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InceptionV3-Based Blood Cell Classification for Cancer Detection

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Abstract: Blood cell morphological analysis plays a vital role in clinical diagnosis, especially in the early detection of leukemia, anemia and other blood system diseases. Conventional image processing techniques are difficult to deal with complex situations such as cell overlap and uneven staining, and basic machine learning methods also have obvious limitations in extracting complex morphological features. Deep learning has shown excellent performance in the field of medical image classification and provides a new technical approach for automated analysis of blood cells. This study aims to develop an efficient and accurate blood cell classification model to assist in the early diagnosis of blood diseases and cancer. By adopting the InceptionV3 network structure and combining the 'Grid Search Enhanced with Coordinate Ascent' hyperparameter optimization method, the study provides a systematic automated classification model training method for blood cell multi-classification tasks. The experiment was based on a dataset containing five types of cells. The results showed that the final model achieved an accuracy of 99.20% on the test set, the AUC of all classes reached 1.00, and the average specificity was as high as 99.80%, providing a reliable technical reference for clinical blood pathology analysis and early cancer screening.

Keywords: Inception, Blood Cell, Image Classification, Deep Learning, Hyperparameters Optimization.

Disciplines: Computer Science. **Subjects:** Image Classification.

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1 INTRODUCTION

With the increasing demand for hematology and clinical diagnosis, accurate and rapid morphological analysis of blood cells has become an important means of diagnosing leukemia, anemia and other blood system diseases. However, traditional manual inspection methods often rely on the experience of pathologists to observe and annotate each cell in the microscopic image one by one, which is not only time-consuming and labor-intensive, but may also cause fluctuations in accuracy due to subjective factors. In addition, in the actual detection process, there are complex situations such as overlap and staining differences between cells. Traditional image processing methods or simple machine learning models are difficult to deal with effectively. A smarter and more efficient automated solution is needed to improve the accuracy and stability of blood cell classification and identification.

To overcome the above limitations, this study proposed a systematic automated classification model training method, the core of which includes model selection, hyperparameter adjustment method selection, and hyperparameter adjustment experimental design, which accurately distinguishes multiple cell types including basophil, erythroblast, monocyte, myeloblast and seg_neutrophil. The experiment will use the InceptionV3 network structure and perform multiple rounds of hyperparameter optimization through Grid Search Enhanced with Coordinate Ascent (GSECA [13]) to improve generalization ability and convergence speed. This method not only ensures efficient model training, but also strives to achieve accurate recognition of different cell types under complex image backgrounds and subtle morphological differences. It is expected that the automated classification process proposed in this study can provide more reliable and practical technical support for the early diagnosis and subsequent treatment of blood diseases, and bring new ideas and methods to clinical testing and scientific research applications.

2 RELATED RESEARCH

2.1 MEDICAL IMAGE PROCESSING METHODS

As an important branch of the intersection of medicine and computer science, medical image processing has made significant progress in recent years. Medical image processing usually includes multiple key links such as image segmentation, registration, detection, enhancement and diagnosis. Its purpose is to improve the quality and accuracy of medical images, thereby assisting in the diagnosis and treatment effect. Wang and Summers (2012) outlined the

application of machine learning in medical image processing, focusing on image segmentation, registration, detection and diagnosis in radiology, and analyzed in detail the key steps such as feature extraction, dimensionality reduction and classification, laying the foundation for the subsequent development of deep learning methods [1].

Sharma and Aggarwal (2010) reviewed the automatic segmentation technology of CT and MR images and discussed the advantages and disadvantages of existing methods [2]. The article pointed out that although simple grayscale and regional methods have limited applications, they can be combined with artificial intelligence technology to improve the effect. The method using texture features and atlas has outstanding results in segmentation, but requires professional knowledge. The fuzzy C-means algorithm is suitable for complex structure segmentation. Although the neural network algorithm has high accuracy in texture segmentation, it relies on a lot of supervision and training. An ideal segmentation algorithm should have accuracy, reliability and robustness.

