A New Genetic Method for Sub-Pixel Mapping Using Hyperspectral Images

Xiaohua Tong\textsuperscript{a,*}, Xiong Xu\textsuperscript{a,b}, Antonio Plaza\textsuperscript{b}, Fellow, IEEE, Huan Xie\textsuperscript{a}, Haiyan Pan\textsuperscript{a}, Wen Cao\textsuperscript{a}, Dong Lv\textsuperscript{a}

\textsuperscript{a}College of Surveying and Geo-Informatics, Tongji University, 1239 Siping Road, Shanghai, P.R. China
\textsuperscript{b}Hyperspectral Computing Laboratory, Department of Technology of Computers and Communications, Escuela Politecnica, University of Exremadura, Cáceres, Spain
* Corresponding author Email: xhtong@tongji.edu.cn
Tel: +86-21-65988851 Fax: +86-21-65981085

Abstract—Sub-pixel mapping techniques aim to obtain the spatial location and distribution of sub-pixels by transforming the information coming from a set of input abundance maps into a classification result with higher spatial resolution. However, traditional sub-pixel mapping algorithms generally ignore the possible errors that are due to abundance estimation inaccuracies by spectral unmixing techniques. In this paper, we propose a new genetic algorithm based sub-pixel mapping technique that solves the sub-pixel mapping problem by correcting the potential errors in the estimated abundance fractions used as input to the sub-pixel mapping process. The proposed algorithm has been compared with other two genetic sub-pixel mapping methods, using both synthetic and real hyperspectral images. Our experimental results demonstrate that the proposed approach outperforms traditional sub-pixel mapping algorithms, thus providing an effective option to improve the accuracy of sub-pixel mapping for remotely sensed hyperspectral images.

Index Terms—Hyperspectral imaging, sub-pixel mapping, spectral unmixing, genetic algorithms.
I. INTRODUCTION

The signal recorded by a hyperspectral sensor is generally a mixture of the reflected radiation scattered by the underlying constituent substances located in a given pixel [1]. Spectral unmixing techniques focus on discriminating different materials in mixed pixels and obtaining the corresponding fractions of the so-called endmembers (pure spectral components). However, the spatial distribution of the endmembers in the pixel cannot be inferred from the estimated endmember abundance maps. For this reason, sub-pixel mapping (or super-resolution mapping) has been introduced to solve this problem by dividing a pixel into sub-pixels and assigning each sub-pixel to a land-cover class, in order to convert the abundance map to a hard classification map with higher spatial resolution [2].

Sub-pixel mapping is an ill-posed problem that attempts to obtain a finer classification map from a coarser abundance image. To tackle this problem, several sub-pixel mapping methods have been proposed based on the concept of spatial dependence [3-31], which refers to the property that pixels which are spatially adjacent in the scene are more likely to be similar than those that appear in spatially disjoint areas. As a typical inverse problem [3], artificial intelligence algorithms have been widely used to automatically label sub-pixels using spatial dependence properties owing to their global optimization abilities [4-14]. For instance, artificial neural networks (ANNs), as powerful tools for nonlinear prediction, have been applied to sub-pixel mapping by constructing the projection relationship between the
abundance map and the sub-pixel mapping output [4-7]. To deal with different types of mixed pixels, Xu et al. [8] designed a multi-agent system algorithm to reconstruct possible features during the sub-pixel mapping procedure. Furthermore, based on the spatial dependence criterion, several objective functions were established and different optimization techniques were utilized in previous works [9-16]. Given a certain objective function, genetic algorithms aim at generating the final result by incorporating different operators [9]. Besides, Villa et al. [10] utilized a simulated annealing technique to finalize the sub-pixel mapping procedure with another different objective function. Based on the objective function proposed in [11], Zhong et al. adopted differential evolution [12] and artificial immune system techniques [13] to perform optimization in the context of sub-pixel mapping respectively. Moreover, a particle swarm optimization algorithm was used in [14] as a post-processing on a previously derived sub-pixel mapping result.

Genetic algorithms have been widely used in various fields and proved to be simple but efficient global optimization methods [32-35]. These kinds of techniques can be used to search for an optimal solution without trying all possible cases [36-37]. Inspired by the principle of “survival of the fittest” in natural evolution processes, the basic idea of the method is that different operators collaborate to generate the optimal solution iteratively for a population of individuals that represent possible solutions. For example, the selection operator aims to pass on genes of better individuals to the next generation; the crossover and the mutation operators can effectively avoid converging to local optima and thus better search for an optimal solution [38]. When
it comes to the sub-pixel mapping problem, different combinations of operators and objective (or fitness) functions have been designed [9, 30-31]. In addition to the selection and crossover operators, Mertens et al. [10] devised an inversion operator that is used to invert the order of the genes of an individual. Zhao et al. [30] utilized the traditional selection operator and a specifically defined crossover operator to generate the final sub-pixel mapping result. Moreover, genetic algorithm based sub-pixel mapping has also been applied for wetland inundation estimation [31].

