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New Normal and Abnormal Red Blood Cells Features for Improved Classification

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Abstract

This paper focused obtaining new features for improved classification of red blood cells (RBCs). RBCs varies according to shapes, colors and sizes. Abnormal RBCs may be caused by anemia. Abnormal RBCs has great similarities among each other causing difficulties in medical diagnosis. In this work, spatial, spectral statistical features and geometrical features of RBCs are extracted from 1000 normal and abnormal RBCs. The extracted features are reduced using Principal Component Analysis (PCA) and tested with different types of machine learning algorithms for classification. Classifications were evaluated for high sensitivity, specificity, and kappa statistical parameters. The classifications yielded accuracy rates of 97.9%, 98% and 98% for discriminative (SVM), generative (RBFNN) and clustering (K-NN) algorithm respectively, which is an improvement over previous works.

Keywords: Principal Component Analysis; RBC classifications; red blood cells features; machine learning algorithms.

1. Introduction

Medical images help identify and treat various blood diseases and perform clinical studies to reach a diagnosis [1]. Blood can have normal and abnormal RBCs, where abnormalities are in the variations in shapes, colors and sizes. RBCs images can determine whether it is normal or abnormal by its external edge and central pallor area which may indicate different types of blood diseases or anemia [2].

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Anemia classification is required due to variations in the morphology of the RBCs images. The variation

morphology of RBCs produces a huge number of features. To efficiently classify them, number of features need to be kept small. This can be achieved when a larger decimation (reduction of features) factor is applied [4]. Classification makes use of machine learning algorithms and feature selection or feature reduction process. The process of decimation is useful in providing acceptable classification accuracy. Principal Component Analysis (PCA) is a statistical technique for feature reduction used in image recognition by almost all scientific disciplines [7]. PCA involves a linear transformation of the data such that, in the new coordinate frame, the projection of the data has its greatest variance along the first axis (the first principal component), its second greatest variance along the second principal component, etc. Variance is retained for representing the data, while higher-order ones are discarded. The number of principal components used depends on the level of accuracy needed to reconstruct the original data set [10]. Nandi and his colleagues [11] presented a survey of the applications of PCA used in the various medical images and the results obtained prove their efficacy. A few other studies were done on RBCs classification using PCA and machine learning algorithms [12]. Park and his colleagues [13] uses three machine learning algorithms to classify abnormal RBCs. Sharma and his colleagues [14] compares different machine learning classifiers of RBCs. Wheelless and his colleagues [15] mentioned that there are no literatures yet with regard to the anaemic RBCs feature selection that has been published leading to this work in studying issues related to this topic.

2. Features reduction of RBCs Images

This work performed studies on the new features for RBCs classification using data as described in the following sections below. The data sets were self-collected and various steps were performed to obtain the necessary samples from the raw data set collected. Features were extracted, then relevant and useful ones were selected to reduce the total number of features. The aim is to suggest the best features for the RBCs data set collected and explain the steps of obtaining them, validated by the results of three choices of classification methods.

2.1 Input Dataset of RBCs

In this study, 100 different anaemic blood smear slides are used. The slides are collected from the Hematology Unit of the Pathology Department, Faculty of Medicine, Serdang Hospital in 2015. An Olympus BX43 U-CAM D3 photo imaging microscope was used to transform peripheral blood smear slides into digital images at the Faculty of Medicine, SEGI University, Malaysia. Samples of normal and abnormal RBCs slides are shown in Figure 1.

2.2 *Materials and Methods*

2.2.1 *Feature Extraction*

This proposed work consists of extracting features and reducing it using PCA model. Initially, several steps were done in segmenting the individual RBCs image from the digital blood smear image. Thousands of individual normal and abnormal RBCs were obtained from the segmentation processes. Figure 2 shows some examples of individual RBCs. Feature extraction were done next. It is a difficult and complex process due to the

similarities in the RBCs. It requires the examination of cells by several features, such as size, area, shape, and internal configurations to distinguish RBCs that have different central pallors but with cells of similar size and shape.

