

RDNet: ResNet-18 with Dropout for blood cell classification

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Abstract: (Aims) Blood cells are hematopoietic pluripotent stem cells derived from bone marrow. Blood diseases occur primarily in the hematopoietic system and can affect the hematopoietic system with abnormal blood changes, characterized by anemia, bleeding, and fever. It is helpful for doctors to diagnose blood diseases by classifying blood cells. However, doctors take a lot of time and energy to classify blood cells. The classification process is easily disturbed by external factors, such as doctors' lack of rest, fatigue, etc. Many researchers use CNN to classify and detect red blood cells or white blood cells. However, using CNN has some problems in the classification or detection process. First, most researchers only classify blood cells into two categories, but there are many different types of blood cells. In addition, some studies are multi-classification of cells, but the results are often not ideal. **(Methods)** We propose a new model (RDNet) for the automatic classification of four types of blood cells to deal with these problems. The proposed RDNet selects the pre-trained ResNet-18 as the backbone. We transfer the pre-trained ResNet-18 because of the difference between the blood cell data set with the ImageNet data set. We add dropout to improve the classification performance. **(Results)** The accuracy of the proposed RDNet is 86.53%. The proposed RDNet obtains better accuracy than the transferred ResNet-18 because we add dropout in RDNet. Based on the accuracy, the proposed model is an effective tool to classify blood cells.

Keywords: blood cells; dropout; ResNet-18; transfer learning; convolutional neural network

1. Introduction

Blood cells are hematopoietic pluripotent stem cells derived from bone marrow. In addition to having the ability to proliferate, stem cells can migrate out of bone marrow hematopoietic tissue under certain circumstances and form hematopoietic cell nodules with blood flow to extramedullary tissue, which is called colony-forming unit.

Blood diseases occur primarily in the hematopoietic system and can affect the hematopoietic system with abnormal blood changes, characterized by anemia, bleeding, and fever. The factors leading to blood diseases may be: 1 Malnutrition can lead to malnutrition anemia, 2 There may also be some external toxic effects, such as chemicals or radiation. It is helpful for doctors to diagnose blood diseases by classifying blood cells. However, it takes a lot of time and energy for doctors to classify blood cells. The classification process is easily disturbed by external factors, such as doctors' lack of rest, fatigue, etc.

More and more researchers use computer technology to classify blood cells. [Tiwari, et al. \[1\]](#) developed a deep learning model, which was based on convolution neural networks (CNN). The CNN-based learning model was to classify the blood cell images. [Long, et al. \[2\]](#) proposed a novel model (BloosCaps) to classify blood cells. The proposed model achieved an accuracy of 99.3%. [Patil, et al. \[3\]](#) presented a method- Canonical Correlation Analysis (CCA) to deal with the problems of multiple cells overlap. The results showed that the proposed model improved accuracy than other blood cell classification models. [Hegde, et al. \[4\]](#) provided the comparison of deep learning models and traditional approaches in the classification of white blood cells. The traditional approach got a 99.8% accuracy. The deep learning models obtained a 99% accuracy. [Kutlu, et al. \[5\]](#) used Regional Convolutional Neural Networks (R-CNN) to identify white blood cells. The R-CNN obtained high accuracy in various types of white blood cells. [Banik, et al. \[6\]](#) proposed a novel WBC nucleus segmentation model based on the k-means algorithm and color space conversion. The proposed model got a 98.61% accuracy. [Lamberti \[7\]](#) proposed a model to classify blood cells. Support vector machine model was used in the proposed model. [Pasupa, et al. \[8\]](#) proposed a model to classify dog red blood cell morphology. The proposed model was based on CNN. [Dhieib, et al. \[9\]](#) presented a model to automatically count blood cells. The model combined CNN, instance segmentation, R-CNN, and transfer learning. [Kassim, et al. \[10\]](#) proposed RBCNet to detect and count blood images. The proposed RBCNet used U-Net and R-CNN. The study obtained an accuracy that was higher than 97%.