However, an important aspect of genetic based sub-pixel mapping methods is that they generally rely on the estimated abundance map as a baseline, which means that the proportions of different classes in mixed pixels will remain unchanged during the process of sub-pixel mapping, and crossover operators are commonly designed under this circumstance to generate the final sub-pixel mapping output without bearing in mind the potential errors that could be introduced by spectral unmixing techniques [39]. Although linear spectral unmixing techniques have shown their effectiveness in decomposing mixed pixels [40], in many situations the estimated abundances may not be completely accurate due to noise, atmospheric interferers, nonlinearity of the mixtures, and so on. As a result, potential inaccuracies in abundance estimation may introduce significant errors in the sub-pixel mapping process and the resulting thematic maps.

This inspired us to propose, as a novel contribution of this work, the use of a mutation operator and therefore a new sub-pixel mapping method based on genetic algorithms which corrects potential abundance inaccuracies to obtain the final
solution. With the introduced mutation operator, which alters the gene value randomly, the proportions of classes in mixed pixel can be adjusted to search for a better result. Although the mutation operator can alter the inaccuracies in abundance maps, the sub-pixel mapping result may suffer from excessive distortion due to the fact that only spatial dependence is utilized in the fitness function and the ability of the mutation operator is hard to confine. Therefore, a weighted spectral term was also formulated and incorporated into the fitness function so that the impact of the original spectral information can still be taken into consideration to avoid excessive mutations.

In conclusion, the proposed genetic method considers sub-pixel mapping as an optimization problem which maximizes spatial dependence (by establishing sub-pixel associations that promote the grouping of pixels which are spatially adjacent in the scene) and minimizes the possibly negative impact of abundance estimation inaccuracies by allowing the genetic algorithm to modify the gene value of individuals, in which case the utilized abundance map can be modified indirectly. In this way, the proposed method is expected to achieve a better solution when compared with traditional genetic sub-pixel mapping methods.

The remainder of this paper is organized as follows. Section II gives a detailed description of the proposed method. Section III presents experimental results obtained using both synthetic and real hyperspectral scenes. Section IV concludes the paper with some remarks and hints at plausible future research lines.
II. PROPOSED SUBPIXEL MAPPING METHOD

The key issue in a sub-pixel mapping problem is how to determine an optimal sub-pixel distribution of each class within a pixel. Inspired from Tobler’s first law [41-42], spatial dependence has been regarded as a relevant criterion. It simply refers to the tendency of spatially close observations to be more alike than more distant observations [2]. As illustrated in Fig. 1, given an abundance map obtained by spectral unmixing techniques, each coarse pixel can be divided into $S \times S$ sub-pixels, where $S$ represents the scale factor. The number of sub-pixels for each land-cover class can be determined by the fractional values of different classes. Fig. 1 shows a sub-pixel mapping example with three classes. As shown in Fig. 1(a), a coarse pixel is divided into 16 ($4 \times 4$) sub-pixels, where the scale factor $S$ equals 4, and 0.5 in the fraction image in red, which means that 8 ($16 \times 0.5$) sub-pixels belong to land-cover class 1. Figs. 1(b) and 1(c) describe two possible distributions of sub-pixels. Given the principle of spatial dependence, the latter is perceived to be less optimal.

![Figure 1. Toy example illustrating sub-pixel mapping methods. (a) Abundance maps (b) Possible distribution 1 (c) Possible distribution 2](image)

- **class 1**
- **class 2**
- **class 3**
extracted for a 3x3-pixel image. (b) A possible distribution of sub-pixels in a finer resolution image in which a coarse pixel is divided into 16 (4×4) sub-pixels. (c) Another distribution which is perceived as less optimal than the one reported in (b).

As mentioned before, for traditional genetic based sub-pixel mapping methods, the spatial dependence is considered as the sole criterion for defining the fitness function, and the constraint on abundance fractions is strictly satisfied (meaning that the initial estimation of abundance fractions will have a great impact on the final sub-pixel mapping result). The main innovation of our proposed method is that possible inaccuracies and errors in abundance estimation are taken into consideration and the mutation operator is utilized to adjust the abundance fractions by modifying the attribution values of sub-pixels. Specially, a weighted spectral term is incorporated into the fitness function to avoid the severe discrepancy between the generated sub-pixel mapping result and the original hyperspectral imagery. In the following, we provide a description of our proposed approach.

Fig. 2 shows a general flow of the proposed method, which can be summarized by the following steps:

- Firstly, an abundance map is obtained from the original hyperspectral scene using a spectral unmixing technique. For each pixel in the abundance map, an initial population of solutions is generated randomly. Each individual of the population is a solution of a possible configuration of different endmembers for a given mixed pixel.
At this point three different kinds of operators, i.e. selection, crossover and mutation are used to increase the fitness of the whole population after iterating (while removing some individuals that did not exhibit a good overall fit).

