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Soft Computing IA 2 Report

Cell Classification Using Convolutional Neural Networks in Medical Hyperspectral Imagery

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1. Introduction

1.1 Introduction

Hyperspectral imaging is a rising imaging modality in the field of medical applications, and the combination of both spectral and spatial information provides wealth information for cell classification. In this paper, deep convolutional neural network (CNN) is employed to achieve blood cell discrimination in medical hyperspectral images (MHSI) Experimental results based on two real medical hyperspectral image data sets demonstrate that cell classification using CNNs is effective

Hyperspectral imagery (HSI) is characterized by hundreds of spectral channels with high resolution. This is beneficial for image processing because each pixel in HSI involves numerous spectrums and conveys more information as compared to color pixels. Currently, hyperspectral imaging technology has been greatly developed not only in the remote sensing field but also for many medical applications, such as cancer detections, cell recognition, and other diagnostics

1.2 Problem Statement

Many different feature extraction methods have been proposed to solve the classification problem in hyperspectral images [6]. Recently, a deep convolutional neural network has been considered a powerful model for image classification, whose classification performance is competitive to some traditional methods, such as support vector machines (SVM). In this work, inspired by we describe a multi-layer CNN architecture that jointly exploits both spatial and spectral features for cell classification, which contains rich spatial-spectral characteristics of hyperspectral pixel vectors

1.3 Objective & Scope

Currently, hyperspectral imaging technology has been greatly developed not only in the remote sensing field but also for many medical applications, such as cancer detections, cell recognition, and other diagnostics

Blood cell discrimination is highly informative for the detection and treatment of many diseases in clinical medicine

An abnormal increase or decrease in counting results may indicate that there are many diseases that can provide an overview of the patient's overall health status

2. Literature Survey

2.1. Research Paper analysis

A medical hyperspectral image with high spatial and spectral resolution may contain more cell information, but image processing may bring complexity and interference due to the high dimension. In order to use the information more efficiently, we need to use dimensionality reduction methods to reduce the image dimension, such as the classic PCA.

In the first step, PCA is introduced to reduce redundant spectral information and reduce the data dimension to an acceptable scale. Because the designed experiment uses CNN, we fully utilize the fact that neighboring pixels in MHSI tend to belong to the same class and extract a large number of small regions (a central pixel with its neighbors).

Furthermore, in order to increase the data for better tuning the multi-layer network, we flip the image and increase the total number of samples. A neighborhood region with a large size not only contains too much redundancy but also is not conducive. Thus, in the second step, the experimental image is divided into the same patches as input, where each patch contains spectral and spatial information.

The spectrum should be considered first because it contains major information for distinguishing different kinds of categories. As for spatial information, we extract a neighborhood region of the pixel after PCA on spectral. After these processes, we "unfold" these patches before the input layer. The proposed net contains eight layers with weights: including the input layer, two convolutional layers, two max-pooling layers, two full connection layers, and the final output layer.

In our designed architecture, convolutional layers and max-pooling layers can be viewed as a trainable feature extractor to the input data, and full connection layers are trainable classifiers to the feature extractor.

3. Implementation

3.1 System Architecture

The proposed CNN multilayer architecture is shown below

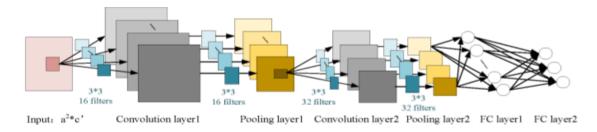


Figure 2. The proposed multi-layer CNN architecture.

3.2 FlowChart

The overall flowchart of the proposed CNN-based method is given below:

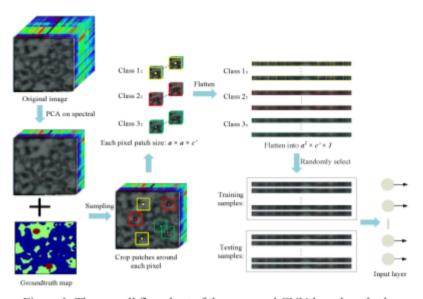


Figure 1. The overall flowchart of the proposed CNN-based method.

