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Compressed Sensing Reconstruction for Hyperspectral Images Using Immune Clone Algorithm Based on Gaussian Dictionary

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Abstract

An immune clone algorithm (ICA) for compressed sensing (CS) reconstruction for hyperspectral images is proposed. The core idea of compressed sensing theory is that, an image of interest is sparse or compressible in some domain, and then it could be reconstructed accurately through a complex optimization algorithm. ICA is a global optimal search algorithm which could ensure the algorithm converges to the optimal solution with probability 1. The paper takes advantage of the ICA to solve a complex optimization problem to reconstruct the images which are sampled by compressed sensing. The proposed algorithm was evaluated on some hyperspectral images and the results illustrate that the reconstructed images has high peak signal-to-noise ratio (PSNR) owing to the merit of ICA.

Keywords

Hyperspectral images, Compressed sensing reconstruction; Immune clone algorithm; Reconstructed peak signal-to-noise ratio.

1. Introduction

The traditional sampling theoretical foundation is the Nyquist sampling theorem, which states that the signal information is preserved if the underlying analogy signal is uniformly sampled above the Nyquist rate. Unfortunately, Nyquist theorem could not satisfy the requirements of process velocity along with the development of the technology, especially during processing the hyperspectral images (HSI) [1]-[3].

Compressed sensing (CS) [4] [5] offers an attractive theory for signal process which could permit accurate reconstruction of the signal via lower sampling rate than Nyquist sampling rate. However, how to reconstruct the signal or image accurately from very few non-adaptive measurements through a complex optimization algorithm is a NP hard problem [5]. Some reconstruct algorithm has appeared these years, such as matching pursuit and iterative hard threshold [6] [7], and some reconstruction algorithms for hyperspectral images [8]-[10].

Although the algorithms above could reconstruct the signal, there are some inherent flaws. The immune clone algorithm (ICA) [11] [12] is a global search algorithm which could be used for electrocardiogram signals analyse or artificial neural networks. In this paper, ICA is introduced to solve the reconstruct optimal problem, which capitalizes on the prior knowledge of the hyperspectral images.

The reminder of the paper is organized as follows. In section 2, the compressed senisng sampling and reconstruction is simply introduced. And then in Section 3, the proposed reconstruction algorithm with immune clone algorithm idea is described, including the Block diagram and the implementation process. Experimental results carried on two hyperspectral images ar shown in Section 4 and conclusions are marked in Section 5.

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2. Description of Compressed Sensing Theory

Consider a real-valued, finite-length, one-dimensional, discrete-time signal x, which can be viewed as an $N \times 1$ column vector in R^N. An image is vectorized into a long one-dimensional vector. Any signal in R^N can be represented in terms of a basis of $N \times 1$ vectors $\{\psi_i\}_{i=1}^N$. Additionally, $\{\psi_i\}$ could also be called as an atom. For simplicity, assume that the basis is orthonormal. Forming the $N \times N$ basis matrix $\Psi = [\psi_1, \psi_2, ..., \psi_N]$ by stacking the vectors $\{\psi_i\}$ as columns, any signal can be expressed as:

$$x = \sum_{i=1}^{N} s_i \psi_i \quad or \quad x = \Psi S \tag{1}$$

where S is the $N \times 1$ column vector of weighting coefficients $s_i = \langle x, \psi_i \rangle = \psi_i^T x$.

If the signal is K-parse or compressible, according to the theory of CS, we consider a more general linear measurement process that computes $M < N$ inner products between x and a collection of vectors $\{\phi_j\}_{j=1}^M$ as in $y_j = \langle x, \phi_j \rangle$. Stacking the measurements y_j into the $M \times 1$ vector y and the measurement vectors ϕ_j^T as rows into an $M \times N$ matrix Φ and substituting in (1), the CS process can be written as and the diagram is shown inFigure 1:

$$y = \Phi x = \Phi \Psi S \tag{2}$$

Note that the measurement process is non-adaptive; Φ does not depend in any way on the signal x. Since $M < N$, the problem of reconstructing x from y is ill conditioned. However, CS theory says that as long as x is sparse in some domain, we can reconstruct the original signal from the condensed measurements exactly by solving a combinational optimization problem [13]:

$$\hat{S} = \operatorname{argmin} \|S\|_0 \quad s.t. \quad \Phi \Psi S = y \tag{3}$$

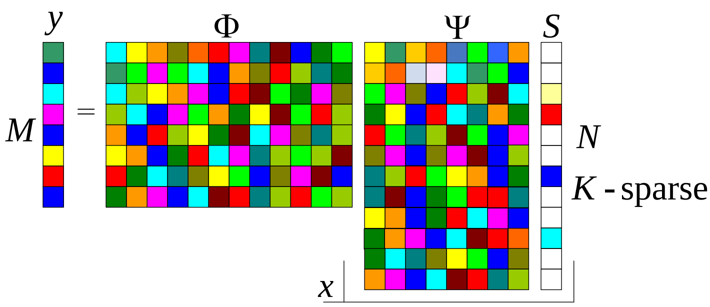

Figure 1. Block diagram of compressed sensing.

