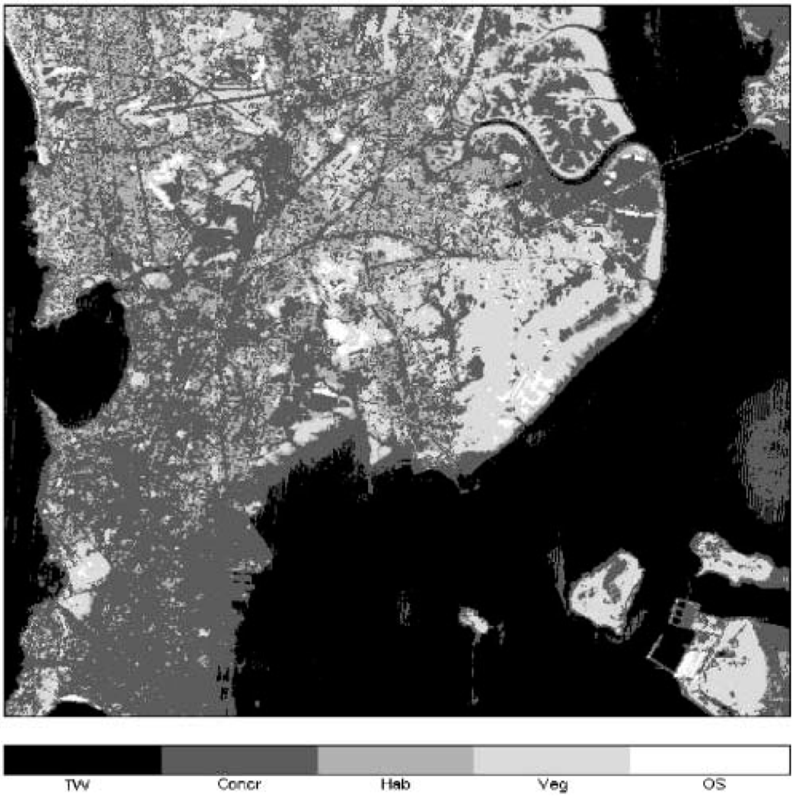

Figure 6. Classified Mumbai image using the Bayes maximum likelihood classifier.

4.2 *Results*

This section presents the results of application of the genetic fuzzy clustering technique on the above-mentioned images. Results are provided both when the spatial information is neglected as well as considered, for the two images.

In the case of the Spanner image, two clusters are obtained when spatial information is not considered. These correspond to the object and the background regions. The resulting clustered image is shown in figure 2. Using the WinTopDown approach, again two clusters are obtained. The J_m values (equation (5)) for the above two cases (both of which provide two clusters) are found to be 870.7243*10^4 and 870.5665*10^4, respectively, indicating a slightly better performance using the WinTopDown approach. For the case when the WinAvg approach is used with a window size of 3×3, three clusters are obtained, one of which belongs to the background and the other two to the object (see figure 3). Interestingly, some portions of the spanner, which are found to have grey-level properties close to that of the background, are segmented as a class separate from both the backgound and object regions (appears in white in the figure). Note that some subsequent postprocessing technique can be applied in order to infer that this segment needs to be merged with the object segment (appears in black in figure 3) before further analysis is carried out.

In the case of the Mumbai image, the algorithm using WinAvg approach for incorporating spatial information was executed for different window sizes, namely

3×3, 5×5 and 7×7, while the WinTopDown approach had a window size of 3×3. In all the cases, the algorithm provided five clusters. This more or less corresponded to the five land-cover types obtained using the supervised classifiers mentioned earlier (figures 5 and 6). The values of J_m (equation (5)) for the different cases is provided in table 1. As can be seen from the table, the J_m values obtained when spatial information is incorporated are generally found to be lower than when spatial information is ignored. For the WinAvg approach, the lowest value is achieved for a window size of 3×3. As expected for this approach, for larger window sizes, increased averaging effect is observed. This leads to the loss of very narrow regions like roads, bridges, etc. Figure 7 shows the result of this approach for

Table 1. Value of J_m for different approaches for Mumbai image.

