Rapid matching algorithm for hyperspectral image based on norm sifting

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We propose a rapid spectral matching method by lowering number of comparisons, processing time can be saved. Firstly, 1-norm is chosen as length measure of spectrum, and with this criterion, a 1-norm database is built. Secondly, a subspace is constructed from the whole reference library by retaining the references with the most similar 1-norm values. Finally, matching operations are performed in the subspace to obtain the match result. Simulations of geological mapping with ASTER spectral library show that the proposed method can significantly reduce processing time and enhance accuracy compared with traditional and dimension reduction methods.

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Hyperspectral images provide both spatial and spectral information with fine resolution. Analysis of hyperspectral data has been applied to environment monitoring, geological mapping, target recognition, etc.[1−3]. Lately the study of hyperspectral image processing has been mainly focused on anomaly detection, mixture analysis and classification methods according to specific applications[4]. On the other hand, as a pre-processing step of these methods, techniques of band selection, feature extraction, and dimension reduction are also topics of interest. They deal with the problem of high dimensionality of hyperspectral data[5], which is of great importance in applications like military target detection where the processing speed really matters[6]. Spectral matching programs also benefit from these methods, compared to traditional spectral matching measures like Euclidean distance (ED) and spectral angle measure (SAM)[7,8], after dimensional reduction, redundant spectral information is removed, therefore the calculation complexity is reduced.

In recent years, numerous dimension reduction methods have been proposed[9−12] to avoid redundancy between bands. For spectral matching tasks, a feasible dimension reduction method is band selection[13−17]. Guo *et al*. proposed a band selection method based on mutual information (MI)[16]. The method estimates MI values using priori knowledge of a reference dataset, and by eliminating bands with low MI values, which result in the reduction of the computational cost of spectral matching. Another method, proposed by Li *et al*. is called adaptive band selection algorithm (ABS)[17], which retains bands with the largest possible amount of information and the least correlation among them. Similarly, the method is capable of reducing the computational cost of matching algorithms.

These methods are designed to reduce the dimensions of every single spectrum by eliminating redundant bands, in this way the calculation time required for each comparison between spectra will be reduced. However, a great number of comparisons are still needed during spectral matching procedure, which is especially true when the spectral library contains a large quantity of reference spectra. Therefore the total processing time for spectral matching is still problematic for certain applications. Band selection methods overlooked this factor, so it is necessary to develop a method to reduce matching time by avoiding unwanted comparisons.

In this letter, a new spectral matching algorithm based on norm information of spectrum is proposed, by lowering the number of comparisons, processing time can be saved. Reference spectra in spectral library are viewed as n-dimensional vectors, which are sparsely distributed in an n-dimensional space. The 1-norm values of these vectors are calculated and used as an index for sifting. When a pixel is analyzed, reference spectra with similar 1-norm values are retained and subsequently compared with the pixel. In this method, spectral matching is processed inside a significantly smaller subspace rather than in the entire n-dimensional space. As fewer comparisons are needed, time consumption is considerably decreased.

In geographical mapping applications, spectral matching algorithm performs a pixel-by-pixel analysis for an image containing N pixels with n bands. Each pixel is compared with M reference spectrums in the library to determine the most similar material. The time needed for these operations can be expressed as follows:

$$T_1 = M \times (T_{\rm d} + T_{\rm c}) \times N, \tag{1}$$

where $T_{\rm d}$ refers to the reading and writing time of a reference spectrum record and $T_{\rm c}$ stands for time spent on comparison operations.

A spectrum with n bands can be viewed as a vector $\mathbf{x}_n = \{x_1, x_2, \cdots, x_n\}$ in n-dimensional space. The distance between target spectrum $\mathbf{x}_n$ and a reference spectrum $\mathbf{y}_n$ can be calculated using spectral similarity measures. Two of the most popular similarity measures are ED and SAM[7]. They are expressed as

$$\mathrm{ED} = \left[\sum_{i=1}^{n}(x_i - y_i)^2\right]^{1/2}, \tag{2}$$

$$\mathrm{SAM} = \cos^{-1}\frac{\sum_{i=1}^{n} x_i y_i}{\sqrt{\sum_{i=1}^{n} x_i^2}\sqrt{\sum_{i=1}^{n} y_i^2}}. \tag{3}$$

Time complexity of comparison operation has been proven to be $O(n^2)$ by Eqs. (2) and (3). Dimension reduction algorithms reduce $O(n^2)$ to $O(l^2)$ by compressing the original n-dimensional space into a smaller one-dimensional space. A comparison operation will be performed $M \times N$ times in Eq. (1) to facilitate the reduction of T_c by the same number of times.