Salem et al. (2019) studied medical image enhancement methods based on histogram algorithms, focusing on improving the visual quality of images to reduce the risk of misdiagnosis [3]. The study developed a variety of histogram-based algorithms and used MATLAB to conduct a comprehensive analysis of the enhancement performance of these algorithms, providing an important reference for image processing methods in the field of medical imaging.

2.2 Blood Cell Image Classification and Detection

Automated classification and detection of blood cell images plays a key role in clinical diagnosis. It can not only effectively distinguish normal from abnormal blood cells, but also be used to monitor the progression of blood diseases and assist in subsequent treatment decisions.

Jambhekar (2011) used a red blood cell morphology recognition method based on image processing and combined it with a multi-layer perceptron model to classify red blood cells and white blood cells[4]. This study excluded overlapping cells through edge detection and segmentation technology, and used morphological features such as cell size, edge shape, and internal dark spots as the main basis for judgment. The experimental results showed that its classification accuracy reached about 81%, and it achieved good results in identifying sickle-shaped red blood cells and regular red blood cells, providing a reference for the subsequent automated detection of blood cell subtypes.

Taherisadr et al. (2013) used an image processing method based on threshold judgment for blood cell classification[5]. By extracting key features such as the area, perimeter, morphological geometric factors, and central pale area of red blood cells, and comparing thresholds layer by layer, the cell class is determined. This method can ultimately classify red blood cells into 12 subtypes, including iron deficiency anemia, β-thalassemia, and sickle cells, reducing over-reliance on expert experience and providing a more operational approach for the automated identification of abnormal blood cell morphology.

Maitra et al. (2012) proposed an automated blood cell detection and counting method based on Hough transform [6]. This method first uses preprocessing steps such as edge detection and adaptive histogram equalization to highlight the outline of red blood cells, and then uses Hough transform to identify circular features to complete the counting, which significantly improves efficiency and accuracy compared to manual methods.

2.3 Blood Cell Image Classification Based on Deep Learning

Deep learning technology has brought a new idea to blood cell image classification. Unlike traditional methods that rely on complete cell contours, CNN can extract features from local areas and achieve high accuracy even when cells are partially overlapped or have poor visibility.

Kutlu et al. (2020) proposed a white blood cell detection and classification scheme based on regional convolutional neural network (R-CNN) and conducted experiments on BCCD and LISC datasets[7]. By comparing multiple networks (AlexNet, VGG16, GoogLeNet, ResNet50), the results showed that ResNet50 combined with transfer learning strategy had the best classification effect, with an accuracy of 99.52% for lymphocytes, 98.40% for monocytes, 98.48% for basophils, 96.16% for eosinophils, and 95.04% for neutrophils.

Fanous et al. (2022) automatically located and classified white blood cells based on stain-free phase imaging (cSLIM) combined with deep learning[8]. The phase image is first converted into a bright field image, and then the target is detected using EfficientNet, and then the segmentation mask is generated with the help of U-Net. The experimental results show that the average accuracy of the detection and classification of neutrophils, eosinophils, lymphocytes and monocytes is 75%, and the pixel-level segmentation F1 score is about 80%, which provides a new technical idea for fast and low-cost blood cell analysis.

3 Material and Methods

3.1 Dataset

The public dataset of blood cell microscopic images used in this study is designed to support the development of automated leukemia detection systems. The dataset contains five cell classes: basophil, erythroblast, monocyte, myeloblast, and seg_neutrophil. The image size of each class is 350-400 pixels, all stained with Wright-Giemsa, and collected under 100× objective oil immersion (total magnification 1000 times), and saved in color format (RGB).

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The data is divided into training set, validation set, and test set at a ratio of 70%, 15%, and 15%, respectively, to ensure a balanced distribution of classes; specifically, each class has approximately 700 images in the training set, 150 images in the validation set, and 150 images in the test set. Figure 1 shows the distribution of the number of samples in each class in the dataset, and Figure 2 shows example images of samples in each class.

