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Artificial immune kernel clustering network for unsupervised image segmentation

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Abstract

An immune kernel clustering network (IKCN) is proposed based on the combination of the artificial immune network and the support vector domain description (SVDD) for the unsupervised image segmentation. In the network, a new antibody neighborhood and an adaptive learning coefficient, which is inspired by the long-term memory in cerebral cortices are presented. Starting from IKCN algorithm, we divide the image feature sets into subsets by the antibodies, and then map each subset into a high dimensional feature space by a mercer kernel, where each antibody neighborhood is represented as a support vector hypersphere. The clustering results of the local support vector hyperspheres are combined to yield a global clustering solution by the minimal spanning tree (MST), where a predefined number of clustering is not needed. We compare the proposed methods with two common clustering algorithms for the artificial synthetic data set and several image data sets, including the synthetic texture images and the SAR images, and encouraging experimental results are obtained.

Keywords: Artificial immune network; Kernel mapping; Nonsubsampled contourlet transform; Unsupervised image segmentation

1. Introduction

Tax and Duin [1] and Schőlkopf et al. [2] proposed a kernel method, also known as the support vector domain description, to characterize the support of a high dimensional distribution. Intuitively, the support vector domain description computes the smallest hypersphere in feature space enclosing the image of the input data. In this paper, we introduce the support vector domain description (SVDD) into a novel structural adaptation artificial immune network for image segmentation. As the total number of pixels in the original image is usually huge, which cannot be directly used as antigens (train pattern), we firstly segment the original image into regions using the watershed segmentation algorithm. Then the mean features energy of each watershed region is calculated, which is regarded as the antigens of the immune kernel clustering network (IKCN). A set of features, including the nonsubsampled contourlet transform (NSCT) [3] and the gray level co-occurrence matrix (GLCM) [4], are extracted from the image. Starting from IKCN, the input image features are firstly divided into subsets by the antibodies, and then each subset is mapped into a hypersphere in a high dimensional feature space by a mercer kernel. Finally, the clustering results of the local support vector hyperspheres are combined to yield a global clustering solution by MST [5] in graph theory, which can automatically cluster the antibody obtained in the output space without a predefined number of clustering. Such an immune kernel approach can deal with problems with unevenly distributed samples. Another advantage of the proposed method is that it can simplify the computation of support vector domain description as well as facilitate a parameter tuning task. Furthermore, noise patterns can be easily detected by the boundary curves

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obtained from support vectors for each antibody, which is represented as a support vector hypersphere.

2. Mathematical preliminaries

2.1. Watershed segmentation

In this work, we use the well-known watershed segmentation [6] to partition an image into nonoverlapping regions. Pixels in a watershed region are homogeneous in the feature space. We then introduce the basic concept of watershed segmentation as follows:

$$MG(f) = \frac{1}{n}\sum_{i=1}^{n}[((f \oplus B_i) - (f \Theta B_i)\Theta B_{i-1})] \tag{1}$$

where $\oplus$ and Θ denote dilation and erosion, respectively, and B_i is called structural element with size $(2i-1)\times(2i-1)$ pixels, and f is the original image.

If the watershed regions are too large, one region may contain more than one focused subject in the image. If the number of regions is too small, texture feature in the region may not be homogeneous, and the computational complexity will increase. In our design, we adopted two parameters: $r = 4$ and $h = 4$. Using this setting, the number of regions was about 1400 in each 256×256 image.

2.2. Feature extraction

We introduce the features used in our work, including the nonsubsampled contourlet transform and the gray level co-occurrence matrix. As for the NSCT features, the original image was firstly transformed into multi-channel images by using a NSCT decomposition, and then texture features have been extracted by moving a window, i.e. for any position in the feature images, mean deviation is estimated in its neighborhood. In this study, we used a small window (e.g. 15×15) to estimate "texture energy feature" from the transformed multi-channel images. As for the GLCM features, we use the entropy, energy, contrast and correlation features for the displacement is 1 and the window's size is 9. The feature vectors from NSCT had a set of 18 features (the resolution level is 3 and the frequency direction is 6), while the feature vector from GLCM had a set of 12 features.

2.3. Support vector domain description

Let $D = (x_i \in R^n, i = 1,2,\cdots,m) \subseteq X$, with $X \subseteq \Re^n$. Using a nonlinear transformation Φ from X to some high-dimensional feature space, it looks for the smallest enclosing hypersphere of radius R. This is described by the constraints

$$\min_{R,a,\xi_i} R^2 + C\sum_i \xi_i \tag{2}$$

Subject to the constraint $\|\Phi(x_i) - a\|^2 \leqslant R^2 + \xi_i$

where $\|\cdot\|$ is the Euclidean norm, a is the center of the hypersphere and $\xi_i \geqslant 0$ is the slack variable, and C is a constant controlling the penalty of noise. The Lagrangian is introduced to find the smallest sphere of radius R

$$L = R^2 - \sum_{i=1}^{m}\left(R^2 + \xi_i - \|\Phi(x_i) - a\|^2\right)\beta_i - \sum_{i=1}^{m}\xi_i\mu_i + C\sum_{i=1}^{m}\xi_i \tag{3}$$

Using (2) and (3), we may turn the constrained minimization of Lagrangian into the Wolfe dual form

$$\max_{\beta_i} W = \sum_{i=1}^{m}\Phi(x_i)^2\beta_i - \sum_{i=1}^{m}\sum_{j=1}^{m}\beta_i\beta_j\Phi(x_i)\cdot\Phi(x_j)$$
$$\text{subject to} \quad \sum_{i=1}^{m}\beta_i = 1 \quad \text{and} \quad 0 \leqslant \beta_i \leqslant C, \ \ i = 1,2,\ldots,m \tag{4}$$

The image of a point x_i with $\xi_i > 0$ and $\beta_i > 0$ lies outside the feature space hypersphere. A point with $\mu_i = 0$ is called a bounded support vector (BSV). A point x_i with $\xi_i = 0$ and $0 < \beta_i < C$ implies that its image $\Phi(x_i)$ lies on the surface of the feature space hypersphere. Such a point will be referred to as a support vector (SV). We compute the dot products $\Phi(x_i)\cdot\Phi(x_j)$ in (4) by an appropriate mercer kernel $G(x_i, x_j)$, and the Gaussian kernel is used in this study.

$$\Phi(x_i)\cdot\Phi(x_j) = G(x_i, x_j) = \mathrm{e}^{-\|x_i - x_j\|^2/\sigma^2}, \quad \sigma \in \Re \tag{5}$$

3. Immune kernel clustering network

The IKCN makes use of several features of the immune response, such as the clonal expansion of the most stimulated cells, death of the non-stimulated cells and the affinity maturation of the repertoire [7]. The network does not have a predefined number of antibodies, which will be determined dynamically based on immune principles. Finally, a MST is used to automatically determine the final number of clusters. The model can adaptively map input data into the antibody output space, which has a better adaptive network structure.

3.1. IKCN algorithm

The IKCN algorithm is summarized in the pseudocode presented below.

Step 1: Initialize randomly the antibodies in the network and define the parameters: $\eta(1)$, α, β, ε and σ. The number of initial antibodies could be set between $0.005N$ and $0.01N$, where N is the number of input data points.

Step 2: While not reached the convergence criterion do:

2.1. For each input pattern do:

(1) present all the antigens to the network;

(2) calculate the Euclidean distance between the antigens and the antibodies;