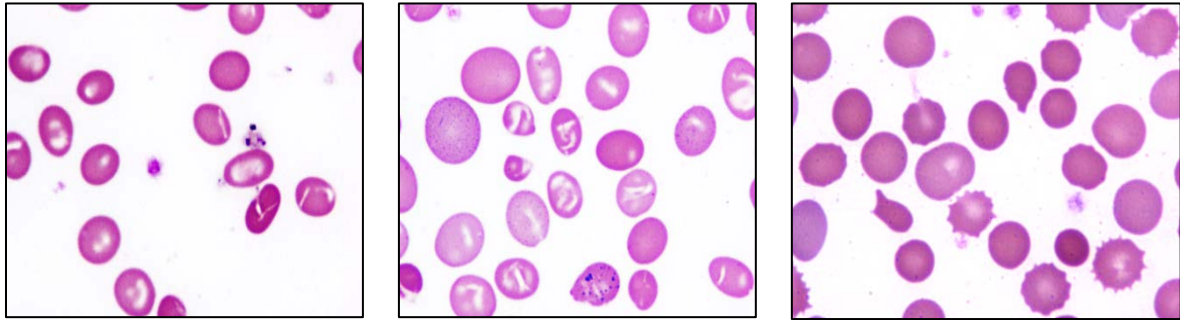


Figure 1: Anaemic blood smear image slide

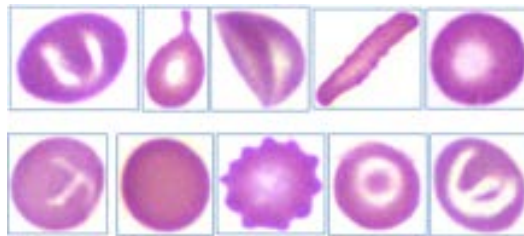


Figure 2: Samples of Individual RBCs

More specifically, feature extraction aimed to obtain a hybrid of statistical, spectral texture, and geometric features based on first, second, or higher-order statistics of the gray level of an image. In the case of spectral methods, textures are defined by the spatial frequencies of the band color image, which are red, green, and blue. Fourier descriptor is extracted as geometrical features to identify the shape of RBCs. Finally, a total of 271 features were extracted from 1000 individual RBCs. These led to a new data set called FRBCs. The features included some redundancies, that is, some of the variables are correlated with one another because they measured the same construct. Thus, reducing the observed variables into a small number of artificial variables (principal components) is important, which will account for most of the variances in the observed variables.

2.2.2 Feature Reduction Using PCA

The new FRBCs dataset included 271 features from 40 types of 1000 samples. PCA will reduce the observed variables into a smaller number of principal components (artificial variables) which will account for most of the variances in the observed variables. The motivations for this is to improve the prediction performance and to provide rapid and cost-effective predictors as well as to provide an improved analysis of the underlying process that generated the data in the ML algorithms. The PCA statistical model includes two phases; the data preparation and component extraction. SPSS version 21 was used in the process. The PCA technique is based on backward reduction features, which starts with all the variables (features) and removes them one by one at each step in order to eliminate the one that decreases the error significantly, until any removal increases the error

significantly. In the data preparation phase, data set underwent normalization using standard deviation method where all feature values are made to be in the same range, between (± 1) and replicated data removed as suggested by Gibson and his colleagues [17].

The normalization step aims to reduce the significant variations in the range of values of raw data in several ML algorithms. The majority of classifiers calculated the distance between two points. When one of the features has a broad range of values, this particular feature will determine the distance. The data set obtained from the scaling process normality test was applied using Gaussian distribution test. Results of Gaussian test of the FRBC dataset shows that 99.7% of feature RBCs data set ranges from -0.4 and 0.8 and 68% of FRBCs data are in the range from 0 and 0.4 and the data has normal distribution.

Before applying PCA to the FRBC data a test whether the FRBC data are suitable for reduction was done using the Kaiser–Meyer–Olkin test. The null hypothesis is tested to prove that the correlation matrix is an identity matrix of FRBC data set by using Bartlett's test of sphericity. Then Pearson test was used to test the correlation coefficients matrix. Subsequently, the extraction of communalities for each feature is conducted. The communalities indicated that the variance in each of the original features is explained by the extracted component. The summaries of 271 variances with relative importance for each feature are shown in Table 1.

