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HEp-2 cells Classification via clustered multi-task learning

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ABSTRACT

This paper proposes a clustered multi-task learning-based method for automated HEp-2 cells Classification. First, the visual feature is extracted for individual sample to represent its appearance characteristics. Then, the models of multiple HEp-2 cell category are jointly trained in the framework of clustered multi-task learning. The extensive experiments on the HEp 2, cell dataset released by the HEp-2 Cells Classification contest, held at the 2012 International Conference on Patter Recognition, show that the proposed method can discover and share the latent relatedness among multiple tasks and consequently augment the performance. The quantitative comparison against the state-of-the-art methods demonstrates the superiority of the proposed method.

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1. Introduction

Over the last few years, image processing and pattern recognition techniques have been widely leveraged to develop the computer-aided diagnosis (CAD) systems. Although these systems cannot make the exact decision, they can work as a pre-selection of the cases for further examining and consequently enable the physician to focus the attention only on the most relevant cases [1–4]. Therefore, humans have applied these systems into multiple fields of life science and medical science both for research purposes and for actual clinical practice [5].

Recently, more and more researchers are paying attention on developing CAD systems to realize automated analysis of indirect immunofluorescence (IIF) images. IIF is a diagnostic methodology based on image analysis that reveals the presence of autoimmune diseases by searching for antibodies in patient's serum [5]. However, physicians can only treat IIF with specific subjective methods which highly rely on the experience and expertise. This has caused significant disagreement for further diagnosis. It has been reported that the inter-laboratories agreement is 92.6% for the simple task of positive/negative intensity classification, while it can drop to 76.0% for the recognition of staining patterns, which is required for a more detailed diagnosis [6]. Therefore, in recent years, lots of work have been done on the related research topics, including image preconditioning [7,8], image segmentation [9,10], mitotic cell recognition [11–17], and pattern recognition [18–20]. Since the success of HEp-2 Cells Classification contest held at 2012 International conference on Pattern Recognition, more and more researchers are being engaged in this task. The current methods of HEp-2 cell classification usually contain three main steps, including feature extraction, feature selection, and model learning. For feature extraction, Cheplygina et al. utilized the variance and covariance of intensity values, the histograms of the red and green channels, and the morphological features of the foreground as visual representation [5]. To improve the discrimination of feature representation, many textual features, such as local binary patterns [21], gray level co-occurrence matrix [22], and discrete cosine transform coefficients, and sophisticated shape features, such as histograms of oriented gradients [23], have been wide leveraged for this task. Since much work extracted multiple features for representation, feature selection is necessary. Kazanov et al. used forward selection to extract the significant features from the basic intensity features and morphological features [5]. Mateos-Garcia et al. leveraged the correlation feature selection and genetic algorithm for feature selection [5]. Rezvani et al. utilized the classic PCA to select the best features from the extracted textual and intensity features [5]. With the discriminative features, lots of powerful classifiers are implemented for cell classification, including k-NN, support vector machine (SVM) [24–26], multiclass SVM [27], ShareBoost [28], AdaBoost [25], and random decision forest [29].

Although much work has been done for HEp-2 cell classification, there still exist two critical problems. To our knowledge, most of the previous methods work in the framework of single-task learning. Although many sophisticated classifiers have been designed, they cannot take the latent relatedness among multiple cell categories into consideration. It is challenging to cluster HEp-2 cells into clusters simply with the visual appearances by humans. Therefore, it is extremely difficult to discriminate several clusters (such as homogeneous, fine speckled, and coarse speckled) with similar patterns. On the other hand, there usually exist limited samples since it is expensive for large-scale dataset preparation and manual segmentation and

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annotation of specific cell regions. Moreover, there also exists significant imbalance of data distribution due to the complicated factors during cell culture. For example, the number of centromere cells is about three times higher than the number of cytoplasmic cells in the HEp-2 cell classification dataset [6]. Therefore the imbalance of data distribution will make it difficult for model learning. Although many researchers are involved to design classifiers with higher generalization ability, model learning is still highly dependent on large scale data since there always exist significant variations of shape, orientation, illumination and other factors as shown in Fig. 2.

To discover the latent relatedness among multiple cell categories and deal with the imbalance of data distribution, in this paper, we propose an automated HEp-2 Cells Classification method based on clustered multi-task learning. First, we extract the visual feature to represent the appearance characteristics of individual sample. Then, we jointly learn the models of 6 HEp-2 cell categories in the framework of clustered multi-task learning [30,31]. The framework of the proposed method is shown in Fig. 1. The extensive experiments on the HEp2 cell dataset released by the HEp-2 Cells Classification contest show that the proposed method can discover and share the latent relatedness among multiple tasks and consequently augment the performance. The quantitative comparison against the state-of-the-art methods demonstrates the superiority of the proposed method. The main contributions lie in two-folds:

1. To our knowledge, this is the first HEp-2 cell classification method based on the theory of multi-task learning. Especially, with the clustering-based regularization, the proposed method can discover the grouping information which will benefit discriminating the cell categories with similar visual patterns.
2. The proposed method can effectively avoid the imbalance of data distribution by leveraging the entire data for joint model learning, which implicitly augments the training data for all models.