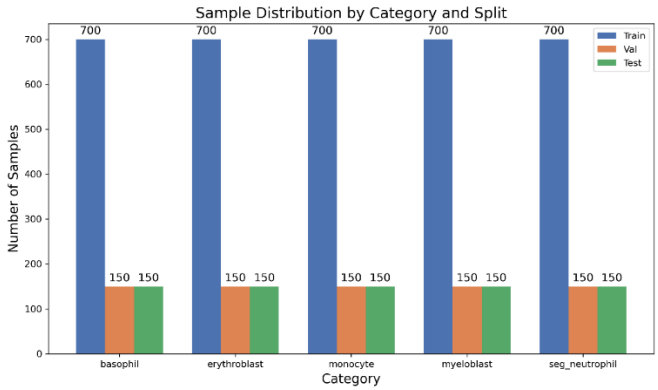

FIG. 1 SAMPLE DISTRIBUTION OF DATASET

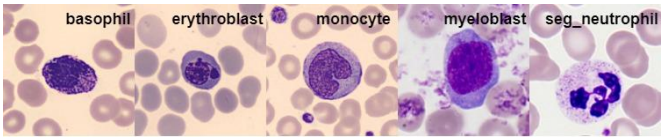

FIG. 2 SAMPLE IMAGES FOR EACH CLASS OF BLOOD CELL

3.2 MODEL SELECTION

In terms of model selection, after a comprehensive comparison of the performance and complexity of various mainstream convolutional neural network structures (such as VGG [9], ResNet [10], etc.), this study finally selected InceptionV3 as the experimental model. The Inception series of networks was originally proposed by Szegedy et al. [11]. Its core idea is to extract features through multi-scale convolution kernels in parallel to better capture key information at different scales. In InceptionV3, factorized convolution and auxiliary classifiers are further introduced to improve the efficiency of feature extraction and the training stability of the model on large-scale images [12]. Compared with earlier deep networks such as VGG, InceptionV3 has shown better parameter utilization and generalization performance in many image classification tasks. At the same time, it effectively controls the network size and computational complexity while maintaining a high accuracy. Given that this study needs to balance training efficiency and classification effect with limited computing resources, InceptionV3's multi-scale parallel structure and good migration performance make it a more suitable choice.

3.3 EXPERIMENT SETS

This experiment used a search method called Grid Search Enhanced with Coordinate Ascent (GSECA) in the hyperparameter optimization process to gradually explore the three dimensions of learning rate, batch size, and number of training rounds [13]. This method can effectively avoid the huge computational overhead of traditional grid search in high-dimensional hyperparameter space. This method dynamically adjusts the hyperparameter values and continuously observes the changes in the accuracy of the validation set by making multiple local increases and decreases in the initial hyperparameters (see Table 1), thereby fully searching the space while taking into account convergence efficiency.

TABLE 1. INITIAL HYPERPARAMETER SET, UPDATE RULES AND BOUNDARY VALUES

Hyperparameters	Initial value	Update Rule	Boundary Values
Learning Rate	1.00E-2	$x_{n+1} = x_n /10$	1.00E-6
Batch Size	10	$x_{n+1} = x_n + 10$	60
Epochs	20	$x_{n+1} = x_n * 1.2$	/

Specifically, combined with the idea of moving only in one dimension at a time in a three-dimensional coordinate system, the experiment uses three parameter adjustments as a cycle, and only adjusts one hyperparameter value each time, and forms a new hyperparameter group with the other two unadjusted parameters for training. From the training results of these three sets of hyperparameter models, the best combination is obtained according to the accuracy of the validation set, and compared with the historical best validation set accuracy. If it is lower than the historical best twice in a row, indicating that the validation set accuracy is blocked, the optimization process is stopped and the local optimal hyperparameter configuration is obtained.

During the experiment, in order to quantify and record the changes in indicators during the hyperparameter optimization process, the experiment saves data such as loss and accuracy of the training, validation and test sets. For each hyperparameter test, the program will perform a complete training, verify the test process, and count the accuracy and loss of each class. After determining the optimal hyperparameter group, the experiment will conduct final training on the InceptionV3 model and evaluate and analyze it on the test set.

3.4 EXPERIMENTAL ENVIRONMENT

The experimental running software environment is cuda11.8, python3.8, pytorch2.1.0, and the hardware platform parameters are shown in Table 2.

