Recognition of milk somatic cells based on dichotomy model

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Abstract. The number of various milk somatic cells can be calculated accurately by using image processing technology. In order to identify four kinds of cells, a method of milk somatic cell recognition based on dichotomy model was proposed. Firstly, eight typical morphological features were extracted from cells. Some morphological features were selected by feature optimization and Bayes classifier was used twice to carry out two binary classification. The texture feature described by HOG and BP neural network were used on the last classify. Finally, 96.02% of the average classification accuracy was achieved in the actual experiment of milk somatic cell image data.

1. Introduction
Usually, the somatic cells in milk are mainly macrophages(Mø), lymphocytes(LYM), neutrophil (NE) and contain a small amount of epithelial cells(EPI). The type and quantity of milk somatic cells is an important index for milk quality evaluation. The percentage of different types of somatic cells in normal milk is 60% macrophage, 25% lymphocyte and 15% neutrophil or polymorphic nuclear neutrophil. When dairy cows suffer from mastitis, the number of somatic cells will increase greatly, especially neutrophils. The proportion of somatic cells varies at different lactation stages[1]. The proportion of somatic cells can be calculated by accurately identifying all kinds of cells, and consequently the lactation stage and the infection degree of mastitis in dairy cows can be judged accordingly.

With the development of computer technology, image processing and pattern recognition have been widely used in medical field. They have achieved good results in human tumor cell recognition[2] and leukocyte classification[3]. However, in the current research on classification of milk somatic cells, most of them first extract morphological and texture features of various cells, and then send these features to classifier for recognition[4]. These methods have large workload and complicated calculation, which easily lead to feature redundancy.

On the basis of literature[5], eight morphological features are extracted and optimized. An algorithm for milk somatic cell recognition based on dichotomous model is proposed in this paper, which uses three classifiers in series to fuse and classify four kinds of cells three times.

2. Feature extraction
The feature extraction of milk somatic cells is very important for identification and classification. By comparing the characteristics of the microscopic images of the four types of milk somatic cells, it was found that there are significant differences in the shape of nucleus between NE and other three types...
of cells, and the nucleus of the LYM was larger. There is little difference in morphology between EPI and Mø, but texture is an objective feature of cell images, which can reflect the structural characteristics of cells.

2.1. Morphological feature extraction
Eight morphological features of common bovine milk somatic cell images were extracted, including somatic area, nucleus area, somatic perimeter, nucleus perimeter, minimum circumferential area, nucleus complexity, circularity and nucleus proportion.

According to the morphological differences mentioned above, the optimal selection of features was carried out. Two parameters, complexity and circularity, were selected from four types of cells. 30 groups of data were extracted from each group. Under the condition of $\alpha=0.05$, the two-factor and repeated variance analysis of four types of cells showed that there were significant differences between NE and the other three types of cells. There were no significant differences between Mø, EPI and LYM. A parameter of cell nucleus proportion was chosen from Mø, EPI and LYM, and 30 groups of data were extracted from each group. Under the condition of $\alpha = 0.05$, one-way ANOVA was performed on these three kinds of cells. It was found that LYM were significantly different from the other two types of cells. There was no significant difference between Mø and EPI. This is the reason why complexity, circularity and nuclear proportion were chosen.

2.2. Texture feature extraction
The direction of edge distribution of pixels can well describe the local appearance or shape of an object in an image. Based on this theory, Dalal and Triggs proposed the describing operator of HOG feature (histogram of oriented gradient) in 2005. Literature[6] gives several specific steps to extract HOG feature.

2.2.1. Standardized Gamma space and color space. Square root Gamma standardization can eliminate the influence of overall illumination and contrast. However, it was found that the standardization process did not significantly improve the final results in the experiment. The reason is that the block normalization process plays the same role and the square root Gamma normalization process is omitted in the general application of HOG features.

2.2.2. The calculation of pixel gradient. The operation of HOG features is very sensitive to template operators. Through experiments and comparisons, it is found that the simplest one-dimensional discrete differential template (-1, 0, +1) and its transposition can achieve the best detection results by calculating the gradient of each pixel in the horizontal and vertical directions. The modulus and direction angle of the gradient can be calculated by the equations (1) and (2) respectively.

$$G(x, y) = \sqrt{(H(x+1,y) - H(x-1,y))^2 + (H(x,y+1) - H(x,y-1))^2} \quad (1)$$

$$\alpha(x,y) = \tan^{-1}\frac{H(x,y+1)-H(x,y-1)}{H(x+1,y)-H(x-1,y)} \quad (2)$$

In the formula, $G(x, y)$, $\alpha(x, y)$, $H(x, y)$ represent the gradient magnitude, gradient direction and gray value of the pixel respectively. For color images, the gradient of each color channel can be calculated separately, and the maximum value of the gradient can be selected as the gradient of the pixel.