Finally, the individual with the best overall fit is identified and retained as the one providing the optimal configuration for a given pixel, after all iterations have been completed.

Let us denote the original hyperspectral image by $y$. This image contains $K$ bands and $m$ pixels, and we use $y_i^k$ to denote the $k$-th band of pixel $i$. Let us also suppose that the spectral unmixing model yields a set of abundance fraction maps $x$ for $C$
endmembers, so that each mixed pixel in the original scene can be divided into $S*S$ sub-pixels, assuming that $S$ is the scale factor. With the aforementioned notations in mind, the number of sub-pixels to be assigned to the class given by endmember $c$ in the mixed pixel $i$ can be calculated as follows:

$$NS_i^c = \text{round}(x_i^c*S*S),$$  \hspace{1cm} (1)

where $x_i^c$ is the abundance fraction of class $c$ in pixel $i$, and $\text{round}()$ is an operator to convert the input to the nearest integer. Then, the initial population of solutions for each mixed pixel $i$ can be generated randomly under a constraint given by the calculated $NS_i^c$, $c\in[1,C]$. Specifically, this sub-pixel number constraint is fulfilled strictly in other genetic sub-pixel mapping methods [9, 30]. Therefore, the widely used mutation operator was generally discarded. However, since our goal is to correct possible abundance estimation inaccuracies, mutation is the best choice for an operator able to adjust these possible errors by altering each gene (sub-pixel) value to an arbitrary class label with a certain probability. Therefore, three operators (selection, crossover and mutation) are utilized in our proposed method. Moreover, in order to restrain the abrupt changes often brought by the mutation operator, a weighted spectral term was integrated with the commonly used spatial dependence term for the considered fitness function.

A. Selection, Crossover and Mutation Operators

Given an initial population of solutions generated randomly, three kinds of operators are utilized to obtain a new generation. The selection operator aims at
retaining the individuals with higher fitness by selecting two individuals as the parents.

In this paper, the roulette wheel method was utilized to select the parents according to a probability that is proportional to the fitness, which means that the better the individuals, the more chances they have to be selected.

Once the two parent individuals have been selected, the crossover operator is used. This crossover operator allows for exchanging the genes between two individuals with a certain probability $P_c$. This operator has the ability to approach the globally optimal solution. In this paper, the one-point crossover method is used for this purpose, and the operator is designed as illustrated in Fig. 3. Specifically, an insert position is first generated randomly, and the latter parts of the two individuals will then perform an exchange of information with each other in order to generate two new individuals.

![Crossover operator](image)

Figure 3. Example of the crossover operator.
An important consideration at this point is that the crossover operation should not break the inherent abundance constraint from the parent individuals, and the number of sub-pixels for different classes should be kept constant between the parent individuals and the generated child individuals. Therefore, after the crossover operation, the two new child individuals have to be adjusted to satisfy the constraint. Our strategy to address this issue is to first assess the differences between parent and child individuals and then exchange class labels of genes until the disagreement is eliminated, as Fig. 4 shows. As a result, two new child individuals are obtained for the new generation.

![Figure 4. Illustration of the adjustment process.](image)

As mentioned above, the crossover operator aims to approach the global optimization problem under the effective adjustment of the abundance constraint. However, when the abundances are taken into consideration, a mutation operator is utilized in the proposed method. This operator changes a gene from one class to
another with a certain probability $P_m$. By this way, the initial abundance fractions may be modified. Fig. 5 illustrates the implementation of the mutation operator in our proposed approach. As shown by Fig. 5, each gene in the parent individual has a chance to change to other class randomly, so that the child individual can be then obtained. By this way, the proposed method has the ability to modify the previously defined abundance fractions and try to find a better solution given the fitness function, thus correcting potential errors in the initial fractional abundance estimations that serve as the starting condition for the method.

![Mutation operator](image)

Figure 5. Example of the mutation operator.

B. **The fitness function**

After introducing the three different operators that the genetic algorithm exploits, we focus now on the fitness function as a key aspect to improve the performance of the proposed method. Generally, the spatial dependence principle is formulated as the only criterion to control the search for a global solution. However, a main innovation of our work is that the mutation operator is utilized to correct the possible abundance estimation errors. Accordingly, the effect of the mutation operator should be refined.
to avoid excessive distortion and ensure the coincidence between the generated sub-pixel mapping result and the information contained in the original hyperspectral image. To address this issue, we incorporate a weighted spectral term (together with the spatial dependence term) in the fitness function of the proposed method.