TABLE 2. HARDWARE ENVIRONMENT FOR EXPERIMENT

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Unit	Model
CPU	12th Gen Intel(R) Core(TM) i7-12700H @ 2.30GHz
GPU	NVIDIA GeForce RTX 3050ti GPU(4G)
RAM	DDR5 4800MHz 16G

4 EXPERIMENTAL RESULTS

TABLE 3. HYPERPARAMETER OPTIMIZATION PROCESS MODEL PERFORMANCE

DE_COUNT	lrate	batch_size	epochs	train_loss	train_acc	val_loss	val_acc	test_loss	test_acc
0	1e-02	10	20	0.0282	0.9096	0.2842	0.8787	0.3020	0.8693
0	1e-02	20	20	0.0137	0.9126	9.5063	0.5293	9.1947	0.5320
0	1e-02	10	24	0.0294	0.9052	0.0671	0.9760	0.0768	0.9787
0	1e-03	10	20	0.0136	0.9581	0.0191	0.9933	0.0228	0.9920
0	1e-03	20	20	0.0058	0.9650	0.0132	0.9933	0.0215	0.9907
0	1e-03	10	24	0.0126	0.9609	0.0475	0.9800	0.0523	0.9880
0	1e-04	10	20	0.0082	0.9751	0.0051	1.0000	0.0075	0.9987
0	1e-04	20	20	0.0033	0.9801	0.0047	0.9987	0.0113	0.9960
0	1e-04	10	24	0.0075	0.9772	0.0123	0.9960	0.0389	0.9907
0	1e-05	10	20	0.0248	0.9246	0.0196	0.9947	0.0220	0.9947
1	1e-04	30	20	0.0020	0.9826	0.0083	0.9960	0.0114	0.9960
1	1e-04	20	24	0.0030	0.9823	0.0155	0.9960	0.0150	0.9947
1	1e-05	20	20	0.0120	0.9299	0.0211	0.9960	0.0311	0.9920

Table 3 shows the loss and accuracy of the InceptionV3 model on the training, validation, and test sets under different hyperparameter combinations. The hyperparameters listed in the table include learning rate (lrate), batch size (batch_size), and number of training rounds (epochs), combined with an annealing counter called DE_COUNT to record situations when the validation set performance stagnates or repeats in multiple iterative searches. It can be observed that as the learning rate gradually decreases or the batch size is adjusted appropriately, the model's accuracy on the validation set can reach up to 100.00%, while maintaining a high accuracy of about 99.87% on the test set; the corresponding training loss and validation loss also show a clear downward trend, indicating that this optimization strategy has a positive effect on improving the generalization performance of the model. By comparing the indicators in different rows, it can be seen that if the learning rate is set too large or too small, the validation loss will fluctuate greatly or even increase significantly, resulting in a decrease in the accuracy of the final test set; when the hyperparameters are selected relatively reasonably, the model can achieve stable and excellent performance on the data sets at each stage, further confirming the role of the optimal hyperparameter group obtained after multiple rounds of search and adjustment in promoting the convergence and generalization of model training.

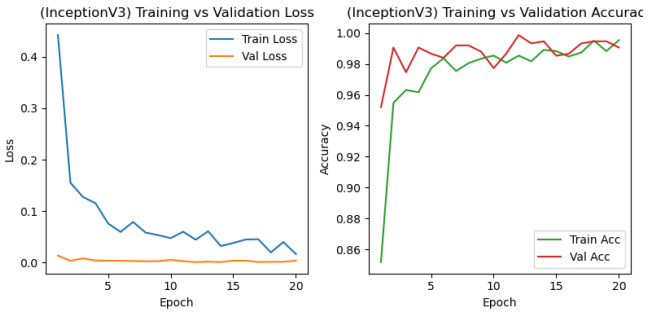

FIG 3. TRAINING AND VALIDATION METRICS PER EPOCH

Figure 3 shows the changing trends of the loss and accuracy of the InceptionV3 model during training. It can be seen that the training loss decreases rapidly with the number of iterations and tends to stabilize in the later stage, and the verification loss is close to 0 and tends to stabilize. In terms of accuracy, both the training and verification curves maintain a high level and steadily improve with iterations, and finally converge around the 20th round, indicating that the model has good convergence efficiency and generalization ability under the current hyperparameter settings.

