A Sub-pixel Mapping Algorithm based on Artificial Immune Systems for Remote Sensing Imagery

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ABSTRACT

The mixed pixel is a common phenomenon in remote sensing classification. The classification accuracy may be severely compromised by the presence of mixed pixels. Spectral unmixing is an effective method to improve the classification accuracy by linear or nonlinear mixing models, in which the measured spectrum of a mixed pixel is decomposed into a collection of constituent spectra, or endmembers, and their corresponding fractional abundances that indicate the proportion of each endmember present in the pixel. However, the output of spectral unmixing provides no indication of how such classes are distributed spatially within these pixels. Sub-pixel mapping (Atkinson 1997) is a technique designed to use the fraction information with the assumption of spatial dependence to specify the location of each class, which divides pixels into sub-pixels and allocates the different classes to these sub-pixels. The key problem of sub-pixel mapping is determining the most likely locations of the fractions of each land cover class within the pixel (Verhoeye and De Wulf 2002). Many different techniques have been proposed to tackle the sub-pixel mapping issue (Boucher et al 2008, Zhang et al 2008).

In this paper, a new search strategy inspired by the clonal selection algorithm (CSA) in artificial immune systems (AIS) is proposed, namely clonal selection sub-pixel mapping (CSSM), for sub-pixel mapping of remote sensing imagery. CSA, derived from the clonal selection theory, is an effective method of AIS and successfully applies to pattern recognition, multimodal optimization, and classification (De Castro and Timmis, 2002). In CSSM, the sub-pixel mapping problem becomes one of assigning land cover classes to the sub-pixels

while maximizing the spatial dependence by clonal selection algorithm. In the initial step, each antibody in CSSM represents the possible sub-pixel configuration of the pixel and is directly described by a string consisting of integer numbers, which the length of each antibody string is equal to the number of sub-pixels. The value of each bit in the string represents the class of each sub-pixel. After initialization, the simulation of the clonal selection process begins. One generation after another antibody is created, and each must prove its affinity to the criterion function. As a criterion function, the proposed algorithm uses the measure for spatial dependence (Verhoeye and De Wulf 2002). In each iteration, a number of possible solutions are generated by means of applying the immune operators such as clone, mutation, and selection in a stochastic process guided by an affinity measure. In specially, the clonal and the mutation operators are two foremost processes. The clonal process can draw the evolutionary process closer to the goal. It raises the average affinity value and gives the following steps a good chance to further move towards the solution, i.e. the optimal sub-pixel distribution. The mutation step generates random changes of single features to the individual solutions and helps the proposed algorithm to avoid local optimal value. In addition, CSSM inherits the memory property of human immune systems to build a memory-cell population with a diverse set of local optimal solutions. Based on the memory-cell population, CSSM outputs the value of the memory cell and find the optimal sub-pixel mapping. The proposed method was tested using the synthetic and degraded real imagery. Experimental results demonstrate that the proposed approach outperform the hard classification algorithm, and hence provide an effective option for sub-pixel mapping of remote sensing imagery.

References:

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