Specifically, we use a metric called spatial dependence index (SDI) proposed in [11]. Let $j$ denote a gene (sub-pixel) in each individual (solution) that corresponds to the original mixed pixel $i$. The SDI of sub-pixel $j$ for endmember class $c$ can be calculated as follows:

$$SDI_j^c = \sum_{t \in N[i]} w_{j,t} \cdot x^c_t,$$

where $N[i]$ denotes the set of neighboring pixels of pixel $i$; $w_{j,t}$ is the weight of neighboring pixel $t$ to sub-pixel $j$; and $x^c_t$ is the abundance fraction of pixel $t$ for class $c$. $w_{j,t}$ is often calculated as the inverse of the distance of the sub-pixel to the corresponding pixel center [2].

The fitness function based on spatial dependence for all sub-pixels of each individual can be formulated as:

$$\text{Fitness(SD)} = \sum_{j=1}^{S \times S} \sum_{c=1}^{C} v_{j,c} \cdot SDI_j^c,$$

where $v_{j,c}$ is used to model if sub-pixel $j$ belongs to endmember class $c$ as follows:

$$v_{j,c} = \begin{cases} 1, & \text{if sub-pixel } j \text{ belongs to class } c \\ 0, & \text{otherwise} \end{cases}$$

The greater the SDI, the better the individual. In order to ensure spectral consistency, we employed the difference between the original spectral signature $y_i$ and the inverse (estimated) spectral signature of the same mixed pixel $i$ (which is also
known as the root-mean-square error (RMSE)) as follows:

$$\text{Fitness}(\text{AI}) = \sqrt{\frac{\|y_i - \hat{y}_i\|^2}{K}},$$

(5)

where $\hat{y}_i$ is the inverse signature of pixel $i$, generated from the configuration of each individual. The smaller the difference between the original and the inverse spectral signature, the better the individual.

With these ideas in mind, the fitness function for the proposed method, hereinafter called genetic algorithm able to correct abundance inaccuracies (GAAI), can be formulated as follows:

$$\text{Fitness}(\text{GAAI}) = \text{Fitness}(\text{SD}) - \lambda \cdot \text{Fitness}(\text{AI})$$

(6)

where $\lambda$ is a weight that controls the trade-off between the spatial dependence and the spectral term.

C. Comparison with genetic algorithms based methods

As mentioned before, there are other genetic sub-pixel mapping algorithms that have been developed in the literature. In this section we provide a brief comparison of the main properties of our proposed GAAI method with regards to these methods. Specifically, we consider the genetic algorithm (GA) in [9] and the modified genetic algorithm (MGA) in [30]. A comparison of the two algorithms with the proposed method is given in Table I.

In Table I, $N_{ij}$ denotes the set of neighboring sub-pixels of sub-pixel $j$, and $N_i$
is the total number of neighboring sub-pixels. \( \delta_{j,p} \) is used to describe if neighboring sub-pixel \( p \) belongs to the same class as sub-pixel \( j \):

\[
\delta_{j,p} = \begin{cases} 
1, & \text{if sub-pixel } p \text{ belongs to the same class with sub-pixel } j \\
0, & \text{otherwise}
\end{cases},
\]

From the comparison presented in Table I, we can see that the utilization of the mutation operator and the inclusion of a spectral term in the fitness function are the most relevant innovations of the proposed method with regards to other techniques. An experimental evaluation of the effectiveness of the proposed method will be discussed in the following section.

### III. EXPERIMENTS AND ANALYSIS

In our experimental evaluation, the proposed GAAI method was compared with three different sub-pixel mapping algorithms: the spatial attraction (SA) model in [15], the GA in [9], and the MGA in [30]. In our experiments, we use both synthetic and

<table>
<thead>
<tr>
<th>Methods</th>
<th>Fitness function</th>
<th>Operator</th>
</tr>
</thead>
<tbody>
<tr>
<td>GA</td>
<td>( \sum_{j \in S} \sum_{p \in I, [j]} \frac{\delta_{j,p}}{N_s} )</td>
<td>√</td>
</tr>
<tr>
<td>MGA</td>
<td>Fitness(SD)</td>
<td>√</td>
</tr>
<tr>
<td>Proposed (GAAI)</td>
<td>Fitness(GAAI)</td>
<td>√</td>
</tr>
</tbody>
</table>
real hyperspectral images. Specifically, the parameters used for the different genetic algorithms were set empirically and made equal in all tests. More specifically, the size of the population was set to 200; the number of generations was set to 100, and the crossover probability $P_c$ was set to 0.5. Moreover, the mutation probability $P_m$ was set to 0.05 for the proposed method. Moreover, to ensure the convergence of the proposed method, we let the iterative process continue until the result remains unchanged, even the pre-defined number of iterations has been completed. Owing to the fact that the number of endmembers in a mixed pixel are proportional to the obtained abundance fractions, and due to the need to impose the sum-to-one constraint on the estimated abundances in order to have meaningful sub-pixel estimates, we have used the fully constraint least squares (FCLS) [43] method to estimate the abundance maps in this work. The accuracy assessment was undertaken using the classification overall accuracy (OA), average accuracy (AA), individual classification accuracies and the Kappa coefficient of the sub-pixel mapping result [44]. At the same time, the abundance map can also be generated from the final sub-pixel mapping result and the root mean square error (RMSE) is utilized in this case to compare the reference abundance fractions with the reference classification map.