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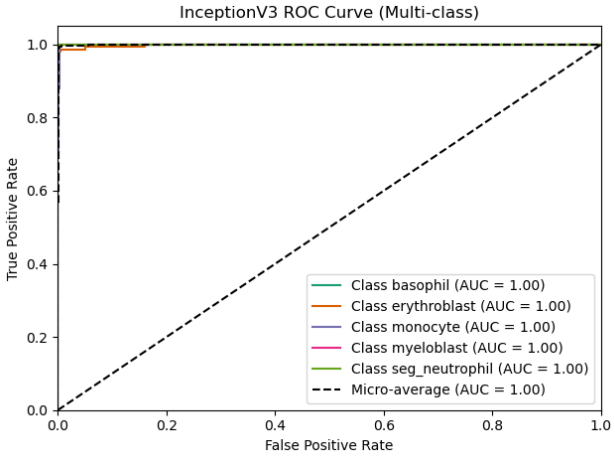

FIG 4. ROC CURVE VISUALIZATION

Figure 4 shows the ROC curve of the model in a multi-classification scenario, where the AUC for each class reaches 1.00, and the micro-average curve also shows almost perfect classification performance. This high confidence result shows that the model has extremely high discrimination in distinguishing different cell types, and can maintain a low false positive rate and a high true positive rate for any given threshold, thereby providing stable and reliable cell recognition performance in clinical or related applications.

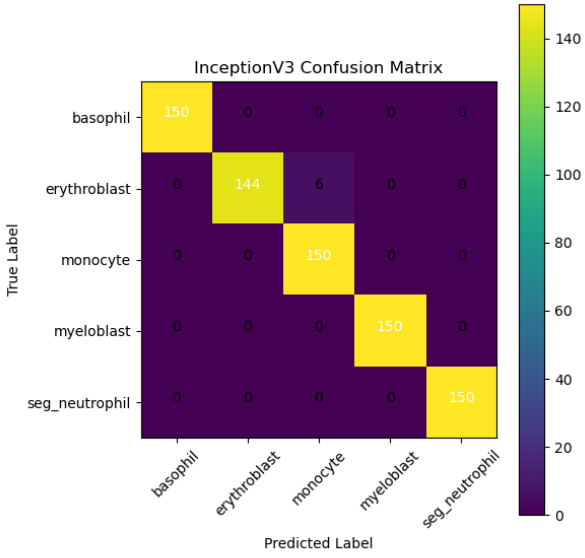

FIG 5. CONFUSION MATRIX ON TEST SET

From the confusion matrix in Figure 5, we can see that except for a few erythroblast samples that were incorrectly predicted as monocytes, there was almost no cross-class confusion in the other classes, indicating that the model can accurately separate different cell types in the test set in most cases. Among them, the classes of basophil, myeloblast, and seg_neutrophil were not misclassified at all, reflecting a relatively high discrimination stability; while the erythroblast class had a small amount of confusion on the boundary with monocytes, suggesting that the two classes may have some similarities in morphological characteristics or staining differences.

TABLE 4. DETAILED EVALUATION METRICS OF THE INCEPTIONV3 MODEL ON EACH CLASS

Class	AUC(%)	Precision(%)	Recall(%)	F1-score(%)	Specificity(%)	Accuracy(%)
basophil	1.00	100.00	100.00	100.00	100.00	
erythroblast	1.00	100.00	96.00	97.96	100.00	
monocyte	1.00	96.15	100.00	98.03	99.00	99.20
myeloblast	1.00	100.00	100.00	100.00	100.00	
seg_neutrophil	1.00	100.00	100.00	100.00	100.00	

Table 4 shows that the Precision, Recall, and F1-score of each class are basically maintained at a high level, with most of the indicators reaching 100% or close to 100%. Only the erythroblast class has a slight decrease in Recall, resulting in a relatively low F1-score. The overall accuracy and macro-average specificity also reached about 99.20% and 99.80%, respectively, indicating that the model has good classification performance and discrimination ability in identifying most cell types, with only a small number of misclassifications between individual classes.