Approach	Window size	J_m
No spatial information	–	228.3718*10^4
WinAvg	3×3	221.26*10^4
	5×5	227.6153*10^4
	7×7	225.0962*10^4
WinTopDown	3×3	219.2152*10^4

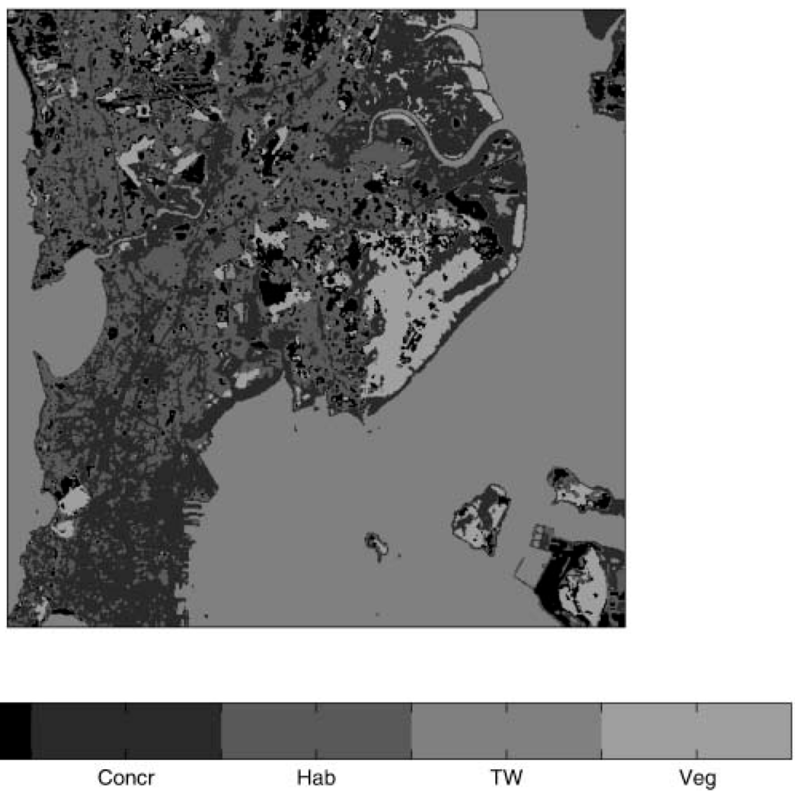

Figure 7. Segmented Mumbai image with spatial information using WinAvg approach for window size of 3×3.

window size equal to 3×3. The result for the WinTopDown approach is provided in figure 8. As can be seen, here a small part of the bridge connecting Mumbai to New Mumbai has been identified. Comparison of figures 7 and 8 with the results obtained using the supervised classifiers (figures 5 and 6) indicates that the unsupervised scheme provides a reasonably good automatic landcover classification into the five classes. As noted earlier (Pal *et al.* 2001), the Bayes maximum likelihood classifier appears to overestimate the concrete classes, resulting in a proper extraction of the bridge connecting Mumbai to New Mumbai, while not being able to retain the structure of the dockyard, or the roads. Both the k-NN rule and the Bayes maximum likelihood classifier provide some spurious regions within the wide Arabian Sea area. In contrast, it can be observed from the results of the unsupervised schemes (figures 7 and 8) that a good balance is maintained within the different classes, with the Arabian Sea coming out as a single waterbody, and the structure of the dockyard extracted properly. This result is quite encouraging since the unsupervised scheme has neither any pre-labelled training data nor knowledge about the number of classes in the image at its disposal.

Table 2 shows, in summary, the number of clusters provided by the genetic fuzzy clustering method both with and without spatial information for the two images.