On the other hand, the decrease of T_c with the help of faster CPUs on PCs has also been demonstrated. A PC equipped with a Core2 Duo CPU has obtained a low T_c of 0.1 ms when measuring the ED of two 210-dimension vectors. In this context, time spent on searching, reading, and writing references (T_d) cannot be ignored. The same PC has achieved the reading/writing time of a vector as $T_\mathrm{d} \approx 0.5$ ms. T_d has taken about 80% of the total time consumed in $(T_\mathrm{d} + T_\mathrm{c})$. Thus, methods that focus on reducing T_c (e.g. dimension reduction) will no longer be effective in reducing total time cost.

Results from utilizing Eq. (1) show that the pixel number N remain unchanged for a certain task, T_d can be bound by hardware limitations and cannot be lowered, and T_c can only have a minimal effect on time reduction, as previously mentioned. Therefore, the remaining possible choice to increase spectral matching efficiency is to lower the number of reference library M. In other words, the number of comparisons should be reduced, and unnecessary comparisons need to be avoided.

A spectral library $Y = \{\mathbf{y}_1, \mathbf{y}_2, \cdots, \mathbf{y}_M\}$ is a set of M n-dimensional vectors distributed in n-dimensional space. Each element in the set stands for a certain kind of material. Suppose a pixel on a hyperspectral image is occupied by material $\mathbf{y}_i$; then data on this pixel collected by a hyperspectral sensor are affected by atmosphere attenuation and instrumental noise. Thus, after atmosphere correction and de-noising, target spectrum $\mathbf{y}'_i$ is obtained. $\mathbf{y}'_i$ is slightly different from $\mathbf{y}_i$ because attenuations and noises are not eradicated. The task of spectral matching is to determine the reference $\mathbf{y}_\mathrm{t}$ in set Y that has the least distance from $\mathbf{y}'_i$. When using ED or SAM measures, the match result $\mathbf{y}_\mathrm{t}$ is given as

$$\mathbf{y}_\mathrm{t}\left|\mathrm{ED}_\mathrm{t} = \min_i \mathrm{ED}_i \text{ or } \mathrm{SAM}_\mathrm{t} = \min_i \mathrm{SAM}_i,\right. \quad i \in (1, 2, \cdots, M). \tag{4}$$

For a finite set Y, all M elements are contained in an n-dimensional sphere with a radius of R, expressed as $O(R^n)$. Elements are uniformly and sparsely distributed. However, as shown in Fig. 1, target spectrum $\mathbf{y}'_i$ deviates slightly from its original reference $\mathbf{y}_i$. Thus, it is inefficient to search for $\mathbf{y}_\mathrm{t}$ within the entire $O(R^n)$. To address this concern, an improved search strategy is proposed. Instead of searching within $O(R^n)$, the search is conducted within a smaller n-dimensional sphere $O(r^n)$ centered at point $\mathbf{y}'_i$ with a radius of r, as shown in Fig. 1. Let Y_{r^n} be the set of references in $O(r^n)$, then, we can determine a suitable r which satisfies:

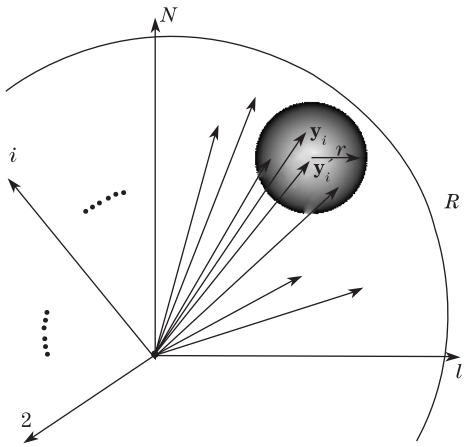

Fig. 1. (Color online) Distribution of references in an n-dimension space. Colored lines stand for references in the library. The dark region is the subspace centered at $\mathbf{y}'_i$. With suitable radius r, the correct match result should be contained in the subspace.

$$Y_{r^n} \in Y \text{ and } \mathbf{y}_i \in Y_{r^n},\ 0 < r \leqslant R. \tag{5}$$

Therefore, Y_{r^n} is a subspace of Y. Y_{r^n} eliminates irrelevant elements in Y and thus, its size m might be smaller than that of M. In this case, spectral matching is performed within Y_{r^n} rather than in Y. Consequently, $\mathbf{y}_t$ in Eq. (4) is obtained simply by m comparisons, which results in significant reduction of the processing time.

Subsequent to the analysis of the proposed search strategy is the development of a feasible method to construct subspace Y_{r^n}. The p-norms can be used as length measures in an n-dimensional space. The simplest form of p-norms is 1-norm, which is expressed as

$$\left|\left|\mathbf{x}_i\right|\right|_1 = \sum_{i=1}^{n} x_i. \tag{6}$$

Target spectrum $\mathbf{y}'_i$ and its match $\mathbf{y}_i$ should have similar lengths, thus their 1-norms should also be similar. Therefore, only references with 1-norm near $||\mathbf{y}'_i||_1$ should be retained for comparison. Based on 1-norm information, the original reference library can be sifted through to obtain subspace Y_{r^n}, which consists of all references in $O(r^n)$. Using 1-norm criterion, $O(r^n)$ can be expressed as

$$O(r^n) = \left\{\mathbf{y}_i \middle| \left|\left|\mathbf{y}'_i\right|\right|_1 - \left|\left|\mathbf{y}_i\right|\right|_1 \middle| \leqslant r\right\}. \tag{7}$$

With the norm sifting method, time consumption for spectral matching is given as

$$T_2 = [T_\mathrm{s} + m \times (T_\mathrm{d} + T_\mathrm{c})] \times N. \tag{8}$$

The number of perform times of T_d and T_c dropped from M in Eq. (1) to m in Eq. (8). For each pixel, additional time T_s is used to calculate $||\vec{\mathbf{y}}'_i||_1$ and to construct Y_{r^n}. As expressed in Eq. (6), the time complexity of calculating $||\vec{\mathbf{y}}'_i||_1$ is $O(n)$. The time complexity of constructing Y_{r^n} is mainly determined by searching actions, the time complexity of which is $O(\log_2 M)$. The time complexity of T_s should be $O(n) + O(\log_2 M) =$

$O(n)$. Comparing this complexity with those of Eqs. (2) and (3), it can be concluded that $T_{\rm s} << T_{\rm d} << T_{\rm c}$. Comparing Eqs. (8) with (1), the ratio of time cost with and without norm-based sifting is given as

$$\frac{T_1}{T_2} = \frac{M \times (T_{\rm d} + T_{\rm c}) \times N}{[T_{\rm s} + m \times (T_{\rm d} + T_{\rm c})] \times N} = \frac{M \times (T_{\rm d} + T_{\rm c})}{T_{\rm s} + m \times (T_{\rm d} + T_{\rm c})} \approx \frac{M}{m}. \quad (9)$$

Therefore, the matching algorithm is M/m times faster when a sifting method is used. This ratio can be estimated using the relationship between the sizes of subspace $O(r^n)$ and space $O(R^n)$. Suppose 1-norm values of all references are uniformly distributed, then the radius R of $O(R^n)$ should be $M/2$. When this is combined with Eq. (7), M/m can be expressed as

$$\frac{M}{m} = \frac{2R}{2r} = \frac{R}{r}. \quad (10)$$

The spectral matching algorithm using norm sifting method is illustrated in detail by the following steps:

1) For each reference spectrum in library Y, 1-norm is calculated using Eq. (6). The results are subsequently rearranged to obtain a sorted 1-norm database, denoted as $\{||\mathbf{y}_i||_1\}$.