Table 1: Descriptive summaries of variance, relative importance features

Varince	Number of features	Relative features importance
0.80-0.99	241	88.95
0.60-0.79	17	6.26
< 9	13	4.79
Total	271	100

The components are extracted after the FRBC data set was prepared. In the component extraction phase, Cattell's scree test was used to select the number of component return, which included plotting the eigenvalues of the component and examining the plot to find a point where the shape of the curve changes its direction. The recommendation is that all components that have large eigenvalues above the certain points (the elbow in the graph) should be retained because they contributed the most for the explanation of variance in the dataset. 8 components were chosen by this way with a threshold value of 0.60 for the loading component matrix [16]. The estimation score (ESS) of the PCA model was tested by using the Bartlett method to test the orthogonal components solution, which is calculated as follows [18,19] .

$$ESS = \sum_{i=1}^8 MLi \tag{1}$$

Where:

ESS: is an estimation of score model

ML: is the maximum loading variable in factor

3. Evaluating Feature Reduction Results

After the feature reduction processes using PCA model we done, the resulting feature sets were tested. The evaluation of the PCA model is described in the following sections and the evaluation procedure of the obtained features using three classification methods are also given.

3.1 Evaluation of the PCA model

The evaluation of the PCA model was performed according to the identity and degree of rotation (DoR) matrices. DoR is measured by the average diameter of the component transformation matrix. It is the efficiency indicator of the rotation process to obtain the orthogonal components. The value of DoR should be more than 0.70. The component transformation matrix is presented in Table 3.

Table 3: Component Transformation or DoR Matrix

Component	1	2	3	4	5	6	7	8
1	.847	.352	-.031	.009	.196	-.010	-.004	.001
2	-.403	.882	.108	-.024	.012	-.008	.005	-.012
3	.089	-.080	.979	.138	-.115	-.004	-.003	-.134
4	-.075	-.001	-.120	.967	-.074	.017	-.002	.214
5	.044	-.158	-.035	-.029	.930	.228	.005	-.129
6	-.008	.042	.017	-.015	.180	.972	.000	.093
7	.024	.060	.016	-.059	-.196	.010	.744	-.157
8	.006	.089	.003	.005	.020	.030	-.461	.890

4. Classification using Obtained features

Classifications were performed using machine learning (ML) algorithms to test the features and component abilities in recognizing different types of RBCs. Three different supervised ML algorithms, each with its own properties, were applied using Weka software. The first algorithm is generative in the form of artificial neural networks (RBFNN), the second algorithm is discriminative in the form of support vector machines(SVM), and the third is a clustering algorithm, which is the K-nearest neighbor algorithm(KNN).

The purpose of using the three algorithms is to enable a fair comparison among them and to measure the efficiency of the extracted feature components. The confusion matrix was used to evaluate the performance of the classification models through discrimination metrics. In addition, evaluation was performed with accuracy, sensitivity, specificity, F-measure, and area under Receiver operating characteristic (ROC), which are the common metrics of comparison in the process of evaluating ML classification algorithms.

5. Classification Results

Feature reduction is computed by using the PCA technique for all features (normal and anemic) RBCs. The PCA technique reduced 271 features to 8 feature components, which created the new data set, CRBCs. Each component contains at least two features with a high loading value and a minimum 0.90 variance. The accuracy of the three ML classifications in the data set of features and components is shown in Table 4.

Table 4: Comparison between three Classification

ML- Algorithms	Data set	Accuracy%	Time Sec.
KNN	FRBCs	90	1.01
	CRBCs	98	0.01
SMO-SVM	FRBCs	92	6.97
	CRBCs	97.9	1.89
RBFNN	FRBCs	91.875	18478
	CRBCs	98	2.36

From table 4, the effected of PCA technique is clear, where increase the accuracy of the results of the classification task. In addition reducing training time especially in the RBFNN algorithm. The evaluation of classification performance of the three ML algorithms is presented in Table 5. It clearly show that the perfect performance of algorithms after using PCA technique

Table 5: Evaluation results of the ML algorithms

ML- Algorithms	Accuracy	Precision	Recall	F-measure
KNN	99.90%	0.979	0.979	0.979
SMO-SVM	98%	0.98	0.98	0.98
RBFNN	98 %	0.98	0.98	0.98

6. Conclusion

This work mainly aimed to establish new features of RBCs that can distinguish normal and abnormal RBCs. Through different types of ML methods, we achieved an improved precision and accuracy for interpreting normal and anaemic RBC images. According to the experimental results, it was concluded that several features

extracted from anemic RBC images are not significant when observed independently but improved the percentage of accuracy when combined with other features. In addition, the reduction in time consumption was very clearly visualized in the training of RBFNN algorithms. The high classification results and the closeness of components indicated their strength.

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