From the above analysis of the research, it can be concluded that many researchers use CNN to classify and detect red blood cells or white blood cells. However, there are some problems in the classification or detection process. First, most researchers only classify blood cells into two categories, but there are many different types of blood cells. In addition, some studies are multi-classification of cells, but the results are often not ideal. To deal with these problems, we propose a new model (RDNet) for the automatic classification of four types of blood cells. The proposed RDNet selects the pre-trained ResNet-18 as the backbone. We transfer the pre-trained ResNet-18 because of the difference between the blood cell data set with the ImageNet data set. The transferred pre-trained ResNet-18 is abbreviated as TRNet. We add dropout to improve the classification performance.

The organization of the rest paper is as follows. Section 2 discusses the blood cell data set used in this paper. The methodology is shown in Section 3. Section 4 is about the results. The conclusion is given in Section 5.

2. Materials

The data set used in this paper can be available on the Kaggle website. There are four types of blood cells, which are Eosinophil, Lymphocyte, Monocyte, and Neutrophil, respectively. Some figures of four types of blood cells are shown in Figure 1.

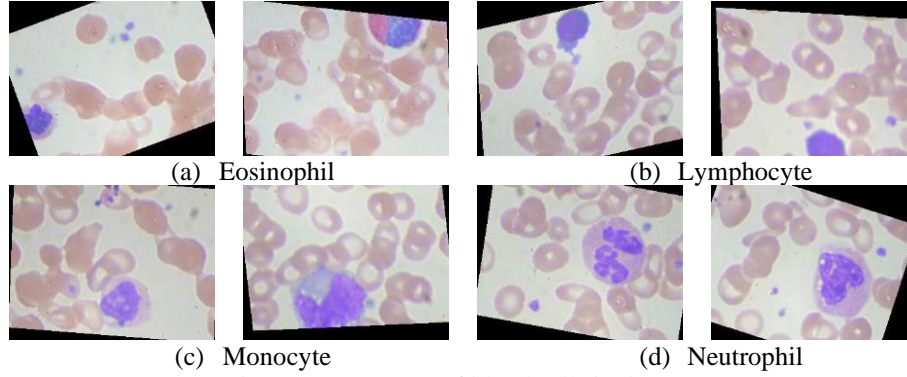


Figure 1 Four types of blood cells in data set

3. Methodology

One of the most important steps in image classification [11] is feature extraction. But it is very difficult for researchers to extract useful information from images because images contain too much information. Previously, researchers generally manually extracted the features of images. However, manually extracting features is time-consuming and usually cannot get good results [12]. With the rapid development of artificial intelligence [13], researchers pay more attention to the feature extraction of images using computer vision technology. More and more excellent artificial intelligence models have been proposed, such as VGG [14], AlexNet [15], etc.

3.1 Proposed RDNet

A novel method (RDNet) is proposed for the automatic classification of blood cells. The pipeline of the proposed RDNet is shown in Figure 2. The pseudocode of our model is given in Table 1. The ResNet-18 is pre-trained on the ImageNet data set. The pre-trained ResNet-18 is chosen as the backbone of the proposed RDNet. We transfer the pre-trained ResNet-18. The transferred pre-trained ResNet-18 is abbreviated as TRNet. We remove the softmax and classification layer from the pre-trained ResNet-18. What's more, we add FC64, FC4, softmax, and classification layers to form the TRNet. We add dropout between FC64 and FC4 to improve the classification performance. The whole network is the proposed RDNet.