2.2.3. Statistics of gradient histograms in cells. The image is divided into several squared cells, each cell contains 8x8 pixels divides the gradient direction of $[-\frac{\pi}{2}, \frac{\pi}{2}]$ into nine intervals. The gradient values of all pixels are histogram counted in each interval, so that a cell can get a 9-dimensional feature vector[7].
2.2.4. Normalized histogram. A block consists of 3×3 cells forms 81-dimensional feature vectors. After that, L2-norm was used to normalize the whole block to get the final feature vectors.

2.2.5. HOG features of images. The image used in the experiment is 64×64 and the cell is 8×8. An image contains (8-3+1)×(8-3+1)=36 blocks which is a 81-dimensional vector. The HOG eigenvectors of a 64×64 image is divided into 81×36=2916. Finally, the extracted HOG features are input into the BP neural network classifier. The image obtained by using HOG is shown in Figure 1. The above parameters are obtained by experiments.

![Original images](image1.png)
(a) Original images.
![HOG-processed images](image2.png)
(b) HOG-processed images.

Figure 1. HOG processing results.

3. Classification model

3.1. Classification model design
Using the idea of dichotomy, the cell types are determined step by step. This classification model can be divided into three main steps:

The first step is to extract morphological features and identify whether the target cell is NE. If the cell is identified, the recognition is completed, otherwise the second step is carried out.

The second step is to extract morphological features and identify whether the target cell is LYM. If the target cell is a lymphocyte, the recognition is completed, otherwise the third step is carried out.

The third step is to extract texture features and identify whether the target cells are Mø or EPI. Finally, target cell recognition is over. The classification model is shown in Figure 2.

![Classification model](image3.png)

Figure 2. Classification model.

3.2. Classification model implementation
Three classifiers in series are used to establish the classification model in this paper. Naïve Bayes classifier (NBC) assumes that the effect of an attribute value on a given class is independent of the value of other attributes. This assumption is called class conditional independence, in this sense, Naïve
Bayesian classifier is called Naive. NBC model is insensitive to missing data not only needs fewer parameters than neural network and support vector machine model, but also has the smallest error rate compared with other classification methods[8]. Because the dimension of morphological features is small, Bayes classifier is used in the first two steps.

BP neural network which has been widely used[9] solves the problem of learning the connection weight of hidden unit layer in multi-layer network systematically. What's more, the reason why BP neural network classifier is selected in the last step is that histogram has a high characteristic dimension. The number of neurons in the hidden layer is related to the number of nodes in the input and output layer. Various solutions and many empirical formulas have been put forward by many scholars to solve this problem [10].

\[ \sum_{i=0}^{n} C_{n_1}^i > k \]  

In the formula, \( k \) is the sample size, \( n_i \) is the number of hidden layer nodes, and \( n \) is the number of input layer nodes. When \( i > n_i, \ C_{n_1}^i = 0 \).  

\[ n_1 = \sqrt{n + m + a} \]  

In the formula, \( n \) is the number of input layer nodes, \( m \) is the number of output layer nodes, and \( a \) is a constant between 1 and 10.  

\[ n_1 = \log_{2^n} \]  

The interval \([a, b]\) about the number of nodes in the hidden layer can be obtained by solving the simultaneous equations 3-5. The structure of BP neural network classifier with the number of hidden layer nodes calculated by literature[11] is shown in table 1.

| Input Layer | Hidden Layer | Output Layer | Transfer Function |
|-------------|--------------|--------------|-------------------|
| 2916        | 16           | 2            | Sigmoid           |

4. Experimental result and analysis

The experimental data was taken from cell images that was segmented by team members[4]. Fifty cell images with magnification of 1000 times were selected from each group. The resolution of each image is 64×64. The hardware configuration of the experiment is 3.60 GHz Intel (R) Core (TM) i7-7700 CPU 8G memory and Windows 10 professional operating system. The software environment is Python 3.6.