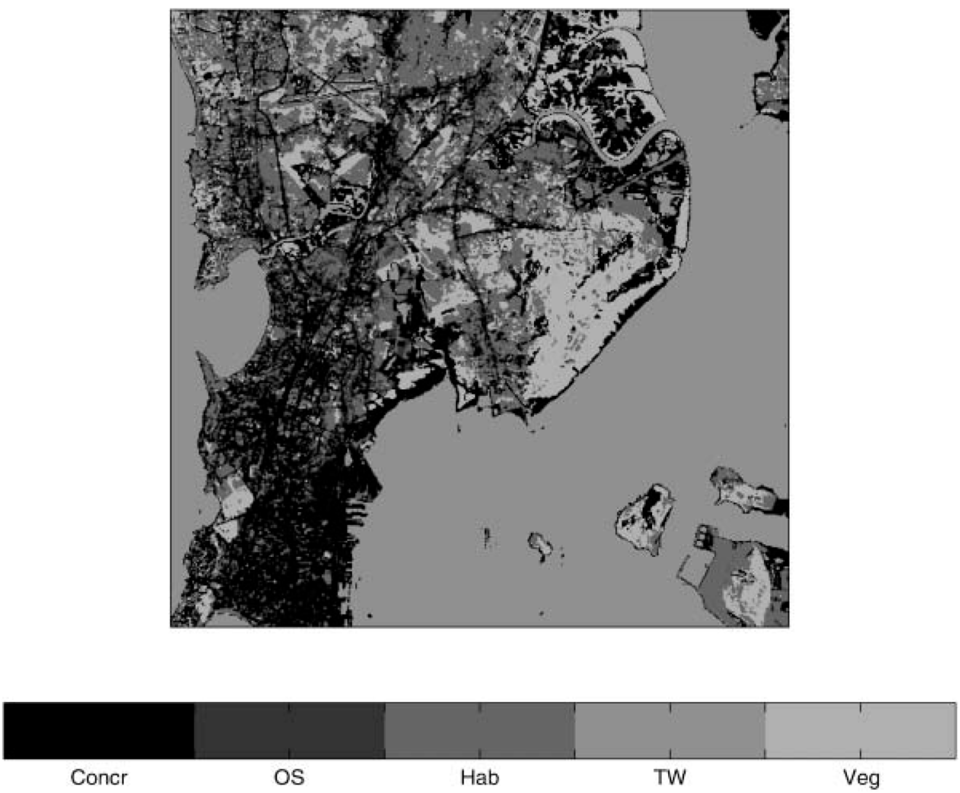

Figure 8. Segmented Mumbai image with spatial information using WinTopDown approach for window size of 3×3.

Table 2. Number of clusters.

Data	Number of clusters		
	With spatial information		Without spatial information
	WinAvg	WinTopDown	
Spanner	3	2	2
Mumbai image	5	5	5

5. Discussion and conclusions

This paper describes an approach for automatic segmentation of images using a fuzzy clustering technique. The genetically guided fuzzy clustering algorithm incorporates spatial information that is inherent in the pixels in order to obtain good segmentation results. Two different approaches, WinAvg and WinTopDown, are implemented for incorporating spatial information. As a result, the feature space is enhanced, so that its dimensionality increases from N (the number of bands in the image) to $2N$ and $3N$, respectively. The clustering method described here can automatically evolve the number of clusters as well as the proper partitioning of the data. A genetic algorithm has been used as the underlying search strategy as it has the capability of coming out of local optima. Since the number of clusters is not known *a priori*, it is kept variable in the chromosomes. Real encoding of the cluster centres in the chromosomes, along with appropriate definition of the genetic operators, is used. Moreover, in order to tackle the concept of variable string lengths, a don't care symbol # is also incorporated in the chromosome representation. The Fukuyama–Sugeno index has been used as the minimizing criterion in order to evolve the appropriate partitioning of the data.

Results are demonstrated on a Spanner image and a satellite image of a part of the city of Mumbai. The effectiveness of incorporating spatial information is demonstrated both qualitatively as well as quantitatively for the images by comparing the results of the algorithm with those where the spatial information is ignored. Results on the Mumbai image demonstrate that the method is automatically able to distinguish between the various land-cover types present. This can be verified by comparing with the results of supervised classification schemes using the Bayes maximum likelihood classifier and the k-NN rule.

There are many ways in which this work may be extended further. As a scope for further research, other ways of incorporating spatial information in the clustering process need to be investigated and compared. Comparison with other classification schemes and/or using features other than simple intensity values needs to be investigated. As an example, texture based image segmentation techniques (Chen *et al.* 2003) may be studied. The fitness function of the GA may be modified appropriately so as to penalize the chromosomes that give rise to highly non-contiguous segments. Moreover, the effect of using other cluster validity indices (Bezdek 1974, 1975, Windham 1982, Xie and Beni 1991, Bensaid *et al.* 1996, Bandyopadhyay and Maulik 2001) needs to be investigated. Other related evolutionary algorithms such as evolutionary strategies (Schwefel 1987), simulated annealing (Kirkpatrick *et al.* 1983, Maulik *et al.* 2001), etc., may be utilized as the underlying search and optimization tool, and the performance may be compared with that of the GA based scheme. Finally, parallelization of the genetic image segmentation scheme is another important direction of further study.

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