Table 1 The pseudocode of our model

Step 1: Load the pre-trained ResNet-18.
Step 2: Transfer the pre-trained ResNet-18.
Step 2.1 Remove, softmax, and classification layer from the pre-trained ResNet-18.
Step 2.2 Add FC64, FC4, softmax, and classification layers.
Step 2.3 The whole network is named TRNet.RDNet

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- Step 3: Add dropout between FC64 and FC4.
- Step 3.1: The whole network is named RDNet.
- Step 4: Train the proposed RDNet.
- Step 4.1: Input is the training set.
- Step 4.2: Target is the labels of the training set.
- Step 5: Test the trained RDNet on the test set.
- Step 6: Report the classification performance of the trained RDNet.
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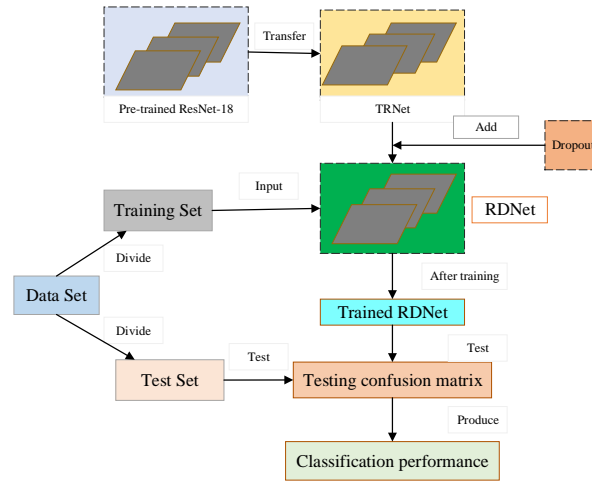
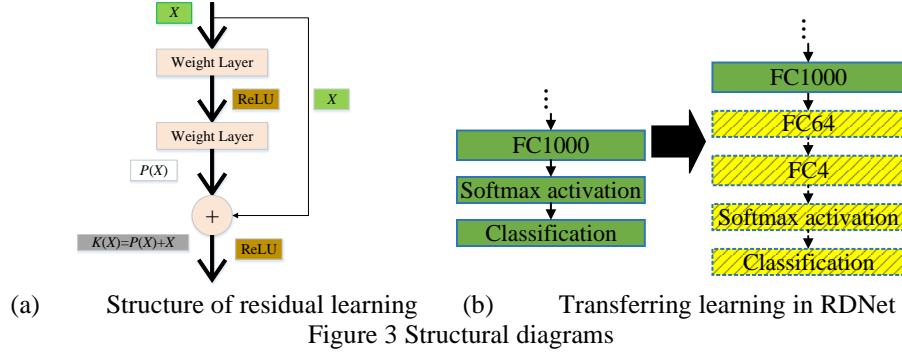


Figure 2 The pipeline of the proposed RDNet

3.2 The backbone of the proposed RDNet

More information can usually be obtained with the deeper network. However, with the deepening of the network, the optimization effect worsens, and the accuracy of test data and training data is reduced. This is because the deepening of the network will cause the problems of gradient explosion and gradient disappearance. [He, et al. \[16\]](#) proposed a new model (residual learning) to reduce these problems. The structure of residual learning is shown in Figure 3(a).



The calculation formula of residual learning is as follows. Suppose the input is X , the learned feature is $K(X)$, and the residual learning result is $P(X)$:

$$P(X) = K(X) - X \quad (1)$$

The formula of the learned feature is:

$$K(X) = P(X) + X \quad (2)$$

Residual learning establishes a direct connection between input and output (identity mapping). Through identity mapping, the performance of the next layer will not decline at least.

We select the pre-trained ResNet-18 as the backbone of the proposed RDNet. We transfer the pre-trained ResNet-18, as shown in Figure 3(b). We add the FC4 layer because of the four types of blood cells in the data set. The FC64 is added between FC1000 and FC4 for reducing the dimensional differences.

3.3 Dropout

In the machine learning model, if the model's parameters are too many and the training samples are too few, the machine learning model is easy to produce the problem of overfitting. The overfitting problem is embodied in: the loss function of the model in the training data is small, and the prediction accuracy is high; but, in the test data, the loss function is relatively large, and the prediction accuracy is low. Therefore, we use dropout to solve the overfitting problem in this paper. The dropout is shown in Figure 4. Dropout can be used as a trick for training the deep neural network. The overfitting problem can be significantly reduced in each training batch by ignoring half of the feature detectors (making half of the hidden layer node value 0). We add the dropout layer between FC64 and FC4 to improve the classification performance.