The rest of the paper is structured as follows. In Section 2, we will detail the method for clustered multi-task learning. The experimental method and results will be respectively detailed in Sections 3 and 4. At last, Conclusions are presented.

2. Clustered multi-task learning (CMTL)

In this section, we will detail the formulation of the objective function, the convex relaxation of the regularization, and the corresponding optimization method.

2.1. Formulation

For HEp-2 Cells Classification, model learning for m cell categories can be considered as m task. During the training step, a set of training data $\{(x_j^i, y_j^i)\}_{j=1}^{n_i}$, where $x_j^i \in \mathbb{R}^d$ is the d-dimension visual representation and $y_j^i \in \mathbb{R}$ is the label, is given for model learning. To classify individual cell category, it is requested to learn a linear predictive function $f_i : f_i(x_j^i) = w_i^\top x_j^i$, where w_i is the model parameter of the i-th task. Supposing m task is given, we use $W = \{w_i\}_{i=1}^m$ as the parameter matrix for model learning. The objective function can usually be formulated as

$$Obj(W) = L(X, Y, W) + \Omega(W) \tag{1}$$

The objective function consists of two components:

- *Empirical loss function*: $L(X, Y, W)$ means the empirical loss function of joint multi-task learning and can be computed by $L(X, Y, W) = \sum_{i=1}^m \frac{1}{n_i}(\sum_{j=1}^{n_i} \| f_i(x_i, w_i) - y_i \|_2^2)$.

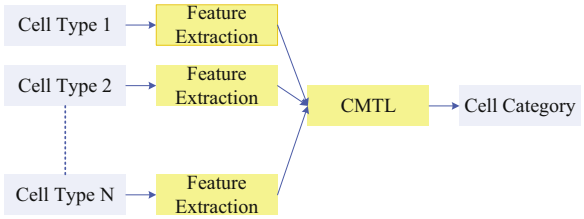

Fig. 1. Framework of the proposed method.

- *Clustering-based regularization*: Different from previous methods, which usually deal with the model learning independently, we assume that all tasks can be grouped into $k < m$ clusters. The index set of the j-th cluster is defined as $\mathcal{I}_j = \{v | v \in \text{Cluster}_j\}$. The mean of the j-th cluster can be formulated as $\overline{w}_j = \frac{1}{n_j}\sum_{v \in \mathcal{I}_j} w_v$. For $W = \{w_i\}_{i=1}^m$, the sum-of-square error (SSE) function utilized in K-means algorithm can be formulated as:

$$\sum_{j=1}^{k} \sum_{v \in \mathcal{I}_j} \| w_v - \overline{w}_j \|_2^2 = \text{tr}(W^T W) - \text{tr}(F^T W^T W F) \tag{2}$$

where $F \in \mathbb{R}^{m \times k}$ is an orthogonal cluster indicator matrix, where $F_{i,j} = \frac{1}{\sqrt{n_j}}$ if $i \in \mathcal{I}_j$ and $F_{i,j} = 0$ otherwise. By ignoring the special structure of F and keeping the orthogonality requirement, the SSE minimization problem can be relaxed as:

$$\min_{F: F^T F = I_k} \text{tr}(W^T W) - \text{tr}(F^T W^T W F) \tag{3}$$

Then the clustering-based regularization term for CMTL can be formulated as:

$$\Omega(W, F) = \alpha(\text{tr}(W^T W) - \text{tr}(F^T W^T W F)) + \beta\, \text{tr}(W^T W) \tag{4}$$

where the first term is derived from the K-means algorithm and the second term is imposed to augment the generalization performance.

To sum up, the objective function of CMTL for joint HEp-2 cells modeling can be formulated as:

$$Obj(W) = \sum_{i=1}^{m} \frac{1}{n_i} \left(\sum_{j=1}^{n_i} \| f_i(x_i, w_i) - y_i \|_2^2 \right) + \alpha(\text{tr}(W^T W) - \text{tr}(F^T W^T W F)) + \beta\, \text{tr}(W^T W) \tag{5}$$

2.2. Convex relaxation

Since the objective function above is not convex, the convex relaxation is performed on Eq. (5). The regularization in Eq. (5) can be reformulated as:

$$\Omega_1(W, F) = \alpha\eta(1+\eta)\, \text{tr}(W(\eta I + FF^T)^{-1} W^T) \tag{6}$$

where $\eta = \beta/\alpha > 0$. Therefore, the optimization of Eq. (5) is equivalent to the following problem:

$$W^* = \arg \min_{W, F: F^\top F = I_k} L(X, Y, W) + \Omega_1(W, F) \tag{7}$$

Following [31], we can achieve the convex relaxation of Eq. (5)

$$W^* = \arg \min_{W, M} \sum_{i=1}^{m} \frac{1}{n_i} \left(\sum_{j=1}^{n_i} \| f_i(x_i, w_i) - y_i \|_2^2 \right) + \alpha\eta(1+\eta)\text{tr}(W(\eta I + M)^{-1} W^T) \quad \text{s.t. } \text{tr}(M) = k, M \preceq I, M \in \mathbb{S}_+^m. \tag{8}$$

The objective function in Eq. (8) is convex with respect to both W and M.

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