However, this problem cannot be solved efficiently since it is non-convex. Current research focuses on compressed sensing is to find a suitable sparse matrix Ψ and observation matrix Φ, and to construct high-performance recovery algorithms. Work on natural image statistics confirms that natural images are sparse under decompositions using Gaussian redundancy dictionary [14]. In the experiments, Gaussian random matrix is used as the sampling matrix which has been demonstrated with high reconstruction accuracy [5].

3. Proposed Reconstruction Algorithm

Utilizing the global search ability of ICA, the proposed algorithm tries to find the optimal atoms to describe the image corresponding to the measured values under a sparse basis through an iterative fashion. Then the sparse coefficients could be calculated and finally the original image would be obtained. The block diagram of the proposed algorithm is depicted in Figure 2. The algorithm mainly

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includes three aspects, namely the initial antibody production, the affinity function design and the main operators design.

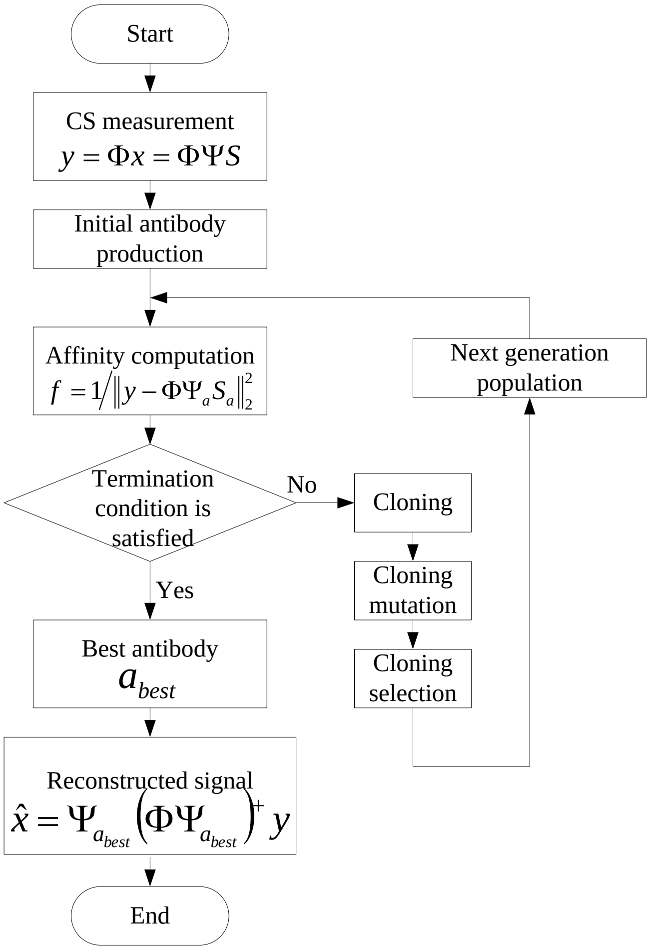

Fig. 2 Block diagram of reconstruction algorithm using ICA.

(1) Initial antibody production

Assume the image sparsity under the sparse basis is k, then the antibody is expressed as a $1 \times k$ row vector, such as $a = \left(aa^1, aa^2, ..., aa^k\right)$, where aa^i is one number of set [1,K], which is one atom of the sparse basis. A population contains a number of antibodies, that is $A = \left(a_1; a_2; ...; a_Q\right)$, where Q is the population size.

(2) Affinity function design

In ICA, affinity function indicates the objective function value of candidate solution, and is used to evaluate the pros and cons of the antibodies, finally to guide the cloning operator. The antibody is more excellent with higher affinity. In order to find the optimal atoms to describe one image under sparse basis, the affinity function is designed as follows:

$$f = 1 / \|y - \Phi \Psi_a S_a\|_2^2 \tag{4}$$

Where, Ψ_a and S_a are the corresponding atoms and coefficients selected by antibody a.

(3) Main operators design

The main operator in ICA is cloning operator which consists of cloning, cloning mutation and cloning selection operation.