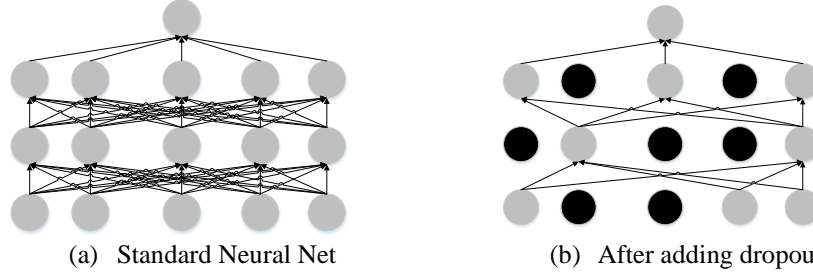


Figure 4 Comparison between using dropout and not using dropout in network structure

4 Results

4.1 Experiment settings

The hyper-parameter settings of the proposed model are modified. We set the minibatch size to 64 to overcome the problem of overfitting. The max-epoch is 1. Based on the experience, the learning rate is set as $1e-4$. The hyper-parameter settings of the proposed model are given in Table 2.

Table 2 The hyper-parameter settings of the proposed model

Hyper-parameter	Value
Minibatch size	64
Max-epoch	1
Learning rate	$1e-4$

4.2 The performance of the proposed model

In this paper, there are four types of blood cells: Eosinophil, Lymphocyte, Monocyte, and Neutrophil, respectively. Each of four different types of blood cells has about 3,000 images. The details of the data set are given in Table 3. The test confusion matrix of our model is shown in Table 4. The accuracy of our model is 86.53%. The specific calculation is:

$$\text{accuracy(RDNet)} = \frac{492 + 618 + 474 + 568}{623 + 620 + 620 + 624} = 86.53\% \quad (3)$$

Table 3 The details of the data set

	Eosinophil	Lymphocyte	Monocyte	Neutrophil
Training set	2497	2483	2478	2499
Test set	623	620	620	624

Table 4 The test confusion matrix of our model

		Predicted class			
		Eosinophil	Lymphocyte	Monocyte	Neutrophil
Actual class	Eosinophil	492	1	0	130
	Lymphocyte	0	618	2	0
	Monocyte	60	0	474	86
	Neutrophil	56	0	0	568

4.3 Comparison of the proposed model with TRNet

To better show the superiority of our model, we compare the proposed RDNet with the TRNet. The test confusion matrix of the TRNet is demonstrated in Table 5. The accuracy of the TRNet is:

$$\text{accuracy}(\text{TRNet}) = \frac{454 + 618 + 457 + 567}{623 + 620 + 620 + 624} = 84.28\% \quad (4)$$

The proposed RDNet obtains better accuracy than the TRNet because we add dropout in RDNet.

Table 5 The test confusion matrix of the TRNet

		Predicted class			
		Eosinophil	Lymphocyte	Monocyte	Neutrophil
Actual class	Eosinophil	454	4	5	160
	Lymphocyte	0	618	2	0
	Monocyte	5	0	457	158
	Neutrophil	57	0	0	567

5 Conclusion

The paper proposes a new model (RDNet) for the automatic classification of four types of blood cells. The proposed RDNet selects the pre-trained ResNet-18 as the backbone. We transfer the pre-trained ResNet-18 because of the difference between the blood cell data set with the ImageNet data set. The transferred pre-trained ResNet-18 is abbreviated as TRNet. We add dropout to improve the classification performance. The accuracy of the proposed RDNet is 86.53%. The proposed RDNet obtains better accuracy than the TRNet because we add dropout in RDNet. Based on the accuracy, the proposed model is an effective tool to classify blood cells.

Even though the proposed model gets good results, there are still some limitations. 1. In this paper, we only test single cells and do not test overlapping cells. 2. Although four kinds of blood cells are classified in this paper, there are many kinds of cells that we have not tested.