In summary, during multiple rounds of hyperparameter optimization, InceptionV3 achieved a maximum accuracy of 100.00% on the validation set, while maintaining a high level of around 99.87% on the test set. Finally, during the training process under the local optimal hyperparameter group, the validation accuracy gradually increased with iterations and converged around 20 rounds. The test results show that the model has basically no misjudgment of classes such as basophil, myeloblast, and seg_neutrophil, with precision and recall both as high as 100%. There was only a small amount of confusion between erythroblast and monocyte, with precision and recall both reaching over 96%. The overall accuracy and average specificity were as high as 99.20% and 99.80%, respectively. In addition, the AUC for all classes reached 1.00, indicating that the model has extremely high discrimination and generalization capabilities in distinguishing different cell types.

5 DISCUSSION AND FUTURE WORK

The blood cell automatic classification model based on InceptionV3 and GSECA hyperparameter optimization method obtained in this study showed high accuracy and robustness in the recognition of multiple types of cells.

Through multiple rounds of iterative optimization and experimental evaluation, the model's performance on both the validation and test sets can be maintained at a high level, indicating that deep learning has significant advantages in dealing with challenges such as blood cell morphological diversity, staining differences and overlapping phenomena. Compared with traditional image processing methods, this study not only achieved deep mining of cell morphological features, but also achieved a good balance between training efficiency, convergence speed and generalization ability, providing a practical technical path for automatic classification of blood cells.

However, there are still some shortcomings and research gaps in the experiment, which need to be further improved and expanded in future work. First, the data set used in this experiment is small in scale and the sample image resolution is low. It is necessary to train and test on larger and more complex data sets to verify the applicability and robustness of the model in actual clinical environments. Secondly, future research should consider including the detection and classification tasks of multiple cells appearing in the same image in the research scope, integrating the target detection and classification process to eliminate the step of manually extracting single cell images and achieve end-to-end automated analysis. Finally, by comparing other advanced deep learning models, such as ResNet, DenseNet, EfficientNet, etc., and exploring model fusion strategies, it is expected to further improve model performance and enhance the ability to distinguish complex blood pathology characteristics.

6 CONCLUSION

This study systematically trained and optimized the model for the classification tasks of five types of cells: basophil, erythroblast, monocyte, myeloblast, and seg_neutrophil. The dataset used contains 5,000 microscopic images of about 350 to 400 pixels in size, and each class is divided into a training set, a validation set, and a test set at a ratio of 70%, 15%, and 15%. In order to reduce the experimental computational overhead, the GSECA method was used for hyperparameter optimization, and the changes in model performance during the optimization process were recorded and analyzed.

The test results show that the model trained under the local optimal hyperparameter group obtained after multiple rounds of iterative search has an AUC of 1.00 for all classes. There is basically no misjudgment for classes such as basophil, myeloblast, and seg_neutrophil, and only a small amount of confusion occurs between erythroblast and monocyte. The overall accuracy and average specificity are as high as 99.20% and 99.80% respectively, indicating that this method has good discrimination and robustness in the identification of different cell types.

Future work will further expand the application scope and performance of this research method. For example, the robustness of the model will be verified on a larger and more diverse dataset to ensure its higher adaptability in actual clinical environments. At the same time, an end-to-end blood cell detection and classification system will be built to automatically locate and identify multiple cells from the original image, reducing the reliance on manual segmentation in the early stage. In addition, by comparing with other advanced networks (such as ResNet, DenseNet, EfficientNet) and exploring model fusion strategies, the classification accuracy can be further improved to provide more solid technical support for clinical intelligent diagnosis.

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DATA AVAILABILITY STATEMENT

The original contributions presented in the study are included in the article/supplementary material, further inquiries can be directed to the corresponding author.

CONFLICT OF INTEREST

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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AUTHOR CONTRIBUTIONS

Not applicable.

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