A. Synthetic experiments

Two synthetic hyperspectral images have been constructed to test the performance of the proposed GAAI method. In our experiments, the low-resolution hyperspectral
image is generated by degrading the available high-resolution hyperspectral image with an averaging filter. In this way, the classification result obtained for the high-resolution image can be used as the ground truth to evaluate different sub-pixel mapping results.

A.1. Synthetic image 1- HJ-1A

To simulate a real world situation under a fully controlled scenario, we used a real hyperspectral data set which was obtained by a Chinese environmental satellite, HJ-1A [45]. The HJ-1A satellite has a hyperspectral sensor with 115 spectral bands (in the spectral range from 0.45 to 0.95 µm) and spatial resolution of 100 m per pixel. The utilized HJ-1A image (150×150 pixels) was acquired on August 19, 2009 and was used as the original image in our experiments. The study site is located in Hanchuan City, Hubei Province, central China, and its surrounding area. Four land-cover classes, i.e., urban, agricultural land, water and vegetation are used to characterize this image as Fig. 6(b) shows. This image was degraded artificially to obtain a low-resolution synthetic image given a scale factor of three in this experiment.

As illustrated in Fig. 6, the abundance map used as initial condition can severely impact the final sub-pixel mapping results. Compared with the reference classification map in Fig. 6(b), obtained using the support vector machine (SVM) method, the results of SA [see Fig. 6(c)], GA [see Fig. 6(d)] and MGA [see Fig. 6(e)] are seriously affected by the errors introduced by the spectral unmixing process, while the proposed
method provides a more smooth classification map due to the correction of abundance estimation inaccuracies [see Fig. 6(f)]. However, it is obvious that some regions in the result of GAAI are over-smoothed. This is because that sub-pixel mapping is an inverse problem and there is a trade-off between the refinement of abundance inaccuracies and the degree of detail preservation. As observed in Fig. 6, a generally better visual result can be obtained with the proposed method.

![Sub-pixel mapping results for the synthetic dataset (HJ-1A): original low-resolution imagery (a); reference classification map obtained by eCognition software (b); sub-pixel mapping result obtained using SA (c), GA (d), MGA (e), GAAI (f).](image)

The sub-pixel mapping accuracies obtained in this experiment are listed in Table II to evaluate the effectiveness of the proposed method in quantitative fashion. As
shown by Table II, the proposed GAAI provided significant improvements in terms of all quantitative indexes when compared with the SA, GA and MGA. Specifically, a better abundance estimation can be generated with the sub-pixel mapping result by GAAI method. It is clear from Table II that the performance of the considered sub-pixel mapping methods was limited by the accuracy of the initial abundance map, but the proposed method exhibited the capacity to improve over the original abundance estimation as compared with the other three tested methods.

Moreover, the CPU time was also reported for each method in Table II. Owing to the fact that the utilized spatial attraction (SA) model is a non-iterative method, this one is the fastest. However, compared with other iterative genetic algorithms based sub-pixel mapping methods, the proposed method exhibits similar performance in terms of time consumption. The modified fitness function and added mutation step did not increase the computational time significantly.

<table>
<thead>
<tr>
<th>Class</th>
<th>Methods</th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>SA</td>
<td>GA</td>
<td>MFA</td>
<td>GAAI</td>
</tr>
<tr>
<td>Individual class accuracy (%)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Urban area</td>
<td>58.46</td>
<td>52.97</td>
<td>58.36</td>
<td>67.75</td>
</tr>
<tr>
<td>Agricultural land</td>
<td>80.62</td>
<td>70.40</td>
<td>79.73</td>
<td>81.70</td>
</tr>
<tr>
<td>Water</td>
<td>63.74</td>
<td>54.81</td>
<td>62.62</td>
<td>63.92</td>
</tr>
<tr>
<td>Vegetation</td>
<td>69.04</td>
<td>59.88</td>
<td>68.37</td>
<td>76.19</td>
</tr>
<tr>
<td>Average class accuracy (%)</td>
<td>67.97%</td>
<td>59.52%</td>
<td>67.27%</td>
<td>72.39%</td>
</tr>
<tr>
<td>Overall Accuracy (%)</td>
<td>64.07%</td>
<td>56.63%</td>
<td>63.56%</td>
<td>70.04%</td>
</tr>
<tr>
<td>Kappa</td>
<td>0.505</td>
<td>0.403</td>
<td>0.498</td>
<td>0.580</td>
</tr>
</tbody>
</table>