2) For spectrum $\mathbf{x}_{i,j}$ received on pixel (i, j), the 1-norm $||\mathbf{x}_{i,j}||_1$ is calculated using Eq. (6). The nearest 1-norm value $||\mathbf{y}_o||_1$ of $||\mathbf{x}_{i,j}||_1$ is determined from 1-norm database $\{||\mathbf{y}_i||_1\}$.

3) The subset $Y_{r^n} = \{\mathbf{y}_{o-r}, \cdots, \mathbf{y}_{o-1}, \mathbf{y}_o, \mathbf{y}_{o+1}, \cdots, \mathbf{y}_{o+r}\}$ is constructed. The subset consists of $2r + 1$ spectrums, including $\mathbf{y}_o$, r spectrums above $\mathbf{y}_o$, and r spectrums below $\mathbf{y}_o$ in $\{||\mathbf{y}_i||_1\}$.

4) The Euclidean distances ED_{xy_i}, $i = o - r, \cdots, o, \cdots, o + r$ are calculated between $\mathbf{x}_{i,j}$ and every reference in Y_{r^n}. The shortest distance $\mathbf{y}_t | \mathrm{ED}_{xy_t} = \min_i \mathrm{ED}_{xy_i}$ is determined, and consequently, $\mathbf{y}_t$ is the match result of $\mathbf{x}_{i,j}$.

Simulations were performed on a PC with a Core 2 Duo CPU to assess the proposed norm sifting (NS) spectral matching algorithm. A total of 1 430 records from an ASTER spectral library were chosen as a reference library. Each record contained 215 bands ranging from 2 to 14 μm. A map of N=145×145 (pixels) was established, and the material of each pixel was randomly chosen from the reference map.

The NS algorithm (subspace radius set to $r = M \times 5\%$) was compared with three spectral matching algorithms, namely, the ED method, MI method[16] with retained bands of 20, and the ABS method[17] with retained bands of 20. To evaluate the performance of these methods under different kinds of reference libraries, library size M was set to 50, 100, 200, 400, 600, 800, 1 000, 1 200, and 1 430. Processing times of these algorithms are shown in Fig. 2.

Figure 2 shows that the time consumption of the four algorithms increases in a linear manner in relation to library size. The traditional ED method achieves the largest time cost under any circumstance. MI and ABS have the same level of performance, both achieving

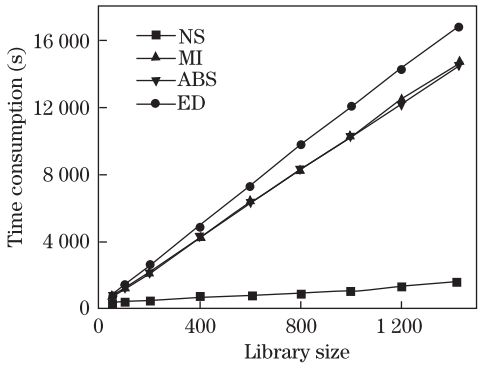

Fig. 2. Time cost of the proposed NS method compared with the ED, MI, and ABS methods. Simulations were performed under different library sizes, M= 50, 100, 200, 400, 600, 800, 1 000, 1 200, and 1 430.

Table 1. Comparison of Accuracies between Proposed NS Method and MI, ABS, and ED Methods

Library Size	NS (%)	MI (%)	ABS (%)	ED (%)
50	92.17	96.09	93.87	98.06
100	89.45	96.57	92.36	99.04
200	91.27	97.84	95.44	99.53
400	94.04	97.68	93.67	99.00
600	95.87	94.36	94.23	99.11
800	96.46	92.80	94.41	98.12
1 000	94.41	88.93	90.42	96.66
1 200	94.71	90.63	91.14	97.18
1 430	93.14	90.05	89.25	96.31

processing time 15% less than that of the ED method. The proposed NS algorithm reduces time consumption significantly, especially when library size is larger. At M=1 430, the NS method completes a matching task in 1 670 s, taking only 9.9% of the processing time of ED.