In the first experiment, BP neural network classifier is used to compare the different block and cell of HOG feature extraction. The results, which is shown in the table 2, the recognition rate is the highest when the number of blocks is 3×3 and cell is 8×8.

| Bin | Cell | Block | Dimension | Recognition Rate (%) |
|-----|------|-------|-----------|----------------------|
| 8×8 |      | 2×2   | 1764      | 88.9                 |
|     |      | 3×3   | 2916      | 89.5                 |
|     |      | 4×4   | 3600      | 84.6                 |
| 9   |      | 2×2   | 900       | 86.9                 |
|     |      | 3×3   | 1296      | 87.0                 |
|     |      | 4×4   | 1296      | 85.4                 |

Considering the small size of bovine milk somatic cell images, choosing appropriate cell and block sizes can not only avoid dimension disasters, but also improve the performance of classifiers.

In order to verify the correct rate of each step of the classification model, three step-by-step experiments were carried out. As we can see from the table 3, the classification results for each layer are ideal.
Table 3. Recognition rate of each layer.

| Layer | Type   | Dimension | Recognition Rate (%) |
|-------|--------|-----------|----------------------|
| 1     | NE     | 2         | 97.0                 |
| 2     | LYM    | 1         | 99.0                 |
| 3     | Mø & EPI | 2916   | 89.5                 |

Finally, several commonly used classification methods are compared in table 4.

Table 4. Experimental comparison of different methods.

| Method   | Dimension | Time(s) | Recognition Rate (%) |
|----------|-----------|---------|----------------------|
| LBP      | 256       | 1.15    | 82.38                |
| HOG      | 2916      | 0.68    | 85.18                |
| MC +LBP\(^a\) | 2+1+256 | 2.26    | 95.11                |
| MC+HOG\(^b\) | 2+1+2916 | 1.73    | 96.02                |

\(^a\) Extraction of texture features by LBP operator.
\(^b\) MC means morphological character.

By comparing with traditional methods, the proposed binary model based on morphological features and HOG can effectively recognize milk somatic cells. Although the running time has been extended, the recognition rate has been improved within the acceptable range.

5. Conclusion
A method of milk somatic cell recognition based on dichotomy model is proposed in this paper. Using morphological features and HOG to recognize step by step, the four classification problems are transformed into three binary classification problems. The multilevel classifier was successfully applied to the classification and recognition of milk somatic cells. Experiments show that the classification effect of dichotomy model is ideal, and the correct rate is 96.02\%. In the follow-up work, increasing the recognition rate of each step of the model can improve the recognition rate of the whole algorithm for milk cells.

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References
[1] Xue, H.R. (2007) Studies on segmentation methods of milk somatic cell color image. D.IMAU.
[2] Lan, G., Yong, H.Z. (2016) Regularized robust coding for tumor cell image recognition based on dictionary learning. J. Journal of Computer Applications., 36(10):2895-2899.
[3] Qin, F., Gao, N., Peng, Y., et al. (2018) Fine-grained leukocyte classification with deep residual learning for microscopic images. J. Computer Methods and Programs in Biomedicine., 162:243-252.
[4] Gao, X.J. (2018) Research of polymorphous bovine somatic cell recognition based on feature fusion. D.IMAU.
[5] Zhang, X.L, Xue, H.R., Gao, X.J., et al. (2018) Milk somatic cells recognition based on multi-feature fusion and random forest. J. Journal of Inner Mongolia Agricultural University., 39(06):87-92.
[6] Dalal, N., Triggs, B. (2005) Histograms of oriented gradients for human detection. // IEEE Computer Society Conference on Computer Vision & Pattern Recognition.
[7] Chen, Y., Wang, M., Chen, X. (2015) Human detection based on HOG-PCA and LBP characteristics. J. Information Technology.,2015(2):101-105.
[8] Zhai, Z.F., Xu, Z., Zhou, X.Q., et al. (2015) Recognition of hazard grade for cotton blind stinkbug based on Naive Bayesian classifier. J. Transactions of the Chinese Society of Agricultural Engineering., 31(01):204-211.

[9] Wang, R.B., Xu, H.Y., Li,B., et al. (2018) Research on Method of Determining Hidden Layer Nodes in BP Neural Network. J. Computer Technology and Development., 28(04):31-35.

[10] Shen, H.Y., Wang, Z.X., Gao, C.Y., et al. (2008) Determining the number of BP network hidden layer units. J. Journal of Tianjin University of Technology., 2008(05):13-15.

[11] Khanlou,H.M., Sadollah, A., Ang, B.C., et al. (2014) Prediction and optimization of electrospinning parameters for polymethyl methacrylate nanofiber fabrication using response surface methodology and artificial neural networks. J. Neural Computing and Applications., 25(3-4):767-777.