1) Cloning: A cloning operator done on the population A:

$$\vartheta(A) = \left(\vartheta(a_1); \vartheta(a_2); ...; \vartheta(a_Q)\right) \tag{5}$$

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Where, $\vartheta(a_i)$ is the clone of a_i. The clone number is defined as:

$$q_i = C * \frac{f(a_i)}{\sum_{j=1}^{Q} f(a_j)} \tag{6}$$

Where, $C > Q$ is the clone consistent.

After cloning operator, the population is:

$$A = (A; A_1'; A_2'; ...; A_Q') \tag{7}$$

Where $A_1' = (a_{i1}; a_{i2}; ...; a_{iq_i-1}), a_{ij} = a_i$, $j = 1,2,...,q_i - 1$.

2) Cloning mutation: In order to retain the original information of the antibody, the mutation operator is only applied to clone antibodies $\vartheta(a_i)$. Specify mutation probability P_{m}, for each component of the antibody, generates a random number pm between 0 and 1. If pm is smaller than P_{m}, then the corresponding component would be re-selected as one number from set [1,K], otherwise the component would not change.

3) Cloning selection: If there exists the outstanding mutation antibody $b = \max\{f(a_{ij}) | j = 1,2,...,q_i - 1\}$ which satisfies,

$$f(a_i) < f(b) \quad a_i \in A \tag{8}$$

Then antibody b is chosen to replace the parent antibody a_i to update the population.

After the three operators, the initial population would be evolved to the next generation population which has higher affinity. The best antibody a_{best} is obtained by implementing the above process in an iterative fashion. Then the original signal would be expressed as:

$$\hat{x} = \Psi_{a_{best}} (\Phi \Psi_{a_{best}})^{+} y \tag{9}$$

Where $\Psi_{a_{best}}$ is the corresponding atoms selected by antibody a_{best}, and symbol '+' means pseudo inverse.

4. Experimental Results

The performance of reconstruction algorithm is evaluated on two hyperspectral datasets from AVIRIS (http://aviris.jpl.nasa.gov), denoted as Cuprite1 and Cuprite2. Removed the noisy and absorbed bands, the aviable bands used in the experiments are 188 and the images are spatially cropped to 256*256 without affecting the performance of the algorithm. The sampling rates are 0.1 to 0.5 with 0.1 as the interval. Considering the reconstruction accuracy and the computational complexity, in the following experiments, the parameters in proposed reconstruction algorithm are set as: population size $Q = 10$, maximum evolution generation $M = 1$, the sparsity $k = 32$, clone consistent $C = 15$ and mutation probability $P_{\mathrm{m}} = 0.2$.

The quality of reconstructed image is measured by peak signal-to-noise ratio (PSNR) [15] between reconstructed and original image. The PSNR measured in dB is defined as,

$$\mathrm{PSNR}(\boldsymbol{x}, \hat{\boldsymbol{x}}) = 20\log_{10} \frac{\max(\boldsymbol{x})}{\sqrt{\mathrm{MSE}(\boldsymbol{x}, \hat{\boldsymbol{x}})}} \tag{10}$$

where $\boldsymbol{x}$ and $\hat{x}$ are the original and reconstructed image, $\max(\boldsymbol{x})$ is the peak value of $\boldsymbol{x}$, $\mathrm{MSE}(\boldsymbol{x}, \hat{\boldsymbol{x}})$ is the mean squared error,

$$\mathrm{MSE}(\boldsymbol{x}, \hat{\boldsymbol{x}}) = \frac{1}{N} \|\boldsymbol{x} - \hat{\boldsymbol{x}}\|_2^2 \tag{11}$$