The accuracy of a matching algorithm is defined by $N_{\rm match}/N$, where $N_{\rm match}$ counts the number of correct matches of N pixels. Comparison of accuracies is illustrated in Table 1. Of the four methods, ED has the highest accuracy because it keeps raw hyperspectral data on every spectrum and shows the upper boundary for all spectral matching algorithms. Other methods show similar results, with accuracies slightly lower than that of the ED method. The NS method performs slightly better than both the MI and ABS algorithms when library size is 600 or more and remains competitive even when library size is smaller.

The radius r affects the performance of NS the method in two ways. First, as shown in Eq. (10), r determines how fast the proposed algorithm runs, wherein a smaller r means less processing time. Second, r is related to match accuracy, and with a smaller r, the correct reference will be more likely to "slip away" from $O(r^n)$, causing the accuracy to decrease. The proposed algorithm was tested at M =1 430 with different radii r=30–90.

Figure 3 shows the time analysis of the results. The growth of r results in the linear growth of total time cost.

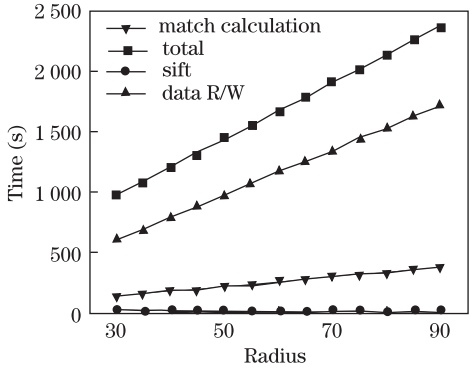

Fig. 3. (Color online) Time analysis of the proposed method. Time spent on sifting operations (red line), reading/writing operations (blue line), and comparing/matching calculations (purple line), together with total time consumptions (black line) with different radii are shown.

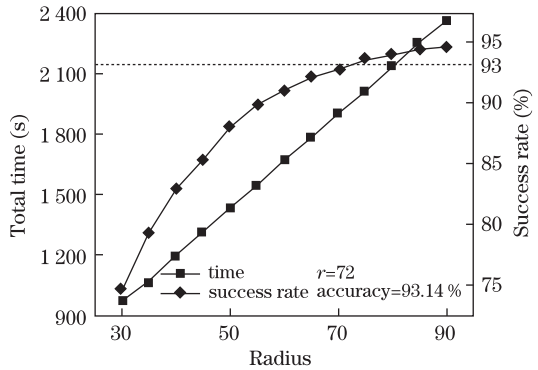

Fig. 4. (Color online) Time cost and accuracy under different radii. Using N-P criterion with a lower limit of acceptable accuracy set to 93%, the optimal radius is found at r=72.

Time spent on comparing/matching and reading/writing also increases linearly, although the latter grows much faster than the former. Processing time for sifting is less than 1 s, which is negligible compared with those of other operations.

Figure 4 shows the relationship between radius and accuracy (blue curve) and between radius and time consumption (red line). With a larger r, better accuracy is obtained, but the growth rate of accuracy shows a tendency to slow down, gradually approaching the limit accuracy of the ED method shown in Table 1.

N-P criterion[18] can be used to achieve a compromise between efficiency and accuracy of the proposed algorithm. First, a lower limit of acceptable accuracy is defined. Subsequently, the smallest r, which satisfies the requirement of accuracy, is chosen as the optimal radius. For instance, if the required accuracy should be above 93% for certain tasks, the optimal radius should be r=72, as shown in Fig. 4.

In conclusion, a matching algorithm for hyperspectral image analysis based on norm sifting has been described. With the construction of a subspace based on 1-norm criterion, the number of comparison operations is minimized. Simulation results show that the proposed algorithm saves approximately 90% of processing time compared with the ED algorithm. Moreover, its accuracy is competitive compared with those of the ED, MI, and ABS algorithms. The proposed method is useful for geological mapping, as well as other applications using the spectral matching method.

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