TABLE II. Accuracy statistics for the HJ-1A image experiment.
The other synthetic image used in experiments is a multispectral aerial data set containing agricultural crop species and land use, obtained in the 620-660 nm wavelengths (band number 12) by an optical mechanical line scanner referred to as the University of Michigan M-7 system. The flightline used in this work (called C-1) was collected on June 28, 1966 [46]. The flightline was taken over the southern part of Tippecanoe County of Indiana. It has eight land cover classes, as illustrated in Figs. 7(a) and 7(b). The size in pixels of the degraded low-resolution image is 20*40 pixels and the reference classification map is 80*160 pixels with a scale factor of four. Moreover, in our experiments the classification map was obtained by classifying the high-resolution image using the commercial eCognition software.

As illustrated in Fig. 7, the impact of the initial abundance map is quite important for the subsequent sub-pixel mapping procedure. The proposed GAAI method [see Fig. 7(f)] has a better performance on visual assessment as compared with the other three methods [see Figs. 7(c) – Fig. 7(e)].

Table III shows a quantitative comparison of the SA, GA, MGA and the proposed GAAI methods. The same conclusions can be drawn as in the experiment with the HJ-1A dataset. Moreover, the ability of the proposed method to generate a smooth classification result is quite significant. For example, a gain of 9.51% in OA is observed for the proposed method with the FLC1 dataset. Moreover, GAAI also
exhibits a better RMSE result, owing to its ability to adjust the initial abundance estimations.

Figure 7. Sub-pixel mapping results for the synthetic dataset (FLC1): original low-resolution imagery (a); reference classification map obtained by eCognition software (b); sub-pixel mapping result obtained using SA (c), GA (d), MGA (e), GAAI (f).
<table>
<thead>
<tr>
<th>Class</th>
<th>Individual class accuracy (%)</th>
<th>Methods</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>SA</td>
</tr>
<tr>
<td>Red cover</td>
<td>54.94</td>
<td>51.14</td>
</tr>
<tr>
<td>Oats</td>
<td>56.75</td>
<td>59.42</td>
</tr>
<tr>
<td>Wheat</td>
<td>93.06</td>
<td>79.68</td>
</tr>
<tr>
<td>Soybeans</td>
<td>79.95</td>
<td>75.89</td>
</tr>
<tr>
<td>Hay (timothy)</td>
<td>53.03</td>
<td>60.22</td>
</tr>
<tr>
<td>Pasture</td>
<td>64.07</td>
<td>70.82</td>
</tr>
<tr>
<td>Alfalfa</td>
<td>71.76</td>
<td>66.12</td>
</tr>
<tr>
<td>Corn</td>
<td>93.11</td>
<td>57.64</td>
</tr>
<tr>
<td><strong>Average class accuracy (%)</strong></td>
<td><strong>70.83</strong></td>
<td><strong>65.12</strong></td>
</tr>
<tr>
<td><strong>Overall Accuracy (%)</strong></td>
<td><strong>66.55</strong></td>
<td><strong>65.13</strong></td>
</tr>
<tr>
<td><strong>Kappa</strong></td>
<td>0.617</td>
<td>0.601</td>
</tr>
<tr>
<td><strong>RMSE</strong></td>
<td>0.142</td>
<td>0.142</td>
</tr>
<tr>
<td><strong>CPU time (s)</strong></td>
<td>1.455</td>
<td>272.649</td>
</tr>
</tbody>
</table>

**A.3. Synthetic image 3- AVIRIS Indian Pines dataset**

The third image used in experiments is the commonly used AVIRIS Indian Pines dataset. Ten land cover classes were considered for classification. The utilized image is composed of 145*145 pixels, and the ground truth data was used as the reference data. The scale factor was set as three and Fig. 8 (a) shows the degraded AVIRIS hyperspectral image cube; Fig. 8 (b) shows the ground truth data in which 10 major land-cover classes can be distinguished. Fig. 8 (c)–(g) illustrate the sub-pixel mapping
results using SA, GA, MGA and the proposed methods, respectively.

Figure 8. Sub-pixel mapping results for the synthetic dataset (AVIRIS): original low-resolution imagery (a); The ground truth data as the reference classification map (b); sub-pixel mapping result obtained using SA (c), GA (d), MGA (e), GAAI (f).

As shown in Fig. 8, the impact of errors from spectral unmixing is significant and therefore many regions were severely misclassified. For example, the Soybeans-min class was hard to be identified owing to its spectral similarity with other classes such as Corn-notill. Therefore, all methods were affected apparently and the sub-pixel
mapping results were limited to the spectral unmixing inaccuracies. However, it can be observed that the proposed method can still improve the final result by modifying the abundance maps.