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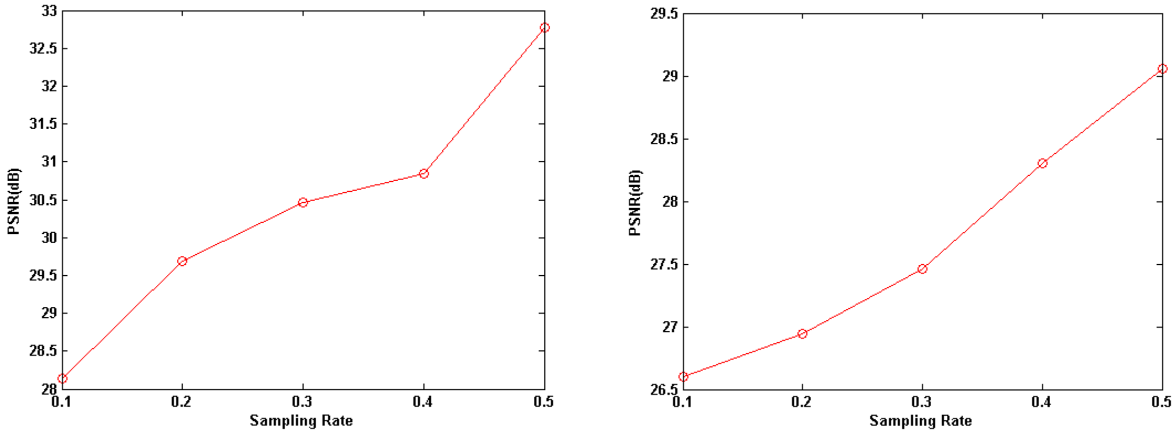
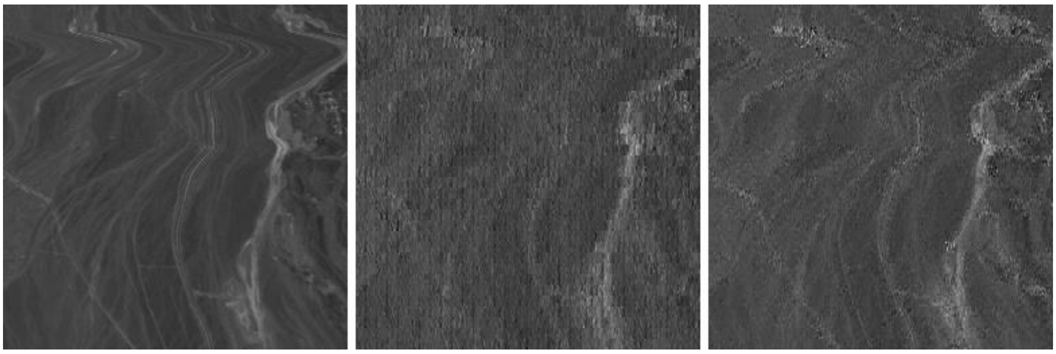
The average PSNR with different sampling rates are shown in Figure 3. Seen from the figures, with the increasing sampling rate, the information could be used in reconstruction are increasing, thus leading the PSNR increasing as well.



(a) Cuprite1 (b) Cuprite2

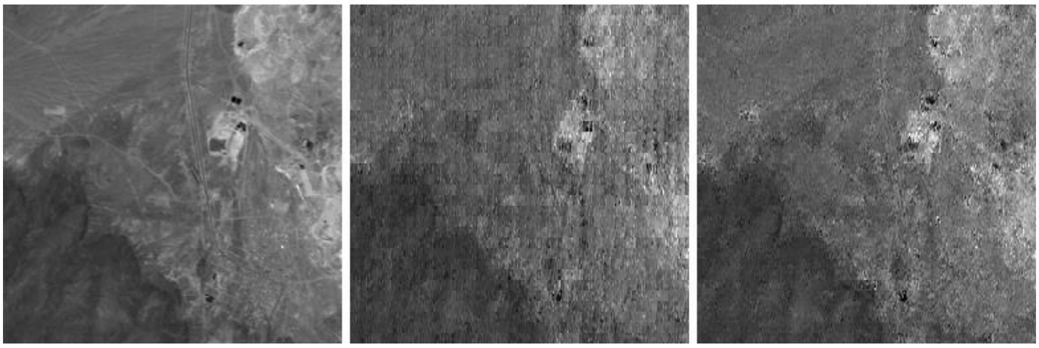
Figure 3. Average PSNR with different sampling rates for Cuprite1 and Cuprite2

The original and reconstructed images (band 50) of Cuprite1 and Cuprite2 are shown in Figure 4 and Figure 5, respectively, which are obtained under sampling rates $M/N = 0.3$ and $M/N = 0.5$. Compared with the original images, when the sampling rate is 0.3, there are some noises and distortion in the reconstructed image as shown in Figure 4(b) and Figure 5(b). When the sampling rate increases to 0.5, the reconstructed images has noticeable improvement and could describe the details of the image to some extent.



(a) (b) (c)

Figure 4. Comparison between original and reconstructed images for Cuprite1. (a) Original image, (b) sampling rate is 0.3 and PSNR is ,(c) sampling rate is 0.3 and PSNR is .



(a) (b) (c)

Figure 5. Comparison between original and reconstructed images for Cuprite1. (a) Original image, (b) sampling rate is 0.3 and PSNR is ,(c) sampling rate is 0.3 and PSNR is .

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5. Conclusion

A compressed sensing reconstruction algorithm of hyperspectral images utilizing ICA based on Gaussian redundancy dictionary is proposed. It was realized in an iterative fashion to select the best atoms to describe the image which is sparse under the dictionary. Experiment results show that the algorithm could reconstruct the images effectively and the PSNR of the reconstructed image could hit 40dB.

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