비지도학습의 딥 컨벌루셔널 자동 인코더를 이용한 셀 이미지 분류

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Cell Images Classification using Deep Convolutional Autoencoder of Unsupervised Learning

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요 약

The present work proposes a classification system for the HEp-2 cell images using an unsupervised deep feature learning method. Unlike most of the state-of-the-art methods in the literature that utilize deep learning in a strictly supervised way, we propose here the use of the deep convolutional autoencoder (DCAE) as the principal feature extractor for classifying the different types of the HEp-2 cell images. The network takes the original cell images as the inputs and learns to reconstruct them in order to capture the features related to the global shape of the cells. A final feature vector is constructed by using the latent representations extracted from the DCAE, giving a highly discriminative feature representation. The created features will be fed to a nonlinear classifier whose output will represent the final type of the cell image. We have tested the discriminability of the proposed features on one of the most popular HEp-2 cell classification datasets, the SNPHEp-2 dataset and the results show that the proposed features manage to capture the distinctive characteristics of the different cell types while performing at least as well as the actual deep learning based state-of-the-art methods.

1. INTRODUCTION

Computer-aided diagnostic (CAD) systems have gained tremendous interests since the unfolding of various machine learning techniques in the past decades. They comprise all the systems that aim to consolidate the automation of the disease diagnostic procedures. One of the most challenging tasks regarding those CAD systems is the complete analysis and understanding of the images representing the biological organisms. In case of the autoimmune diseases, the automatic classification of the different types of the Human Epithelial type 2 (HEp-2) cell patterns is one of the most important steps of the diagnosis procedure.

Automatic feature learning methods have been widely adopted since the unfolding of deep learning [1]. They have shown outstanding results in the object recognition problems [2] and many researchers have adopted them as principal tool for the HEp-2 cell classification. Unlike conventional methods whose accuracy depends on the subjective choice of the features, deep learning methods, such as deep convolutional neural networks (CNNs), have the advantage of offering an automatic feature learning process. In fact, many works have demonstrated the superiority of the deep learning based features over the hand-crafted ones for the HEp-2 cell classification task.

We propose an unsupervised deep feature learning process that uses the deep convolutional autoencoder (DCAE) as the principal feature extractor. The DCAE, which learns to reproduce the original cellular images *via* a deep encoding-decoding scheme, is used for extracting the features. The DCAE takes the original cell image as an input and will learn to reproduce it by extracting the meaningful features needed for the discrimination part of the method. The latent representations trapped between the encoder and the decoder of the DCAE will be extracted and used as the final high-level features of the system.

The DCAE will help to encode the geometrical details of the cells contained in the original pictures. The discrimination potentiality carried by the extracted features allows us to feed them as the inputs of a shallow nonlinear classifier, which will certainly find a way to discriminate them. The proposed method was tested on the SNP Hep-2 Cell dataset [3] and the results show that the proposed features outperform by far the conventional and popular handcrafted features and perform at least as well as the state-of-the-art supervised deep learning based methods.

2. METHOD

Auto-encoders [4] are unsupervised learning methods that are used for the purpose of feature extraction and dimensionality reduction of data. Neural network based auto-

encoder consists of an encoder and a decoder. The encoder takes an input x of dimension d, and maps it to a hidden representation y, of dimension r, using a deterministic mapping function f such that:

$$y = f(\boldsymbol{W}x + \boldsymbol{b}), \quad (1)$$

where the parameters $\boldsymbol{W}$ and $\boldsymbol{b}$ are the weights and bias associated with the layer that takes the input x. They must be learned by the encoder. The decoder then takes the output y of the encoder and uses the same mapping function f in order to provide a reconstruction z that must be of the same shape or in the same form (which means almost equal to) as x. Using equation (1), the output of the decoder is also given by:

$$z = f(\boldsymbol{W}'y + \boldsymbol{b}'), \quad (2)$$

where the parameters **W'** and **b'** are the weights and bias associated with the decoder layer. In final, the network must learn the parameters **W**, **W'**, **b** and **b'** so that z must be close or, if possible, equal to x. Though, the network leans to minimize the differences between the input x and the output z.

This encoding-decoding process can be done with the use convolutional neural networks by using what we call the DCAE. Unlike conventional neural networks, where you can set the size of the output that you want to get, the convolutional neural networks are characterized by the process of down-sampling, accomplished by the pooling layers, which is incorporated in their architecture. As explained in the first section of the paper, this sub-sampling process induces the loss of spatial information while we go deeper inside the network.

To tackle this problem, we can use DCAE instead of conventional convolutional neural networks. The DCAE, after the down-sampling process accomplished by the encoder, the decoder tries to up-sample the representation until we reconstruct the original size. This can be made by backwards convolution often called "deconvolution" operations. The final solution of the network can be written in the form:

$$(\mathbf{W}, \mathbf{W}', \mathbf{b}, \mathbf{b}') = \underset{W,W',b,b'}{\operatorname{argmin}} L(xz), \quad (3)$$

where z denotes the decoder's output and x is the original image.

3. RESULTS

There are 1,884 cellular images in the dataset, all of them extracted from the 40 different specimen images. Different specimens were used for constructing the training and testing image sets, and both sets were created in such a way that they cannot contain images from the same specimen. From the 40 specimen, 20 were used for the training sets and the remaining 20 were used for the testing sets. In total there are 905 and 979 cell images for the training and testing sets, respectively. Each set (training and testing) contains five-fold validation splits of randomly selected images. In each set, the different splits are used for cross validating the different models, each split containing 450 images approximatively. The SNPHEp-2 dataset was present by Wiliem et al. [3].

As presented before, the created feature vectors extracted from the DCAE contain 4096 elements. So, our network will have 4096 neurons in the input layer. The best results were obtained using a 4096-250-50-5 architecture, meaning that we have 4096 neurons in the input layer, 250 neurons in the first hidden layer, 50 neurons in the second hidden layer and a final layer containing 5 neurons corresponding to the 5 cell types of our dataset. The total accuracy reached by the network was 88.08 %. The details of the results are shown in the confusion matrix shown in Fig. 1.

Output Class \ Target Class	Homo	Coarse	Fine	Nucl	Centro
Homo	**91.07**	0.53	9.97	0	0
Coarse	0.46	**88.27**	0	5.77	6.54
Fine	6.11	2.24	**86.42**	0	0.10
Nucl	1.38	3.79	0.94	**85.09**	0.17
Centro	0.98	5.17	2.67	9.14	**93.19**

Fig. 1. Confusion matrix of the results.

4. CONCLUSION

We have presented a cell classification method for the microscopy that uses the DCAE as the principal feature extractor. Unlike most of the methods in the literature that are based on the supervised learning, we have used the DCAE in order to construct the feature vectors. These obtained vectors were then given to a nonlinear classifier whose outputs determine the cell type of the image. The results show that the proposed feature extraction really captures the characteristics of each cell type. The comparative study demonstrates that our proposed features perform far better than the handcrafted ones and slightly better than the supervised deep learning method.

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