The quantitative comparison in Table IV gives similar conclusion as the visual assessment. It is obvious that the sub-pixel mapping results were greatly affected by the spectral unmixing errors. If we take the Grass/Pasture class as an example, it can

<table>
<thead>
<tr>
<th>Class</th>
<th>Methods</th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>SA</td>
<td>GA</td>
<td>MFA</td>
<td>GAAI</td>
</tr>
<tr>
<td>Individual class accuracy (%)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corn-notill</td>
<td>44.00</td>
<td>44.34</td>
<td>45.78</td>
<td>49.24</td>
</tr>
<tr>
<td>Corn-min</td>
<td>12.52</td>
<td>12.67</td>
<td>12.22</td>
<td>10.86</td>
</tr>
<tr>
<td>Grass/Pasture</td>
<td>6.79</td>
<td>6.53</td>
<td>5.74</td>
<td>4.70</td>
</tr>
<tr>
<td>Grass/Trees</td>
<td>52.87</td>
<td>49.04</td>
<td>53.91</td>
<td>58.09</td>
</tr>
<tr>
<td>Hay-windrowed</td>
<td>92.70</td>
<td>91.57</td>
<td>94.10</td>
<td>96.91</td>
</tr>
<tr>
<td>Soybeans-notill</td>
<td>61.86</td>
<td>61.71</td>
<td>62.15</td>
<td>62.89</td>
</tr>
<tr>
<td>Soybeans-min</td>
<td>25.58</td>
<td>25.03</td>
<td>26.51</td>
<td>28.64</td>
</tr>
<tr>
<td>Soybeans-clean</td>
<td>39.56</td>
<td>40.05</td>
<td>39.56</td>
<td>41.52</td>
</tr>
<tr>
<td>woods</td>
<td>94.78</td>
<td>94.10</td>
<td>95.07</td>
<td>96.52</td>
</tr>
<tr>
<td>Average class accuracy (%)</td>
<td>47.93</td>
<td>47.44</td>
<td>48.33</td>
<td>50.26</td>
</tr>
<tr>
<td>Overall Accuracy (%)</td>
<td>46.41</td>
<td>45.92</td>
<td>47.04</td>
<td>48.97</td>
</tr>
<tr>
<td>Kappa</td>
<td>0.391</td>
<td>0.386</td>
<td>0.398</td>
<td>0.419</td>
</tr>
<tr>
<td>RMSE</td>
<td>0.080</td>
<td>0.080</td>
<td>0.080</td>
<td>0.077</td>
</tr>
<tr>
<td>CPU time (s)</td>
<td>2.432</td>
<td>965.346</td>
<td>2143.534</td>
<td>840.286</td>
</tr>
</tbody>
</table>
be seen that the individual accuracies for this class were even lower than 10%. Therefore, the sub-pixel mapping results for this image are not as satisfactory as for the other datasets tested owing to the difficulty of spectral unmixing for this particular scene, in which spectra of different classes were very similar to each other. However, it can also be concluded from our experiment that the proposed method can improve the sub-pixel mapping performance by incorporating the abundance map accuracies.

B. Real experiments—Nuance dataset

Our real experiments were conducted using a pair of low and high spatial resolution images collected simultaneously over the same area. The low spatial resolution image (of size 50*50 pixels) was collected using the Nuance NIR imaging spectrometer [see Fig. 9(a)]. The acquired image has 46 bands, collected in the spectral range from 650–1100 nm and with 10 nm spectral sampling interval. The high spatial resolution color image (of size 150*150 pixels) was obtained by a digital camera for the same area [see Fig. 9(b)], and the scale factor was exactly three with regards to the low spatial resolution hyperspectral image. Three major land-cover classes can be distinguished in this scene: withered vegetation, fresh vegetation, and black paper, used as the background. A reference classification map was obtained by using the SVM technique on the high spatial resolution color image, which gave the result reported on Fig. 9(c). The sub-pixel mapping results (obtained with different methods) are reported on Figs. 9(d-g).

As shown in Fig. 9, the proposed method can provide a better visual result.
However, some important details may also be removed due to unmixing errors and excessive smoothing as mentioned before. This kind of trade-off between smoothing and detail preservation is inevitable for sub-pixel mapping.

![Sub-pixel mapping results for the real experiment](image)

**Figure 9.** Sub-pixel mapping results for the real experiment: low spatial resolution image obtained by the Nuance NIR imaging spectrometer (a); High spatial resolution color image obtained by a high-resolution digital camera (b); Reference classification result obtained by the SVM (c). Sub-pixel mapping results obtained by SA (d), GA (e), MGA (f), GAAI (g).

As illustrated in Table V, the proposed GAAI also provided improvements in this experiment in terms of all indexes when compared with the SA, GA and MGA. The RMSE index also showed improvements. Unlike the synthetic experiments, additional error sources were introduced in the real experiment such as the registration error between the low resolution hyperspectral image and the high resolution color image. However, GAAI method still was able to obtain the highest accuracy under the same
circumstances.