3.3 Results & Analysis

All the experimental data sets are collected by composing the VariSpec Liquid Crystal Tunable Filters (LCTFs) with microscope and silicon charge-coupled devices. Two datasets have been taken named blood cell 1-3 and bloodcell2-2 containing images with size 973x799x33 and 462x451x33 respectively.

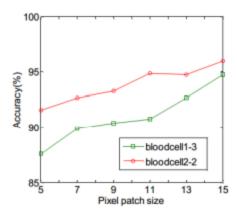
Images contain three classes - white cells, red cells and background.

With the CNN-based cell classification, the classification performance may mainly be influenced by three factors: the pixel patch size, the degree of dimension reduction, and training sample ratio.

In order to study the effect of pixel patch, it is varied from 5x5 to 15x15 Experimental Results:

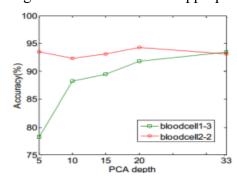
Accuracy of the first experimental data (i.e., bloodcell-3) achieves to 94.75% using 15xl5xlO pixel patch, and the one of the second experimental data (i.e., bloodcell-2) achieves the highest using 15x15xlO.

Results of comparison with different Pixel patch sizes on the experimental data is as shown below.



Data Set	bloodcell1-3	bloodcell2-2
5×5×10	87.58%	91.59%
7×7×10	89.92%	92.70%
9×9×10	90.42%	93.27%
11×11×10	90.77%	94.86%
13×13×10	92.68%	94.75%
15×15×10	94.75%	95.99%

During the preprocessing, in order to improve the experimental efficiency, we reduce the data dimension to an acceptable scale by PCA. We validate the experiment samples with different reduced dimensions for PCA: 5, 10, 15, 20, and original dimension 33 with other parameters unchanged. It is empirically studied that the dimensionality reduction from the range of 10 to 20 is a more appropriate choice.



Finally, we vary the quantity of training samples per class from 10% to 60% to see how varied numbers of training samples per class affect classification accuracy.

Figure 6 depicts the outcomes of the experiment.

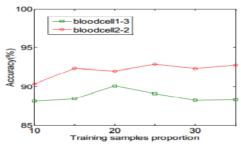


Figure 6. Classification performance of different ratios of training samples to the total labeled samples.

When the ratio of training samples hits 30%, the accuracy of the blood cells-3 reaches its peak and subsequently begins to decline.

When the ratio of training samples is 30%, the accuracy of the remaining bloodceII2-2 remains stable. The explanation for this could be that training too much data causes network over-fitting, which causes accuracy to drop rather than rise.

In general, a training sample ratio of roughly 30% will yield better outcomes.

We compare the proposed method to standard classification methods such as SVM to ensure that it has a superior representation on cell categorization. For each test data set, we repeat the tests three times and calculate the average error.

The CNN-based model goes through around 2000 iterations of training. Table III shows a detailed comparison of the proposed approach with the classic SVM classifier in terms of classification performance.

TABLE III. CLASSIFICATION PERFORMANCE OF THE PROPOSED CNN AND SVM USING TWO EXPERIMENTAL DATA

Data	The proposed CNN	SVM
bloodcell1-3	89.92%±0.0028	56.35%±0.0021
bloodcell2-2	92.70%±0.0027	63.11%±0.0046

By comparison, the suggested CNN model consistently outperforms the SVM, with an average accuracy of around 93 percent, a 30 percent improvement over the SVM.

4. Conclusion

The findings show that deep CNN has a lot of potential when it comes to dealing with medical hyperspectral images.

Paper suggested a deep CNN-based approach for separating white cells and red cells in human blood cells in this research.

We presented a CNN-based approach for integrating hyperspectral pictures' spectral and spatial information. Due to the limited number of training samples, the suggested CNN-based cell classifier had two convolutional layers and two fully connected layers.

On the one hand, we looked into the impact of numerous characteristics affecting classification precision.

Paper compared the proposed approach to the SVM classifier, possibly improving the accuracy by combining the two experimental methods sets of data.

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