In future research, we will collect more kinds of blood cells for classification. What's more, we will classify single cells and include overlapping cells in the next paper.

Reference

- [1] P. Tiwari *et al.*, "Detection of subtype blood cells using deep learning," *Cognitive Systems Research*, vol. 52, pp. 1036-1044, 2018.
- [2] F. Long, J.-J. Peng, W. Song, X. Xia, and J. Sang, "BloodCaps: A capsule network based model for the multiclassification of human peripheral blood cells," *Computer Methods and Programs in Biomedicine*, vol. 202, p. 105972, 2021.
- [3] A. Patil, M. Patil, and G. Birajdar, "White blood cells image classification using deep learning with canonical correlation analysis," *IRBM*, vol. 42, no. 5, pp. 378-389, 2021.
- [4] R. B. Hegde, K. Prasad, H. Hebbar, and B. M. K. Singh, "Comparison of traditional image processing and deep learning approaches for classification of white blood cells in peripheral blood smear images," *Biocybernetics and Biomedical Engineering*, vol. 39, no. 2, pp. 382-392, 2019.
- [5] H. Kutlu, E. Avci, and F. Özyurt, "White blood cells detection and classification based on regional convolutional neural networks," *Medical hypotheses*, vol. 135, p. 109472, 2020.
- [6] P. P. Banik, R. Saha, and K.-D. Kim, "An automatic nucleus segmentation and CNN model based classification method of white blood cell," *Expert Systems with Applications*, vol. 149, p. 113211, 2020.
- [7] W. F. Lamberti, "Blood cell classification using interpretable shape features: A Comparative study of SVM models and CNN-Based approaches," *Computer Methods and Programs in Biomedicine Update*, vol. 1, p. 100023, 2021.
- [8] K. Pasupa, S. Vathanaavaro, and S. Tungjitnob, "Convolutional neural networks based focal loss for class imbalance problem: A case study of canine red blood cells morphology classification," *Journal of Ambient Intelligence and Humanized Computing*, pp. 1-17, 2020.
- [9] N. Dhieb, H. Ghazzai, H. Besbes, and Y. Massoud, "An automated blood cells counting and classification framework using mask R-CNN deep learning model," in *2019 31st International Conference on Microelectronics (ICM)*, 2019: IEEE, pp. 300-303.
- [10] Y. M. Kassim *et al.*, "Clustering-based dual deep learning architecture for detecting red blood cells in malaria diagnostic smears," *IEEE Journal of Biomedical and Health Informatics*, vol. 25, no. 5, pp. 1735-1746, 2020.
- [11] S. Lu, Z. Zhu, J. M. Gorriz, S. H. Wang, and Y. D. Zhang, "NAGNN: Classification of COVID-19 based on neighboring aware representation from deep graph neural network," *International Journal of Intelligent Systems*, 2021.
- [12] S.-Y. Lu, S. C. Satapathy, S.-H. Wang, and Y.-D. Zhang, "PBTNet: A New Computer-Aided Diagnosis System for Detecting Primary Brain Tumors," *Frontiers in Cell and Developmental Biology*, p. 2926, 2021.
- [13] J. M. Górriz *et al.*, "Artificial intelligence within the interplay between natural and artificial computation: Advances in data science, trends and applications," *Neurocomputing*, vol. 410, pp. 237-270, 2020.
- [14] K. Simonyan and A. Zisserman, "Very deep convolutional networks for large-scale image recognition," *arXiv preprint arXiv:1409.1556*, 2014.
- [15] A. Krizhevsky, I. Sutskever, and G. E. Hinton, "Imagenet classification with deep convolutional neural networks," *Advances in neural information processing systems*, vol. 25, pp. 1097-1105, 2012.

- [16] K. He, X. Zhang, S. Ren, and J. Sun, "Deep residual learning for image recognition," in *Proceedings of the IEEE conference on computer vision and pattern recognition*, 2016, pp. 770-778.