TABLE V. Accuracy statistics for the Nuance image experiment.

<table>
<thead>
<tr>
<th>Class</th>
<th>SA</th>
<th>GA</th>
<th>MFA</th>
<th>GAAI</th>
</tr>
</thead>
<tbody>
<tr>
<td>Urban area</td>
<td>84.75</td>
<td>81.04</td>
<td>84.50</td>
<td>86.62</td>
</tr>
<tr>
<td>Agricultural land</td>
<td>61.72</td>
<td>59.74</td>
<td>61.64</td>
<td>66.58</td>
</tr>
<tr>
<td>Water</td>
<td>66.73</td>
<td>64.62</td>
<td>66.51</td>
<td>73.31</td>
</tr>
<tr>
<td>Average class accuracy (%)</td>
<td>71.07</td>
<td>68.47</td>
<td>70.88</td>
<td>75.50</td>
</tr>
<tr>
<td>Overall Accuracy (%)</td>
<td>69.95</td>
<td>67.42</td>
<td>69.78</td>
<td>74.38</td>
</tr>
<tr>
<td>Kappa</td>
<td>0.545</td>
<td>0.507</td>
<td>0.542</td>
<td>0.612</td>
</tr>
<tr>
<td>RMSE</td>
<td>0.196</td>
<td>0.196</td>
<td>0.196</td>
<td>0.189</td>
</tr>
<tr>
<td>CPU time (s)</td>
<td>1.572</td>
<td>617.307</td>
<td>1633.60</td>
<td>614.831</td>
</tr>
</tbody>
</table>

C. Parameter Analysis

1) Impact of the weighted parameter $\lambda$

In this subsection, we evaluate the impact of parameter $\lambda$ on the accuracy of the proposed GAAI method. Fig. 10 shows the OA as a function of different values of this parameter for two of the considered hyperspectral scenes (HJ-1A and Nuance datasets). As shown by Fig. 10, the curves for both images exhibit a similar shape.

Generally speaking, small values of parameter $\lambda$ result in stable OAs and the optimal parameter value is around two for the proposed GAAI method. As $\lambda$ increases greatly, the OA scores decrease and become less stable. However, a better result can be obtained for most parameter values compared with the other three traditional
methods.

(a) Synthetic image experiment  (b) Real image experiment

Figure 10. Impact of parameter $\lambda$ on the classification accuracy obtained by the proposed GAAI method. (a) Synthetic image experiment (HJ-1A). (b) Real image experiment (Nuance).

2) Impact of the combination of fitness function and operators

In this subsection we evaluate the utilization of the mutation operator and the weighted spectral term. To verify the effectiveness of the two modifications in the proposed GAAI method, different combinations of the fitness function and operators were tested for both images (HJ-1A and Nuance datasets) as Fig. 11 depicts.

Figure 11. Impact of using different fitness functions and operators on the classification accuracy. (a) Proposed GAAI method. (b) Fitness(GAAI) + Operator(GA). (c)
Fitness(GAAI)+Operator(MGA). (d) Fitness(SD)+Operator(GAAI).

Apparently, both the mutation operator and the spectral term contribute to the performance of the GAAI method greatly. Although the mutation operator can lead to greater improvements as compared with the spectral term, it is essential to introduce the spectral term to retain the consistency between the original hyperspectral imagery and the generated sub-pixel mapping result.

IV. CONCLUSIONS AND FUTURE RESEARCH LINES

This paper has introduced a novel sub-pixel mapping method based on genetic algorithms which has the potential to correct possible errors in the initial abundance estimations by means of a mutation operator. As a result, a new feature of our proposed approach is that it can correct possibly inaccurate abundance estimations used as the initial condition in the sub-pixel mapping process. In this regard, a major difference of the proposed approach with regards to other traditional sub-pixel mapping methods is that we do not assume that the initial abundance map is completely accurate, but instead use a mutation operator to adjust the attribution of sub-pixels in order to refine the final mapping result. Moreover, our method incorporates a weighted spectral term into the fitness function that is combined with the spatial term commonly adopted by other methods. Our experimental results, conducted using both synthetic and real hyperspectral images, indicate that our method provides comparable or better results than those obtained by other three
traditional sub-pixel mapping algorithms. A detailed parameter analysis also shows that both the mutation operator and the weighted spectral term introduced by our proposed method play significant key roles in obtaining a better sub-pixel mapping result.

Another important observation is that the proposed method can only adjust the abundance map and the final sub-pixel mapping result slightly, and therefore unmixing may still contribute significantly to the final sub-pixel mapping results. Future research will focus on conducting additional experiments with other data sets, designing strategies for adaptively setting the input parameter $\lambda$, and testing the impact of different kinds of spectral unmixing techniques in the task of generating the initial abundance map used for sub-pixel mapping purposes.

REFERENCES


